Package ‘lefko3’

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R topics documented:

- add_lM ........................................ 3
- aflefko2 .................................... 8
- cond_hmpm .................................. 16
- create_lM ................................... 18
- cypdata ..................................... 25
- cypvert ...................................... 28
- delete_lM ................................... 30
- density_input ................................. 34
- elasticity3 .................................. 37
- elasticity3.lefkoMat ......................... 40
- elasticity3.list .............................. 43
- elasticity3.matrix ........................... 46
- flefko2 ...................................... 48
- flefko3 ...................................... 58
- historicalize3 ............................... 67
- image3 ....................................... 75
- image3.lefkoElas ............................ 77
- image3.lefkoMat ............................. 80
- image3.lefkoSens ............................ 82
- image3.list .................................. 84
- image3.matrix ................................ 87
- lambda3 ..................................... 89
- lambda3.lefkoMat ............................ 91
- lambda3.matrix .............................. 94
- lathyrus ..................................... 97
- lefko3 ....................................... 100
- lmean ......................................... 101
- ltre3 ......................................... 104
- ltre3.lefkoMat ............................... 106
- modelsearch ................................ 109
- overwrite .................................... 118
- projection3 .................................. 121
- repvalue3 ................................... 125
- repvalue3.lefkoMat ......................... 127
- repvalue3.matrix ............................ 131
- rlefko2 ...................................... 134
- rlefko3 ...................................... 139
- sensitivity3 ................................. 144
- sensitivity3.lefkoMat ....................... 147
- sensitivity3.list ............................ 150
- sensitivity3.matrix .......................... 153
- sf_create ................................... 155
- sf_distrib ................................... 161
- slambda3 .................................... 164
- stablestage3 ................................ 167
- stablestage3.lefkoMat ..................... 169
Function `add_lM()` adds matrices to `lefkoMat` objects.

### Description

Function `add_lM()` adds matrices to `lefkoMat` objects.

### Usage

```r
add_lM(
  lM,
  Amats = NA,
  Umats = NA,
  Fmats = NA,
  UFdecomp = FALSE,
  entrystage = 1,
  pop = NA,
  patch = NA,
  year = NA
)
```

### Arguments

- **lM**: The `lefkoMat` object to add matrices to.
- **Amats**: Either a single `A` matrix, or a list of `A` matrices. Not necessary if `Umats` and `Fmats` are both provided.
- **Umats**: Either a single `U` matrix, or a list of `U` matrices. Not necessary if `Amats` and `Fmats` are both provided, or if `UFdecomp = TRUE` and `entrystage` is provided.
- **Fmats**: Either a single `F` matrix, or a list of `U` matrices. Not necessary if `Amats` and `Umats` are both provided, or if `UFdecomp = TRUE` and `entrystage` is provided.
- **UFdecomp**: A logical value indicating whether `U` and `F` matrices should be inferred from `A` matrices and the given `entrystage`. Defaults to `TRUE`. 
entrystage: The stage or stages produced by reproductive individuals. Used to determine which transitions are reproductive for U-F decomposition. Defaults to 1, which corresponds to the first stage in the stageframe.

pop: The population designation for each matrix. If object lM includes only a single population, then defaults to that designation. Otherwise requires a designation as input.

patch: The patch designation for each matrix. If object lM includes only a single patch, then defaults to that designation. Otherwise requires a designation as input.

year: The designation for occasion at time *t* corresponding to each matrix. Cannot be left empty.

Value

A lefkoMat object incorporating the new matrices within the object input in lM.

Notes

This function will not allow matrices of different dimension from those input in object lM to be added to that object.

Two of Amats, Umats, and Fmats must be provided for this function to proceed. Also, if Amats, Umats, and Fmats are all provided, then this function will default to replacing Amats with the sum of the respective Umats and Fmats.

See Also

create_lM()
delete_lM()
subset_lM()

Examples


sizevector <- c(1, 1, 2, 3) # These sizes are not from the original paper
stagevector <- c("Sdl", "Veg", "SmFlo", "Lflo")
reppvector <- c(0, 0, 1, 1)
obsvector <- c(1, 1, 1, 1)
matvector <- c(0, 1, 1, 1)
immvector <- c(1, 0, 0, 0)
propvector <- c(0, 0, 0, 0)
indataset <- c(1, 1, 1, 1)
binvec <- c(0.5, 0.5, 0.5, 0.5)

anthframe <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = reppvector, obsstatus = obsvector, matstatus = matvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec, propstatus = propvector)
# POPN C 2003-2004
XC3 <- matrix(c(0, 0, 1.74, 1.74,
0.208333333, 0, 0, 0.057142857,
0.041666667, 0.076923077, 0, 0,
0.083333333, 0.076923077, 0.066666667, 0.028571429), 4, 4, byrow = TRUE)

# 2004-2005
XC4 <- matrix(c(0, 0, 0.3, 0.6,
0.32183908, 0.142857143, 0, 0,
0.16091954, 0.285714286, 0, 0,
0.252873563, 0.285714286, 0.5, 0.6), 4, 4, byrow = TRUE)

# 2005-2006
XC5 <- matrix(c(0, 0, 0.50625, 0.675,
0, 0, 0.035714286,
0.1, 0.068965517, 0.0625, 0.107142857,
0.3, 0.137931034, 0, 0.071428571), 4, 4, byrow = TRUE)

# POPN E 2003-2004
XE3 <- matrix(c(0, 0, 2.44, 6.569230769,
0.196428571, 0, 0, 0,
0.125, 0.5, 0, 0,
0.160714286, 0.5, 0.133333333, 0.076923077), 4, 4, byrow = TRUE)

XE4 <- matrix(c(0, 0, 0.45, 0.646153846,
0.06557377, 0.090909091, 0.125, 0,
0.032786885, 0, 0.125, 0.076923077,
0.049180328, 0, 0.125, 0.230769231), 4, 4, byrow = TRUE)

XE5 <- matrix(c(0, 0, 2.85, 3.99,
0.083333333, 0, 0, 0,
0, 0, 0, 0,
0.416666667, 0.1, 0, 0.1), 4, 4, byrow = TRUE)

# POPN F 2003-2004
XF3 <- matrix(c(0, 0, 1.815, 7.058333333,
0.075949367, 0, 0.05, 0.083333333,
0.139240506, 0, 0, 0.25,
0.075949367, 0, 0, 0.083333333), 4, 4, byrow = TRUE)

XF4 <- matrix(c(0, 0, 1.233333333, 7.4,
0.223880597, 0, 0.111111111, 0.142857143,
0.134328358, 0.272727273, 0.166666667, 0.142857143,
0.119402985, 0.366666667, 0.055555556, 0.142857143), 4, 4, byrow = TRUE)

XF5 <- matrix(c(0, 0, 1.06, 3.372727273,
0.073170732, 0.025, 0.033333333, 0,
0.03658366, 0.15, 0.1, 0.136363636,
0.06097561, 0.225, 0.166666667, 0.272727273), 4, 4, byrow = TRUE)

# POPN G 2003-2004
XG3 <- matrix(c(0, 0, 0.245454545, 2.1,
addLM

\[
XG4 \leftarrow \text{matrix}(c(0, 0, 1.1, 1.54, \\
0.111111111, 0, 0, 0, \\
0.125, 0, 0, 0, \\
0.125, 0, 0.090909091, 0.333333333), 4, 4, \text{byrow = TRUE})
\]

\[
XG5 \leftarrow \text{matrix}(c(0, 0, 1.5, \\
0, 0, 0, 0, \\
0.111111111, 0, 0, 0, \\
0.545454545, 0.5, 0, 0.5), 4, 4, \text{byrow = TRUE})
\]

# POPN L 2003-2004

\[
XL3 \leftarrow \text{matrix}(c(0, 0, 1.785365854, 1.856521739, \\
0.128571429, 0, 0, 0.010869565, \\
0.028571429, 0, 0, 0, \\
0.014285714, 0, 0, 0.02173913), 4, 4, \text{byrow = TRUE})
\]

\[
XL4 \leftarrow \text{matrix}(c(0, 0, 14.25, 16.625, \\
0.131443299, 0.057142857, 0, 0.25, \\
0.144329897, 0, 0, 0, \\
0.09273505, 0.2, 0, 0.25), 4, 4, \text{byrow = TRUE})
\]

\[
XL5 \leftarrow \text{matrix}(c(0, 0, 0.594642857, 1.765909091, \\
0, 0, 0.017857143, 0, \\
0.021052632, 0.018518519, 0.035714286, 0.045454545, \\
0.021052632, 0.018518519, 0.035714286, 0.068181818), 4, 4, \text{byrow = TRUE})
\]

# POPN O 2003-2004

\[
XO3 \leftarrow \text{matrix}(c(0, 0, 11.5, 2.775862069, \\
0.6, 0.285714286, 0.333333333, 0.24137931, \\
0.04, 0.142857143, 0, 0, \\
0.16, 0.285714286, 0, 0.172413793), 4, 4, \text{byrow = TRUE})
\]

\[
XO4 \leftarrow \text{matrix}(c(0, 0, 3.78, 1.225, \\
0.28358209, 0.171052632, 0, 0.166666667, \\
0.084577114, 0.026315789, 0, 0.055555556, \\
0.139303483, 0.447368421, 0, 0.385555556), 4, 4, \text{byrow = TRUE})
\]

\[
XO5 \leftarrow \text{matrix}(c(0, 0, 1.542857143, 1.035616438, \\
0.126084127, 0.105263158, 0.047619048, 0.054794521, \\
0.095238095, 0.157894737, 0.19047619, 0.082191781, \\
0.111111111, 0.223684211, 0, 0.356164384), 4, 4, \text{byrow = TRUE})
\]

# POPN Q 2003-2004

\[
XQ3 \leftarrow \text{matrix}(c(0, 0, 0.15, 0.175, \\
0, 0, 0, 0, \\
0, 0, 0, 0, \\
1, 0, 0, 0), 4, 4, \text{byrow = TRUE})
\]

\[
XQ4 \leftarrow \text{matrix}(c(0, 0, 0.25, \\
0, 0, 0.045454545, 0, \\
0.125, 0, 0.090909091, 0, \\
0.125, 0, 0.090909091, 0.333333333), 4, 4, \text{byrow = TRUE})
\]
add.IM

0, 0, 0, 0,
0, 0, 0, 0,
1, 0.666666667, 0, 1), 4, 4, byrow = TRUE)

XQ5 <- matrix(c(0, 0, 1.428571429,
0, 0, 0.142857143,
0.25, 0, 0, 0,
0.25, 0, 0, 0.571428571), 4, 4, byrow = TRUE)

# POPN R 2003-2004
XR3 <- matrix(c(0, 0, 0.7, 0.6125,
0.25, 0, 0, 0.125,
0, 0, 0, 0,
0.25, 0, 0.166666667, 0.25), 4, 4, byrow = TRUE)

XR4 <- matrix(c(0, 0, 0, 0.6,
0.285714286, 0, 0, 0,
0.285714286, 0.333333333, 0, 0,
0.285714286, 0.333333333, 0, 1), 4, 4, byrow = TRUE)

XR5 <- matrix(c(0, 0, 0.7, 0.6125,
0, 0, 0, 0,
0, 0, 0, 0,
0.333333333, 0, 0.333333333, 0.625), 4, 4, byrow = TRUE)

# POPN S 2003-2004
XS3 <- matrix(c(0, 0, 2.1, 0.816666667,
0.166666667, 0, 0, 0,
0, 0, 0, 0,
0, 0, 0, 0.166666667), 4, 4, byrow = TRUE)

XS4 <- matrix(c(0, 0, 0, 7,
0.333333333, 0.5, 0, 0,
0, 0, 0, 0,
0.333333333, 0, 0, 1), 4, 4, byrow = TRUE)

XS5 <- matrix(c(0, 0, 0, 1.4,
0, 0, 0, 0,
0, 0, 0, 0.2,
0.111111111, 0.75, 0, 0.2), 4, 4, byrow = TRUE)

mats_list <- list(XC3, XC4, XC5, XE3, XE4, XE5, XF3, XF4, XF5, XG3, XG4, XG5, 
XL3, XL4, XL5, XO3, XO4, XO5, XQ3, XQ4, XQ5, XR3, XR4, XR5, XS3, XS4, XS5)

yr_ord <- c(1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3)

pch_ord <- c(1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4, 5, 5, 5, 6, 6, 6, 7, 7, 7, 
8, 8, 8, 9, 9, 9)

anth_lefkoMat <- create.IM(mats_list, anthframe, hstages = NA, historical = FALSE, 
poporder = 1, patchorder = pch_ord, yearorder = yr_ord)
# POPN H (EXCD FROM ANALYSIS B/C OF UNREALISTIC ELASTICITIES)
XH3 <- matrix(c(0, 0, 0.1125, 1.05,
0.2, 0, 0, 0,
0, 0.5, 0, 0,
0.2, 0.5, 0, 0), 4, 4, byrow = TRUE)

XH3u <- matrix(c(0, 0, 0, 0,
0.2, 0, 0, 0,
0, 0.5, 0, 0,
0.2, 0.5, 0, 0), 4, 4, byrow = TRUE)

XH4 <- matrix(c(0, 0, 0, 0,
0, 0.5, 0,
0.8, 0.5, 0.25, 0.25,
0.2, 0, 0.75), 4, 4, byrow = TRUE)

XH4u <- matrix(c(0, 0, 0, 0,
0, 0.5, 0,
0.8, 0.5, 0.25, 0.25,
0.2, 0, 0.75), 4, 4, byrow = TRUE)

XH5 <- matrix(c(0, 0, 0.2, 1.05,
0, 0, 0, 0,
0.001, 0.001, 0.333333333, 0, #ELEMENTS (3,1),(4,1),(3,2) REPLACED W NONZERO
0.001, 0, 0, 0), 4, 4, byrow = TRUE)

XH5u <- matrix(c(0, 0, 0, 0,
0, 0, 0,
0.001, 0.001, 0.333333333, 0, #ELEMENTS (3,1),(4,1),(3,2) REPLACED W NONZERO
0.001, 0, 0, 0), 4, 4, byrow = TRUE)

anth_lefkoMat <- add_lM(anth_lefkoMat, Amats = list(XH3, XH4, XH5),
Umats = list(XH3u, XH4u, XH5u), patch = c(10, 10, 10), year = c(1, 2, 3))

anth_lefkoMat

---

aflefko2

Create Function-based Ahistorical Age x Stage Matrix Projection Model

Description

Function aflefko2() returns ahistorical age x stage MPMs corresponding to the patches and occasion times given, including the associated component transition and fecundity matrices, data frames detailing the characteristics of ahistorical stages and the exact age-stage combinations corresponding to rows and columns in estimated matrices, and a data frame characterizing the patch and occasion time combinations corresponding to these matrices.
Usage

```r
aflefko2(
  year = "all",
  patch = "all",
  stageframe,
  supplement = NULL,
  repmatrix = NULL,
  overwrite = NULL,
  data = NA,
  modelsuite = NA,
  surv_model = NA,
  obs_model = NA,
  size_model = NA,
  sizeb_model = NA,
  sizec_model = NA,
  repst_model = NA,
  fec_model = NA,
  jsurv_model = NA,
  jobs_model = NA,
  jsize_model = NA,
  jsizeb_model = NA,
  jsizec_model = NA,
  jrepst_model = NA,
  paramnames = NA,
  ina = NULL,
  indb = NULL,
  indc = NULL,
  surv_dev = 0,
  obs_dev = 0,
  size_dev = 0,
  sizeb_dev = 0,
  sizec_dev = 0,
  repst_dev = 0,
  fec_dev = 0,
  jsurv_dev = 0,
  jobs_dev = 0,
  jsize_dev = 0,
  jsizeb_dev = 0,
  jsizec_dev = 0,
  jrepst_dev = 0,
  density = NA,
  repmod = 1,
  yearcol = NA,
  patchcol = NA,
  year.as.random = FALSE,
  patch.as.random = FALSE,
  random.ina = FALSE,
  random.indb = FALSE,
)```
random.indc = FALSE,
final_age = 10,
continue = TRUE,
randomseed = NA,
nefgec = FALSE,
reduce = FALSE,
err_check = FALSE,
exp_tol = 700,
theta_tol = 1e+08
}

Arguments

**year**
A variable corresponding to observation occasion, or a set of such values, given in values associated with the year term used in linear model development. Defaults to "all", in which case matrices will be estimated for all occasions.

**patch**
A variable designating which patches or subpopulations will have matrices estimated. Defaults to "all", but can also be set to specific patch names.

**stageframe**
A stageframe object that includes information on the size, observation status, propagule status, immaturity status, and maturity status of each ahistorical stage. Should also incorporate bin widths if size is continuous.

**supplement**
An optional data frame of class lefkoSD that provides supplemental data that should be incorporated into the MPM. Three kinds of data may be integrated this way: transitions to be estimated via the use of proxy transitions, transition overwrites from the literature or supplemental studies, and transition multipliers for survival and fecundity. This data frame should be produced using the `supplemental()` function. Can be used in place of or in addition to an overwrite table (see `overwrite` below) and a reproduction matrix (see `repmatrix` below).

**repmatrix**
An optional reproduction matrix. This matrix is composed mostly of 0s, with non-zero entries acting as element identifiers and multipliers for fecundity (with 1 equaling full fecundity). If left blank, and no `supplement` is provided, then `aflefko2()` will assume that all stages marked as reproductive produce offspring at 1x that of estimated fecundity, and that offspring production will yield the first stage noted as propagule or immature. To prevent this behavior, input just 0, which will result in fecundity being estimated only for transitions noted in `supplement` above. Must be the dimensions of an ahistorical stage-based matrix.

**overwrite**
An optional data frame developed with the `overwrite()` function describing transitions to be overwritten either with given values or with other estimated transitions. Note that this function supplements overwrite data provided in `supplement`.

**data**
The historical vertical demographic data frame used to estimate vital rates (class `hfvdata`). The original data frame is required in order to initialize occasions and patches properly.

**modelsuite**
An optional `lefkoMod` object holding the vital rate models. If given, then `surv_model`, `obs_model`, `size_model`, `sizeb_model`, `sizec_model`, `repst_model`, `fec_model`,
jsurv_model, jobs_model, jsize_model, jsizb_model, jsizc_model, jrepsr_model, pa-ramnames, yearcol, and patchcol are not required. No models should include size or reproductive status in occasion \( t-1 \).

**surv_model**
A linear model predicting survival probability. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any survival probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**obs_model**
A linear model predicting sprouting or observation probability. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any observation probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**size_model**
A linear model predicting primary size. This can be a model of class `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `vglm`, `lm`, or `lmer`. If given, then will overwrite any primary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**sizeb_model**
A linear model predicting secondary size. This can be a model of `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `vglm`, `lm`, or `lmer`. If given, then will overwrite any secondary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**sizec_model**
A linear model predicting tertiary size. This can be a model of `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `vglm`, `lm`, or `lmer`. If given, then will overwrite any tertiary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**repsr_model**
A linear model predicting reproduction probability. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any reproduction probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**fec_model**
A linear model predicting fecundity. This can be a model of `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `vglm`, `lm`, or `lmer`. If given, then will overwrite any fecundity model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**jsurv_model**
A linear model predicting juvenile survival probability. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any juvenile survival probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**jobs_model**
A linear model predicting juvenile sprouting or observation probability. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any juvenile observation probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**jsize_model**
A linear model predicting juvenile primary size. This can be a model of class `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `vglm`, `lm`, or `lmer`. If given, then will overwrite
any juvenile primary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion $t$.

**jsizeb_model** A linear model predicting juvenile secondary size. This can be a model of class glm, glmer, glmmTMB, zeroinf1, vglm, lm, or lmer. If given, then will overwrite any juvenile secondary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion $t$.

**jsizec_model** A linear model predicting juvenile tertiary size. This can be a model of class glm, glmer, glmmTMB, zeroinf1, vglm, lm, or lmer. If given, then will overwrite any juvenile tertiary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion $t$.

**jrepst_model** A linear model predicting reproduction probability of a mature individual that was immature in the previous year. This can be a model of class glm or glmer, and requires a predicted binomial variable under a logit link. If given, then will overwrite any reproduction probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion $t$.

**paramnames** A dataframe with three columns, the first describing all terms used in linear modeling, the second (must be called mainparams), showing the general model terms that will be used in matrix creation (users should use modelsearch() at least once to see the proper names to be used in this column), and the third showing the equivalent terms used in modeling (must be named modelparams). Only required if modelsuite is not supplied.

**inda** Can be a single value to use for individual covariate a in all matrices, a pair of values to use for times $t$ and $t-1$ in historical matrices, or a vector of such values corresponding to each occasion in option year. Defaults to NULL.

**indb** Can be a single value to use for individual covariate b in all matrices, a pair of values to use for times $t$ and $t-1$ in historical matrices, or a vector of such values corresponding to each occasion in option year. Defaults to NULL.

**indc** Can be a single value to use for individual covariate c in all matrices, a pair of values to use for times $t$ and $t-1$ in historical matrices, or a vector of such values corresponding to each occasion in option year. Defaults to NULL.

**surv_dev** A numeric value to be added to the y-intercept in the linear model for survival probability.

**obs_dev** A numeric value to be added to the y-intercept in the linear model for observation probability.

**size_dev** A numeric value to be added to the y-intercept in the linear model for primary size.

**sizeb_dev** A numeric value to be added to the y-intercept in the linear model for secondary size.

**sizec_dev** A numeric value to be added to the y-intercept in the linear model for tertiary size.

**repst_dev** A numeric value to be added to the y-intercept in the linear model for probability of reproduction.

**fec_dev** A numeric value to be added to the y-intercept in the linear model for fecundity.
jsurv_dev  A numeric value to be added to the y-intercept in the linear model for juvenile survival probability.

jobs_dev  A numeric value to be added to the y-intercept in the linear model for juvenile observation probability.

jsize_dev  A numeric value to be added to the y-intercept in the linear model for juvenile primary size.

jsizeb_dev  A numeric value to be added to the y-intercept in the linear model for juvenile secondary size.

jsizec_dev  A numeric value to be added to the y-intercept in the linear model for juvenile tertiary size.

jrepst_dev  A numeric value to be added to the y-intercept in the linear model for juvenile reproduction probability.

density  A numeric value indicating density value to use to propagate matrices. Only needed if density is an explanatory term used in linear models. Defaults to NA.

repmad  A scalar multiplier of fecundity. Defaults to 1.

yearcol  The variable name or column number corresponding to year in occasion \( t \) in the dataset. Not needed if a model suite is supplied.

patchcol  The variable name or column number corresponding to patch in the dataset. Not needed if a model suite is supplied.

year.as.random  A logical term indicating whether coefficients for missing occasions within vital rate models should be estimated as random intercepts. Defaults to FALSE, in which case missing monitoring occasion coefficients are set to 0.

patch.as.random  A logical term indicating whether coefficients for missing patches within vital rate models should be estimated as random intercepts. Defaults to FALSE, in which case missing patch coefficients are set to 0.

random.ina  A logical value denoting whether to treat individual covariate \( a \) as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.

random.inb  A logical value denoting whether to treat individual covariate \( b \) as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.

random.inc  A logical value denoting whether to treat individual covariate \( c \) as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.

final_age  The final age to model in the matrix, where the first age will be age 0.

continue  A logical value designating whether to allow continued survival of individuals past the final age noted in the stageframe, using the demographic characteristics of the final age.

randomseed  A numeric value used as a seed to generate random estimates for missing occasion and patch coefficients, if either year.as.random or patch.as.random is set to TRUE. Defaults to `set.seed()` default.

negfec  A logical value denoting whether fecundity values estimated to be negative should be reset to 0. Defaults to FALSE.
reduce
A logical value denoting whether to remove ahistorical stages associated solely with 0 transitions. These are only removed in cases where the associated row and column sums in ALL matrices estimated equal 0. Defaults to FALSE.

err_check
A logical value indicating whether to append matrices of vital rate probabilities associated with each matrix to the `lefkoMat` object generated. These matrices are developed internally and can be used for error checking. Defaults to FALSE.

exp_tol
A numeric value used to indicate a maximum value to set exponents to in the core kernel to prevent numerical overflow. Defaults to 700.

theta_tol
A numeric value used to indicate a maximum value to theta as used in the negative binomial probability density kernel. Defaults to 100000000, but can be reset to other values during error checking.

Value
If all inputs are properly formatted, then this function will return an object of class `lefkoMat`, which is a list that holds the matrix projection model and all of its metadata. Its structure is a list with the following elements:

A
A list of full projection matrices in order of sorted patches and occasions. All matrices output in R's `matrix` class.

U
A list of survival transition matrices sorted as in A. All matrices output in R's `matrix` class.

F
A list of fecundity matrices sorted as in A. All matrices output in R's `matrix` class.

hstages
A data frame matrix showing the pairing of ahistorical stages used to create historical stage pairs. Set to NA for ahistorical matrices.

agestages
A data frame showing the stage number and stage name corresponding to hstages, as well as the associated age, of each actual row in each age-by-stage matrix.

ahstages
A data frame detailing the characteristics of associated ahistorical stages, in the form of a modified stageframe that includes status as an entry stage through reproduction.

labels
A data frame giving the patch and year of each matrix in order. In `aflefko2()`, only one population may be analyzed at once, and so pop = NA

matrixqc
A short vector describing the number of non-zero elements in U and F matrices, and the number of annual matrices.

modelqc
This is the qc portion of the modelsuite input.

prob_out
An optional element only added if err_check = TRUE. This is a list of vital rate probability matrices, with 6 columns in the order of survival, observation probability, reproduction probability, primary size transition probability, secondary size transition probability, and tertiary size transition probability.

Notes
Unlike `rlefko2()` and `rlefko3()`, this function does not currently distinguish populations.
This function will yield incorrect estimates if the models utilized incorporate state in occasion t-1. Only use models developed testing for ahistorical effects.
The default behavior of this function is to estimate fecundity with regards to transitions specified via associated fecundity multipliers in either supplement or repmatrix. If both of these fields are left empty, then fecundity will be estimated at full for all transitions leading from reproductive stages to immature and propagule stages. However, if a supplement is provided and a repmatrix is not, or if repmatrix is set to 0, then only fecundity transitions noted in the supplement will be set to non-zero values. To use the default behavior of setting all reproductive stages to reproduce at full fecundity into immature and propagule stages but also incorporate given or proxy survival transitions, input those given and proxy transitions through the overwrite option.

The reproduction matrix (field repmatrix) may only be supplied as ahistorical. If provided as historical, then aplefko2() will fail and produce an error.

Users may at times wish to estimate MPMs using a dataset incorporating multiple patches or sub-populations, but without discriminating between those patches or subpopulations. Should the aim of analysis be a general MPM that does not distinguish these patches or subpopulations, the patchcol variable should be set to NA, which is the default.

Input options including multiple variable names must be entered in the order of variables in occasion \(t+1\) and \(t\). Rearranging the order will lead to erroneous calculations, and may lead to fatal errors.

Care should be taken to match the random status of year and patch to the states of those variables within the modelsuite. If they do not match, then they will be treated as zeroes in vital rate estimation.

Using the err_check option will produce a matrix of 6 columns, each characterizing a different vital rate. The product of each row yields an element in the associated $U$ matrix. The number and order of elements in each column of this matrix matches the associated matrix in column vector format. Use of this option is generally for the purposes of debugging code.

Users may produce age-based (Leslie) MPMs using this function. In that case, stages must be defined as occurring serially within single ages in the stageframe, with the possible exception of the final stage (which sometimes involves a perpetual stasis transition).

**Examples**

```r
data(lathyrus)
sizevector <- c(0, 4.6, 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 1, 2, 3, 4, 5, 6, 7, 8, 9)
stagevector <- c("Sd", "Sdl", "Dorm", "Sz1nr", "Sz2nr", "Sz3nr", "Sz4nr", 
                  "Sz5nr", "Sz6nr", "Sz7nr", "Sz8nr", "Sz9nr", "Sz1r", "Sz2r", 
                  "Sz3r", "Sz4r", "Sz5r", "Sz6r", "Sz7r", "Sz8r")
revector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
minima <- c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
maxima <- c(NA, 1, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA)
binvec <- c(0, 4.6, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)
```
cond_hmpm <- sf_create(sizes = sizevector, stagenames = stagevector, 
  repstatus = repvector, obsstatus = obsvector, matstatus = matvector, 
  immstatus = immvector, indataset = indataset, binhalfwidth = binvec, 
  propstatus = propvector, minage = minima, maxage = maxima)

lathvertln <- verticalize3(lathyrus, noyears = 4, firstyear = 1988, 
  patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9, 
  juvcol = "Seedling1988", sizeacol = "lnVol88", repstracol = "Intactseed88", 
  fecacol = "Intactseed88", deadacol = "Dead1988", 
  nonobsacol = "Dormant1988", stageassign = lathframeln, 
  stagesize = "sizea", censorcol = "Missing1988", censorkeep = NA, 
  NAas0 = TRUE, censor = TRUE)

lathvertln$feca2 <- round(lathvertln$feca2)
lathvertln$fecal1 <- round(lathvertln$fecal1)
lathvertln$feca3 <- round(lathvertln$feca3)

lathmodelsln2 <- modelsearch(lathvertln, historical = FALSE, 
  approach = "mixed", suite = "main", 
  vitalrates = c("surv", "obs", "size", "repst", "fec"), juvestimate = "Sdl", 
  bestfit = "AICc&k", sizedist = "gaussian", fecdist = "poisson", 
  indiv = "individ", patch = "patchid", year = "year2", age = "obsage", 
  year.as.random = TRUE, patch.as.random = TRUE, show.model.tables = TRUE, 
  quiet = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
lathsupp2 <- supplemental(stage3 = c("Sd", "Sdl", "Sd", "Sdl"), 
  stage2 = c("Sd", "Sdl", "rep", "rep"), 
  givenrate = c(0.345, 0.054, NA, NA), 
  multiplier = c(NA, NA, 0.345, 0.054), 
  type = c(1, 1, 3, 3), stageframe = lathframeln, historical = FALSE)

lathomat2age <- aflefko2(year = "all", patch = "all", 
  stageframe = lathframeln, modelsuite = lathmodelsln2, data = lathvertln, 
  supplement = lathsupp2, patchcol = "patchid", 
  yearcol = "year2", year.as.random = FALSE, patch.as.random = FALSE, 
  final_age = 2, continue = TRUE, reduce = FALSE)

summary(lathomat2age)
cond_hmpm

object, and forms one ahistorical matrix for each stage in time t-1.

Usage

cond_hmpm(hmpm, matchoice = NULL, err_check = NULL)

Arguments

hmpm A historical matrix projection model of class lefkoMat.
matchoice A character denoting whether to use A, U, or F matrices. Defaults to A matrices.
err_check A logical value denoting whether to include a data frame of element equivalence from the conditional matrices to the original matrices. Used only for debugging purposes. Defaults to FALSE.

Value

A lefkoCondMat object, with the following elements:

Acond A multi-level list holding the conditional A matrices derived from the input lefkoMat object. The top level of the list corresponds to each historical matrix in turn, and the lower level corresponds to each stage in time t-1, with individual conditional matrices named for the latter.
hstages A data frame matrix showing the pairing of ahistorical stages used to create historical stage pairs.
ahstages A data frame detailing the characteristics of associated ahistorical stages.
labels A data frame showing the patch and year of each input full A matrix in order.

Examples

data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
reppvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, propstatus = propvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004, patchidcol = "patch", individcol = "plantid", blocksize = 4, sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04", sizevector = c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5), stagevector = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg"), repvector = c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1), obsvector = c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1), matvector = c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1), immvector = c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0), propvector = c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0), indataset = c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1), binvec = c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7))
create_lM

Create lefkoMat Object from Given Input Matrices

Description

Function create_lM() creates lefkoMat objects from supplied matrices and extra information.

Usage

create_lM(
  mats,
  stageframe,
  hstages = NA,
  agestages = NA,
  historical = FALSE,
  agebystage = FALSE,
create_IM

UFdecomp = TRUE,
entrystage = 1,
poporder = 1,
patchorder = 1,
yearorder = NA
)

Arguments

mats A list of A matrices.
stageframe A stageframe describing all stages utilized.
hstages A data frame outlining the order of historical stages, if matrices provided in mats are historical. Defaults to NA.
agestages A data frame outlining the order of ahistorical age-stages, if age-by-stage matrices are provided.
historical A logical value indicating whether input matrices are historical or not. Defaults to FALSE.
agebystage A logical value indicating whether input matrices are ahistorical age-by-stage matrices. If TRUE, then object agestages is required. Defaults to FALSE.
UFdecomp A logical value indicating whether U and F matrices should be inferred. Defaults to TRUE.
entrystage The stage or stages produced by reproductive individuals. Used to determine which transitions are reproductive for U-F decomposition. Defaults to 1, which corresponds to the first stage in the stageframe.
poporder The order of populations in the list supplied in object mats. Defaults to 1.
patchorder The order of patches in the list supplied in object mats. Defaults to 1.
yearorder The order of monitoring occasions in the list supplied in object mats. Defaults to NA, which leads to each matrix within each population-patch combination being a different monitoring occasion.

Value

A lefkoMat object incorporating the matrices input in object mats as object A, their U and F decompositions in objects U and F (if requested), the provided stageframe as object hstages, the order of historical stages as object hstages (if historical = TRUE), the order of matrices as object labels, and a short quality control section used by the summary.lefkoMat() function.

Notes

U and F decomposition assumes that elements holding fecundity values are to be interpreted solely as fecundity rates. Users wishing to split these elements between fecundity and survival should do so manually after running this function.

Age-by-stage MPMs require an agestages data frame outlining the order of age-stages. This data frame has 3 variables: stage.id, which is the number of the stage as labelled by the equivalently named variable in the stageframe; stage, which is the official name of the stage as given in the equivalently named variable in the stageframe; and age, which of course gives the age associated
with the stage at that time. The number of rows must be equal to the number of rows and columns of each entered matrix.

See Also

add_lM()
delete_lM()
subset_lM()

Examples

# These matrices are of 9 populations of the plant species Anthyllis
# vulneraria, and were originally published in Davison et al. (2010) Journal

sizevector <- c(1, 1, 2, 3) # These sizes are not from the original paper
stagevector <- c("Sdl", "Veg", "SmFlo", "LFlo")
reppvector <- c(0, 0, 1, 1)
obsvector <- c(0, 1, 1, 1)
matvector <- c(0, 1, 1, 1)
immvector <- c(1, 0, 0, 0)
propvector <- c(0, 0, 0, 0)
indataset <- c(1, 1, 1, 1)
binvec <- c(0.5, 0.5, 0.5, 0.5)

anthframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

# POPN C 2003-2004
XC3 <- matrix(c(0, 0, 1.74, 1.74,
0.208333333, 0, 0, 0.057142857,
0.041666667, 0.076923077, 0, 0,
0.083333333, 0.076923077, 0.066666667, 0.028571429), 4, 4, byrow = TRUE)

# 2004-2005
XC4 <- matrix(c(0, 0, 0.3, 0.6,
0.32183908, 0.142857143, 0, 0,
0.16091954, 0.285714286, 0, 0,
0.252873563, 0.285714286, 0.5, 0.6), 4, 4, byrow = TRUE)

# 2005-2006
XC5 <- matrix(c(0, 0, 0.50625, 0.675,
0, 0, 0, 0.035714286,
0, 0.068965517, 0.0625, 0.107142857,
0.3, 0.137931034, 0, 0.071428571), 4, 4, byrow = TRUE)

# POPN E 2003-2004
XE3 <- matrix(c(0, 0, 2.44, 6.569230769,
0.196428571, 0, 0, 0,
0.125, 0.5, 0, 0,
create.LM

0.160714286, 0.5, 0.133333333, 0.076923077), 4, 4, byrow = TRUE)

XE4 <- matrix(c(0, 0, 0.45, 0.646153846, 0.06557377, 0.090909091, 0.125, 0, 0.032786885, 0, 0.125, 0.076923077, 0.049180328, 0.0, 0.230769231), 4, 4, byrow = TRUE)

XE5 <- matrix(c(0, 0, 2.85, 3.99, 0.083333333, 0, 0, 0, 0.032786885, 0, 0.125, 0.076923077, 0.049180328, 0, 0.125, 0.230769231), 4, 4, byrow = TRUE)

# POPN F 2003-2004
XF3 <- matrix(c(0, 0, 1.815, 7.058333333, 0.075949367, 0, 0.05, 0.083333333, 0.139240506, 0, 0, 0.25, 0.075949367, 0, 0, 0.083333333), 4, 4, byrow = TRUE)

XF4 <- matrix(c(0, 0, 1.233333333, 7.4, 0.223880597, 0, 0.111111111, 0.142857143, 0.134328358, 0.272727273, 0.166666667, 0.142857143, 0.119402985, 0.363636364, 0.055555556, 0.142857143), 4, 4, byrow = TRUE)

XF5 <- matrix(c(0, 0, 1.06, 3.372727273, 0.073170732, 0.025, 0.033333333, 0, 0.036585366, 0.15, 0.1, 0.136666667, 0.06097561, 0.225, 0.166666667, 0.272727273), 4, 4, byrow = TRUE)

# POPN G 2003-2004
XG3 <- matrix(c(0, 0, 0.245454545, 2.1, 0, 0.045454545, 0, 0.125, 0, 0.090909091, 0, 0.125, 0, 0.090909091, 0.333333333), 4, 4, byrow = TRUE)

XG4 <- matrix(c(0, 0, 1.1, 1.54, 0.111111111, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0.111111111, 0, 0, 0), 4, 4, byrow = TRUE)

XG5 <- matrix(c(0, 0, 0, 1.5, 0, 0, 0, 0, 0.090909091, 0, 0, 0, 0.545454545, 0.5, 0, 0.5), 4, 4, byrow = TRUE)

# POPN L 2003-2004
XL3 <- matrix(c(0, 0, 1.785365854, 1.856521739, 0.128571429, 0, 0, 0.01869565, 0.028571429, 0, 0, 0, 0.014285714, 0, 0, 0.02173913), 4, 4, byrow = TRUE)

XL4 <- matrix(c(0, 0, 14.25, 16.625, 0.131443299, 0.057142857, 0, 0.25, 0.144329897, 0, 0, 0,
\begin{verbatim}
create_lM

0.092783505, 0.2, 0, 0.25), 4, 4, byrow = TRUE)

XL5 <- matrix(c(0, 0, 0.594642857, 1.765909091, 0, 0, 0.017857143, 0, 0.021052632, 0.018518519, 0.035714286, 0.045454545, 0.021052632, 0.018518519, 0.035714286, 0.068181818), 4, 4, byrow = TRUE)

# POPN O 2003-2004
XO3 <- matrix(c(0, 0, 11.5, 2.775862069, 0.6, 0.285714286, 0.333333333, 0.24137931, 0.04, 0.142857143, 0, 0, 0.16, 0.285714286, 0, 0.172413793), 4, 4, byrow = TRUE)

XO4 <- matrix(c(0, 0, 3.78, 1.225, 0.28358209, 0.171052632, 0, 0.166666667, 0.084577114, 0.026315789, 0, 0.055555556, 0.139303483, 0.447368421, 0, 0.305555556), 4, 4, byrow = TRUE)

XO5 <- matrix(c(0, 0, 1.542857143, 1.035616438, 0.126984127, 0.105263158, 0.047619048, 0.054794521, 0.095238095, 0.157894737, 0.19047619, 0.082191781, 0.111111111, 0.223684211, 0, 0.35664384), 4, 4, byrow = TRUE)

# POPN Q 2003-2004
XQ3 <- matrix(c(0, 0, 0.15, 0.175, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0), 4, 4, byrow = TRUE)

XQ4 <- matrix(c(0, 0, 0, 0.25, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0.666666667, 0, 1), 4, 4, byrow = TRUE)

XQ5 <- matrix(c(0, 0, 0, 1.428571429, 0, 0, 0, 0.142857143, 0.25, 0, 0, 0, 0.25, 0, 0, 0.571428571), 4, 4, byrow = TRUE)

# POPN R 2003-2004
XR3 <- matrix(c(0, 0, 0.7, 0.6125, 0.25, 0, 0, 0.125, 0, 0, 0, 0, 0.25, 0.166666667, 0, 0.25), 4, 4, byrow = TRUE)

XR4 <- matrix(c(0, 0, 0, 0.6, 0.285714286, 0, 0, 0, 0.285714286, 0.333333333, 0, 0, 0.285714286, 0.333333333, 0, 0, 0), 4, 4, byrow = TRUE)

XR5 <- matrix(c(0, 0, 0, 0.7, 0.6125, 0, 0, 0, 0, 0, 0, 0), 4, 4, byrow = TRUE)
\end{verbatim}
# POPN S 2003-2004
XS3 <- matrix(c(0, 0, 2.1, 0.816666667,
0.166666667, 0, 0, 0,
0, 0, 0, 0.166666667), 4, 4, byrow = TRUE)

XS4 <- matrix(c(0, 0, 7,
0.333333333, 0.5, 0, 0,
0, 0, 0, 0.166666667), 4, 4, byrow = TRUE)

XS5 <- matrix(c(0, 0, 0, 1.4,
0, 0, 0, 0,
0, 0, 0, 0.2,
0.111111111, 0.75, 0, 0.2), 4, 4, byrow = TRUE)

mats_list <- list(XC3, XC4, XC5, XE3, XE4, XE5, XF3, XF4, XF5, XG3, XG4, XG5,
XL3, XL4, XL5, XQ3, XQ4, XQ5, XR3, XR4, XR5, XS3, XS4, XS5)

yr_ord <- c(1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3)
pch_ord <- c(1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4, 5, 5, 5, 6, 6, 6, 7, 7, 7,
8, 8, 8, 9, 9, 9)

anth_lefkoMat <- create_lM(mats_list, anthframe, hstages = NA, historical = FALSE,
poporder = 1, patchorder = pch_ord, yearorder = yr_ord)

anth_lefkoMat

# A theoretical example showcasing historical matrices

sizevector <- c(1, 2, 3) # These sizes are not from the original paper
stagevector <- c("Sdl", "Veg", "Flo")
repsvector <- c(0, 0, 1)
obsvector <- c(1, 1, 1)
matvector <- c(0, 1, 1)
immvector <- c(1, 0, 0)
propvector <- c(1, 0, 0)
indataset <- c(1, 1, 1)
binvec <- c(0.5, 0.5, 0.5)

exframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repsstatus = repsvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

A1 <- matrix(c(0.10, 0, 0, 0.12, 0, 0, 0.15, 0, 0,
0.15, 0, 0, 0.17, 0, 0, 0.20, 0, 0,
0.20, 0, 0, 0.22, 0, 0, 0.25, 0, 0,
0, 0.20, 0, 0, 0.22, 0, 0, 0.25, 0,
0, 0, 0, 0, 0, 0, 0, 0, 0), 9, 9, byrow = TRUE)
```
0, 0.25, 0, 0, 0.27, 0, 0, 0.30, 0,
0, 0.30, 0, 0, 0.32, 0, 0, 0.35, 0,
0, 0, 2.00, 0, 0, 3.00, 0, 0, 4.00,
0, 0, 0.35, 0, 0, 0.37, 0, 0, 0.40,
0, 0, 0.40, 0, 0, 0.42, 0, 0, 0.45), 9, 9, byrow = TRUE)
```

```
A2 <- matrix(c(0.10, 0, 0, 0.12, 0, 0, 0.15, 0, 0,
0.15, 0, 0, 0.17, 0, 0, 0.20, 0, 0,
0.20, 0, 0, 0.22, 0, 0, 0.25, 0, 0,
0, 0.20, 0, 0, 0.22, 0, 0, 0.25, 0,
0, 0.25, 0, 0, 0.27, 0, 0, 0.30, 0,
0, 0.30, 0, 0, 0.32, 0, 0, 0.35, 0,
0, 0, 5.00, 0, 0, 6.00, 0, 0, 7.00,
0, 0, 0.35, 0, 0, 0.37, 0, 0, 0.40,
0, 0, 0.40, 0, 0, 0.42, 0, 0, 0.45), 9, 9, byrow = TRUE)
```

```
A3 <- matrix(c(0.10, 0, 0, 0.12, 0, 0, 0.15, 0, 0,
0.15, 0, 0, 0.17, 0, 0, 0.20, 0, 0,
0.20, 0, 0, 0.22, 0, 0, 0.25, 0, 0,
0, 0.20, 0, 0, 0.22, 0, 0, 0.25, 0,
0, 0.25, 0, 0, 0.27, 0, 0, 0.30, 0,
0, 0.30, 0, 0, 0.32, 0, 0, 0.35, 0,
0, 0, 8.00, 0, 0, 9.00, 0, 0, 10.00,
0, 0, 0.35, 0, 0, 0.37, 0, 0, 0.40,
0, 0, 0.40, 0, 0, 0.42, 0, 0, 0.45), 9, 9, byrow = TRUE)
```

```
B1 <- matrix(c(0.10, 0, 0, 0.12, 0, 0, 0.15, 0, 0,
0.15, 0, 0, 0.17, 0, 0, 0.20, 0, 0,
0.20, 0, 0, 0.22, 0, 0, 0.25, 0, 0,
0, 0.20, 0, 0, 0.22, 0, 0, 0.25, 0,
0, 0.25, 0, 0, 0.27, 0, 0, 0.30, 0,
0, 0.30, 0, 0, 0.32, 0, 0, 0.35, 0,
0, 0, 11.00, 0, 0, 12.00, 0, 0, 13.00,
0, 0, 0.35, 0, 0, 0.37, 0, 0, 0.40,
0, 0, 0.40, 0, 0, 0.42, 0, 0, 0.45), 9, 9, byrow = TRUE)
```

```
B2 <- matrix(c(0.10, 0, 0, 0.12, 0, 0, 0.15, 0, 0,
0.15, 0, 0, 0.17, 0, 0, 0.20, 0, 0,
0.20, 0, 0, 0.22, 0, 0, 0.25, 0, 0,
0, 0.20, 0, 0, 0.22, 0, 0, 0.25, 0,
0, 0.25, 0, 0, 0.27, 0, 0, 0.30, 0,
0, 0.30, 0, 0, 0.32, 0, 0, 0.35, 0,
0, 0, 14.00, 0, 0, 15.00, 0, 0, 16.00,
0, 0, 0.35, 0, 0, 0.37, 0, 0, 0.40,
0, 0, 0.40, 0, 0, 0.42, 0, 0, 0.45), 9, 9, byrow = TRUE)
```

```
B3 <- matrix(c(0.10, 0, 0, 0.12, 0, 0, 0.15, 0, 0,
0.15, 0, 0, 0.17, 0, 0, 0.20, 0, 0,
0.20, 0, 0, 0.22, 0, 0, 0.25, 0, 0,
0, 0.20, 0, 0, 0.22, 0, 0, 0.25, 0,
0, 0.25, 0, 0, 0.27, 0, 0, 0.30, 0,
0, 0.30, 0, 0, 0.32, 0, 0, 0.35, 0,
0, 0, 17.00, 0, 0, 18.00, 0, 0, 19.00,
```
cypdata

Demographic Dataset of Cypripedium candidum Population, in Horizontal Format

Description
A dataset containing the states and fates of *Cypripedium candidum* (white lady’s slipper orchids), family Orchidaceae, from a population in Illinois, USA, resulting from monitoring that occurred annually between 2004 and 2009.

Usage
data(cypdata)

Format
A data frame with 77 individuals and 27 variables. Each row corresponds to an unique individual, and each variable from `size.04` on refers to the state of the individual in a particular year.

- **plantid**  A numeric variable giving a unique number to each individual.
- **patch**  A variable referring to patch within the population.
- **censor**  A variable coding for whether the data point is valid. An entry of 1 means that it is so.
- **Inf2.04** Number of double inflorescences in 2004.
- **Inf.04** Number of inflorescences in 2004.
- **Veg.04** Number of stems without inflorescences in 2004.
- **Pod.04** Number of fruits in 2004.
- **Inf2.05** Number of double inflorescences in 2005.
- **Inf.05** Number of inflorescences in 2005.
- **Veg.05** Number of stems without inflorescences in 2005.
- **Pod.05** Number of fruits in 2005.
- **Inf2.06** Number of double inflorescences in 2006.
**Inf.06** Number of inflorescences in 2006.

**Veg.06** Number of stems without inflorescences in 2006.

**Pod.06** Number of fruits in 2006.

**Inf2.07** Number of double inflorescences in 2007.

**Inf.07** Number of inflorescences in 2007.

**Veg.07** Number of stems without inflorescences in 2007.

**Pod.07** Number of fruits in 2007.

**Inf2.08** Number of double inflorescences in 2008.

**Inf.08** Number of inflorescences in 2008.

**Veg.08** Number of stems without inflorescences in 2008.

**Pod.08** Number of fruits in 2008.

**Inf2.09** Number of double inflorescences in 2009.

**Inf.09** Number of inflorescences in 2009.

**Veg.09** Number of stems without inflorescences in 2009.

**Pod.09** Number of fruits in 2009.

**Source**


**Examples**

```r
# Cypripedium example using blocksize
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagvector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagvector,
                          repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                          propstatus = propvector, immstatus = immvector, indataset = indataset,
                          binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
                        patchidcol = "patch", individcol = "plantid", blocksize = 4,
                        sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
```

```
cypdata <- data_frame(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, propstatus = propvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004, patchidcol = "patch", individcol = "plantid", blocksize = 4, sizea0 = "Inf.04", sizeb0 = "Inf2.04", sizec0 = "Veg.04", repstrac0 = c("Inf.04", "Inf.05", "Inf.06", "Inf.07", "Inf.08", "Inf.09"), repstrb0 = c("Inf2.04", "Inf2.05", "Inf2.06", "Inf2.07", "Inf2.08", "Inf2.09"), fecac0 = "Pod.04", stageassign = cypraw_v1, stagesize = "sizeadded", NAas0 = TRUE, NRasRep = TRUE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypraw_v1, year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"), size = c("size3added", "size2added"), supplement = cypsupp2r, yearcol = "year", patchcol = "patchid", individcol = "individ")

cypmatrix2r$A[intersect(which(cypmatrix2r$labels$patch == "A"), which(cypmatrix2r$labels$year == 2004))]

data(cypdata)
sizevector <- c(0, 0, 0, 0, 0, 0, 1.5, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SL", "rep")
repsvector <- c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)
cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")
cypmatrix2r$$A[[intersect(which(cypmatrix2r$labels$patch == "A"),
which(cypmatrix2r$labels$year2 == 2004))]]

lambda3(cypmatrix2r)

---

cypvert

**Demographic Dataset of Cypripedium candidum Population, in Vertical Format**

**Description**

A dataset containing the states and fates of *Cypripedium candidum* (white lady’s slipper orchids), family Orchidaceae, from a population in Illinois, USA, resulting from monitoring that occurred annually between 2004 and 2009. Same dataset as cypdata, but arranged in an ahistorical vertical format.

**Usage**

data(cypvert)

**Format**

A data frame with 77 individuals, 331 rows, and 12 variables. Each row corresponds to a specific two-year transition for a specific individual. Variable codes are similar to those for cypdata, but use .2 to identify occasion t and .3 to identify occasion t+1.

- **plantid** A numeric variable giving a unique number to each individual.
- **patch** A variable referring to patch within the population.
- **censor** A variable coding for whether the data point is valid. An entry of 1 means that it is so.
- **year2** Year in occasion t.
- **Inf2.2** Number of double inflorescences in occasion t.
- **Inf.2** Number of inflorescences in occasion t.
Veg.2 Number of stems without inflorescences in occasion $t$.

Pod.2 Number of fruits in occasion $t$.

Inf2.3 Number of double inflorescences in occasion $t+1$.

Inf.3 Number of inflorescences in occasion $t+1$.

Veg.3 Number of stems without inflorescences in occasion $t+1$.

Pod.3 Number of fruits in occasion $t+1$.

Source


Examples

data(cypvert)

```r
sizevector <- c(0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypframe_raw

cypraw_v2 <- historicalize3(data = cypvert, patchidcol = "patch",
individcol = "plantid", year2col = "year2", sizea2col = "Inf2.2",
sizea1col = "Inf2.3", sizeb2col = "Inf.2", sizeb3col = "Inf.3",
sizec2col = "Veg.2", sizec3col = "Veg.3", repstra2col = "Inf2.2",
repstra3col = "Inf2.3", repstrb2col = "Inf.2", repstrb3col = "Inf.3",
feca2col = "Pod.2",eca3col = "Pod.3", repstrrel = 2,
stageassign = cypframe_raw, stagesize = "sizeadded", censorcol = "censor",
censor = FALSE, NAas0 = TRUE, NRasRep = TRUE, reduce = TRUE)

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
```
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type =c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stagframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v2, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

cypmatrix2r$A[[intersect(which(cypmatrix2r$labels$patch == "A"),
which(cypmatrix2r$labels$year2 == 2004))]]

lambda3(cypmatrix2r)

delete_lM

Delete Matrices from lefkoMat Object

Description

Function delete_lM() deletes matrices from lefkoMat objects.

Usage

delete_lM(lM, mat_num = NA, pop = NA, patch = NA, year = NA)

Arguments

- **lM**: The lefkoMat object to delete matrices from.
- **mat_num**: Either a single integer corresponding to the matrix to remove within the labels element of lM, or a vector of such integers.
- **pop**: The population designation for matrices to remove. Only used if mat_num is not given.
- **patch**: The patch designation for matrices to remove. Only used if mat_num is not given.
- **year**: The time *t* designation for matrices to remove. Only used if mat_num is not given.

Value

A lefkoMat object in which the matrices specified in lM have been removed.

Notes

If mat_num is not provided, then at least one of pop, patch, or year must be provided. If at least two of pop, patch, and year are provided, then function delete_lM() will identify matrices to remove as the intersection of provided inputs.
See Also

create_lM()
add_lM()
subset_lM()

Examples

# These matrices are of 9 populations of the plant species Anthyllis
# vulneraria, and were originally published in Davison et al. (2010) Journal

sizevector <- c(1, 1, 2, 3)  # These sizes are not from the original paper
stagevector <- c("Sdl", "Veg", "SmFlo", "LFlo")
repvector <- c(0, 0, 1, 1)
obsvector <- c(1, 1, 1, 1)
matvector <- c(0, 1, 1, 1)
immvector <- c(1, 0, 0, 0)
propvector <- c(0, 0, 0, 0)
indataset <- c(1, 1, 1, 1)
binvec <- c(0.5, 0.5, 0.5, 0.5)

anthframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

# POPN C 2003-2004
XC3 <- matrix(c(0, 0, 1.74, 1.74,
               0.208333333, 0, 0, 0.057142857,
               0.041666667, 0.076923077, 0, 0,
               0.083333333, 0.076923077, 0.066666667, 0.028571429), 4, 4, byrow = TRUE)

# 2004-2005
XC4 <- matrix(c(0, 0, 0.3, 0.6,
               0.32183908, 0.142857143, 0, 0,
               0.16091954, 0.285714286, 0, 0,
               0.252873563, 0.285714286, 0.5, 0.6), 4, 4, byrow = TRUE)

# 2005-2006
XC5 <- matrix(c(0, 0, 0.50625, 0.675,
               0, 0, 0, 0.035714286,
               0.1, 0.068965517, 0.0625, 0.107142857,
               0.3, 0.137931034, 0, 0.071428571), 4, 4, byrow = TRUE)

# POPN E 2003-2004
XE3 <- matrix(c(0, 0, 2.44, 6.569230769,
               0.196428571, 0, 0, 0,
               0.125, 0.5, 0, 0,
               0.160714286, 0.5, 0.133333333, 0.076923077), 4, 4, byrow = TRUE)
XE4 <- matrix(c(0, 0, 0.45, 0.646153846,
0.06557377, 0.090909091, 0.125, 0, 0.032786885, 0, 0.125, 0.076923077, 0.049180328, 0, 0.125, 0.230769231), 4, 4, byrow = TRUE)

XE5 <- matrix(c(0, 0, 2.85, 3.99, 0.032786885, 0, 0.125, 0.076923077, 0.049180328, 0, 0.125, 0.230769231), 4, 4, byrow = TRUE)

# POPN F 2003-2004
XF3 <- matrix(c(0, 0, 1.815, 7.058333333, 0.075949367, 0, 0.05, 0.083333333, 0.139240506, 0, 0, 0.25, 0.075949367, 0, 0, 0.083333333), 4, 4, byrow = TRUE)

XF4 <- matrix(c(0, 0, 1.233333333, 7.4, 0.223880597, 0, 0.111111111, 0.142857143, 0.134328358, 0.272727273, 0.166666667, 0.142857143, 0.119402985, 0.363636364, 0.055555556, 0.142857143), 4, 4, byrow = TRUE)

XF5 <- matrix(c(0, 0, 1.06, 3.372727273, 0.073170732, 0.025, 0.033333333, 0, 0.036585366, 0.15, 0.1, 0.166666667, 0.142857143, 0.06097561, 0.225, 0.166666667, 0.272727273), 4, 4, byrow = TRUE)

# POPN G 2003-2004
XG3 <- matrix(c(0, 0, 0.245454545, 2.1, 0, 0, 0.045454545, 0, 0.125, 0, 0.090909091, 0, 0.125, 0, 0.090909091, 0.333333333), 4, 4, byrow = TRUE)

XG4 <- matrix(c(0, 0, 1.1, 1.54, 0.111111111, 0, 0, 0, 0.090909091, 0, 0, 0.20, 0, 0.25), 4, 4, byrow = TRUE)

XG5 <- matrix(c(0, 0, 0, 1.5, 0, 0, 0, 0.045454545, 0.5, 0, 0.5), 4, 4, byrow = TRUE)

# POPN L 2003-2004
XL3 <- matrix(c(0, 0, 1.785365854, 1.856521739, 0.128571429, 0, 0, 0.010869565, 0.028571429, 0, 0, 0, 0.014285714, 0, 0, 0.02173913), 4, 4, byrow = TRUE)

XL4 <- matrix(c(0, 0, 14.25, 16.625, 0.131443299, 0.057142857, 0, 0.25, 0.144329897, 0, 0, 0, 0.092783505, 0.2, 0, 0.25), 4, 4, byrow = TRUE)

XL5 <- matrix(c(0, 0, 0.594642857, 1.765909091,
# POPN O 2003-2004
XO3 <- matrix(c(0, 0, 11.5, 2.775862069, 0.6, 0.285714286, 0.333333333, 0.24137931, 0.04, 0.142857143, 0, 0, 0.017857143, 0, 0.021052632, 0.018518519, 0.035714286, 0.045454545, 0.017857143, 0, 0.021052632, 0.018518519, 0.035714286, 0.068181818), 4, 4, byrow = TRUE)

# POPN Q 2003-2004
XQ3 <- matrix(c(0, 0, 0.15, 0.175, 0, 0, 0, 0, 1, 0, 0, 0), 4, 4, byrow = TRUE)
XQ4 <- matrix(c(0, 0, 0, 0.25, 0.285714286, 0, 0, 0, 0.285714286, 0.333333333, 0, 0, 0.142857143, 0.166666667, 0, 0.166666667, 0, 0.172413793), 4, 4, byrow = TRUE)
XQ5 <- matrix(c(0, 0, 0, 1.428571429, 0, 0, 0, 0.142857143, 0.25, 0, 0, 0.25, 0, 0, 0.571428571), 4, 4, byrow = TRUE)

# POPN R 2003-2004
XR3 <- matrix(c(0, 0, 0.7, 0.6125, 0.25, 0, 0, 0.125, 0, 0, 0, 0.25, 0.166666667, 0, 0.25), 4, 4, byrow = TRUE)
XR4 <- matrix(c(0, 0, 0, 0.6, 0.285714286, 0, 0, 0, 0.285714286, 0.333333333, 0, 0, 0.285714286, 0.333333333, 0, 1), 4, 4, byrow = TRUE)
XR5 <- matrix(c(0, 0, 0, 0.7, 0.6125, 0, 0, 0, 0, 0, 0, 0.333333333, 0, 0.333333333, 0.625), 4, 4, byrow = TRUE)

# POPN S 2003-2004
density_input

Create a Data Frame of Elements Subject to Density Dependence

Description

Function density_input() provides all necessary data to incorporate density dependence into a lefkomat object, a list of matrices, or a single matrix. Three forms of density dependence are allowed, including the Ricker function, the Beverton-Holt function, the Usher function, and the logistic function. In each case, density must have an effect with at least a one time-step delay (see Notes).

Usage

density_input(
  mpm,
  stage3,
  stage2,
  stage1 = NA,
density_input

age2 = NA,
style = 1,
time_delay = 1,
alpha = NA,
beta = NA,
type = NA,
type_t12 = NA
}

Arguments

mpm
The lefkoMat object that will be subject to density dependent projection.

stage3
A vector showing the name or number of the stage in occasion t+1 in the transitions to be affected by density. Abbreviations for groups of stages are also usable (see Notes).

stage2
A vector showing the name or number of the stage in occasion t in the transition to be affected by density. Abbreviations for groups of stages are also usable (see Notes).

stage1
A vector showing the name or number of the stage in occasion t-1 in the transition to be affected by density. Only needed if a historical MPM is used. Abbreviations for groups of stages are also usable (see Notes).

age2
A vector showing the age of the stage in occasion t in the transition to be affected by density. Only needed if an age-by-stage MPM is used.

style
A vector coding for the style of density dependence on each transition subject to density dependence. Options include 1, ricker, ric, or r for the Ricker function; 2, beverton, bev, and b for the Beverton-Holt function; 3, usher, ush, and u for the Usher function; and 4, logistic, log, and l for the logistic function. If only a single code is provided, then all noted transitions are assumed to be subject to this style of density dependence. Defaults to ricker.

time_delay
A vector indicating the number of occasions back on which density dependence operates. Defaults to 1, and may not equal any number less than 1. If a single number is input, then all noted transitions are assumed to be subject to this time delay.

alpha
A vector indicating the numeric values to use as the alpha term in the two parameter Ricker, Beverton-Holt, or Usher function, or the value of the carrying capacity K to use in the logistic equation (see Notes section for more on this term). If a single number is provided, then all noted transitions are assumed to be subject to this value of alpha.

beta
A vector indicating the numeric values to use as the beta term in the two parameter Ricker, Beverton-Holt, or Usher function. Not used in the logistic equation. If a single number is provided, then all noted transitions are assumed to be subject to this value of beta.

type
A vector denoting the kind of transition between occasions t and t+1 to be replaced. This should be entered as 1, S, or s for the replacement of a survival transition; or 2, F, or f for the replacement of a fecundity transition. If empty or not provided, then defaults to 1 for survival transition.
density_input

**type_t12**

An optional vector denoting the kind of transition between occasions \( t-1 \) and \( t \). Only necessary if a historical MPM in deVries format is desired. This should be entered as 1, S, or s for a survival transition; or 2, F, or f for a fecundity transitions. Defaults to 1 for survival transition, with impacts only on the construction of deVries-format hMPMs.

**Value**

A data frame of class `lefkoDens`. This object can be used as input in function `projection3()`.

Variables in this object include the following:

- **stage3**: Stage at occasion \( t+1 \) in the transition to be replaced.
- **stage2**: Stage at occasion \( t \) in the transition to be replaced.
- **stage1**: Stage at occasion \( t-1 \) in the transition to be replaced, if applicable.
- **age2**: Age at occasion \( t \) in the transition to be replaced, if applicable.
- **style**: Style of density dependence, coded as 1, 2, 3, or 4 for the Ricker, Beverton-Holt, Usher, or logistic function, respectively.
- **time_delay**: The time delay on density dependence, in time steps.
- **alpha**: The value of alpha in the Ricker, Beverton-Holt, or Usher function, or the value of carrying capacity, \( K \), in the logistic function.
- **beta**: The value of beta in the Ricker, Beverton-Holt, or Usher function.
- **type**: Designates whether the transition from occasion \( t \) to occasion \( t+1 \) is a survival transition probability (1), or a fecundity rate (2).
- **type_t12**: Designates whether the transition from occasion \( t-1 \) to occasion \( t \) is a survival transition probability (1), a fecundity rate (2).

**Notes**

The parameters alpha and beta are applied according to the two-parameter Ricker function, the two-parameter Beverton-Holt function, the two-parameter Usher function, or the one-parameter logistic function. Although the default is that a 1 time step delay is assumed), greater time delays can be set through the `time_delay` option.

Entries in `stage3`, `stage2`, and `stage1` can include abbreviations for groups of stages. Use `rep` if all reproductive stages are to be used, `nrep` if all mature but non-reproductive stages are to be used, `mat` if all mature stages are to be used, `immat` if all immature stages are to be used, `prop` if all propagule stages are to be used, `nprop` if all non-propagule stages are to be used, and leave empty or use `all` if all stages in stageframe are to be used.

**See Also**

- `start_input()`
- `projection3()`
Examples

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                        immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobscol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sdl", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sdl"),
eststage3 = c(NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA),
givenrate = c(0.345, 0.345, 0.054, 0.054),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
type = c(1, 1, 1, 1, 3, 3),
type_t12 = c(1, 1, 1, 2, 2, 1),
stageframe = lathframe, historical = TRUE)

ehr3d <- density_input(ehr3dmean, stage3 = c("Sd", "Sdl"),
stage2 = c("rep", "rep"), stage1 = c("all", "all"), style = 1,
time_delay = 1, alpha = 1, beta = 0, type = c(2, 2), type_t12 = c(1, 1))
```

elasticity3

Estimate Elasticity of Population Growth Rate to Matrix Elements
elasticity3() is a generic function that returns the elasticity of the population growth rate to the elements of the matrices in a matrix population model. Currently, this function estimates both deterministic and stochastic elasticities, where the growth rate is $\lambda$ in the former case and the log of the stochastic $\lambda$ in the latter case. This function is made to handle very large and sparse matrices supplied as lefkoMat objects, as lists of matrices, and as individual matrices.

Usage

```r
elasticity3(mats, ...)
```

Arguments

- `mats` A lefkoMat object, or population projection matrix, for which the stable stage distribution is desired.
- `...` Other parameters.

Value

The value returned depends on the class of the `mats` argument.

See Also

- `elasticity3.lefkoMat()`
- `elasticity3.matrix()`
- `elasticity3.list()`

Examples

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VL\alpha", "Flo", "Dorm")
repsvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector, 
                        repstatus = repsvector, obsstatus = obsvector, matstatus = matvector, 
                        immstatus = immvector, indataset = indataset, binhalfwidth = binvec, 
                        propstatus = propvector)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988, 
                           patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9, 
                           juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88", 
                           youngcol = "Seedling1988", propcol = "FCODE88", 
                           indataset = indataset, binhalfwidth = binvec)
```

elasticity3

fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
elasticity3(ehrlen3mean)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypraw_v1, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "SD", "P1"),
rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)
cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
  year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
  size = c("size3added", "size2added"), supplement = cypsupp2r,
  yearcol = "year2", patchcol = "patchid", individcol = "individ")
elasticity3(cypmatrix2r)

Description

elasticity3.lefkoMat() returns the elasticities of population growth rate to elements of all $A$ matrices in an object of class lefkoMat. If deterministic, then $\lambda$ is taken as the population growth rate. If stochastic, then stochastic $\lambda$, or the stochastic growth rate, is taken as the population growth rate. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as smaller ahistorical matrices.

Usage

## S3 method for class 'lefkoMat'
elasticity3(
  mats,
  stochastic = FALSE,
  steps = 10000,
  time_weights = NA,
  sparse = "auto",
  append_mats = FALSE,
  ...
)

Arguments

mats An object of class lefkoMat.
stochastic A logical value determining whether to conduct a deterministic (FALSE) or stochastic (TRUE) elasticity analysis. Defaults to FALSE.
steps The number of occasions to project forward in stochastic simulation. Defaults to 10,000.
time_weights Numeric vector denoting the probabilistic weightings of annual matrices. Defaults to equal weighting among occasions.
sparse  A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
append_mats  A logical value indicating whether to include the original A, U, and F matrices in the output lefkoElas object.
...  Other parameters.

Value
This function returns an object of class lefkoElas, which is a list with 8 elements. The first, h_elasmats, is a list of historical elasticity matrices (NULL if an ahMPM is used as input). The second, ah_elasmats, is a list of either ahistorical elasticity matrices if an ahMPM is used as input, or, if an hMPM is used as input, then the result is a list of elasticity matrices in which historical elasticities have been summed by the stage in occasions $t$ and $t+1$ to produce historically-corrected elasticity matrices, which are equivalent in dimension to ahistorical elasticity matrices but reflect the effects of stage in occasion $t-1$. The third element, h_stages, is a data frame showing historical stage pairs (NULL if ahMPM used as input). The fourth element, agestages, shows age-stage combinations in the order used in age-by-stage MPMs, if supplied. The fifth element, ah_stages, is a data frame showing the order of ahistorical stages. The last 3 elements are the A, U, and F portions of the input.

Notes
Deterministic elasticities are estimated as eqn. 9.72 in Caswell (2001, Matrix Population Models). Stochastic elasticities are estimated as eqn. 14.99 in Caswell (2001). Note that stochastic elasticities are of the stochastic $\lambda$, while stochastic sensitivities are with regard to the log of the stochastic $\lambda$.

See Also
elasticity3()
elasticity3.matrix()
elasticity3.list()
summary.lefkoElas()

Examples
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 0, 0, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 0)
immvector <- c(1, 0, 1, 1, 1, 1, 1)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, 0.054),
type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

elasticity3(ehrlen3, stochastic = TRUE)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
"XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypraw_v1, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"),
eststage3 = c(NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type =c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

elasticity3(cypmatrix2r)

---

elasticity3.list  Estimate Elasticity of Population Growth Rate of a List of Matrices

Description

elasticity3.list() returns the elasticities of lambda to elements of a single matrix. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as smaller ahistorical matrices.

Usage

## S3 method for class 'list'
elasticity3(
mats,
stochastic = FALSE,
steps = 10000,
time_weights = NA,
historical = FALSE,
sparse = "auto",
append_mats = FALSE,
...
)

Arguments

mats  A list of objects of class matrix.
stochastic  A logical value determining whether to conduct a deterministic (FALSE) or stochastic (TRUE) elasticity analysis. Defaults to FALSE.
The number of occasions to project forward in stochastic simulation. Defaults to 10,000.

Numeric vector denoting the probabilistic weightings of annual matrices. Defaults to equal weighting among occasions.

A logical value denoting whether the input matrices are historical. Defaults to FALSE.

A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".

A logical value indicating whether to include the original matrices input as object mats in the output lefkoElas object.

Other parameters.

This function returns an object of class lefkoElas, which is a list with 8 elements. The first, h_elasmats, is a list of historical elasticity matrices, though in the standard list case it returns a NULL value. The second, ah_elasmats, is a list of ahistorical elasticity matrices. The third element, h_stages, the fourth element, agestages, and the fifth element, ah_stages, are set to NULL. The last 3 elements are the original A matrices in element A, followed by NULL values for the U and F elements.

Deterministic elasticities are estimated as eqn. 9.72 in Caswell (2001, Matrix Population Models). Stochastic elasticities are estimated as eqn. 14.99 in Caswell (2001). Note that stochastic elasticities are of stochastic $\lambda$, while stochastic sensitivities are with regard to the log of the stochastic $\lambda$.

See Also

elasticity3()
elasticity3.lefkoMat()
elasticity3.matrix()

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repevector <- c(0, 0, 0, 0, 1, 0)
obsvect <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvect <- c(1, 0, 0, 0, 0, 0, 0)
propvect <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(1, 0, 0, 0, 0, 0, 0)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec, propstatus = propvector)


lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sdl", "mat"), stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"), stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"), eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"), eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"), eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"), givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA), multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA), type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1), stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all", stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3, yearcol = "year2", indivcol = "individ")

elasticity3(ehrlen3$A, stochastic = TRUE)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframerate <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004, patchidcol = "patch", individcol = "plantid", blocksize = 4, sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04", repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04"
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)
cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", individcol = "individ")
elasticity3(cypmatrix2r$A)

elasticity3.matrix  Estimate Elasticity of Population Growth Rate of a Single Matrix

Description

elasticity3.matrix() returns the elasticities of lambda to elements of a single matrix. Because
this handles only one matrix, the elasticities are inherently deterministic and based on the dominant
eigen value as the best metric of the population growth rate. This function can handle large and
sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as
well as smaller ahistorical matrices.

Usage

## S3 method for class 'matrix'
elasticity3(mats, sparse = "auto", ...)

Arguments

mats  An object of class matrix.
sparse  A text string indicating whether to use sparse matrix encoding ("yes") or dense
matrix encoding ("no"). Defaults to "auto".
...

Value

This function returns a single elasticity matrix.
elasticity3.matrix

See Also

elasticity3()
elasticity3.lefkoMat()
elasticity3.list()

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repsvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
            repstatus = repsvector, obsstatus = obsvector, matstatus = matvector,
            immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
            propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
            patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
            juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
            fecacol = "Intactseed88", deadacol = "Dead1988",
            nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
            censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
            stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
            stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
            eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
            eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
            eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
            givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
            multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
            type = c(1, 1, 1, 1, 3, 1, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
            stageframe = lathframe, historical = TRUE)

ehrten3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
            stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
            yearcol = "year2", individcol = "individ")

ehrten3mean <- lmean(ehrten3)
elasticity3(ehrten3mean$A[[1]])

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, propstatus = propvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004, patchidcol = "patch", individcol = "plantid", blocksize = 4, sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04", repstracol = "Inf2.04", repstrbcol = "Inf.04", fecacol = "Pod.04", stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE, NRasRep = TRUE)

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"), stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"), eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA), eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA), givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA), multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA), type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3), stageframe = cypframe_raw, historical = FALSE)

cymatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw, year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"), size = c("size3added", "size2added"), supplement = cypsupp2r, yearcol = "year2", patchcol = "patchid", indivcol = "individ")

elasticity3(cymatrix2r$A[[1]])
Description

Function `flefko2()` returns ahistorical MPMs corresponding to the patches and occasion times given, including the associated component transition and fecundity matrices, a data frame detailing the characteristics of the ahistorical stages used, and a data frame characterizing the patch and occasion time combinations corresponding to these matrices.

Usage

```r
flefko2(
  year = "all", patch = "all",
  stageframe, supplement = NULL,
  repmatrix = NULL, overwrite = NULL,
  data = NA, modelsuite = NA,
  surv_model = NA, obs_model = NA,
  size_model = NA, sizeb_model = NA,
  sizec_model = NA, repst_model = NA,
  fec_model = NA, jsurv_model = NA,
  jobs_model = NA, size_model = NA,
  jsize_model = NA, jsizeb_model = NA,
  jsizec_model = NA, jrepst_model = NA,
  paramnames = NA, inda = NULL,
  indb = NULL, indc = NULL,
  surv_dev = 0, obs_dev = 0,
  size_dev = 0, sizeb_dev = 0,
  sizec_dev = 0, repst_dev = 0,
  fec_dev = 0, jsurv_dev = 0,
  jobs_dev = 0, jsize_dev = 0,
  jsizeb_dev = 0, jsizec_dev = 0,
  jrepst_dev = 0,
  density = NA,
```

Arguments

year A variable corresponding to observation occasion, or a set of such values, given in values associated with the year term used in linear model development. Defaults to "all", in which case matrices will be estimated for all occasion times.

patch A variable designating which patches or subpopulations will have matrices estimated. Defaults to "all", but can also be set to specific patch names.

stageframe A stageframe object that includes information on the size, observation status, propagule status, immaturity status, and maturity status of each ahistorical stage. Should also incorporate bin widths if size is continuous.

supplement An optional data frame of class lefkoSD that provides supplemental data that should be incorporated into the MPM. Three kinds of data may be integrated this way: transitions to be estimated via the use of proxy transitions, transition overwrites from the literature or supplemental studies, and transition multipliers for survival and fecundity. This data frame should be produced using the supplement() function. Can be used in place of or in addition to an overwrite table (see overwrite below) and a reproduction matrix (see repmatrix below).

repmatrix An optional reproduction matrix. This matrix is composed mostly of 0s, with non-zero entries acting as element identifiers and multipliers for fecundity (with 1 equaling full fecundity). If left blank, and no supplement is provided, then flefko2() will assume that all stages marked as reproductive produce offspring at 1x that of estimated fecundity, and that offspring production will yield the first stage noted as propagule or immature. To prevent this behavior, input just 0, which will result in fecundity being estimated only for transitions noted in supplement above. Must be the dimensions of an ahistorical matrix.

overwrite An optional data frame developed with the overwrite() function describing transitions to be overwritten either with given values or with other estimated transitions. Note that this function supplements overwrite data provided in supplement.
data

The historical vertical demographic data frame used to estimate vital rates (class hfvdata). The original data frame is required in order to initialize times and patches properly.

modelsuite

An optional lefkoMod object holding the vital rate models. If given, then surv_model, obs_model, size_model, sizeb_model, sizec_model, repst_model, fec_model, jsurv_model, jobs_model, jsize_model, jsizeb_model, jsizec_model, jrepst_model, paramnames, yearcol, and patchcol are not required. No models should include size or reproductive status in occasion t-1.

surv_model

A linear model predicting survival probability. This can be a model of class glm or glmr, and requires a predicted binomial variable under a logit link. If given, then will overwrite any survival probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion t.

obs_model

A linear model predicting sprouting or observation probability. This can be a model of class glm or glmr, and requires a predicted binomial variable under a logit link. If given, then will overwrite any observation probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion t.

size_model

A linear model predicting primary size. This can be a model of class glm, glmer, glmmTMB, zeroinfl, vglm, lm, or lmer. If given, then will overwrite any primary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion t.

sizeb_model

A linear model predicting secondary size. This can be a model of class glm, glmer, glmmTMB, zeroinfl, vglm, lm, or lmer. If given, then will overwrite any secondary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion t.

sizec_model

A linear model predicting tertiary size. This can be a model of class glm, glmer, glmmTMB, zeroinfl, vglm, lm, or lmer. If given, then will overwrite any tertiary size model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion t.

repst_model

A linear model predicting reproduction probability. This can be a model of class glm or glmr, and requires a predicted binomial variable under a logit link. If given, then will overwrite any reproduction probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion t.

fec_model

A linear model predicting fecundity. This can be a model of class glm, glmer, glmmTMB, zeroinfl, vglm, lm, or lmer. If given, then will overwrite any fecundity model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion t.

jsurv_model

A linear model predicting juvenile survival probability. This can be a model of class glm or glmr, and requires a predicted binomial variable under a logit link. If given, then will overwrite any juvenile survival probability model given in modelsuite. This model must have been developed in a modeling exercise testing only the impacts of occasion t.

jobs_model

A linear model predicting juvenile sprouting or observation probability. This can be a model of class glm or glmr, and requires a predicted binomial variable under a logit link. If given, then will overwrite any juvenile observation
probability model given in `modelsuite`. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**jsize_model** A linear model predicting juvenile primary size. This can be a model of class `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `vglm`, `lm`, or `lmer`. If given, then will overwrite any juvenile primary size model given in `modelsuite`. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**jsizb_model** A linear model predicting juvenile secondary size. This can be a model of class `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `vglm`, `lm`, or `lmer`. If given, then will overwrite any juvenile secondary size model given in `modelsuite`. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**jsizc_model** A linear model predicting juvenile tertiary size. This can be a model of class `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `vglm`, `lm`, or `lmer`. If given, then will overwrite any juvenile tertiary size model given in `modelsuite`. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**jrepst_model** A linear model predicting reproduction probability of a mature individual that was immature in the previous year. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any reproduction probability model given in `modelsuite`. This model must have been developed in a modeling exercise testing only the impacts of occasion \( t \).

**paramnames** A dataframe with three columns, the first describing all terms used in linear modeling, the second (must be called `mainparams`), showing the general model terms that will be used in matrix creation (users should use `modelsearch()` at least once to see the proper names to be used in this column), and the third showing the equivalent terms used in modeling (must be named `modelparams`). Only required if `modelsuite` is not supplied.

**inda** Can be a single value to use for individual covariate \( a \) in all matrices, a pair of values to use for times \( t \) and \( t-1 \) in historical matrices, or a vector of such values corresponding to each occasion in option `year`. Defaults to NULL.

**indb** Can be a single value to use for individual covariate \( b \) in all matrices, a pair of values to use for times \( t \) and \( t-1 \) in historical matrices, or a vector of such values corresponding to each occasion in option `year`. Defaults to NULL.

**indc** Can be a single value to use for individual covariate \( c \) in all matrices, a pair of values to use for times \( t \) and \( t-1 \) in historical matrices, or a vector of such values corresponding to each occasion in option `year`. Defaults to NULL.

**surv_dev** A numeric value to be added to the y-intercept in the linear model for survival probability.

**obs_dev** A numeric value to be added to the y-intercept in the linear model for observation probability.

**size_dev** A numeric value to be added to the y-intercept in the linear model for primary size.

**sizeb_dev** A numeric value to be added to the y-intercept in the linear model for secondary size.

**sizec_dev** A numeric value to be added to the y-intercept in the linear model for tertiary size.
repst_dev  A numeric value to be added to the y-intercept in the linear model for probability of reproduction.

fec_dev    A numeric value to be added to the y-intercept in the linear model for fecundity.

jsurv_dev  A numeric value to be added to the y-intercept in the linear model for juvenile survival probability.

jobs_dev   A numeric value to be added to the y-intercept in the linear model for juvenile observation probability.

jsize_dev  A numeric value to be added to the y-intercept in the linear model for juvenile primary size.

jsizeb_dev A numeric value to be added to the y-intercept in the linear model for juvenile secondary size.

jsizec_dev A numeric value to be added to the y-intercept in the linear model for juvenile tertiary size.

jrepst_dev A numeric value to be added to the y-intercept in the linear model for juvenile reproduction probability.

density    A numeric value indicating density value to use to propagate matrices. Only needed if density is an explanatory term used in linear models. Defaults to NA.

repmnd     A scalar multiplier of fecundity. Defaults to 1.

yearcol    The variable name or column number corresponding to year in occasion t in the dataset. Not needed if a modelsuite is supplied.

patchcol   The variable name or column number corresponding to patch in the dataset. Not needed if a modelsuite is supplied.

year.as.random A logical term indicating whether coefficients for missing occasions within vital rate models should be estimated as random intercepts. Defaults to FALSE, in which case missing monitoring occasion coefficients are set to 0.

patch.as.random A logical term indicating whether coefficients for missing patches within vital rate models should be estimated as random intercepts. Defaults to FALSE, in which case missing patch coefficients are set to 0.

random.inda A logical value denoting whether to treat individual covariate a as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.

random.indb A logical value denoting whether to treat individual covariate b as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.

random.indc A logical value denoting whether to treat individual covariate c as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.

randomseed A numeric value used as a seed to generate random estimates for missing occasion and patch coefficients, if either year.as.random or patch.as.random is set to TRUE. Defaults to set.seed() default.

negfec     A logical value denoting whether fecundity values estimated to be negative should be reset to 0. Defaults to FALSE.
reduce: A logical value denoting whether to remove ahistorical stages associated solely with 0 transitions. These are only removed in cases where the associated row and column sums in ALL matrices estimated equal 0. Defaults to `FALSE`.

err_check: A logical value indicating whether to append matrices of vital rate probabilities associated with each matrix to the `lefkoMat` object generated. These matrices are developed internally and can be used for error checking. Defaults to `FALSE`.

exp_tol: A numeric value used to indicate a maximum value to set exponents to in the core kernel to prevent numerical overflow. Defaults to 700.

theta_tol: A numeric value used to indicate a maximum value to theta as used in the negative binomial probability density kernel. Defaults to 100000000, but can be reset to other values during error checking.

Value

If all inputs are properly formatted, then this function will return an object of class `lefkoMat`, which is a list that holds the matrix projection model and all of its metadata. Its structure is a list with the following elements:

- **A**: A list of full projection matrices in order of sorted patches and occasion times. All matrices output in R's `matrix` class.
- **U**: A list of survival transition matrices sorted as in **A**. All matrices output in R's `matrix` class.
- **F**: A list of fecundity matrices sorted as in **A**. All matrices output in R's `matrix` class.
- **hstages**: A data frame matrix showing the pairing of ahistorical stages used to create historical stage pairs. Set to `NA` for ahistorical matrices.
- **agestages**: A data frame showing age-stage pairs. In this function, it is set to `NA`. Only used in output to function `aflfko2()`.
- **ahstages**: A data frame detailing the characteristics of associated ahistorical stages, in the form of a modified stageframe that includes status as an entry stage through reproduction.
- **labels**: A data frame giving the population, patch, and year of each matrix in order. In `flefko2()`, only one population may be analyzed at once, and so `pop = NA`.
- **matrixqc**: A short vector describing the number of non-zero elements in **U** and **F** matrices, and the number of matrices.
- **modelqc**: This is the qc portion of the modelsuite input.
- **prob_out**: An optional element only added if `err_check = TRUE`. This is a list of vital rate probability matrices, with 6 columns in the order of survival, observation probability, reproduction probability, primary size transition probability, secondary size transition probability, and tertiary size transition probability.

Notes

Unlike `rlefko2()` and `rlefko3()`, this function does not currently distinguish populations. This function will yield incorrect estimates if the models utilized incorporate state in occasion \( t-1 \). Only use models developed testing for ahistorical effects.
The default behavior of this function is to estimate fecundity with regards to transitions specified via associated fecundity multipliers in either supplement or repmatrix. If both of these fields are left empty, then fecundity will be estimated at full for all transitions leading from reproductive stages to immature and propagule stages. However, if a supplement is provided and a repmatrix is not, or if repmatrix is set to 0, then only fecundity transitions noted in the supplement will be set to non-zero values. To use the default behavior of setting all reproductive stages to reproduce at full fecundity into immature and propagule stages, but also incorporate given or proxy survival transitions, input those given and proxy transitions through the overwrite option.

The reproduction matrix (field repmatrix) may only be supplied as ahistorical. If provided as historical, then flefko2() will fail and produce an error.

Users may at times wish to estimate MPMs using a dataset incorporating multiple patches or subpopulations, but without discriminating between those patches or subpopulations. Should the aim of analysis be a general MPM that does not distinguish these patches or subpopulations, the patchcol variable should be set to NA, which is the default.

Input options including multiple variable names must be entered in the order of variables in occasion \(t+1\) and \(t\). Rearranging the order will lead to erroneous calculations, and may lead to fatal errors.

Care should be taken to match the random status of year and patch to the states of those variables within the modelsuite. If they do not match, then they will be treated as zeroes in vital rate estimation.

Using the err_check option will produce a matrix of 6 columns, each characterizing a different vital rate. The product of each row yields an element in the associated $U$ matrix. The number and order of elements in each column of this matrix matches the associated matrix in column vector format. Use of this option is generally for the purposes of debugging code.

**Examples**

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 4.6, 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 1, 2, 3, 4, 5, 6, 7, 8, 9)
stagevector <- c("Sd", "Sd1", "Dorm", "Sz1nr", "Sz2nr", "Sz3nr", "Sz4nr", "Sz5nr", "Sz6nr", "Sz7nr", "Sz8nr", "Sz9nr", "Sz1r", "Sz2r", "Sz3r", "Sz4r", "Sz5r", "Sz6r", "Sz7r", "Sz8r", "Sz9r")
revector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
immvector <- c(1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 4.6, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)
lathframeln <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = revector, obsstatus = obsvector, matstatus = matvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec, propstatus = propvector)
```
```r
lathvertln <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "lnVol88", repstracol = "Intactseed88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframeln,
stagesize = "sizea", censorcol = "Missing1988", censorkeep = NA,
NAas0 = TRUE, censor = TRUE)

lathvertln$feca2 <- round(lathvertln$feca2)
lathvertln$feca1 <- round(lathvertln$feca1)
lathvertln$feca3 <- round(lathvertln$feca3)

lathmodelsln2 <- modelsearch(lathvertln, historical = FALSE,
approach = "mixed", suite = "main",
vitalrates = c("surv", "obs", "size", "repst", "fec"), juvestimate = "Sdl",
bestfit = "AICc&k", sizedist = "gaussian", fecdist = "poisson",
indiv = "individ", patch = "patchid", year = "year2",
year.as.random = TRUE, patch.as.random = TRUE, show.model.tables = TRUE,
quiet = TRUE)

# Here we use supplemental to provide overwrite and reproductive info
lathsupp2 <- supplemental(stage3 = c("Sd", "Sdl", "Sd", "Sdl"),
stage2 = c("Sd", "Sd", "rep", "rep"),
givenrate = c(0.345, 0.054, NA, NA),
multiplier = c(NA, NA, 0.345, 0.054),
type = c(1, 1, 3, 3), stageframe = lathframeln, historical = FALSE)

lathmat2ln <- flefko2(year = "all", patch = "all", stageframe = lathframeln,
modelsuite = lathmodelsln2, data = lathvertln, supplement = lathsupp2,
patchcol = "patchid", yearcol = "year2", year.as.random = FALSE,
patch.as.random = FALSE, reduce = FALSE)

summary(lathmat2ln)

#Cypripedium example using three size metrics for classification
rm(list=ls(all=TRUE))

data(cypdata)

sizevector.f <- c(0, 0, 0, 0, 0, 0, seq(1, 12, by = 1), seq(0, 9, by = 1),
seq(0, 8, by = 1), seq(0, 7, by = 1), seq(0, 6, by = 1), seq(0, 5, by = 1),
seq(0, 4, by = 1), seq(0, 3, by = 1), 0, 1, 2, 0, 1, 0,
0, 0, 1, 0)

sizevector.f <- c(0, 0, 0, 0, 0, 0, rep(0, 12), rep(1, 10), rep(2, 9),
rep(3, 8), rep(4, 7), rep(5, 6), rep(6, 5), rep(7, 4), rep(8, 3), 9, 9, 10,
0, 1, 1, 2)

sizevector.f <- c(0, 0, 0, 0, 0, 0, rep(0, 12), rep(0, 10), rep(0, 9),
rep(0, 8), rep(0, 7), rep(0, 6), rep(0, 5), rep(0, 4), 0, 0, 0, 0, 0, 0,
1, 1, 1, 1)

stagevector.f <- c("DS", "P1", "P2", "P3", "Sd", "Dorm", "V1 I0 D0",
"V2 I0 D0", "V3 I0 D0", "V4 I0 D0", "V5 I0 D0", "V6 I0 D0", "V7 I0 D0",
"V8 I0 D0", "V9 I0 D0", "V10 I0 D0", "V11 I0 D0", "V12 I0 D0", "V0 I1 D0",
"V1 I1 D0", "V2 I1 D0", "V3 I1 D0", "V4 I1 D0", "V5 I1 D0", "V6 I1 D0", "V7 I1 D0",
"V8 I1 D0", "V9 I1 D0", "V10 I1 D0", "V11 I1 D0", "V12 I1 D0", "V0 I2 D0",
"V1 I2 D0", "V2 I2 D0", "V3 I2 D0", "V4 I2 D0", "V5 I2 D0", "V6 I2 D0", "V7 I2 D0",
"V8 I2 D0", "V9 I2 D0", "V10 I2 D0", "V11 I2 D0", "V12 I2 D0", "V0 I3 D0",
"V1 I3 D0", "V2 I3 D0", "V3 I3 D0", "V4 I3 D0", "V5 I3 D0", "V6 I3 D0", "V7 I3 D0",
"V8 I3 D0", "V9 I3 D0", "V10 I3 D0", "V11 I3 D0", "V12 I3 D0", "V0 I4 D0",
"V1 I4 D0", "V2 I4 D0", "V3 I4 D0", "V4 I4 D0", "V5 I4 D0", "V6 I4 D0", "V7 I4 D0",
"V8 I4 D0", "V9 I4 D0", "V10 I4 D0", "V11 I4 D0", "V12 I4 D0", "V0 I5 D0",
"V1 I5 D0", "V2 I5 D0", "V3 I5 D0", "V4 I5 D0", "V5 I5 D0", "V6 I5 D0", "V7 I5 D0",
"V8 I5 D0", "V9 I5 D0", "V10 I5 D0", "V11 I5 D0", "V12 I5 D0", "V0 I6 D0",
"V1 I6 D0", "V2 I6 D0", "V3 I6 D0", "V4 I6 D0", "V5 I6 D0", "V6 I6 D0", "V7 I6 D0",
"V8 I6 D0", "V9 I6 D0", "V10 I6 D0", "V11 I6 D0", "V12 I6 D0", "V0 I7 D0",
"V1 I7 D0", "V2 I7 D0", "V3 I7 D0", "V4 I7 D0", "V5 I7 D0", "V6 I7 D0", "V7 I7 D0",
"V8 I7 D0", "V9 I7 D0", "V10 I7 D0", "V11 I7 D0", "V12 I7 D0", "V0 I8 D0",
"V1 I8 D0", "V2 I8 D0", "V3 I8 D0", "V4 I8 D0", "V5 I8 D0", "V6 I8 D0", "V7 I8 D0",
"V8 I8 D0", "V9 I8 D0", "V10 I8 D0", "V11 I8 D0", "V12 I8 D0", "V0 I9 D0",
"V1 I9 D0", "V2 I9 D0", "V3 I9 D0", "V4 I9 D0", "V5 I9 D0", "V6 I9 D0", "V7 I9 D0",
"V8 I9 D0", "V9 I9 D0", "V10 I9 D0", "V11 I9 D0", "V12 I9 D0", "V0 I10 D0",
"V1 I10 D0", "V2 I10 D0", "V3 I10 D0", "V4 I10 D0", "V5 I10 D0", "V6 I10 D0", "V7 I10 D0",
"V8 I10 D0", "V9 I10 D0", "V10 I10 D0", "V11 I10 D0", "V12 I10 D0", "V0 I11 D0",
"V1 I11 D0", "V2 I11 D0", "V3 I11 D0", "V4 I11 D0", "V5 I11 D0", "V6 I11 D0", "V7 I11 D0",
"V8 I11 D0", "V9 I11 D0", "V10 I11 D0", "V11 I11 D0", "V12 I11 D0", "V0 I12 D0",
"V1 I12 D0", "V2 I12 D0", "V3 I12 D0", "V4 I12 D0", "V5 I12 D0", "V6 I12 D0", "V7 I12 D0", 
}````
"V7 I1 D0", "V8 I1 D0", "V9 I1 D0", "V0 I2 D0", "V1 I2 D0", "V2 I2 D0",
"V3 I2 D0", "V4 I2 D0", "V5 I2 D0", "V6 I2 D0", "V7 I2 D0", "V8 I2 D0",
"V0 I3 D0", "V1 I3 D0", "V2 I3 D0", "V3 I3 D0", "V4 I3 D0", "V5 I3 D0",
"V6 I3 D0", "V7 I3 D0", "V0 I4 D0", "V1 I4 D0", "V2 I4 D0", "V3 I4 D0",
"V4 I4 D0", "V5 I4 D0", "V6 I4 D0", "V0 I5 D0", "V1 I5 D0", "V2 I5 D0",
"V3 I5 D0", "V4 I5 D0", "V5 I5 D0", "V0 I6 D0", "V1 I6 D0", "V2 I6 D0",
"V3 I6 D0", "V4 I6 D0", "V0 I7 D0", "V1 I7 D0", "V2 I7 D0", "V3 I7 D0",
"V0 I8 D0", "V1 I8 D0", "V2 I8 D0", "V0 I9 D0", "V1 I9 D0", "V0 I10 D0",
"V0 I0 D1", "V0 I1 D1", "V1 I1 D1", "V0 I2 D1")

repvector.f <- c(0, 0, 0, 0, 0, rep(0, 13), rep(1, 59))
obsvector.f <- c(0, 0, 0, 0, 0, 0, rep(1, 71))
matvector.f <- c(0, 0, 0, 0, 0, rep(1, 72))
immvector.f <- c(0, 1, 1, 1, 1, rep(0, 72))
propvector.f <- c(1, rep(0, 76))
indataset.f <- c(0, 0, 0, 0, 0, rep(1, 72))
binvec.f <- c(0, 0, 0, 0, 0, rep(0.5, 72))
binbvec.f <- c(0, 0, 0, 0, 0, rep(0.5, 72))
binvec.f <- c(0, 0, 0, 0, 0, rep(0.5, 72))

vertframe.f <- sf_create(sizes = sizevector.f, sizesb = sizebvector.f,
sizesc = sizevector.f, stagenames = stagevector.f, repstatus = repvector.f,
obsstatus = obsvector.f, propstatus = propvector.f, immstatus = immvector.f,
matstatus = matvector.f, indataset = indataset.f, binhalfwidth = binvec.f,
binhalfwidthb = binbvec.f, binhalfwidthc = binvec.f)

vert.data.f <- verticalize3(cypdata, noyears = 6, firstyear = 2004,
individcol = "plantid", blocksize = 4, sizeacol = "Veg.04",
sizebcol = "Inf.04", sizeccol = "Inf2.04", repstracol = "Inf.04",
repstrbcol = "Inf2.04", fecacol = "Pod.04", censorcol = "censor",
censorkeep = 1, censorRepeat = FALSE, stageassign = vertframe.f,
stagesize = "sizeabc", NAas0 = TRUE, censor = FALSE)

vertmodels2f <- modelsearch(vert.data.f, historical = FALSE, suite = "main",
sizeb = c("sizeb3", "sizeb2", "sizeb1"), sizec = c("sizec3", "sizec2", "sizec1"),
approach = "glm", vitalrates = c("surv", "obs", "size", "reps", "fec"),
sizedist = "negbin", sizebdist = "poisson", sizedist = "poisson",
fecdist = "poisson", patch.as.random = TRUE, year.as.random = TRUE)

vertsupp2f <- supplemental(stage3 = c("DS", "P1", "P2", "P3", "SD1", "SD1",
"Dorm", "V1 I0 D0", "V2 I0 D0", "V3 I0 D0", "DS", "P1"),
stage2 = c("DS", "DS", "P2", "P2", "SD1", "SD1", "SD1", "SD1",
"rep", "rep"),
eststage3 = c(NA, NA, NA, NA, NA, "Dorm", "V1 I0 D0", "V2 I0 D0",
"V3 I0 D0", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, "V1 I0 D0", "V1 I0 D0",
"V1 I0 D0", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, 0.40, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, 0.5 * 5000, 0.5 * 5000),
type =c(1, 1, 1, 1, 1, 1, 1, 3, 3), stageframe = vertframe.f,
historical = FALSE)

vert.mats.f2 <- flefko2(stageframe = vertframe.f, supplement = vertsupp2f,
data = vert.data.f, modelsuite = vertmodels2f)
flefko3

Create Function-based Historical Matrix Projection Model

Description

Function `flefko3()` returns function-based historical MPMs corresponding to the patches and occasion times given, including the associated component transition and fecundity matrices, data frames detailing the characteristics of the ahistorical stages used and historical stage pairs created, and a data frame characterizing the patch and occasion time combinations corresponding to these matrices.

Usage

```r
flefko3(
  year = "all",
  patch = "all",
  stageframe,
  supplement = NULL,
  repmatrix = NULL,
  overwrite = NULL,
  data = NA,
  modelsuite = NA,
  surv_model = NA,
  obs_model = NA,
  size_model = NA,
  sizeb_model = NA,
  sizec_model = NA,
  repst_model = NA,
  fec_model = NA,
  jsurv_model = NA,
  jobs_model = NA,
  jsize_model = NA,
  jsizeb_model = NA,
  jsizec_model = NA,
  jrepst_model = NA,
  paramnames = NA,
  inda = NULL,
  indb = NULL,
  indc = NULL,
  surv_dev = 0,
  obs_dev = 0,
  size_dev = 0,
  sizeb_dev = 0,
```
sizec_dev = 0,
repst_dev = 0,
fec_dev = 0,
jsurv_dev = 0,
jobs_dev = 0,
jsize_dev = 0,
jsizeb_dev = 0,
jsizec_dev = 0,
jrepst_dev = 0,
density = NA,
repmod = 1,
yearcol = NA,
patchcol = NA,
year.as.random = FALSE,
patch.as.random = FALSE,
random.inda = FALSE,
random.indb = FALSE,
random.indc = FALSE,
randomseed = NA,
negfec = FALSE,
format = "ehrlen",
reduce = FALSE,
err_check = FALSE,
exp_tol = 700,
theta_tol = 1e+08
)

Arguments

year
A variable corresponding to the observation occasion, or a set of such values, given in values associated with the year term used in linear model development. Defaults to "all", in which case matrices will be estimated for all occasion times.

patch
A variable designating which patches or subpopulations will have matrices estimated. Defaults to "all", but can also be set to specific patch names.

stageframe
A stageframe object that includes information on the size, observation status, propagule status, immaturity status, and maturity status of each ahistorical stage. Should also incorporate bin widths if size is continuous.

supplement
An optional data frame of class \texttt{lefkoSD} that provides supplemental data that should be incorporated into the MPM. Three kinds of data may be integrated this way: transitions to be estimated via the use of proxy transitions, transition overwrites from the literature or supplemental studies, and transition multipliers for survival and fecundity. This data frame should be produced using the \texttt{supplemental()} function. Can be used in place of or in addition to an overwrite table (see overwrite below) and a reproduction matrix (see \texttt{repmatrix} below).

repmatrix
An optional reproduction matrix. This matrix is composed mostly of 0s, with non-zero entries acting as element identifiers and multipliers for fecundity (with
l equaling full fecundity). If left blank, and no supplement is provided, then `flefko3()` will assume that all stages marked as reproductive produce offspring at 1x that of estimated fecundity, and that offspring production will yield the first stage noted as propagule or immature. To prevent this behavior, input just 0, which will result in fecundity being estimated only for transitions noted in supplement above. May be the dimensions of either a historical or an ahistorical matrix. If the latter, then all stages will be used in occasion \( t-1 \) for each suggested ahistorical transition.

**overwrite**

An optional data frame developed with the `overwrite()` function describing transitions to be overwritten either with given values or with other estimated transitions. Note that this function supplements overwrite data provided in supplement.

**data**

The historical vertical demographic data frame used to estimate vital rates (class `hfvddata`), which is required to initialize times and patches properly.

**modelsuite**

An optional `lefkoMod` object holding the vital rate models. If given, then `surv_model`, `obs_model`, `size_model`, `sizeb_model`, `sizec_model`, `repst_model`, `jsurv_model`, `jobs_model`, `jsize_model`, `jsizeb_model`, `jsizec_model`, `jrepst_model`, `paramnames`, `yearcol`, and `patchcol` are not required. One or more of these models should include size or reproductive status in occasion \( t \).

**surv_model**

A linear model predicting survival probability. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any survival probability model given in `modelsuite`. This model must have been developed in a modeling exercise testing the impacts of occasions \( t \) and \( t-1 \).

**obs_model**

A linear model predicting sprouting or observation probability. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any observation probability model given in `modelsuite`. This model must have been developed in a modeling exercise testing the impacts of occasions \( t \) and \( t-1 \).

**size_model**

A linear model predicting primary size. This can be a model of class `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `glm`, `lm`, or `lmer`. If given, then will overwrite any primary size model given in `modelsuite`. This model must have been developed in a modeling exercise testing the impacts of occasions \( t \) and \( t-1 \).

**sizeb_model**

A linear model predicting secondary size. This can be a model of class `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `glm`, `lm`, or `lmer`. If given, then will overwrite any secondary size model given in `modelsuite`. This model must have been developed in a modeling exercise testing the impacts of occasions \( t \) and \( t-1 \).

**sizec_model**

A linear model predicting tertiary size. This can be a model of class `glm`, `glmer`, `glmmTMB`, `zeroinfl`, `glm`, `lm`, or `lmer`. If given, then will overwrite any tertiary size model given in `modelsuite`. This model must have been developed in a modeling exercise testing the impacts of occasions \( t \) and \( t-1 \).

**repst_model**

A linear model predicting reproduction probability. This can be a model of class `glm` or `glmer`, and requires a predicted binomial variable under a logit link. If given, then will overwrite any reproduction probability model given in `modelsuite`. This model must have been developed in a modeling exercise testing the impacts of occasions \( t \) and \( t-1 \).
fec_model  A linear model predicting fecundity. This can be a model of class glm, glmer, glmmTMB, zeroInfl, vglm, lm, or lmer. If given, then will overwrite any fecundity model given in modelsuite. This model must have been developed in a modeling exercise testing the impacts of occasions $t$ and $t-1$.

jsurv_model  A linear model predicting juvenile survival probability. This can be a model of class glm or glmer, and requires a predicted binomial variable under a logit link. If given, then will overwrite any juvenile survival probability model given in modelsuite. This model must have been developed in a modeling exercise testing the impacts of occasions $t$ and $t-1$.

jobs_model  A linear model predicting juvenile sprouting or observation probability. This can be a model of class glm or glmer, and requires a predicted binomial variable under a logit link. If given, then will overwrite any juvenile observation probability model given in modelsuite. This model must have been developed in a modeling exercise testing the impacts of occasions $t$ and $t-1$.

jsize_model  A linear model predicting juvenile primary size. This can be a model of class glm, glmer, glmmTMB, zeroInfl, vglm, lm, or lmer. If given, then will overwrite any juvenile primary size model given in modelsuite. This model must have been developed in a modeling exercise testing the impacts of occasions $t$ and $t-1$.

jsizeb_model  A linear model predicting juvenile secondary size. This can be a model of class glm, glmer, glmmTMB, zeroInfl, vglm, lm, or lmer. If given, then will overwrite any juvenile secondary size model given in modelsuite. This model must have been developed in a modeling exercise testing the impacts of occasions $t$ and $t-1$.

jsizec_model  A linear model predicting juvenile tertiary size. This can be a model of class glm, glmer, glmmTMB, zeroInfl, vglm, lm, or lmer. If given, then will overwrite any juvenile tertiary size model given in modelsuite. This model must have been developed in a modeling exercise testing the impacts of occasions $t$ and $t-1$.

jrephst_model  A linear model predicting reproduction probability of a mature individual that was immature in the previous year. This can be a model of class glm or glmer, and requires a predicted binomial variable under a logit link. If given, then will overwrite any reproduction probability model given in modelsuite. This model must have been developed in a modeling exercise testing the impacts of occasions $t$ and $t-1$.

paramnames  A dataframe with three columns, the first describing all terms used in linear modeling, the second (must be called mainparams), showing the general model terms that will be used in matrix creation (users should use modelsearch() at least once to see the proper names to be used in this column), and the third showing the equivalent terms used in modeling (must be named modelparams). Only required if modelsuite is not supplied.

inda  Can be a single value to use for individual covariate $a$ in all matrices, a pair of values to use for times $t$ and $t-1$ in historical matrices, or a vector of such values corresponding to each occasion in option year. Defaults to NULL.

indb  Can be a single value to use for individual covariate $b$ in all matrices, a pair of values to use for times $t$ and $t-1$ in historical matrices, or a vector of such values corresponding to each occasion in option year. Defaults to NULL.

indc  Can be a single value to use for individual covariate $c$ in all matrices, a pair of values to use for times $t$ and $t-1$ in historical matrices, or a vector of such values corresponding to each occasion in option year. Defaults to NULL.
surv_dev  A numeric value to be added to the y-intercept in the linear model for survival probability.
obs_dev   A numeric value to be added to the y-intercept in the linear model for observation probability.
size_dev  A numeric value to be added to the y-intercept in the linear model for primary size.
sizeb_dev A numeric value to be added to the y-intercept in the linear model for secondary size.
sizec_dev A numeric value to be added to the y-intercept in the linear model for tertiary size.
reps_dev  A numeric value to be added to the y-intercept in the linear model for probability of reproduction.
fec_dev   A numeric value to be added to the y-intercept in the linear model for fecundity.
jsurv_dev A numeric value to be added to the y-intercept in the linear model for juvenile survival probability.
jobs_dev  A numeric value to be added to the y-intercept in the linear model for juvenile observation probability.
jsize_dev A numeric value to be added to the y-intercept in the linear model for juvenile primary size.
jsizeb_devA numeric value to be added to the y-intercept in the linear model for juvenile secondary size.
jsizec_devA numeric value to be added to the y-intercept in the linear model for juvenile tertiary size.
jreps_dev A numeric value to be added to the y-intercept in the linear model for juvenile reproduction probability.
density  A numeric value indicating density value to use to propagate matrices. Only needed if density is an explanatory term used in linear models. Defaults to NA.
repsmod  A scalar multiplier of fecundity. Defaults to 1.
yearcol  The variable name or column number corresponding to year in occasion t in the dataset. Not needed if modelsuite is supplied.
patchcol  The variable name or column number corresponding to patch in the dataset. Not needed if modelsuite is supplied.
year.as.random  A logical term indicating whether coefficients for missing occasions within vital rate models should be estimated as random intercepts. Defaults to FALSE, in which case missing monitoring occasion coefficients are set to 0.
patch.as.random A logical term indicating whether coefficients for missing patches within vital rate models should be estimated as random intercepts. Defaults to FALSE, in which case missing patch coefficients are set to 0.
random.inda A logical value denoting whether to treat individual covariate a as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.
random.indb: A logical value denoting whether to treat individual covariate b as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.

random.indc: A logical value denoting whether to treat individual covariate c as a random, categorical variable. Otherwise is treated as a fixed, numeric variable. Defaults to FALSE.

randomseed: A numeric value used as a seed to generate random estimates for missing occasion and patch coefficients, if either year.as.random or patch.as.random is set to TRUE. Defaults to set.seed() default.

negfec: A logical value denoting whether fecundity values estimated to be negative should be reset to 0. Defaults to FALSE.

format: A string indicating whether to estimate matrices in ehrlen format or deVries format. The latter adds one extra prior stage to account for the prior state of newborns. Defaults to ehrlen format.

reduce: A logical value denoting whether to remove historical stages associated solely with 0 transitions. These are only removed in cases where the associated row and column sums in ALL matrices estimated equal 0. Defaults to FALSE.

err_check: A logical value indicating whether to append matrices of vital rate probabilities associated with each matrix to the lefkoMat object generated. These matrices are developed internally and can be used for error checking. Defaults to FALSE.

exp_tol: A numeric value used to indicate a maximum value to set exponents to in the core kernel to prevent numerical overflow. Defaults to 700.

theta_tol: A numeric value used to indicate a maximum value to theta as used in the negative binomial probability density kernel. Defaults to 100000000, but can be reset to other values during error checking.

Value

If all inputs are properly formatted, then this function will return an object of class lefkoMat, which is a list that holds the matrix projection model and all of its metadata. Its structure is a list with the following elements:

A: A list of full projection matrices in order of sorted patches and occasion times. All matrices output in R’s matrix class.

U: A list of survival transition matrices sorted as in A. All matrices output in R’s matrix class.

F: A list of fecundity matrices sorted as in A. All matrices output in R’s matrix class.

hstages: A data frame matrix showing the pairing of ahistorical stages used to create historical stage pairs.

agestages: A data frame showing age-stage pairs. In this function, it is set to NA. Only used in output to function aflefko2().

ahstages: A data frame detailing the characteristics of associated ahistorical stages, in the form of a modified stageframe that includes status as an entry stage through reproduction.
labels A data frame giving the population, patch, and year of each matrix in order. In `flefko3()`, only one population may be analyzed at once, and so `pop = NA`.

matrixqc A short vector describing the number of non-zero elements in $U$ and $F$ matrices, and the number of annual matrices.

modelqc This is the `qc` portion of the `modelsuite` input.

prob_out An optional element only added if `err_check = TRUE`. This is a list of vital rate probability matrices, with 6 columns in the order of survival, observation probability, reproduction probability, primary size transition probability, secondary size transition probability, and tertiary size transition probability.

Notes

Unlike `rlefko3()`, this function currently does not distinguish populations within the same dataset.

The default behavior of this function is to estimate fecundity with regards to transitions specified via associated fecundity multipliers in either `supplement` or `repmatrix`. If both of these fields are left empty, then fecundity will be estimated at full for all transitions leading from reproductive stages to immature and propagule stages. However, if a supplement is provided and a `repmatrix` is not, or if `repmatrix` is set to 0, then only fecundity transitions noted in the supplement will be set to non-zero values. To use the default behavior of setting all reproductive stages to reproduce at full fecundity into immature and propagule stages, but also incorporate given or proxy survival transitions, input those given and proxy transitions through the `overwrite` option.

The reproduction matrix (field `repmatrix`) may be supplied as either historical or ahistorical. If provided as ahistorical, then `flefko3()` will assume that all historical transitions involving stages noted for occasions $t$ and $t+1$ should be set to the respective fecundity multipliers noted.

Users may at times wish to estimate MPMs using a dataset incorporating multiple patches or sub-populations, but without discriminating between those patches or sub-populations. Should the aim of analysis be a general MPM that does not distinguish these patches or sub-populations, the `patchcol` variable should be set to `NA`, which is the default.

Input options including multiple variable names must be entered in the order of variables in occasion $t+1$, $t$, and $t-1$. Rearranging the order will lead to erroneous calculations, and will may lead to fatal errors.

Care should be taken to match the random status of year and patch to the states of those variables within the `modelsuite`. If they do not match, then they will be treated as zeroes in vital rate estimation.

Using the `err_check` option will produce a matrix of 6 columns, each characterizing a different vital rate. The product of each row yields an element in the associated $U$ matrix. The number and order of elements in each column of this matrix matches the associated matrix in column vector format. Use of this option is generally for the purposes of debugging code.

Examples

```r
# Lathyrus example
data(lathyrus)
sizevector <- c(0, 4.6, 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 1, 2, 3, 4, 5, 6, 7, 8, 9)
```

stagevector <- c("Sd", "Sdl", "Dorm", "Sz1nr", "Sz2nr", "Sz3nr", "Sz4nr", 
"Sz5nr", "Sz6nr", "Sz7nr", "Sz8nr", "Sz9nr", "Sz1r", "Sz2r", "Sz3r", 
"Sz4r", "Sz5r", "Sz6r", "Sz7r", "Sz8r", "Sz9r")
repvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 4.6, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)
lathframeln <- sf_create(sizes = sizevector, stagenames = stagevector, 
reppstatus = repvector, obsstatus = obsvector, matstatus = matvector, 
imstatus = immvector, indataset = indataset, binhalfwidth = binvec, 
propstatus = propvector)
lathvertln <- verticalize3(lathyrus, noyears = 4, firstyear = 1988, 
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9, 
juven = "Seedling1988", sizeacol = "lnVol88", repstracol = "Intactseed88", 
fecacol = "Intactseed88", deadacol = "Dead1988", 
onobscol = "Dormant1988", stageassign = lathframeln, stagesize = "sizea", 
censorcol = "Missing1988", censorkeep = NA, NAas0 = TRUE, censor = TRUE)
lathvertln$feca2 <- round(lathvertln$feca2)
lathvertln$feca1 <- round(lathvertln$feca1)
lathvertln$feca3 <- round(lathvertln$feca3)
lathmodelsln3 <- modelsearch(lathvertln, historical = TRUE, 
approach = "mixed", suite = "main", 
vitalrates = c("surv", "obs", "size", "reps", "fec"), juvestimate = "Sdl", 
bestfit = "AICc&k", sizedist = "gaussian", fecdist = "poisson", 
indiv = "individ", patch = "patchid", year = "year2", year.as.random = TRUE, 
patch.as.random = TRUE, show.model.tables = TRUE, quiet = TRUE)
lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "mat", "Sd", "Sdl"), 
stage2 = c("Sdl", "Sdl", "Sdl", "Sdl", "repst", "Sdl", "repst"), 
stage1 = c("Sdl", "repst", "Sdl", "repst", "Sdl", "mat", "mat"), 
eststage3 = c(NA, NA, NA, NA, "mat", NA, NA), 
eststage2 = c(NA, NA, NA, NA, "Sdl", NA, NA), 
eststage1 = c(NA, NA, NA, NA, "Sdl", NA, NA), 
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA), 
multiplier = c(NA, NA, NA, NA, 0.345, 0.054), 
type = c(1, 1, 1, 1, 1, 3, 3), type_t12 = c(1, 2, 1, 2, 1, 1, 1), 
stageframe = lathframeln, historical = TRUE)
lathmat3ln <- flefko3(year = "all", patch = "all", stageframe = lathframeln, 
modelsuite = lathmodelsln3, data = lathvertln, supplement = lathsupp3, 
patchcol = "patchid", yearcol = "year2", year.as.random = TRUE, 
patch.as.random = TRUE, reduce = FALSE)
summary(lathmat3ln)
# Cypripedium example using three size metrics for classification
rm(list=ls(all=TRUE))

data(cypdata)
sizevector.f <- c(0, 0, 0, 0, 0, seq(1, 12, by = 1), seq(0, 9, by = 1),
seq(0, 8, by = 1), seq(0, 7, by = 1), seq(0, 6, by = 1), seq(0, 5, by = 1),
seq(0, 4, by = 1), seq(0, 3, by = 1), 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,
0, 1, 2)
sizebvector.f <- c(0, 0, 0, 0, 0, rep(0, 12), rep(1, 10), rep(2, 9),
rep(3, 8), rep(4, 7), rep(5, 6), rep(6, 5), rep(7, 4), rep(8, 3), 9, 9, 10,
0, 1, 1, 2)
sizecvector.f <- c(0, 0, 0, 0, 0, rep(0, 12), rep(0, 10), rep(0, 9),
rep(0, 8), rep(0, 7), rep(0, 6), rep(0, 5), rep(0, 4), 0, 0, 0, 0, 0, 0,
1, 1, 1, 1)
stagevector.f <- c("DS", "P1", "P2", "P3", "Dorm", "V1 I0 D0", 
"V2 I0 D0", "V3 I0 D0", "V4 I0 D0", "V5 I0 D0", "V6 I0 D0", "V7 I0 D0", 
"V8 I0 D0", "V9 I0 D0", "V10 I0 D0", "V11 I0 D0", 
"V12 I0 D0", "V0 I1 D0", 
"V1 I1 D0", "V2 I1 D0", "V3 I1 D0", "V4 I1 D0", "V5 I1 D0", 
"V6 I1 D0", "V7 I1 D0", "V8 I1 D0", "V9 I1 D0", "V0 I2 D0", "V1 I2 D0", 
"V2 I2 D0", "V3 I2 D0", "V4 I2 D0", "V5 I2 D0", "V6 I2 D0", "V7 I2 D0", 
"V8 I2 D0", "V9 I2 D0", "V0 I3 D0", "V1 I3 D0", "V2 I3 D0", "V3 I3 D0", 
"V4 I3 D0", "V5 I3 D0", "V6 I3 D0", "V7 I3 D0", "V8 I3 D0", "V9 I3 D0", 
"V0 I4 D0", "V1 I4 D0", "V2 I4 D0", "V3 I4 D0", "V4 I4 D0", "V5 I4 D0", 
"V6 I4 D0", "V7 I4 D0", "V8 I4 D0", "V9 I4 D0", "V0 I5 D0", "V1 I5 D0", 
"V2 I5 D0", "V3 I5 D0", "V4 I5 D0", "V5 I5 D0", "V6 I5 D0", "V7 I5 D0", 
"V8 I5 D0", "V9 I5 D0", "V0 I6 D0", "V1 I6 D0", "V2 I6 D0", "V3 I6 D0", 
"V4 I6 D0", "V5 I6 D0", "V6 I6 D0", "V7 I6 D0", "V8 I6 D0", "V9 I6 D0", 
"V0 I7 D0", "V1 I7 D0", "V2 I7 D0", "V3 I7 D0", "V4 I7 D0", "V5 I7 D0", 
"V6 I7 D0", "V7 I7 D0", "V8 I7 D0", "V9 I7 D0", "V0 I8 D0", "V1 I8 D0", 
"V2 I8 D0", "V3 I8 D0", "V0 I9 D0", "V1 I9 D0", "V2 I9 D0", "V3 I9 D0", 
"V4 I9 D0", "V5 I9 D0", "V6 I9 D0", "V7 I9 D0", "V8 I9 D0", "V9 I9 D0", 
"V0 I10 D0", "V1 I10 D0", "V2 I10 D0", "V3 I10 D0", "V0 I11 D0", "V1 I11 D0", 
"V2 I11 D0")
repvector.f <- c(0, 0, 0, 0, 0, rep(0, 13), rep(1, 59))
obsvector.f <- c(0, 0, 0, 0, 0, 0, rep(1, 71))
matvector.f <- c(0, 0, 0, 0, 0, rep(1, 72))
immvector.f <- c(0, 1, 1, 1, 1, rep(0, 72))
propvector.f <- c(1, rep(0, 76))
indataset.f <- c(0, 0, 0, 0, 0, rep(1, 72))
binvec.f <- c(0, 0, 0, 0, 0, rep(0.5, 72))
binvecb.f <- c(0, 0, 0, 0, 0, rep(0.5, 72))
binvecf.f <- c(0, 0, 0, 0, 0, rep(0.5, 72))
vertframe.f <- sf_create(sizes = sizevector.f, sizesb = sizebvector.f,
sizesc = sizecvector.f, stagenames = stagevector.f, repstatus = repvector.f,
obsstatus = obsvector.f, propstatus = propvector.f, immstatus = immvector.f,
matstatus = matvector.f, indataset = indataset.f, binhalfwidth = binvec.f,
binhalfwidthb = binvecb.f, binhalfwidthf = binvecf.f)

vert.data.f <- verticalize3(cypdata, noyears = 6, firstyear = 2004,
idividcol = "plantid", blocksize = 4, sizeacol = "Veg.04", 
sizebcol = "Inf.04", sizeccol = "Inf2.04", repstracol = "Inf.04", 
repstrbcol = "Inf2.04", fecacol = "Pod.04", censorcol = "censor", 
censorkeep = 1, censorRepeat = FALSE, stageassign = vertframe.f, 
 stagesize = "sizeabc", NAas0 = TRUE, censor = FALSE)

vertmodels3f <- modelsearch(vert.data.f, historical = TRUE, suite = "main", 
sizeb = c("sizeb3", "sizeb2", "sizeb1"), sizec = c("sizec3", "sizec2", "sizec1"), 
sizea = c("sizea3", "sizea2", "sizea1"), 
stage assign = "stage", 
NAas0 = TRUE, censor = FALSE)
historicalize3

Create Historical Vertical Data Frame from Ahistorical Vertical Data Frame

Description

Function historicalize3() returns a vertically formatted demographic data frame organized to create historical projection matrices, given a vertically but ahistorically formatted data frame. This data frame is in standard hfvdata format and can be used in all functions in the package.

Usage

historicalize3(
  data,
  popidcol = 0,
  patchidcol = 0,
  individcol,
  year2col = 0,
  year3col = 0,
xcol = 0,
ycol = 0,
sizea2col = 0,
sizea3col = 0,
sizeb2col = 0,
sizeb3col = 0,
sizec2col = 0,
sizec3col = 0,
repstra2col = 0,
repstra3col = 0,
repstrb2col = 0,
repstrb3col = 0,
feca2col = 0,
feca3col = 0,
fecb2col = 0,
fecb3col = 0,
indcova2col = 0,
indcova3col = 0,
indcovb2col = 0,
indcovb3col = 0,
indcovc2col = 0,
indcovc3col = 0,
alive2col = 0,
alive3col = 0,
dead2col = 0,
dead3col = 0,
obs2col = 0,
obs3col = 0,
onobs2col = 0,
onobs3col = 0,
repstrrel = 1,
fecrel = 1,
stage2col = 0,
stage3col = 0,
juv2col = 0,
juv3col = 0,
stageassign = NA,
stagesize = NA,
censor = FALSE,
censorcol = 0,
censorkeep = 0,
spacing = NA,
NAas0 = FALSE,
NRasRep = FALSE,
reduce = TRUE
Arguments

data
   The horizontal data file.
popidcol
   A variable name or column number corresponding to the identity of the population for each individual.
patchidcol
   A variable name or column number corresponding to the identity of the patch or subpopulation for each individual, if patches have been designated within populations.
individcol
   A variable name or column number corresponding to the unique identity of each individual.
year2col
   A variable name or column number corresponding to occasion \( t \) (year or time).
year3col
   A variable name or column number corresponding to occasion \( t+1 \) (year or time).
xcol
   A variable name or column number corresponding to the X coordinate of each individual in Cartesian space.
ycol
   A variable name or column number corresponding to the Y coordinate of each individual in Cartesian space.
sizea2col
   A variable name or column number corresponding to the primary size entry in occasion \( t \).
sizea3col
   A variable name or column number corresponding to the primary size entry in occasion \( t+1 \).
sizeb2col
   A variable name or column number corresponding to the secondary size entry in occasion \( t \).
sizeb3col
   A variable name or column number corresponding to the secondary size entry in occasion \( t+1 \).
sizec2col
   A variable name or column number corresponding to the tertiary size entry in occasion \( t \).
sizec3col
   A variable name or column number corresponding to the tertiary size entry in occasion \( t+1 \).
repstra2col
   A variable name or column number corresponding to the production of reproductive structures, such as flowers, in occasion \( t \). This can be binomial or count data, and is used to in analysis of the probability of reproduction.
repstra3col
   A variable name or column number corresponding to the production of reproductive structures, such as flowers, in occasion \( t+1 \). This can be binomial or count data, and is used to in analysis of the probability of reproduction.
repstrb2col
   A second variable name or column number corresponding to the production of reproductive structures, such as flowers, in occasion \( t \). This can be binomial or count data.
repstrb3col
   A second variable name or column number corresponding to the production of reproductive structures, such as flowers, in occasion \( t+1 \). This can be binomial or count data.
fec2col
   A variable name or column number corresponding to fecundity in occasion \( t \). This may represent egg counts, fruit counts, seed production, etc.
feca3col  A variable name or column number corresponding to fecundity in occasion \( t+1 \). This may represent egg counts, fruit counts, seed production, etc.

fecb2col  A second variable name or column number corresponding to fecundity in occasion \( t \). This may represent egg counts, fruit counts, seed production, etc.

fecb3col  A second variable name or column number corresponding to fecundity in occasion \( t+1 \). This may represent egg counts, fruit counts, seed production, etc.

indcova2col  A variable name or column number corresponding to an individual covariate to be used in analysis, in occasion \( t \).

indcova3col  A variable name or column number corresponding to an individual covariate to be used in analysis, in occasion \( t+1 \).

indcovb2col  A variable name or column number corresponding to a second individual covariate to be used in analysis, in occasion \( t \).

indcovb3col  A variable name or column number corresponding to a second individual covariate to be used in analysis, in occasion \( t+1 \).

indcovc2col  A variable name or column number corresponding to a third individual covariate to be used in analysis, in occasion \( t \).

indcovc3col  A variable name or column number corresponding to a third individual covariate to be used in analysis, in occasion \( t+1 \).

alive2col  A variable name or column number that provides information on whether an individual is alive in occasion \( t \). If used, living status must be designated as binomial (living = 1, dead = 0).

alive3col  A variable name or column number that provides information on whether an individual is alive in occasion \( t+1 \). If used, living status must be designated as binomial (living = 1, dead = 0).

dead2col  A variable name or column number that provides information on whether an individual is dead in occasion \( t \). If used, dead status must be designated as binomial (living = 0, dead = 1).

dead3col  A variable name or column number that provides information on whether an individual is dead in occasion \( t+1 \). If used, dead status must be designated as binomial (living = 0, dead = 1).

obs2col  A variable name or column number providing information on whether an individual is in an observable stage in occasion \( t \). If used, observation status must be designated as binomial (observed = 1, not observed = 0).

obs3col  A variable name or column number providing information on whether an individual is in an observable stage in occasion \( t+1 \). If used, observation status must be designated as binomial (observed = 1, not observed = 0).

nonobs2col  A variable name or column number providing information on whether an individual is in an unobservable stage in occasion \( t \). If used, observation status must be designated as binomial (observed = 0, not observed = 1).

nonobs3col  A variable name or column number providing information on whether an individual is in an unobservable stage in occasion \( t+1 \). If used, observation status must be designated as binomial (observed = 0, not observed = 1).
repstrrel This is a scalar multiplier making the variable represented by repstrb2col equivalent to the variable represented by repstra2col. This can be useful if two reproductive status variables have related but unequal units, for example if repstrb2col refers to one-flowered stems while repstra2col refers to two-flowered stems.

fecrel This is a scalar multiplier making the variable represented by fechb2col equivalent to the variable represented by feca2col. This can be useful if two fecundity variables have related but unequal units.

stage2col Optional variable name or column number corresponding to life history stage in occasion t.

stage3col Optional variable name or column number corresponding to life history stage in occasion t+1.

juv2col A variable name or column number that marks individuals in immature stages in occasion t. Function historicalize3() assumes that immature individuals are identified in this variable marked with a number equal to or greater than 1, and that mature individuals are marked as 0 or NA.

juv3col A variable name or column number that marks individuals in immature stages in occasion t+1. Function historicalize3() assumes that immature individuals are identified in this variable marked with a number equal to or greater than 1, and that mature individuals are marked as 0 or NA.

stageassign The stageframe object identifying the life history model being operationalized. Note that if stage2col is provided, then this stageframe is not utilized in stage designation.

stagesize A variable name or column number describing which size variable to use in stage estimation. Defaults to NA, and can also take sizea, sizeb, sizec, sizeab, sizebc, sizeac, sizeabc, or sizeadded, depending on which size variable within the input dataset is chosen. Note that the variable(s) chosen should be presented in the order of the primary, secondary, and tertiary variables in the stageframe input with stageassign. For example, choosing sizeb assumes that this size variable in the dataset is the primary variable in the stageframe.

censor A logical variable determining whether the output data should be censored using the variable defined in censorcol. Defaults to FALSE.

censorcol A variable name or column number corresponding to a censor variable within the dataset, used to distinguish between entries to use and those to discard from analysis, or to designate entries with special issues that require further attention.

censorkeep The value of the censoring variable identifying data that should be included in analysis. Defaults to 0, but may take any value including NA.

spacing The spacing at which density should be estimated, if density estimation is desired and X and Y coordinates are supplied. Given in the same units as those used in the X and Y coordinates given in xcol and ycol. Defaults to NA.

NAas0 If TRUE, then all NA entries for size and fecundity variables will be set to 0. This can help increase the sample size analyzed by modelsearch(), but should only be used when it is clear that this substitution is biologically realistic. Defaults to FALSE.
NRasRep

If set to TRUE, then this function will treat non-reproductive but mature individuals as reproductive during stage assignment. This can be useful when a matrix is desired without separation of reproductive and non-reproductive but mature stages of the same size. Only used if stageassign is set to a valid stageframe. Defaults to FALSE.

reduce

A logical variable determining whether unused variables and some invariant state variables should be removed from the output dataset. Defaults to TRUE.

Value

If all inputs are properly formatted, then this function will output a historical vertical data frame (class hfvdata), meaning that the output data frame will have three consecutive years of size and reproductive data per individual per row. This data frame is in standard format for all functions used in lefko3, and so can be used without further modification. Note that determination of state in occasions t-1 and t+1 gives preference to condition in occasion t within the input dataset. Conflicts in condition in input datasets that have both occasions t and t+1 listed per row are resolved by using condition in occasion t.

Variables in this data frame include the following:

- **rowid**: Unique identifier for the row of the data frame.
- **popid**: Unique identifier for the population, if given.
- **patchid**: Unique identifier for patch within population, if given.
- **individ**: Unique identifier for the individual.
- **year2**: Year or time in occasion t.
- **firstseen**: Occasion of first observation.
- **lastseen**: Occasion of last observation.
- **obsage**: Observed age in occasion t, assuming first observation corresponds to age = 0.
- **obslifespan**: Observed lifespan, given as lastseen - firstseen + 1.
- **xpos1, xpos2, xpos3**: X position in Cartesian space in occasions t-1, t, and t+1, respectively, if provided.
- **ypos1, ypos2, ypos3**: Y position in Cartesian space in occasions t-1, t, and t+1, respectively, if provided.
- **sizea1, sizea2, sizea3**: Main size measurement in occasions t-1, t, and t+1, respectively.
- **sizeb1, sizeb2, sizeb3**: Secondary size measurement in occasions t-1, t, and t+1, respectively.
- **sizec1, sizec2, sizec3**: Tertiary size measurement in occasions t-1, t, and t+1, respectively.
- **size1added, size2added, size3added**: Sum of primary, secondary, and tertiary size measurements in occasions t-1, t, and t+1, respectively.
- **repstra1, repstra2, repstra3**: Main numbers of reproductive structures in occasions t-1, t, and t+1, respectively.
repstrb1, repstrb2, repstrb3
Secondary numbers of reproductive structures in occasions $t-1$, $t$, and $t+1$, respectively.

repstr1added, repstr2added, repstr3added
Sum of primary and secondary reproductive structures in occasions $t-1$, $t$, and $t+1$, respectively.

fec1, feca2, feca3
Main numbers of offspring in occasions $t-1$, $t$, and $t+1$, respectively.

fecb1, fecb2, fecb3
Secondary numbers of offspring in occasions $t-1$, $t$, and $t+1$, respectively.

feca1added, fec2added, fec3added
Sum of primary and secondary fecundity in occasions $t-1$, $t$, and $t+1$, respectively.

censor1, censor2, censor3
Censor status values in occasions $t-1$, $t$, and $t+1$, respectively.

juvgiven1, juvgiven2, juvgiven3
Binomial variable indicating whether individual is juvenile in occasions $t-1$, $t$, and $t+1$. Only given if juvcol is provided.

obsstatus1, obsstatus2, obsstatus3
Binomial observation status in occasions $t-1$, $t$, and $t+1$, respectively.

repstatus1, repstatus2, repstatus3
Binomial reproductive status in occasions $t-1$, $t$, and $t+1$, respectively.

fecstatus1, fecstatus2, fecstatus3
Binomial offspring production status in occasions $t-1$, $t$, and $t+1$, respectively.

matstatus1, matstatus2, matstatus3
Binomial maturity status in occasions $t-1$, $t$, and $t+1$, respectively.

alive1, alive2, alive3
Binomial status as alive in occasions $t-1$, $t$, and $t+1$, respectively.

density
Density of individuals per unit designated in spacing. Only given if spacing is not NA.

Notes

Warnings that some individuals occur in state combinations that do not match any stages in the stageframe used to assign stages, and that some individuals match characteristics of several stages in the stageframe, are common when first working with a dataset. Typically, these situations can be identified as NoMatch entries in stage3, although such entries may crop up in stage1 and stage2, as well. In some cases, these warnings will arise with no concurrent NoMatch entries. These are important warnings and suggest that there is likely a problem with the stageframe. The most common such problems are: 1) stages have significant overlap in characteristics, with the most common being overlapping size bins caused by erroneous definitions of size bin halfwidths; and 2) some individuals exist in states not defined within the stageframe.

In some datasets with unobservable stages, observation status (obsstatus) might not be inferred properly if a single size variable is used that does not yield sizes greater than 0 in all cases in which individuals were observed. Such situations may arise, for example, in plants when leaf number is the dominant size variable used, but individuals occasionally occur with inflorescences but no
leaves. In this instances, it helps to mark related variables as sizeb and sizec, because observation status will be interpreted in relation to all 3 size variables. Alternatively, observation status may be input via obs2col and obs3col to force computation with given values (although this requires all instances of observation and non-observation to be known and coded ahead of time). Further analysis can then utilize only a single size variable, of the user’s choosing. Similar issues can arise in reproductive status (repstatus).

Juvenile designation should only be used when juveniles fall outside of the size classification scheme used in determining stages. If juveniles are to be size classified along the size spectrum that adults also fall on, then it is best to treat juveniles as mature but not reproductive.

Care should be taken to avoid variables with negative values indicating size, fecundity, or reproductive or observation status. Negative values can be interpreted in different ways, typically reflecting estimation through other algorithms rather than actual measured data. Variables holding negative values can conflict with data management algorithms in ways that are difficult to predict.

Unusual errors (e.g. “Error in pjf...”) may occur in cases where the variables are improperly passed, or where seemingly numeric variables include text and so get automatically converted to string variables.

Density estimation is performed as a count of individuals alive and within the radius specified in spacing of the respective individual at some point in time.

Examples

data(cypvert)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)

stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")

repsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)

obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)

matvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1)

immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)

propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)

indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)

binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repsvector, obsstatus = obsvector, matstatus = matvector, propstatus = propvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)

cypframe_raw

cyprow_v2 <- historicalize3(data = cypvert, patchidcol = "patch", individcol = "plantid", year2col = "year2", sizea2col = "Inf2.2", sizea3col = "Inf2.3", sizeb2col = "Inf.2", sizeb3col = "Inf.3", sizec2col = "Veg.2", sizec3col = "Veg.3", repstra2col = "Inf2.2", repstra3col = "Inf2.3", repstrb2col = "Inf.2", repstrb3col = "Inf.3", feca2col = "Pod.2", feca3col = "Pod.3", repstrrel = 2, stageassign = cypframe_raw, stagesize = "sizeadded", censorcol = "censor", censor = FALSE, NAas0 = TRUE, NRasRep = TRUE, reduce = TRUE)
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v2, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

cypmatrix2r$A[intersect(which(cypmatrix2r$labels$patch == "A"),
which(cypmatrix2r$labels$year2 == 2004))]

lambda3(cypmatrix2r)

---

**image3**

*Create Matrix Image*

**Description**

Function `image3()` is a generic function that creates matrix plots. It acts as a wrapper for the `image()` function in package SparseM, conducting all necessary conversions and automating image production across all or just specific matrices.

**Usage**

```r
image3(mats, ...)
```

**Arguments**

- `mats` A lefkoMat object, or a single projection matrix, for which the dominant eigenvalue is desired.
- `...` Other parameters

**Value**

Produces a single matrix image, or a series of images, depending on the input. Non-zero elements appear as red space, while zero elements appear as white space.

**See Also**

- `image3.lefkoMat()`
- `image3.matrix()`
Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 1, 0)
obsvectors <- c(0, 1, 1, 1, 1, 1, 0)
matsvectors <- c(0, 0, 1, 1, 1, 1, 1)
immsvectors <- c(1, 1, 0, 0, 0, 0, 0)
propvectors <- c(1, 0, 0, 0, 0, 0, 0)
indsets <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvectors, obsstatus = obsvectors, matstatus = matsvectors,
immstatus = immsvectors, indataset = indsets, binhalfwidth = binvec,
propstatus = propvectors)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)
lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sdl", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 1, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)
ehr3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")
image3(ehr3, used = 1, type = "U")

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
"XLg")
reppvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec  <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.20, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type =c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

image3(cypmatrix2r, used = 1, type = "U")

---

**image3.lefkoElas**

*Create Matrix Image(s) for lefkoElas Object*

**Description**

Function `image3.lefkoElas` plots matrix images for elasticity matrices supplied within `lefkoElas` objects. This function operates as a wrapper the `image()` function in package `SparseM`, conducting all necessary conversions and automating image production across all or just specific matrices.
Usage

## S3 method for class 'lefkoElas'
image3(mats, used = "all", type = "a", ...)

Arguments

mats  A lefkoElas object.
used  A numeric value or vector designating the matrices to plot. Can also take the value "all", which plots all matrices. Defaults to "all".
type  Character value indicating whether to plot "a"historical or "h"istorical elasticity matrices. Defaults to "a"historical, but will plot a historical elasticity matrix image if no ahistorical elasticity matrix exists.

Value

Plots a matrix image, or series of matrix images, denoting non-zero elements as red space and zero elements as white space.

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "SdI", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
               repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
               immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
               propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
               patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
               juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
               fecacol = "Intactseed88", deadacol = "Dead1988",
               nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
               censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "SdI", "SdI", "Sd", "SdI", "mat"),
               stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "SdI"),
               stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
               eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1),
stageframe = lattice, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lattice,
year = c(1989, 1990), stages = c("stage3", "stage2", "stage1"),
supplement = lathsupp3, yearcol = "year2", individcol = "individ")

ehrlen_elas <- elasticity3(ehrlen3)
image3(ehrlen_elas, used = 1, type = "h")

# Cypripedium example
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg",
"XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 1, 1, 1, 1, 1)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "Sd", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)
image3.lefkoMat

Create Matrix Image(s) for lefkoMat Object

Description
Function image3.lefkoMat plots matrix images for matrices supplied within lefkoMat objects. This function operates as a wrapper for the image() function in package SparseM, conducting all necessary conversions and automating image production across all or just specific matrices.

Usage
### S3 method for class 'lefkoMat'
image3(mats, used = "all", type = "A", ...)

Arguments
- **mats**: A lefkoMat object.
- **used**: A numeric value or vector designating the matrices to plot. Can also take the value "all", which plots all matrices. Defaults to "all".
- **type**: Character value indicating whether to plot A, U, or F matrices. Defaults to "A".
- **...**: Other parameters.

Value
Plots a matrix image, or series of matrix images, denoting non-zero elements as red space and zero elements as white space.

Examples
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repsvector <- c(0, 0, 0, 0, 0, 0, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3800, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)
lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)
ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")
image3(ehrlen3, used = 1, type = "U")
# Cypripedium example
data(cypdata)
sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 1, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 0.5, 1, 2.5, 7)
cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,  
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",  
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",  
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,  
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",  
"XSm", "Sm", "P1"),  
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",  
"rep"),  
eststage3 = c(NA, NA, NA, NA, NA, D", "XSm", "Sm", NA, NA),  
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),  
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.20, NA, NA, NA, NA),  
multiplier = c(NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),  
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),  
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,  
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),  
size = c("size3added", "size2added"), supplement = cypsupp2r,  
yearcol = "year2", patchcol = "patchid", individcol = "individ")

image3(cypmatrix2r, used = 1, type = "U")

---

image3.lefkoSens Create Matrix Image(s) for lefkoSens Object

Description

Function image3.lefkoSens plots matrix images for sensitivity matrices supplied within lefkoSens objects. This function operates as a wrapper the image() function in package SparseM, conducting all necessary conversions and automating image production across all or just specific matrices.

Usage

```r
## S3 method for class 'lefkoSens'
image3(mats, used = "all", type = "a", ...)
```

Arguments

- **mats**: A lefkoSens object.
- **used**: A numeric value or vector designating the matrices to plot. Can also take the value "all", which plots all matrices. Defaults to "all".
- **type**: Character value indicating whether to plot "a"historical or "h"istorical sensitivity matrices. Defaults to "a"historical, but will plot a historical sensitivity matrix image if no ahistorical sensitivity matrix exists.
- **...**: Other parameters.
Value

Plots a matrix image, or series of matrix images, denoting non-zero elements as red space and zero elements as white space.

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvect <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = reppvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe,
year = c(1989, 1990), stages = c("stage3", "stage2", "stage1"),
supplement = lathsupp3, yearcol = "year2", indivcol = "individ")

ehrlen_sens <- sensitivity3(ehrlen3)

image3(ehrlen_sens, used = 1, type = "h")

# Cypripedium example
data(cypdata)
sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XS\text{Sm}", "Sm", "Md", "Lg", "XLg")
repsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repsvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)
# Here we use supplemental() to provide overwrite and reproductive info
cypesupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XS\text{Sm}", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XS\text{Sm}", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XS\text{Sm}", "XS\text{Sm}", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)
cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size\text{3added}", "size\text{2added}"), supplement = cypesupp2r,
yearcol = "year2", patchcol = "patchid", individcol = "individ")
cypsens <- sensitivity3(cypmatrix2r)
image3(cypsens, used = 1, type = "a")
Description

Function `image3.matrix` plots matrix images for matrices contained in a list of matrices. This function operates as a wrapper for the `image()` function in package `SparseM`, conducting all necessary conversions and automating image production across all or just specific matrices.

Usage

```r
## S3 method for class 'list'
image3(mats, used = "all", ...)
```

Arguments

- `mats` - A list class object.
- `used` - A numeric vector of projection matrices within `mats` to represent as matrix images. Can also take the text value "all", which will produce images of all matrices. Defaults to "all".
- `...` - Other parameters.

Value

Plots a matrix image, or series of matrix images, denoting non-zero elements as red space and zero elements as white space.

Examples

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                        immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                         patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                         juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                         fecacol = "Intactseed88", deadacol = "Dead1988",
                         nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                         censorcol = "Missing1988", censorkeep = NA, censor = TRUE)
```
lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl"),
stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep"),
stage1 = c("Sd", "rep", "Sd", "rep", "all", "all"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
type = c(1, 1, 1, 1, 3, 3),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"),
supplement = lathsupp3,
yearcol = "year2", individcol = "individ")

ehrlen3$A, used = 1)

# Cypripedium example
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg",
"XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE, 
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cyps2r <- supplemental(stage3 = c("Sd", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
Function `image3.matrix` plots a matrix image for a single matrix. This function operates as a wrapper for the `image()` function in package `SparseM`, conducting all necessary conversions and automating image production across all or just specific matrices.

### Usage
```r
## S3 method for class 'matrix'
image3(mats, ...)
```

### Arguments
- **mats**: A matrix class object.
- **...**: Other parameters.

### Value
Plots a matrix image, or series of matrix images, denoting non-zero elements as red space and zero elements as white space.

### Examples
```r
# Lathyrus example
data(lathyrus)
sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
```
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type.t12 = c(1, 2, 1, 2, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

# Cypripedium example
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cyprframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
bincarewidth = binvec)

cyprraw.v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cyprframe_raw, stagesize = "sizeadded", NaNas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
lambda3

```
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
    stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"),
    eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
    eststage2 = c(NA, NA, NA, NA, NA, "XS m", "XS m", "XS m", NA, NA),
    givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
    multiplier = c(NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
    type = c(1, 1, 1, 1, 1, 1, 1, 3, 3),
    stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
    year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
    size = c("size3added", "size2added"), supplement = cypsupp2r,
    yearcol = "year2", patchcol = "patchid", indivcol = "individ")

image3(cypmatrix2r$U[[1]])
```

Description

lambda3() is a generic function that returns the dominant eigenvalue of a matrix, and set of dominant eigenvalues of a set of matrices. It can handle very large and sparse matrices supplied as lefkoMat objects or as individual matrices, and can be used with large historical matrices, IPMs, age x stage matrices, as well as smaller ahistorical matrices.

Usage

```
lambda3(mats, ...)
```

Arguments

- `mats`: A lefkoMat object, or a single projection matrix, for which the dominant eigenvalue is desired.
- `...`: Other parameters.

Value

The value returned depends on the class of the `mats` argument.

See Also

- `lambda3.lefkoMat()`
- `lambda3.matrix()`
- `slambda3()`
Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)

binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                        immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                          patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                          juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                          fecacol = "Intactseed88", deadacol = "Dead1988",
                          nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                          censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
                          stage2 = c("Sd", "Sd", "Sdl", "Sd", "rep", "rep", "Sdl"),
                          stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
                          eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
                          eststage2 = c(NA, NA, NA, NA, NA, NA, "mat"),
                          eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
                          givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
                          multiplier = c(NA, NA, NA, NA, NA, 0.345, NA),
                          type = c(1, 1, 1, 3, 3, 1, 1),
                          stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
                   stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
                   yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
lambda3(ehrlen3mean)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cymatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", individcol = "individ")

lambda3(cymatrix2r)

### lambda3.lefkoMat

**Estimate Deterministic Population Growth Rates of lefkoMat Matrices**

#### Description

`lambda3.lefkoMat()` returns the dominant eigenvalues of all projection matrices supplied within `lefkoMat` objects. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as ahistorical matrices.
Usage

```r
## S3 method for class 'lefkoMat'
lambda3(mats, sparse = "auto", ...)
```

Arguments

- `mats`: An object of class `lefkoMat`.
- `sparse`: A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
- `...`: Other parameters.

Value

This function returns the dominant eigenvalue of each $A$ matrix in `mats`. The output includes a data frame showing the population, patch, and lambda estimate for each $A$ matrix. Row names correspond to the order of the matrix within the $A$ element of `mats`.

Notes

The `sparse` option allows the function to utilize underlying methods of either dense or sparse matrix manipulation in order to speed up processing time and prevent memory shortages. Under the auto setting, the function will determine whether the matrix is sparse and act accordingly. For extremely large, sparse matrices, the user may simply set `sparse = "yes"` to save time further and force the use of sparse format in calculations.

See Also

- `lambda3()`
- `lambda3.matrix()`
- `slambda3()`

Examples

```r
# Lathyrus example
data(lathyrus)
sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reptector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
             repstatus = reptector, obsstatus = obsvector, matstatus = matvector,
             immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
```
propstatus = propvector

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sd"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA, NA),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
lambda3(ehrlen3mean)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)
Here we use supplemental() to provide overwrite and reproductive info:

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

lambda3(cypmatrix2r)

---

**lambda3.matrix**

**Estimate Deterministic Population Growth Rate of Single Projection Matrix**

**Description**

lambda3.matrix() returns the dominant eigenvalue of a single projection matrix. This function can handle large and sparse matrices, so can be used with large historical matrices, IPMs, age x stage matrices, as well as ahistorical matrices.

**Usage**

```r
## S3 method for class 'matrix'
lambda3(mats, sparse = "auto", ...)
```

**Arguments**

- `mats` A population projection matrix of class `matrix`.
- `sparse` A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
- `...` Other parameters.

**Value**

This function returns the dominant eigenvalue of the matrix.
Notes

The sparse option allows the function to utilize underlying methods of either dense or sparse matrix manipulation in order to speed up processing time and prevent memory shortages. Under the auto setting, the function will determine whether the matrix is sparse and act accordingly. For extremely large sparse matrices, the user may simply set sparse = "yes" to save time further and force the use of sparse format in calculations.

See Also

lambda3()
lambda3.lefkoMat()
slambda3()

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl"),
stage1 = c("Sd", "rep", "Sdl", "rep", "npr", "Sdl"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)
ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
lambda3(ehrlen3mean$A[[1]])

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
reppvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P2", "P3", "SL", "SL", "SL", "SL", "rep"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("sizeadded", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

lambda3(cypmatrix2r$A[[1]])
Description

A dataset containing the states and fates of *Lathyrus vernus* (spring vetch), family Fabaceae, from a population in Sweden monitored annually from 1988 to 1991 in six study plots.

Usage

data(lathyrus)

Format

A data frame with 1119 individuals and 34 variables. Each row corresponds to a unique individual, and each variable from `Volume88` on refers to the state of the individual in a given year.

- **SUBPLOT** A variable referring to patch within the population.
- **GENET** A numeric variable giving a unique number to each individual.
- **Volume88** Aboveground volume in cubic mm in 1988.
- **lnVol88** Natural logarithm of `Volume88`.
- **FCODE88** Equals 1 if flowering and 0 if not flowering in 1988.
- **Flow88** Number of flowers in 1988.
- **Intactseed88** Number of intact mature seeds produced in 1988. Not always an integer, as in some cases seed number was estimated via linear modeling.
- **Dead1988** Marked as 1 if known to be dead in 1988.
- **Dormant1988** Marked as 1 if known to be alive but vegetatively dormant in 1988.
- **Missing1988** Marked as 1 if not found in 1988.
- **Seedling1988** Marked as 1, 2, or 3 if observed as a seedling in year `t`. Numbers refer to certainty of assignment: 1 = certain that plant is a seedling in 1988, 2 = likely that plant is a seedling in 1988, 3 = probable that plant is a seedling in 1988.
- **Volume89** Aboveground volume in cubic mm in 1989.
- **lnVol89** Natural logarithm of `Volume89`.
- **FCODE89** Equals 1 if flowering and 0 if not flowering in 1989.
- **Flow89** Number of flowers in 1989.
- **Intactseed89** Number of intact mature seeds produced in 1989. Not always an integer, as in some cases seed number was estimated via linear modeling.
- **Dead1989** Marked as 1 if known to be dead in 1989.
- **Dormant1989** Marked as 1 if known to be alive but vegetatively dormant in 1989.
- **Missing1989** Marked as 1 if not found in 1989.
Seedling1989 Marked as 1, 2, or 3 if observed as a seedling in year \( t \). Numbers refer to certainty of assignment: 1 = certain that plant is a seedling in 1989, 2 = likely that plant is a seedling in 1989, 3 = probable that plant is a seedling in 1989.

Volume90 Aboveground volume in \( \text{mm}^3 \) in 1990.

lnVol90 Natural logarithm of Volume90.

FCODE90 Equals 1 if flowering and 0 if not flowering in 1990.

Flow90 Number of flowers in 1990.

Intactseed90 Number of intact mature seeds produced in 1990. Not always an integer, as in some cases seed number was estimated via linear modeling.

Dead1990 Marked as 1 if known to be dead in 1990.

Dormant1990 Marked as 1 if known to be alive but vegetatively dormant in 1990.

Missing1990 Marked as 1 if not found in 1990.

Seedling1990 Marked as 1, 2, or 3 if observed as a seedling in year \( t \). Numbers refer to certainty of assignment: 1 = certain that plant is a seedling in 1990, 2 = likely that plant is a seedling in 1990, 3 = probable that plant is a seedling in 1990.

Volume91 Aboveground volume in \( \text{mm}^3 \) in 1991.

lnVol91 Natural logarithm of Volume91.

FCODE91 Equals 1 if flowering and 0 if not flowering in 1991.

Flow91 Number of flowers in 1991.

Intactseed91 Number of intact mature seeds produced in 1991. Not always an integer, as in some cases seed number was estimated via linear modeling.

Dead1991 Marked as 1 if known to be dead in 1991.

Dormant1991 Marked as 1 if known to be alive but vegetatively dormant in 1991.

Missing1991 Marked as 1 if not found in 1991.

Seedling1991 Marked as 1, 2, or 3 if observed as a seedling in year \( t \). Numbers refer to certainty of assignment: 1 = certain that plant is a seedling in 1991, 2 = likely that plant is a seedling in 1991, 3 = probable that plant is a seedling in 1991.

Source


Examples

# Lathyrus example using blocksize - when repeated patterns exist in variable
# order
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
lathyrus <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
feccol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1),
stype_t12 = c(1, 2, 1, 2, 1, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
ehrlen3mean[[1]]

lambda3(ehrlen3mean)

# Lathyrus example without blocksize - when no repeated patterns exist in
# variable order and all variables names are specified
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
lefko3

Historical and Ahistorical Population Projection Matrix Analysis

Description

This package creates population matrix projection models (MPMs) for use in population ecological analyses. Its specialty is the estimation of historical MPMs, which are 2-dimensional matrices comprising 3 monitoring occasions (2 time steps or periods) of demographic information. The package constructs both function-based and raw MPMs for both standard ahistorical (i.e. 2 occasions, 1 period) and historical analyses, and can also produce age-by-stage MPMs and IPMs. It also includes powerful functions to standardize demographic datasets.

Details

The lefko3 package provides six categories of functions:
1. Data transformation and handling functions
2. Functions determining population characteristics from vertical data
3. Model building and selection
4. Matrix / integral projection model creation functions
5. Population dynamics analysis functions
6. Functions describing, summarizing, or visualizing MPMs and derived structures

lefko3 also includes example datasets complete with sample code.

Author(s)

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Johan Ehrlén

References


### lmean

*Estimate Mean Projection Matrices*

#### Description

lmean() estimates mean projection matrices as element-wise arithmetic means.

#### Usage

```r
lmean(mats, matsout = "all")
```

#### Arguments

- **mats**: A `lefkoMat` object.
- **matsout**: A string identifying which means to estimate. Option "pop" indicates population-level only, "patch" indicates patch-level only, and "all" indicates that both patch- and population-level means should be estimated. Defaults to "all".

#### Value

Yields a `lefkoMat` object with the following characteristics:

- **A**: A list of full mean projection matrices in order of sorted populations, patches, and years. These are typically estimated as the sums of the associated mean U and F matrices. All matrices output in the `matrix` class.
- **U**: A list of mean survival-transition matrices sorted as in A. All matrices output in the `matrix` class.
F

A list of mean fecundity matrices sorted as in A. All matrices output in the matrix class.

hstages

A data frame showing the pairing of ahistorical stages used to create historical stage pairs. Given if the MPM is historical.

ahstages

A data frame detailing the characteristics of associated ahistorical stages.

labels

A data frame detailing the order of population, patch, and year of each mean matrix. If pop, patch, or year2 are NA in the original labels set, then these will be re-labeled as A, 1, or 1, respectively.

matrixqc

A short vector describing the number of non-zero elements in U and F mean matrices, and the number of annual matrices.

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 0)
immvector <- c(1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
imstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                        patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                        juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type_tl2 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
ehrlen3mean$A[[1]]

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "Md", "Lg"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "Sm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type =c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

cyp2mean <- lmean(cypmatrix2r)
cyp2mean
**ltre3**  
*Conduct a Life Table Response Experiment*

**Description**

`ltre3()` is a generic function that returns life table response experiment (LTRE) or stochastic LTRE matrices for the input projection matrices.

**Usage**

```r
ltre3(mats, refmats, ...)  
```

**Arguments**

- `mats`: A `lefkoMat` object, population projection matrix, or list of population projection matrices.
- `refmats`: A reference `lefkoMat` object, or matrix, for use as the control. If missing, then is set to the same object as `mats`.
- `...`: Other parameters.

**Value**

The value returned depends on the class of the `mats` argument.

**Notes**


**See Also**

- `ltre3.lefkoMat()`
- `summary.lefkoLTRE()`

**Examples**

```r
# Lathyrus example  
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)  
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")  
revector <- c(0, 0, 0, 0, 1, 0)  
obsvector <- c(0, 1, 1, 1, 1, 1)  
matvector <- c(0, 0, 1, 1, 1, 1)  
immvector <- c(1, 1, 0, 0, 0, 0)  
propvector <- c(1, 0, 0, 0, 0, 0)
```
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                         repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                         immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                         propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                         patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                         juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                         fecacol = "Intactseed88", deadacol = "Dead1988",
                         nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                         censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sdl", "mat"),
                           stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
                           stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sdl"),
                           eststage3 = c(NA, NA, NA, NA, NA, NA, NA),
                           eststage2 = c(NA, NA, NA, NA, NA, NA, NA),
                           eststage1 = c(NA, NA, NA, NA, NA, NA, NA),
                           givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
                           multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
                           type = c(1, 1, 1, 1, 3, 3, 1),
                           type_t12 = c(1, 2, 1, 2, 1, 1, 1),
                           stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
                   stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
                   yearcol = "year2", individcol = "individ")
ltre3(ehrlen3)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg",
                 "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
                           repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                           propstatus = propvector, immstatus = immvector, indataset = indataset,
                           binhalfwidth = binvec)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
### ltre3.lefkoMat

**Conduct a Life Table Response Experiment of a lefkoMat Object**

**Description**

ltr3.lefkoMat() returns a set of matrices of one-way LTRE (life table response experiment) or stochastic LTRE matrices contributions.

**Usage**

```r
# S3 method for class 'lefkoMat'
ltr3(
  mats,
  refmats = NA,
  ref = NA,
  stochastic = FALSE,
  steps = 10000,
  burnin = 3000,
  time_weights = NA,
  sparse = "auto",
  rseed = NA,
  append_mats = FALSE,
  ...
)
```
**ltre3.lefkoMat**

**Arguments**

- **mats**: An object of class `lefkoMat`.
- **refmats**: A reference `lefkoMat` object, or matrix, for use as the control. If missing, then is set to the same object as `mats`.
- **ref**: A numeric value indicating which matrix or matrices in `refmats` to use as the control. The numbers used must correspond to the number of the matrices in the `labels` element of the associated `lefkoMat` object. The default setting, NA, uses all entries in `refmats`.
- **stochastic**: A logical value determining whether to conduct a deterministic (FALSE) or stochastic (TRUE) elasticity analysis. Defaults to FALSE.
- **steps**: The number of occasions to project forward in stochastic simulation. Defaults to 10,000.
- **burnin**: The number of initial steps to ignore in stochastic projection when calculating stochastic elasticities. Must be smaller than `steps`. Defaults to 3000.
- **time_weights**: Numeric vector denoting the probabilistic weightings of all matrices. Defaults to equal weighting among matrices.
- **sparse**: A string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
- **rseed**: Optional numeric value corresponding to the random seed for stochastic simulation.
- **append_mats**: A logical value denoting whether to include the original A, U, and F matrices in the returned `lefkoLTRE` object. Defaults to FALSE.
- **...**: Other parameters.

**Value**

This function returns an object of class `lefkoLTRE`. This includes a list of LTRE matrices as object `ltre_det` if a deterministic LTRE is called for, or a list of mean-value LTRE matrices as object `ltre_mean` and a list of SD-value LTRE matrices as object `ltre_sd` if a stochastic LTRE is called for. This is followed by the stageframe as object `ahstages`, the order of historical stages as object `hstages`, the age-by-stage order as object `agestages`, the order of matrices as object `labels`, and, if requested, the original A, U, and F matrices.

**Notes**


Default behavior for stochastic LTRE uses the full population provided in `mats` as the reference if no `refmats` and `ref` is provided. If no `refmats` is provided but `ref` is, then the matrices noted in `ref` are used as the reference matrix set. Year and patch order is utilized from object `mats`, but not from object `refmats`, in which each matrix is assumed to represent a different year from one population. This function cannot currently handle multiple populations within the same `mats` object (although such analysis is possible if these populations are designated as patches instead).
See Also

tre3()
summary.lefkoLTRE()

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
revector <- c(0, 0, 1, 0, 0, 1, 0)
obsvector <- c(0, 1, 0, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                       repstatus = revector, obsstatus = obsvector, matstatus = matvector,
                       immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                       propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                         patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                         juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                         fecacol = "Intactseed88", deadacol = "Dead1988",
                         nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                         censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
                           stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
                           stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
                           eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
                           eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
                           eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
                           givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
                           multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
                           type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
                           stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
                   stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
                   yearcol = "year2", individcol = "individ")

ltre3(ehrlen3, stochastic = TRUE)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)
sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
revector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
                          repstatus = revector, obsstatus = obsvector, matstatus = matvector,
                          propstatus = propvector, immstatus = immvector, indataset = indataset,
                          binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
                          patchidcol = "patch", individcol = "plantid", blocksize = 4,
                          sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
                          repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
                          stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
                          NRasRep = TRUE)
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
                                "XSm", "Sm", "SD", "P1"),
                          stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
                                "rep"),
                          eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA),
                          eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", NA, NA),
                          givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA),
                          multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
                          type = c(1, 1, 1, 1, 1, 1, 3, 3),
                          stageframe = cypframe_raw, historical = FALSE)
cymatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
                        year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
                        size = c("size3added", "size2added"), supplement = cypsupp2r,
                        yearcol = "year2", patchcol = "patchid", individcol = "individ")
ltre3(cymatrix2r)

**Description**

Function `modelsearch()` runs exhaustive model building and selection for each vital rate needed to estimate a function-based MPM or IPM. It returns best-fit models for each vital rate, model table showing all models tested, and model quality control data. The final output can be used as input in other functions within this package.
Usage

modelsearch(
  data,
  stageframe = NULL,
  historical = TRUE,
  approach = "mixed",
  suite = "size",
  bestfit = "AICc\&k",
  vitalrates = c("surv", "size", "fec"),
  surv = c("alive3", "alive2", "alive1"),
  obs = c("obsstatus3", "obsstatus2", "obsstatus1"),
  size = c("sizea3", "sizea2", "sizea1"),
  sizeb = c(NA, NA, NA),
  sizec = c(NA, NA, NA),
  repst = c("repstatus3", "repstatus2", "repstatus1"),
  fec = c("feca3", "feca2", "feca1"),
  stage = c("stage3", "stage2", "stage1"),
  indiv = "individ",
  patch = NA,
  year = "year2",
  density = NA,
  sizedist = "gaussian",
  sizebdist = NA,
  sizecdist = NA,
  fecdist = "gaussian",
  size.zero = FALSE,
  sizeb.zero = FALSE,
  sizec.zero = FALSE,
  size.trunc = FALSE,
  sizeb.trunc = FALSE,
  sizec.trunc = FALSE,
  fec.zero = FALSE,
  fec.trunc = FALSE,
  patch.as.random = TRUE,
  year.as.random = TRUE,
  juvestimate = NA,
  juvsize = FALSE,
  jsize.zero = FALSE,
  jsizeb.zero = FALSE,
  jsizec.zero = FALSE,
  jsizetrunc = FALSE,
  jsizeb.trunc = FALSE,
  jsizec.trunc = FALSE,
  fectime = 2,
  censor = NA,
  age = NA,
  indcova = NA,
  indcovb = NA,
modelsearch

indcovc = NA,
random.indcova = FALSE,
random.indcovb = FALSE,
random.indcovc = FALSE,
test.group = FALSE,
show.model.tables = TRUE,
global.only = FALSE,
quiet = FALSE
)

Arguments

data
The vertical dataset to be used for analysis. This dataset should be of class hvdata, but can also be a data frame formatted similarly to the output format provided by functions verticalize3() or historicalize3(), as long as all needed variables are properly designated.

stageframe
The stageframe characterizing the life history model used. Optional unless test.group = TRUE, in which case it is required. Defaults to NULL.

historical
A logical variable denoting whether to assess the effects of state in occasion t-1, in addition to state in occasion t. Defaults to TRUE.

approach
The statistical approach to be taken for model building. The default is "mixed", which uses the mixed model approach utilized in packages lme4 and glmmTMB. Other options include "glm", which uses generalized linear modeling assuming that all factors are fixed.

suite
This describes the global model for each vital rate estimation, and has the following possible values: full, includes main effects and all two-way interactions of size and reproductive status; main, includes main effects only of size and reproductive status; size, includes only size (also interactions between size in historical model); rep, includes only reproductive status (also interactions between status in historical model); and cons, all vital rates estimated only as y-intercepts. If approach = "glm" and year.as.random = FALSE, then year is also included as a fixed effect, and, in the case of full, included in two-way interactions. Defaults to size.

bestfit
A variable indicating the model selection criterion for the choice of best-fit model. The default is AICc&k, which chooses the best-fit model as the model with the lowest AICc or, if not the same model, then the model that has the lowest degrees of freedom among models with \( \Delta AICc < 2 \). Alternatively, AICc may be chosen, in which case the best-fit model is simply the model with the lowest AICc value.

vitalrates
A vector describing which vital rates will be estimated via linear modeling, with the following options: surv, survival probability; obs, observation probability; size, overall size; repst, probability of reproducing; and fec, amount of reproduction (overall fecundity). Defaults to c("surv","size","fec").

surv
A vector indicating the variable names coding for status as alive or dead in occasions t+1, t, and t-1, respectively. Defaults to c("alive3","alive2","alive1").

obs
A vector indicating the variable names coding for observation status in occasions t+1, t, and t-1, respectively. Defaults to c("obsstatus3","obsstatus2","obsstatus1").
size  A vector indicating the variable names coding for the primary size variable on occasions $t+1, t,$ and $t-1,$ respectively. Defaults to c("sizea3","sizea2","sizea1").

sizeb A vector indicating the variable names coding for the secondary size variable on occasions $t+1, t,$ and $t-1,$ respectively. Defaults to c(NA,NA,NA), in which case sizeb is not used.

sizec A vector indicating the variable names coding for the tertiary size variable on occasions $t+1, t,$ and $t-1,$ respectively. Defaults to c(NA,NA,NA), in which case sizec is not used.

repst A vector indicating the variable names coding for reproductive status in occasions $t+1, t,$ and $t-1,$ respectively. Defaults to c("repstatus3","repstatus2","repstatus1").

fec A vector indicating the variable names coding for fecundity in occasions $t+1, t,$ and $t-1,$ respectively. Defaults to c("feca3","feca2","feca1").

stage A vector indicating the variable names coding for stage in occasions $t+1, t,$ and $t-1.$ Defaults to c("stage3","stage2","stage1").

indiv A text value indicating the variable name coding individual identity. Defaults to "individ".

patch A text value indicating the variable name coding for patch, where patches are defined as permanent subgroups within the study population. Defaults to NA.

year A text value indicating the variable coding for observation occasion $t.$ Defaults to year2.

density A text value indicating the name of the variable coding for spatial density, should the user wish to test spatial density as a fixed factor affecting vital rates. Defaults to NA.

sizedist The probability distribution used to model primary size. Options include "gaussian" for the Normal distribution (default), "poisson" for the Poisson distribution, "negbin" for the negative binomial distribution (quadratic parameterization), and "gamma" for the Gamma distribution.

sizebdist The probability distribution used to model secondary size. Options include "gaussian" for the Normal distribution, "poisson" for the Poisson distribution, "negbin" for the negative binomial distribution (quadratic parameterization), and "gamma" for the Gamma distribution. Defaults to NA.

sizecdist The probability distribution used to model tertiary size. Options include "gaussian" for the Normal distribution, "poisson" for the Poisson distribution, "negbin" for the negative binomial distribution (quadratic parameterization), and "gamma" for the Gamma distribution. Defaults to NA.

fecdist The probability distribution used to model fecundity. Options include "gaussian" for the Normal distribution (default), "poisson" for the Poisson distribution, "negbin" for the negative binomial distribution (quadratic parameterization), and "gamma" for the Gamma distribution.

size.zero A logical variable indicating whether the primary size distribution should be zero-inflated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE.

sizeb.zero A logical variable indicating whether the secondary size distribution should be zero-inflated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE.
modelsearch

sizec.zero  A logical variable indicating whether the tertiary size distribution should be zero-inflated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE.

size.trunc  A logical variable indicating whether the primary size distribution should be zero-truncated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE. Cannot be TRUE if size.zero = TRUE.

sizeb.trunc  A logical variable indicating whether the secondary size distribution should be zero-truncated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE. Cannot be TRUE if sizeb.zero = TRUE.

sizec.trunc  A logical variable indicating whether the tertiary size distribution should be zero-truncated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE. Cannot be TRUE if size.c.zero = TRUE.

fec.zero  A logical variable indicating whether the fecundity distribution should be zero-inflated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE.

fec.trunc  A logical variable indicating whether the fecundity distribution should be zero-truncated. Only applies to the Poisson and negative binomial distributions. Defaults to FALSE. Cannot be TRUE if fec.zero = TRUE.

patch.as.random  If set to TRUE and approach = "mixed", then patch is included as a random factor. If set to FALSE and approach = "glm", then patch is included as a fixed factor. All other combinations of logical value and approach lead to patch not being included in modeling. Defaults to TRUE.

year.as.random  If set to TRUE and approach = "mixed", then year is included as a random factor. If set to FALSE, then year is included as a fixed factor. All other combinations of logical value and approach lead to year not being included in modeling. Defaults to TRUE.

juvestimate  An optional variable denoting the stage name of the juvenile stage in the vertical dataset. If not NA, and stage is also given (see below), then vital rates listed in vitalrates other than fec will also be estimated from the juvenile stage to all adult stages. Defaults to NA, in which case juvenile vital rates are not estimated.

juvsize  A logical variable denoting whether size should be used as a term in models involving transition from the juvenile stage. Defaults to FALSE, and is only used if juvestimate does not equal NA.

dzsize.zero  A logical variable indicating whether the primary size distribution of juveniles should be zero-inflated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE.

dzsizeb.zero  A logical variable indicating whether the secondary size distribution of juveniles should be zero-inflated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE.

dzsizec.zero  A logical variable indicating whether the tertiary size distribution of juveniles should be zero-inflated. Only applies to Poisson and negative binomial distributions. Defaults to FALSE.

dzsize.trunc  A logical variable indicating whether the primary size distribution in juveniles should be zero-truncated. Defaults to FALSE. Cannot be TRUE if dzsize.zero = TRUE.
A logical variable indicating whether the secondary size distribution in juveniles should be zero-truncated. Defaults to FALSE. Cannot be TRUE if jsizeb.zero = TRUE.

A logical variable indicating whether the tertiary size distribution in juveniles should be zero-truncated. Defaults to FALSE. Cannot be TRUE if jsizec.zero = TRUE.

A variable indicating which year of fecundity to use as the response term in fecundity models. Options include 2, which refers to occasion $t$, and 3, which refers to occasion $t+1$. Defaults to 2.

A vector denoting the names of censoring variables in the dataset, in order from occasion $t+1$, followed by occasion $t$, and lastly followed by occasion $t-1$. Defaults to NA.

Designates the name of the variable corresponding to age in the vertical dataset. Defaults to NA, in which case age is not included in linear models. Should only be used if building Leslie or age x stage matrices.

Vector designating the names in occasions $t+1$, $t$, and $t-1$ of an individual covariate. Defaults to NA.

Vector designating the names in occasions $t+1$, $t$, and $t-1$ of a second individual covariate. Defaults to NA.

Vector designating the names in occasions $t+1$, $t$, and $t-1$ of a third individual covariate. Defaults to NA.

A logical value indicating whether indcova should be treated as a random categorical factor, rather than as a fixed factor. Defaults to FALSE.

A logical value indicating whether indcovb should be treated as a random categorical factor, rather than as a fixed factor. Defaults to FALSE.

A logical value indicating whether indcovc should be treated as a random categorical factor, rather than as a fixed factor. Defaults to FALSE.

A logical value indicating whether to include the group variable from the input stageframe as a fixed categorical variable in linear models. Defaults to FALSE.

If set to TRUE, then includes full modeling tables in the output. Defaults to TRUE.

If set to TRUE, then only global models will be built and evaluated. Defaults to FALSE.

If set to TRUE, then model building and selection will proceed with most warnings and diagnostic messages silenced. Defaults to FALSE.

This function yields an object of class `lefkoMod`, which is a list in which the first 13 elements are the best-fit models for survival, observation status, primary size, secondary size, tertiary size, reproductive status, fecundity, juvenile survival, juvenile observation, juvenile primary size, juvenile secondary size, juvenile tertiary size, and juvenile transition to reproduction, respectively, followed by 13 elements corresponding to the model tables for each of these vital rates, in order, followed
by a data frame showing the order and names of variables used in modeling, followed by a single character element denoting the criterion used for model selection, and ending on a data frame with quality control data:

**survival_model**  
Best-fit model of the binomial probability of survival from occasion $t$ to occasion $t+1$. Defaults to 1.

**observation_model**  
Best-fit model of the binomial probability of observation in occasion $t+1$ given survival to that occasion. Defaults to 1.

**size_model**  
Best-fit model of the primary size metric on occasion $t+1$ given survival to and observation in that occasion. Defaults to 1.

**sizeb_model**  
Best-fit model of the secondary size metric on occasion $t+1$ given survival to and observation in that occasion. Defaults to 1.

**sizec_model**  
Best-fit model of the tertiary size metric on occasion $t+1$ given survival to and observation in that occasion. Defaults to 1.

**repstatus_model**  
Best-fit model of the binomial probability of reproduction in occasion $t+1$, given survival to and observation in that occasion. Defaults to 1.

**fecundity_model**  
Best-fit model of fecundity in occasion $t+1$ given survival to, and observation and reproduction in that occasion. Defaults to 1.

**juv_survival_model**  
Best-fit model of the binomial probability of survival from occasion $t$ to occasion $t+1$ of an immature individual. Defaults to 1.

**juv_observation_model**  
Best-fit model of the binomial probability of observation in occasion $t+1$ given survival to that occasion of an immature individual. Defaults to 1.

**juv_size_model**  
Best-fit model of the primary size metric on occasion $t+1$ given survival to and observation in that occasion of an immature individual. Defaults to 1.

**juv_sizeb_model**  
Best-fit model of the secondary size metric on occasion $t+1$ given survival to and observation in that occasion of an immature individual. Defaults to 1.

**juv_sizec_model**  
Best-fit model of the tertiary size metric on occasion $t+1$ given survival to and observation in that occasion of an immature individual. Defaults to 1.

**juv_reproduction_model**  
Best-fit model of the binomial probability of reproduction in occasion $t+1$, given survival to and observation in that occasion of an individual that was immature in occasion $t$. This model is technically not a model of reproduction probability for individuals that are immature, rather reproduction probability here is given for individuals that are mature in occasion $t+1$ but immature in occasion $t$. Defaults to 1.

**survival_table**  
Full dredge model table of survival probability.

**observation_table**  
Full dredge model table of observation probability.

**size_table**  
Full dredge model table of the primary size variable.
sizeb_table  Full dredge model table of the secondary size variable.
sizec_table  Full dredge model table of the tertiary size variable.
reppstatus_table  Full dredge model table of reproduction probability.
fecundity_table  Full dredge model table of fecundity.
juv_survival_table  Full dredge model table of immature survival probability.
juv_observation_table  Full dredge model table of immature observation probability.
juv_size_table  Full dredge model table of primary size in immature individuals.
juv_sizeb_table  Full dredge model table of secondary size in immature individuals.
juv_sizec_table  Full dredge model table of tertiary size in immature individuals.
juv_reproduction_table  Full dredge model table of immature reproduction probability.
criterion  Character variable denoting the criterion used to determine the best-fit model.
qc  Data frame with four variables: 1) Name of vital rate, 2) number of individuals used to model that vital rate, 3) number of individual transitions used to model that vital rate, and 4) accuracy of model expressed as percent of predicted responses equal to actual responses (only in binomial models).

Notes

The mechanics governing model building are fairly robust to errors and exceptions. The function attempts to build global models, and simplifies models automatically should model building fail. Model building proceeds through the functions `lm()` (GLM with Gaussian response), `glm()` (GLM with Poisson, Gamma, or binomial response), `glm.nb()` (GLM with negative binomial response), `zeroinfl()` (GLM with zero-inflated Poisson or negative binomial response), `vglm()` (GLM with zero-truncated Poisson or negative binomial response), `lmer()` (mixed model with Gaussian response), `glmer()` (mixed model with binomial, Poisson, or Gamma response), and `glmmTMB()` (mixed model with negative binomial, or zero-truncated or zero-inflated Poisson or negative binomial response). See documentation related to these functions for further information. Any response term that is invariable in the dataset will lead to a best-fit model for that response represented by a single constant value.

Exhaustive model building and selection proceeds via the `dredge()` function in package `MuMIn`. This function is verbose, so that any errors and warnings developed during model building, model analysis, and model selection can be found and dealt with. Interpretations of errors during global model analysis may be found in documentation for the functions and packages mentioned. Package `MuMIn` is used for model dredging (see `dredge()`), and errors and warnings during dredging can be interpreted using the documentation for that package. Errors occurring during dredging lead to the adoption of the global model as the best-fit, and the user should view all logged errors and warnings to determine the best way to proceed. The `quiet = TRUE` option can be used to silence dredge warnings, but users should note that automated model selection can be viewed as a black box, and
so care should be taken to ensure that the models run make biological sense, and that model quality is prioritized.

Exhaustive model selection through dredging works best with larger datasets and fewer tested parameters. Setting `suite = "full"` may initiate a dredge that takes a dramatically long time, particularly if the model is historical, individual covariates are used, or a zero-inflated distribution is assumed. In such cases, the number of models built and tested will run at least in the millions. Small datasets will also increase the error associated with these tests, leading to adoption of simpler models overall.

Care must be taken to build models that test the impacts of state in occasion t-1 for historical models, and that do not test these impacts for ahistorical models. Ahistorical matrix modeling particularly will yield biased transition estimates if historical terms from models are ignored. This can be dealt with at the start of modeling by setting `historical = FALSE` for the ahistorical case, and `historical = TRUE` for the historical case.

This function handles generalized linear models (GLMs) under zero-inflated distributions using the `zeroinfl()` function, and zero-truncated distributions using the `vglm()` function. Model dredging may fail with these functions, leading to the global model being accepted as the best-fit model. However, model dredges of mixed models work for all distributions. We encourage the use of mixed models in all cases.

The negative binomial and truncated negative binomial distributions use the quadratic structure emphasized in Hardin and Hilbe (2018, 4th Edition of Generalized Linear Models and Extensions). The truncated negative binomial distribution may fail to predict size probabilities correctly when dispersion is near that expected of the Poisson distribution. To prevent this problem, we have integrated a cap on the overdispersion parameter. However, when using this distribution, please check the matrix column sums to make sure that they do not predict survival greater than 1.0. If they do, then please use either the negative binomial distribution or the zero-truncated Poisson distribution.

If density dependence is explored through function `modelsearch()`, then the interpretation of density is not the full population size but rather the spatial density term included in the dataset.

**Examples**

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 4.6, 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 1, 2, 3, 4, 5, 6, 7, 8, 9)
stagevector <- c("Sd", "Sdl", "Dorm", "Sz1nr", "Sz2nr", "Sz3nr", "Sz4nr",
                  "Sz5nr", "Sz6nr", "Sz7nr", "Sz8nr", "Sz9nr", "Sz1r", "Sz2r", "Sz3r",
                  "Sz4r", "Sz5r", "Sz6r", "Sz7r", "Sz8r", "Sz9r")
repvector <- c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 4.6, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)
```
overwrite <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec, propstatus = propvector)


lathvertln$feca2 <- round(lathvertln$feca2)
lathvertln$feca1 <- round(lathvertln$feca1)
lathvertln$feca3 <- round(lathvertln$feca3)
lathmodelsln3 <- modelsearch(lathvertln, historical = TRUE, approach = "mixed", suite = "main", vitalrates = c("surv", "obs", "size", "repst", "fec"), juvestimate = "Sdl", bestfit = "AICc&k", sizedist = "gaussian", fecdist = "poisson", indiv = "individ", patch = "patchid", year = "year2", year.as.random = TRUE, patch.as.random = TRUE, show.model.tables = TRUE, quiet = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "mat", "Sdl", "Sdl"), stage2 = c("Sd", "Sd", "Sdl", "Sdl", "rep", "rep"), stage1 = c("Sd", "rep", "Sd", "rep", "Sd", "mat", "mat"), eststage3 = c(NA, NA, NA, NA, "mat", NA, NA), eststage2 = c(NA, NA, NA, NA, "Sdl", NA, NA), eststage1 = c(NA, NA, NA, NA, "Sdl", NA, NA), givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA), multiplier = c(NA, NA, NA, NA, NA, 0.345, 0.054), type = c(1, 1, 1, 1, 3, 3), stageframe = lathframeln, historical = TRUE)
lathmat3ln <- flefko3(year = "all", patch = "all", stageframe = lathframeln, modelsuite = lathmodelsln3, data = lathvertln, supplement = lathsupp3, patchcol = "patchid", yearcol = "year2", year.as.random = TRUE, patch.as.random = TRUE, reduce = FALSE)

summary(lathmat3ln)

---

### overwrite

#### Create Overwrite Table for MPM Development

**Description**

overwrite() returns a data frame describing which particular transitions within an ahistorical or
overwrite

historical projection matrix to overwrite with either given rates and probabilities, or other estimated transitions.

Usage

overwrite(
    stage3,
    stage2,
    stage1 = NA,
    eststage3 = NA,
    eststage2 = NA,
    eststage1 = NA,
    givenrate = NA,
    type = NA,
    type_t12 = NA
)

Arguments

stage3 The name of the stage in occasion \( t+1 \) in the transition to be replaced. Abbreviations for groups of stages are also allowed (see Notes).

stage2 The name of the stage in occasion \( t \) in the transition to be replaced. Abbreviations for groups of stages are also allowed (see Notes).

stage1 The name of the stage in occasion \( t-1 \) in the transition to be replaced. Only needed if a historical matrix is to be produced. Abbreviations for groups of stages are also allowed (see Notes).

eststage3 The name of the stage to replace stage3. Only needed if a transition will be replaced by another estimated transition.

eststage2 The name of the stage to replace stage2. Only needed if a transition will be replaced by another estimated transition.

eststage1 The name of the stage to replace stage1. Only needed if a transition will be replaced by another estimated transition, and the matrix to be estimated is historical.

givenrate A fixed rate or probability to replace for the transition described by stage3, stage2, and stage1.

type A vector denoting the kind of transition between occasions \( t \) and \( t+1 \) to be replaced. This should be entered as 1, S, or s for the replacement of a survival transition; or 2, F, or f for the replacement of a fecundity transition. If empty or not provided, then defaults to 1 for survival transition.

type_t12 An optional vector denoting the kind of transition between occasions \( t-1 \) and \( t \). Only necessary if a historical MPM in DeVries format is desired. This should be entered as 1, S, or s for a survival transition; or 2, F, or f for a fecundity transitions. Defaults to 1 for survival transition, with impacts only on the construction of DeVries-format hMPMs.
Value

A data frame that puts the above vectors together and can be used as input in `flefko3()` , `flefko2()` , `rlefko3()` , `rlefko2()` , and `aflefko2()` .

Variables in this data frame include the following:

- **stage3**: Stage at occasion \( t+1 \) in the transition to be replaced.
- **stage2**: Stage at occasion \( t \) in the transition to be replaced.
- **stage1**: Stage at occasion \( t-1 \) in the transition to be replaced.
- **eststage3**: Stage at occasion \( t+1 \) in the transition to replace the transition designated by stage3, stage2, and stage1.
- **eststage2**: Stage at occasion \( t \) in the transition to replace the transition designated by stage3, stage2, and stage1.
- **eststage1**: Stage at occasion \( t-1 \) in the transition to replace the transition designated by stage3, stage2, and stage1.
- **givenrate**: A constant to be used as the value of the transition.
- **convtype**: Designates whether the transition from occasion \( t \) to occasion \( t+1 \) is a survival-transition probability (1) or a fecundity rate (2).
- **convtype_t12**: Designates whether the transition from occasion \( t-1 \) to occasion \( t \) is a survival transition probability (1), a fecundity rate (2).

Notes

Entries in stage3, stage2, and stage1 can include abbreviations for groups of stages. Use rep if all reproductive stages are to be used, nrep if all mature but non-reproductive stages are to be used, mat if all mature stages are to be used, immat if all immature stages are to be used, prop if all propagate stages are to be used, npr if all non-propagate stages are to be used, and leave empty or use all if all stages in stageframe are to be used.

Examples

cypover2r <- overwrite(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm"),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm"),
givenrate = c(0.1, 0.2, 0.2, 0.2, 0.25, NA, NA, NA),
)
cypover2r
cypover2r <- overwrite(stage3 = c("SD", "SD", "P1", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "D", "XSm", "Sm", "D", "XSm", "Sm"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA))
projection3

Conduct Population Projection Simulations

Description

Function projection3() runs projection simulations. It projects the population and patches forward in time by a user-defined number of occasions. Projections may be deterministic or stochastic, and may be density dependent either way. If deterministic, then projections will be cyclical if matrices exist covering multiple occasions for each population or patch. If stochastic, then annual matrices will be shuffled within patches and populations. Replicates may also be requested.

Usage

projection3(
  mpm,
  nreps = 1L,
  times = 10000L,
  stochastic = FALSE,
  standardize = FALSE,
  growthonly = TRUE,
  integeronly = FALSE,
  substoch = 0L,
  start_vec = NULL,
  start_frame = NULL,
  tweights = NULL,
  density = NULL
)

Arguments

mpm A matrix projection model of class lefkoMat, or a list of full matrix projection matrices.
nreps The number of replicate projections.
times Number of occasions to iterate per replicate. Defaults to 10,000.
stochastic A logical value denoting whether to conduct a stochastic projection or a deterministic / cyclical projection.
standardize A logical value denoting whether to re-standardize the population size to 1.0 at each occasion. Defaults to FALSE.

growthonly A logical value indicating whether to produce only the projected population size at each occasion, or a vector showing the stage distribution followed by the reproductive value vector followed by the full population size at each occasion. Defaults to TRUE.

integeronly A logical value indicating whether to round the number of individuals projected in each stage at each occasion to the nearest integer. Defaults to FALSE.

substoch An integer value indicating whether to force survival-transition matrices to be substochastic in density dependent simulations. Defaults to 0, which does not force substochasticity. Alternatively, 1 forces all survival-transition elements to range from 0.0 to 1.0, and 2 forces all column rows to total no more than 1.0.

start_vec An optional numeric vector denoting the starting stage distribution for the projection. Defaults to a single individual of each stage.

start_frame An optional data frame characterizing stages, age-stages, or stage-pairs that should be set to non-zero values in the starting vector, and what those values should be. Can only be used with lefkoMat objects.

tweights An optional numeric vector denoting the probabilistic weightings of annual matrices. Defaults to equal weighting among occasions.

density An optional data frame describing the matrix elements that will be subject to density dependence, and the exact kind of density dependence that they will be subject to. The data frame used should be an object of class lefkoDens, which is the output from function density_input().

Value

A list of class lefkoProj, which always includes the first three elements of the following, and also includes the remaining elements below when a lefkoMat object is used as input:

projection A list of lists of matrices showing the total number of individuals per stage per occasion. The first list corresponds to each pop-patch followed by each population. The inner list corresponds to replicates within each pop-patch or population.

stage_dist A list of lists of the actual stage distribution in each occasion in each replicate in each pop-patch or population. The list order is the same as in projection.

rep_value A list of lists of the actual reproductive value in each occasion in each replicate in each pop-patch or population. The list order is the same as in projection.

pop_size A list of data frames showing the total population size in each occasion per replicate (row within data frame) per pop-patch or population (list element).

labels A data frame showing the order of populations and patches in item projection.

control A short vector indicating the number of replicates and the number of occasions projected per replicate.

ahstages The original stageframe used in the study.

hstages A data frame showing the order of historical stage pairs.

agestages A data frame showing the order of age-stage pairs.
Notes

Projections are run both at the patch level and at the population level. Population level estimates will be noted at the end of the data frame with 0 entries for patch designation.

Weightings given in `tweights` do not need to sum to 1. Final weightings used will be based on the proportion per element of the sum of elements in the user-supplied vector.

Starting vectors can be input in one of two ways: 1) as `start_vec` input, which is a vector of numbers of the numbers of individuals in each stage, stage pair, or age-stage, with the length of the vector necessarily as long as there are rows in the matrices of the MPM; or 2) as `start_frame` input, which is a data frame showing only those stages, stage pairs, or age-stages that should begin with more than 0 individuals, and the numbers of individuals that those stages should start with (this object is created using the `start_input()` function). If both are provided, then `start_frame` takes precedence and `start_vec` is ignored. If neither is provided, then `projection3()` automatically assumes that each stage, stage pair, or age-stage begins with a single individual. Importantly, if a `lefkoMat` object is not used, and a list of matrices is provided instead, then `start_frame` cannot be utilized and a full `start_vec` must be provided to conduct a simulation with starting numbers of individuals other than 1 per stage.

The resulting data frames in element `projection` are separated by pop-patch according to the order provided in element `labels`, but the matrices for each element of `projection` have the result of each replicate stacked in order on top of one another without any break or indication. Results for each replicate must be separated using the information provided in elements `control` and the 3 stage descriptor elements.

Density dependent projections are automatically set up if object `density` is input. If this object is not included, then density independent projections will be set up. Note that currently, density dependent projections can only be performed with `lefkoMat` objects.

The stage distributions and reproductive values produced are not the asymptotic values as would be given by the standardized right and left eigenvectors associated with the dominant eigenvalue of a matrix, but are vectors describing these values at the specific points in time projected. See equations 14.86 and 14.88 and section 14.4 on Sensitivity and Elasticity Analysis under Environmental Stochasticity in Caswell (2001, Matrix Population Models, Sinauer Associates) for more details.

See Also

`start_input()`
`density_input()`

Examples

```r
# Lathyrus example
data(lathyrus)
sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 0)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
```
projection3

indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
 fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep"),
stage1 = c("Sd", "rep", "Sd", "rep", "all", "all"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
type = c(1, 1, 1, 1, 3, 3), type_t12 = c(1, 2, 1, 2, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe,
year = c(1989, 1990), stages = c("stage3", "stage2", "stage1"),
supplement = lathsupp3, yearcol = "year2", individcol = "individ")

lathproj <- projection3(ehrlen3, nreps = 5, stochastic = TRUE)

# Cypripedium example
rm(list = ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",)
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE, NRasRep = TRUE)

cypsupp3r <- supplemental(stage3 = c("SD", "SD", "P1", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "D", "XSm", "Sm", "SD", "P1"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, D", "XSm", "Sm", "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
givenrate = c(0.1, 0.1, 0.2, 0.2, 0.2, 0.2, 0.25, NA, NA, NA, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
type_t12 = c(1, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1),
stageframe = cypframe_raw, historical = TRUE)

cypmatrix3r <- rlefko3(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added", "size1added"),
supplement = cypsupp3r, yearcol = "year2",
patchcol = "patchid", indivcol = "individ")

cypstoch <- projection3(cypmatrix3r, nreps = 5, stochastic = TRUE)

### repvalue3

**Description**

`repvalue3()` is a generic function that estimates returns the reproductive values of stages in a population projection matrix or a set of matrices. The specifics of estimation vary with the class of input object. This function is made to handle very large and sparse matrices supplied as lefkoMat objects or as individual matrices, and can be used with large historical matrices, IPMs, age x stage matrices, as well as ahistorical matrices.

**Usage**

`repvalue3(mats, ...)`

**Arguments**

- **mats**
  A lefkoMat object, or population projection matrix.

- **...**
  Other parameters.
Value

The value returned depends on the class of the mats argument. See related functions for details.

See Also

repvalue3.lefkoMat()
repvalue3.matrix()

Examples

# Lathyrus deterministic example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
reppstatus = reppvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl"),
stage1 = c("Sd", "Sd", "Sdl", "Sdl", "npr", "npr", "Sdl"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 1, 1, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrren3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

ehrren3mean <- lmean(ehrren3)
repvalue3(ehrren3mean)
# Cypripedium stochastic example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", individcol = "individ")

repvalue3(cypmatrix2r, stochastic = TRUE)
Description

repvalue3.lefkoMat() returns the reproductive values for stages in a set of population projection matrices provided as a lefkoMat object. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as ahihistorical matrices.

Usage

## S3 method for class 'lefkoMat'
repvalue3(
mats,
stochastic = FALSE,
times = 10000,
tweights = NA,
seed = NA,
sparse = "auto",
...
)

Arguments

mats An object of class lefkoMat object.
stochastic A logical value indicating whether to use deterministic (FALSE) or stochastic (TRUE) analysis. Defaults to FALSE.
times An integer variable indicating number of occasions to project if using stochastic analysis. Defaults to 10000.
tweights An optional vector indicating the probability weighting to use for each matrix in stochastic simulations. If not given, then defaults to equal weighting.
seed A number to use as a random number seed.
sparse A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
...
Other parameters.

Value

This function returns the asymptotic reproductive value vectors if deterministic analysis is chosen, and long-run mean reproductive value vectors if stochastic analysis is chosen.

The output depends on whether the lefkoMat object used as input is ahihistorical or historical, and whether the analysis is deterministic or stochastic. If deterministic and ahihistorical, then a single data frame is output, which includes the number of the matrix within the A element of the input lefkoMat object, followed by the stage id (numeric and assigned through sf_create()), the stage name, and the estimated proportion of the reproductive value vector (rep_value). If stochastic and ahihistorical, then a single data frame is output starting with the number of the population-patch (matrix_set), a string concatenating the names of the population and the patch (poppatch), the assigned stage id number (stage_id), and the stage name (stage), and the long-run mean reproductive value vector (rep_value).
If a historical matrix is used as input, then two data frames are output into a list object. The hist element describes the historical stage-pair reproductive values, while the ahist element describes the stage reproductive values. If deterministic, then hist contains a data frame including the matrix number (matrix), the numeric stage designations for stages in occasions \( t \) and \( t-1 \) (stage_id_2 and stage_id_1, respectively), followed by the respective stage names (stage_2 and stage_1), and ending with the estimated reproductive values (rep_value). The associated ahist element is as before. If stochastic, then the hist element contains a single data frame with the number of the population-patch (matrix_set), a string concatenating the names of the population and the patch (poppatch), the assigned stage id numbers in times \( t \) and \( t-1 \) (stage_id_2 and stage_id_2, respectively), and the associated stage names (stage_2 and stage_1, respectively), and the long-run mean reproductive values (rep_value). The associated ahist element is as before in the ahistorical, stochastic case.

In addition to the data frames noted above, stochastic analysis will result in the additional output of a list of matrices containing the actual projected reproductive value vectors across all projected occasions, in the order of population-patch combinations in the lefkoMat input.

**Notes**

In stochastic analysis, the projected mean reproductive value vector is the arithmetic mean across the final projected 1000 occasions if the simulation is at least 2000 projected occasions long. If between 500 and 2000 projected occasions long, then only the final 200 are used, and if fewer than 500 occasions are used, then all are used. Note that because reproductive values in stochastic simulations can change greatly in the initial portion of the run, we encourage a minimum 2000 projected occasions per simulation, with 10000 preferred.

**See Also**

repvalue3()
repvalue3.matrix()

**Examples**

# Lathyrus deterministic example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reps vector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sdl", "mat"), stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"), stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"), eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"), eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"), eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"), givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA), multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA), type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1), stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all", stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3, yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
repvalue3(ehrlen3mean)

# Cypripedium stochastic example
rm(list=ls(all=TRUE))
data(cypdata)
sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cyframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, propstatus = propvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004, patchidcol = "patch", individcol = "plantid", blocksize = 4, sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04", repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04", stageassign = cypraw_v1, stagesize = "sizeadded", NAas0 = TRUE, NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "D", "P1"), stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"), eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA), eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA), givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA), multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA), type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3), stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw, year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"), size = c("size3added", "size2added"), supplement = cypsupp2r, yearcol = "year2", patchcol = "patchid", indivcol = "individ")

repvalue3(cypmatrix2r, stochastic = TRUE)

repvalue3.matrix

Estimate Reproductive Value Vector for a Single Population Projection Matrix

Description

repvalue3.matrix() returns the reproductive values for stages in a population projection matrix. The function makes no assumptions about whether the matrix is ahistorical and simply provides standard reproductive values corresponding to each row, meaning that the overall reproductive values of basic life history stages in a historical matrix are not provided (the repvalue3.lefkoMat() function estimates these on the basis of stage description information provided in the lefkoMat object used as input in that function). This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as smaller ahistorical matrices.

Usage

## S3 method for class 'matrix'
repvalue3(mats, sparse = "auto", ...)

Arguments

mats A population projection matrix.

sparse A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".

... Other parameters.
Value

This function returns a vector data frame characterizing the reproductive values for stages of a population projection matrix. This is given as the left eigenvector associated with largest real part of the dominant eigenvalue, divided by the first non-zero element of the left eigenvector.

See Also

repvalue3()
repvalue3.lefkoMat()

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
pachidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)
lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1),
stageframe = lathframe, historical = TRUE)
ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")
ehrlen3mean <- lmean(ehrlen3)
repvalue3(ehrlen3mean$A[[1]])

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
inddataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
 repstatus = repsvector, obsstatus = obsvector, matstatus = matvector,
 propstatus = propvector, immstatus = immvector, indataset = inddataset,
 binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
 patchidcol = "patch", individcol = "plantid", blocksize = 4,
 sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
 repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
 stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
 NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", 
 "XSm", "Sm", "SD", "P1"),
 stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", 
 "rep"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
 year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
 size = c("size3added", "size2added"), supplement = cypsupp2r,
 yearcol = "year2", patchcol = "patchid", individcol = "individ")

repvalue3(cypmatrix2r$A[[1]])
Description

Function `rlefko2()` returns raw ahistorical MPMs, including the associated component transition and fecundity matrices, a data frame describing the ahistorical stages used, and a data frame describing the population, patch, and occasion time associated with each matrix.

Usage

```r
rlefko2(
  data,
  stageframe,
  year = "all",
  pop = NA,
  patch = NA,
  censor = FALSE,
  stages = NA,
  alive = c("alive3", "alive2"),
  size = c("sizea3", "sizea2"),
  sizeb = c(NA, NA),
  sizec = c(NA, NA),
  repst = c("repstatus3", "repstatus2"),
  matst = c("matstatus3", "matstatus2"),
  fec = c("feca3", "feca2"),
  supplement = NULL,
  repmatrix = NULL,
  overwrite = NULL,
  yearcol = NA,
  popcol = NA,
  patchcol = NA,
  indivcol = NA,
  censorcol = NA,
  censorkeep = 0,
  reduce = FALSE
)
```

Arguments

data: A vertical demographic data frame, with variables corresponding to the naming conventions in `verticalize3()`.

stageframe: A stageframe object that includes information on the size, observation status, propagule status, immaturity status, and maturity status of each ahistorical stage. Should also incorporate bin widths if size is continuous.
year
A variable corresponding to observation occasion, or a set of such values, given in values associated with the year term used in vital rate model development. Can also equal all, in which case matrices will be estimated for all occasion times. Defaults to all.

pop
A variable designating which populations will have matrices estimated. Should be set to specific population names, or to all if all populations should have matrices estimated.

patch
A variable designating which patches or subpopulations will have matrices estimated. Should be set to specific patch names, or to all if matrices should be estimated for all patches. Defaults to all.

censor
If TRUE, then data will be removed according to the variable set in censorcol, such that only data with censor values equal to 1 will remain. Defaults to FALSE.

stages
An optional vector denoting the names of the variables within the main vertical dataset coding for the stages of each individual in occasions t+1, t, and t-1. The names of stages in these variables should match those used in the stageframe exactly. If left blank, then rlefko3() will attempt to infer stages by matching values of alive, size, repst, and matst to characteristics noted in the associated stageframe.

alive
A vector of names of binomial variables corresponding to status as alive (1) or dead (0) in occasions t+1 and t, respectively.

size
A vector of names of variables coding the primary size variable in occasions t+1 and t, respectively. Defaults to c("sizea3","sizea2").

sizeb
A vector of names of variables coding the secondary size variable in occasions t+1 and t, respectively. Defaults to c(NA,NA).

sizec
A vector of names of variables coding the tertiary size variable in occasions t+1 and t, respectively. Defaults to c(NA,NA).

repst
A vector of names of variables coding reproductive status in occasions t+1 and t, respectively. Defaults to c("repstatus3","repstatus2"). Must be supplied if stages is not provided.

matst
A vector of names of variables coding maturity status in occasions t+1 and t, respectively. Defaults to c("matstatus3","matstatus2"). Must be supplied if stages is not provided.

fec
A vector of names of variables coding fecundity in occasions t+1 and t, respectively. Defaults to c("feca3","feca2").

supplement
An optional data frame of class lefkoSD that provides supplemental data that should be incorporated into the MPM. Three kinds of data may be integrated this way: transitions to be estimated via the use of proxy transitions, transition overwrites from the literature or supplemental studies, and transition multipliers for fecundity. This data frame should be produced using the supplemental() function. Should be used in place of or in addition to an overwrite table (see overwrite below) and a reproduction matrix (see repmatrix below).

repmatrix
An optional reproduction matrix. This matrix is composed mostly of 0s, with non-zero entries acting as element identifiers and multipliers for fecundity (with 1 equaling full fecundity). If left blank, and no supplement is provided, then
rlefko2() will assume that all stages marked as reproductive produce offspring at 1x that of estimated fecundity, and that offspring production will yield the first stage noted as propagule or immature. To prevent this behavior, input just 0, which will result in fecundity being estimated only for transitions noted in supplement above. Must be the dimensions of an ahistorical matrix.

overwrite  
An optional data frame developed with the overwrite() function describing transitions to be overwritten either with given values or with other estimated transitions. Note that this function supplements overwrite data provided in supplement.

yearcol  
The variable name or column number corresponding to occasion \( t \) in the dataset.

popcol  
The variable name or column number corresponding to the identity of the population.

patchcol  
The variable name or column number corresponding to patch in the dataset.

indivcol  
The variable name or column number coding individual identity.

censorcol  
The variable name or column number denoting the censor status. Only needed if censor = TRUE.

censorkeep  
The value of the censor variable denoting data elements to keep. Defaults to 0.

reduce  
A logical value denoting whether to remove historical stages associated with only zero transitions. These are removed only if the respective row and column sums in ALL matrices estimated equal 0. Defaults to FALSE.

Value

If all inputs are properly formatted, then this function will return an object of class lefkoMat, which is a list that holds the matrix projection model and all of its metadata. Its structure is a list with the following elements:

A  
A list of full projection matrices in order of sorted populations, patches, and occasions. All matrices output in the matrix class.

U  
A list of survival transition matrices sorted as in A. All matrices output in the matrix class.

F  
A list of fecundity matrices sorted as in A. All matrices output in the matrix class.

hstages  
A data frame matrix showing the pairing of ahistorical stages used to create historical stage pairs. Set to NA for ahistorical matrices.

agestages  
A data frame showing age-stage pairs. In this function, it is set to NA. Only used in output to function aflefko2().

ahstages  
A data frame detailing the characteristics of associated ahistorical stages, in the form of a modified stageframe that includes status as an entry stage through reproduction.

labels  
A data frame giving the population, patch, and year of each matrix in order.

matrixqc  
A short vector describing the number of non-zero elements in U and F matrices, and the number of annual matrices.

dataqc  
A vector showing the numbers of individuals and rows in the vertical dataset used as input.
Notes

The default behavior of this function is to estimate fecundity with regards to transitions specified via associated fecundity multipliers in either supplement or repmatrix. If both of these fields are left empty, then fecundity will be estimated at full for all transitions leading from reproductive stages to immature and propagule stages. However, if a supplement is provided and a repmatrix is not, or if repmatrix is set to 0, then only fecundity transitions noted in the supplement will be set to non-zero values. To use the default behavior of setting all reproductive stages to reproduce at full fecundity into immature and propagule stages but also incorporate given or proxy survival transitions, input those given and proxy transitions through the overwrite options.

The reproduction matrix (field repmatrix) may only be supplied as ahistorical. If provided as historical, then rlefko2() will fail and produce an error.

Users may at times wish to estimate MPMs using a dataset incorporating multiple patches or sub-populations. Should the aim of analysis be a general MPM that does not distinguish these patches or subpopulations, the patchcol variable should be left to NA, which is the default. Otherwise the variable identifying patch needs to be named.

Input options including multiple variable names must be entered in the order of variables in occasion $t+1$ and $t$. Rearranging the order WILL lead to erroneous calculations, and may lead to fatal errors.

Although this function is capable of assigning stages given an input stageframe, it lacks the power of verticalize3() and historicalize3() in this regard. Users are strongly encouraged to use the latter two functions for stage assignment.

Examples

```r
# Lathyrus example
data(lathyrus)
sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repsvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                        immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                        patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                        juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                        fecacol = "Intactseed88", deadacol = "Dead1988", nonobsacol = "Dormant1988",
                        stageassign = lathframe, stagesize = "sizea", censorcol = "Missing1988",
                        censorkeep = NA, censor = TRUE)
lathsupp2 <- supplemental(stage3 = c("Sd", "Sdl", "Sd", "Sdl"),
```
stage2 = c("Sd", "Sd", "rep", "rep"),
givenrate = c(0.345, 0.054, NA, NA),
multiplier = c(NA, NA, 0.345, 0.054),
type = c(1, 1, 3, 3), stageframe = lathframe, historical = FALSE)

ehrlen2 <- rlefko2(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2"), supplement = lathsupp2, yearcol = "year2",
indivcol = "individ")

summary(ehrlen2)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
rlefko3

Create Raw Historical Matrix Projection Model

Description

Function rlefko3() returns raw historical MPMs, including the associated component transition and fecundity matrices, data frames describing the ahistorical stages used and the historical paired stages, and a data frame describing the population, patch, and occasion time associated with each matrix.

Usage

rlefko3(
  data,
  stageframe,
  year = "all",
  pop = NA,
  patch = NA,
  censor = FALSE,
  stages = NA,
  alive = c("alive3", "alive2", "alive1"),
  size = c("sizea3", "sizea2", "sizea1"),
  sizeb = c(NA, NA, NA),
  sizec = c(NA, NA, NA),
  repst = c("repstatus3", "repstatus2", "repstatus1"),
  matst = c("matstatus3", "matstatus2", "matstatus1"),
  fec = c("feca3", "feca2", "feca1"),
  supplement = NULL,
  repmatrix = NULL,
  overwrite = NULL,
  yearcol = NA,
  popcol = NA,
  patchcol = NA,
  indivcol = NA,
  censorcol = NA,
  censorkeep = 0,
  format = "ehrlen",
  reduce = FALSE,
  err_check = FALSE
)
Arguments

data  A vertical demographic data frame, with variables corresponding to the naming conventions in `verticalize3()`.

stageframe  A stageframe object that includes information on the size, observation status, propagule status, immaturity status, and maturity status of each ahistorical stage. Should also incorporate bin widths if size is continuous.

year  A variable corresponding to observation occasion, or a set of such values, given in values associated with the `year` term used in vital rate model development. Can also equal all, in which case matrices will be estimated for all occasions. Defaults to all.

pop  A variable designating which populations will have matrices estimated. Should be set to specific population names, or to all if all populations should have matrices estimated.

patch  A variable designating which patches or subpopulations will have matrices estimated. Should be set to specific patch names, or to all if matrices should be estimated for all patches. Defaults to all.

censor  If TRUE, then data will be removed according to the variable set in `censorcol`, such that only data with censor values equal to 1 will remain. Defaults to FALSE.

stages  An optional vector denoting the names of the variables within the main vertical dataset coding for the stages of each individual in occasions \(t+1, t, \) and \(t-1\). The names of stages in these variables should match those used in the `stageframe` exactly. If left blank, then `rlefko3()` will attempt to infer stages by matching values of alive, size, repst, and matst to characteristics noted in the associated stageframe.

alive  A vector of names of binomial variables corresponding to status as alive (1) or dead (0) in occasions \(t+1, t, \) and \(t-1\), respectively.

size  A vector of names of variables coding the primary size variable in occasions \(t+1, t, \) and \(t-1\), respectively. Defaults to c("sizea3", "sizea2", "sizea1").

sizeb  A vector of names of variables coding the secondary size variable in occasions \(t+1, t, \) and \(t-1\), respectively. Defaults to c(NA, NA, NA).

sizec  A vector of names of variables coding the tertiary size variable in occasions \(t+1, t, \) and \(t-1\), respectively. Defaults to c(NA, NA, NA).

repst  A vector of names of variables coding reproductive status in occasions \(t+1, t, \) and \(t-1\), respectively. Defaults to c("repstatus3", "repstatus2", "repstatus1"). Must be supplied if stages is not provided.

matst  A vector of names of variables coding maturity status in occasions \(t+1, t, \) and \(t-1\), respectively. Defaults to c("matstatus3", "matstatus2", "matstatus1"). Must be supplied if stages is not provided.

fec  A vector of names of variables coding fecundity in occasions \(t+1, t, \) and \(t-1\), respectively. Defaults to c("feca3", "feca2", "feca1").

supplement  An optional data frame of class `lefkoSD` that provides supplemental data that should be incorporated into the MPM. Three kinds of data may be integrated this way: transitions to be estimated via the use of proxy transitions, transition overwrites from the literature or supplemental studies, and transition multipliers.
for fecundity. This data frame should be produced using the `supplemental()` function. Should be used in place of or in addition to an overwrite table (see `overwrite` below) and a reproduction matrix (see `repmatrix` below).

**repmatrix**  
An optional reproduction matrix. This matrix is composed mostly of 0s, with non-zero entries acting as element identifiers and multipliers for fecundity (with 1 equaling full fecundity). If left blank, and no supplement is provided, then `rlefko3()` will assume that all stages marked as reproductive produce offspring at 1x that of estimated fecundity, and that offspring production will yield the first stage noted as propagate or immature. To prevent this behavior, input just 0, which will result in fecundity being estimated only for transitions noted in supplement above. May be the dimensions of either a historical or an ahistorical matrix. If the latter, then all stages will be used in occasion t-1 for each suggested ahistorical transition.

**overwrite**  
An optional data frame developed with the `overwrite()` function describing transitions to be overwritten either with given values or with other estimated transitions. Note that this function supplements overwrite data provided in supplement.

**yearcol**  
The variable name or column number corresponding to occasion t in the dataset.

**popcol**  
The variable name or column number corresponding to the identity of the population.

**patchcol**  
The variable name or column number corresponding to patch in the dataset.

**indivcol**  
The variable name or column number coding individual identity.

**censorcol**  
The variable name or column number denoting the censor status. Only needed if `censor = TRUE`.

**censorkeep**  
The value of the censor variable denoting data elements to keep. Defaults to 0.

**format**  
A string indicating whether to estimate matrices in ehrlen format or deVries format. The latter adds one unborn prior stage to account for the prior state of newborns. Defaults to ehrlen format.

**reduce**  
A logical value denoting whether to remove historical stages associated exclusively with zero transitions. These are removed only if the respective row and column sums in ALL matrices estimated equal 0. Defaults to FALSE.

**err_check**  
A logical value indicating whether to append extra information used in matrix calculation within the output list. Used for development debugging purposes. Defaults to FALSE.

**Value**

If all inputs are properly formatted, then this function will return an object of class `lefkoMat`, which is a list that holds the matrix projection model and all of its metadata. Its structure is a list with the following elements:

**A**  
A list of full projection matrices in order of sorted populations, patches, and occasions. All matrices output in the `matrix` class.

**U**  
A list of survival transition matrices sorted as in A. All matrices output in the `matrix` class.
A list of fecundity matrices sorted as in A. All matrices output in the matrix class.

A data frame matrix showing the pairing of ahistorical stages used to create historical stage pairs.

A data frame showing age-stage pairs. In this function, it is set to NA. Only used in output to function aflefko2().

A data frame detailing the characteristics of associated ahistorical stages, in the form of a modified stageframe that includes status as an entry stage through reproduction.

A data frame giving the population, patch, and year of each matrix in order.

A short vector describing the number of non-zero elements in U and F matrices, and the number of annual matrices.

A vector showing the numbers of individuals and rows in the vertical dataset used as input.

The default behavior of this function is to estimate fecundity with regards to transitions specified via associated fecundity multipliers in either supplement or repmatrix. If both of these fields are left empty, then fecundity will be estimated at full for all transitions leading from reproductive stages to immature and propagule stages. However, if a supplement is provided and a repmatrix is not, or if repmatrix is set to 0, then only fecundity transitions noted in the supplement will be set to non-zero values. To use the default behavior of setting all reproductive stages to reproduce at full fecundity into immature and propagule stages but incorporate given or proxy survival transitions, input those given and proxy transitions through the overwrite option.

The reproduction matrix (field repmatrix) may be supplied as either historical or ahistorical. If provided as ahistorical, then flefko3() will assume that all historical transitions involving stages noted for occasions $t$ and $t+1$ should be set to the respective fecundity multipliers noted.

Users may at times wish to estimate MPMs using a dataset incorporating multiple patches or sub-populations. Should the aim of analysis be a general MPM that does not distinguish these patches or subpopulations, the patchcol variable should be left to NA, which is the default. Otherwise the variable identifying patch needs to be named.

Input options including multiple variable names must be entered in the order of variables in occasion $t+1$, $t$, and $t-1$. Rearranging the order WILL lead to erroneous calculations, and may lead to fatal errors.

Although this function is capable of assigning stages given an input stageframe, it lacks the power of verticalize3() and historicalize3() in this regard. Users are strongly encouraged to use the latter two functions for stage assignment.

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 110, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988", nonobsacol = "Dormant1988",
stageassign = lathframe, stagesize = "sizea", censorcol = "Missing1988",
censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1),
type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")

summary(ehrlen3)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
"XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
sensitivity3

Estimate Sensitivity of Population Growth Rate to Matrix Elements

Description

sensitivity3() is a generic function that returns the sensitivity of the population growth rate to the elements of the matrices in a matrix population model. Currently, this function estimates both deterministic and stochastic sensitivities, where the growth rate is $\lambda$ in the former case and the log of the stochastic $\lambda$ in the latter case. This function is made to handle very large and sparse matrices supplied as lefkoMat objects, as lists of matrices, and as individual matrices.
sensitivity3

Usage

sensitivity3(mats, ...)

Arguments

mats A lefkoMat object, or population projection matrix, for which the stable stage distribution is desired.

... Other parameters

Value

The value returned depends on the class of the mats argument.

See Also

sensitivity3.lefkoMat()

sensitivity3.matrix()

sensitivity3.list()

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repsvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0)
matsvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 1, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repsvector, obsstatus = obsvector, matstatus = matsvector,
immmstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
feaconal = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sdl", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)
ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")
ehrlen3mean <- lmean(ehrlen3)
sensitivity3(ehrlen3mean)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)
sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypframe_raw <- sf_create(sizes = sizevector, stagevector = stagevector,
repstatus = repsvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf.04", sizebcol = "Inf2.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE, NRasRep = TRUE)
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", NA, NA, NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1),
stageframe = cypframe_raw, historical = FALSE)
cymatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
sensitivity3.lefkoMat

Estimate Sensitivity of Population Growth Rate of a lefkoMat Object

Description

sensitivity3.lefkoMat() returns the sensitivities of population growth rate to elements of all $A$ matrices in an object of class lefkoMat. If deterministic, then $\lambda$ is taken as the population growth rate. If stochastic, then the log of stochastic $\lambda$, or the log stochastic growth rate, is taken as the population growth rate. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as smaller ahistorical matrices.

Usage

## S3 method for class 'lefkoMat'
sensitivity3(
mats,
  stochastic = FALSE,
  steps = 10000,
  time_weights = NA,
  sparse = "auto",
  append_mats = FALSE,
  ...
)

Arguments

mats An object of class lefkoMat.
stochastic A logical value determining whether to conduct a deterministic (FALSE) or stochastic (TRUE) sensitivity analysis. Defaults to FALSE.
steps The number of occasions to project forward in stochastic simulation. Defaults to 10,000.
time_weights Numeric vector denoting the probabilistic weightings of annual matrices. Defaults to equal weighting among occasions.
sparse A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
append_mats A logical value indicating whether to include the original A, U, and F matrices in the output lefkoSens object.
... Other parameters.
Value

This function returns an object of class `lefkoSens`, which is a list of 8 elements. The first, `h_sensmats`, is a list of historical sensitivity matrices (NULL if an ahMPM is used as input). The second, `ah_elasmats`, is a list of either ahistorical sensitivity matrices if an ahMPM is used as input, or, if an hMPM is used as input, then the result is a list of ahistorical matrices based on the equivalent historical dependencies assumed in the input historical matrices. The third element, `h_stages`, is a data frame showing historical stage pairs (NULL if ahMPM used as input). The fourth element, `agestages`, show the order of age-stage combinations, if age-by-stage MPMs have been supplied. The fifth element, `ah_stages`, is a data frame showing the order of ahistorical stages. The last 3 elements are the A, U, and F portions of the input.

Notes

Deterministic sensitivities are estimated as eqn. 9.14 in Caswell (2001, Matrix Population Models). Stochastic sensitivities are estimated as eqn. 14.97 in Caswell (2001). Note that stochastic sensitivities are of the log of the stochastic $\lambda$.

See Also

`sensitivity3()`
`sensitivity3.matrix()`
`sensitivity3.list()`

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                       repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                       immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                       propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                         patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                         juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                         fecacol = "Intactseed88", deadacol = "Dead1988",
                         nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                         censorcol = "Missing1988", censorkeep = NA, censor = TRUE)
lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
    stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
    stage1 = c("Sd", "rep", "Sd", "rep", "npr", "Sd"),
    eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
    eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
    eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
    givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
    multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
    type = c(1, 1, 1, 1, 3, 3, 1),
    type_t12 = c(1, 2, 1, 2, 1, 1, 1),
    stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
    stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
    yearcol = "year2", indivcol = "individ")
sensitivity3(ehrlen3, stochastic = TRUE)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
    patchidcol = "patch", individcol = "plantid", blocksize = 4,
    sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
    repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
    stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
    NRasRep = TRUE)
cypprep3r <- supplemental(stage3 = c("Sd", "P1", "P2", "P3", "SL", "D",
        "XSm", "Sm", "SD", "P1"),
        "rep"),
    eststage3 = c(NA, NA, NA, NA, NA, NA, NA, NA),
    eststage2 = c(NA, NA, NA, NA, NA, NA, NA, NA),
    givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA),
    multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA),
    type = c(1, 1, 1, 1, 3, 3, 1, 1),
    stageframe = lathframe, historical = TRUE)
```r
sensitivity3.list

Estimate Sensitivity of Population Growth Rate of a List of Matrices

Description

sensitivity3.list() returns the sensitivities of population growth rate to elements of matrices supplied in a list. The sensitivity analysis can be deterministic or stochastic, but if the latter then at least two A matrices must be included in the list. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as smaller ahistorical matrices.

Usage

## S3 method for class 'list'
sensitivity3(
mats,
stochastic = FALSE,
steps = 10000,
time_weights = NA,
historical = FALSE,
sparse = "auto",
append_mats = FALSE,
...
)

Arguments

mats               An object of class matrix.
stochastic         A logical value determining whether to conduct a deterministic (FALSE) or stochastic (TRUE) sensitivity analysis. Defaults to FALSE.
steps              The number of occasions to project forward in stochastic simulation. Defaults to 10,000.
time_weights       Numeric vector denoting the probabilistic weightings of annual matrices. Defaults to equal weighting among occasions.
historical         A logical value indicating whether matrices are historical. Defaults to FALSE.
sparse              A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
```
append_mats  A logical value indicating whether to include the original matrices input as object mats in the output \texttt{lefkoSense} object. Defaults to FALSE.

... Other parameters.

Value

This function returns an object of class \texttt{lefkoSens}, which is a list of 8 elements. The first, \texttt{h_sensmats}, is a list of historical sensitivity matrices (NULL if an ahMPM is used as input). The second, \texttt{ah_elasmats}, is a list of ahistorical sensitivity matrices if an ahMPM is used as input (NULL if an hMPM is used as input). The third element, \texttt{h_stages}, the fourth element, \texttt{agestages}, and the fifth element, \texttt{ah_stages}, are NULL. The last 3 elements include the original A matrices supplied (as the \texttt{A} element), followed by NULLs for the U and F elements.

Notes

Deterministic sensitivities are estimated as eqn. 9.14 in Caswell (2001, Matrix Population Models). Stochastic sensitivities are estimated as eqn. 14.97 in Caswell (2001). Note that stochastic sensitivities are with regard to the log of the stochastic $\lambda$.

Currently, this function does not estimate equivalent ahistorical stochastic sensitivities for input historical matrices, due to the lack of guidance input on the order of stages (such guidance is provided within \texttt{lefkoMat} objects).

See Also

\texttt{sensitivity3(} \texttt{)}

\texttt{sensitivity3.lefkoMat(} \texttt{)}

\texttt{sensitivity3.matrix(} \texttt{)}

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repsvector <- c(0, 0, 0, 0, 1, 0, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
feccol = "Intactseed88", deadacol = "Dead1988",
onobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA), eststage2 = c(NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")
sensitivity3(ehrlen3$A)

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)
sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvecto <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypraw_v1, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "SD", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage1 = c("SD", "SD", "SD", "P3", "SL", "SL", "SL", "rep",
"rep"),
...
eststage3 = c(NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)
cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", individcol = "individ")
sensitivity3(cypmatrix2r$A)

sensitivity3.matrix  Estimate Sensitivity of Population Growth Rate of a Single Matrix

Description

sensitivity3.matrix() returns the sensitivities of \( \lambda \) to elements of a single matrix. Because this handles only one matrix, the sensitivities are inherently deterministic and based on the dominant eigen value as the best metric of the population growth rate. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as smaller ahistorical matrices.

Usage

```r
## S3 method for class 'matrix'
sensitivity3(mats, sparse = "auto", ...)
```

Arguments

- `mats`  
  An object of class matrix.
- `sparse`  
  A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
- `...`  
  Other parameters.

Value

This function returns a single deterministic sensitivity matrix.

See Also

- `sensitivity3()`
- `sensitivity3.lefkoMat()`
- `sensitivity3.list()`
Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
type = c(1, 1, 1, 1, 3, 3, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
sensitivity3(ehrlen3mean$A[[1]])

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg",
"XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
Function sf_create() returns a data frame describing each ahistorical life history stage in the life history model. This data frame can be used as input into MPM creation functions including flefko3(), flefko2(), aflefko2(), rlefko3(), and rlefko2(), in which it determines how each stage is treated during matrix estimation.
Usage

```
sf_create(
  sizes,
  stagenames = NULL,
  sizesb = NULL,
  sizesc = NULL,
  repstatus = NULL,
  obsstatus = NULL,
  propstatus = NULL,
  matstatus = NULL,
  immstatus = NULL,
  minage = NULL,
  maxage = NULL,
  indataset = NULL,
  binhalfwidth = NULL,
  binhalfwidthb = NULL,
  binhalfwidthc = NULL,
  group = NULL,
  comments = NULL,
  roundsize = 5L,
  roundsizeb = 5L,
  roundsizec = 5L,
  ipmbins = 100L,
  ipmbinsb = NA_integer_,
  ipmbinsc = NA_integer_
)
```

Arguments

- **sizes**: A numeric vector of the typical or representative size of each life history stage. If making function-based MPMs, then this should be a vector composed of the midpoints of each size bin. If denoting the boundary of an automated size classification group, then should denote the absolute minimum size of that group, or the absolute size of that group (see Notes).

- **stagenames**: A vector of stage names, in the same order as elements in sizes. Can also be set to `ipm` for automated size classification (see Notes section).

- **sizesb**: An optional numeric vector for a second size metric for each life history stage. Only to be used if stages are defined by at least two size metrics in all cases. Same issues apply as in `sizes`.

- **sizesc**: An optional numeric vector for a third size metric for each life history stage. Only to be used if stages are defined by at least three size metrics in all cases. Same issues apply as in `sizes`.

- **repstatus**: A vector denoting the binomial reproductive status of each life history stage. Defaults to 1.

- **obsstatus**: A vector denoting the binomial observation status of each life history stage. Defaults to 1, but may be changed for unobservable stages.
propstatus  A vector denoting whether each life history stage is a propagule. Such stages are generally only used in fecundity estimation. Defaults to 0.

matstatus  A vector denoting whether each stage is mature. Must be composed of binomial values if given. Defaults to 1 for all stages defined in sizes.

immstatus  A vector denoting whether each stage is immature. Must be composed of binomial values if given. Defaults to the complement of vector matstatus.

minage  An optional vector denoting the minimum age at which a stage can occur. Only used in age x stage matrix development. Defaults to NA.

maxage  An optional vector denoting the maximum age at which a stage should occur. Only used in age x stage matrix development. Defaults to NA.

indataset  A vector designating which stages are found within the dataset. While rlefko2() and rlefko3() can use all stages in the input dataset, flefko3() and flefko2() can only handle size-classified stages with non-overlapping combinations of size and status variables. Stages that do not actually exist within the dataset should be marked as 0 in this vector.

binhalfwidth  A numeric vector giving the half-width of size bins. Required to classify individuals appropriately within size classes. Defaults to 0.5 for all sizes.

binhalfwidthb  A numeric vector giving the half-width of size bins used for the optional second size metric. Required to classify individuals appropriately with two or three size classes. Defaults to 0.5 for all sizes.

binhalfwidthc  A numeric vector giving the half-width of size bins used for the optional third size metric. Required to classify individuals appropriately with three size classes. Defaults to 0.5 for all sizes.

group  An integer vector providing information on each respective stage’s size classification group. If used, then function-based MPM creation functions flefko2(), flefko3(), and aflefko2() will estimate transitions only within these groups and for allowed cross-group transitions noted within the supplement table. Defaults to 0.

comments  An optional vector of text entries holding useful text descriptions of all stages.

roundsize  This parameter sets the precision of size classification, and equals the number of digits used in rounding sizes. Defaults to 5.

roundsizeb  This parameter sets the precision of size classification in the optional second size metric, and equals the number of digits used in rounding sizes. Defaults to 5.

roundsizec  This parameter sets the precision of size classification in the optional third size metric, and equals the number of digits used in rounding sizes. Defaults to 5.

ipmbins  An integer giving the number of size bins to create using the primary size classification variable. This number is in addition to any stages that are not size classified. Defaults to 100, and numbers greater than this yield a warning about the loss of statistical power and increasing chance of matrix over-parameterization resulting from increasing numbers of stages.

ipmbinsb  An optional integer giving the number of size bins to create using the secondary size classification variable. This number is in addition to any stages that are not size classified, as well as in addition to any automated size classification using
the primary and tertiary size variables. Defaults to NA, and must be set to a positive integer for automated size classification to progress.

**ipmbinsc**

An optional integer giving the number of size bins to create using the tertiary size classification variable. This number is in addition to any stages that are not size classified, as well as in addition to any automated size classification using the primary and secondary size variables. Defaults to NA, and must be set to a positive integer for automated size classification to progress.

**Value**

A data frame of class `stageframe`, which includes information on the stage name, size, reproductive status, observation status, propagule status, immaturity status, maturity status, presence within the core dataset, stage group classification, raw bin half-width, and the minimum, center, and maximum of each size bin, as well as its width. If minimum and maximum ages were specified, then these are also included. Also includes an empty string variable that can be used to describe stages meaningfully. This object can be used as the stageframe input for `flefko3()`, `flefko2()`, `rlefko3()`, and `rlefko2()`.

Variables in this data frame include the following:

- **stage** The unique names of the stages to be analyzed.
- **size** The typical or representative size at which each stage occurs.
- **size_b** Size at which each stage occurs in terms of a second size variable, if one exists.
- **size_c** Size at which each stage occurs in terms of a third size variable, if one exists.
- **min_age** The minimum age at which the stage may occur.
- **max_age** The maximum age at which the stage may occur.
- **repstatus** A binomial variable showing whether each stage is reproductive.
- **obsstatus** A binomial variable showing whether each stage is observable.
- **propstatus** A binomial variable showing whether each stage is a propagule.
- **immstatus** A binomial variable showing whether each stage can occur as immature.
- **matstatus** A binomial variable showing whether each stage occurs in maturity.
- **indataset** A binomial variable describing whether each stage occurs in the input dataset.
- **binhalfwidth_raw** The half-width of the size bin, as input.
- **sizebin_min** The minimum size at which the stage may occur.
- **sizebin_max** The maximum size at which the stage may occur.
- **sizebin_center** The midpoint of the size bin at which the stage may occur.
- **sizebin_width** The width of the size bin corresponding to the stage.
- **binhalfwidthb_raw** The half-width of the size bin of a second size variable, as input.
- **sizebinb_min** The minimum size at which the stage may occur.
- **sizebinb_max** The maximum size at which the stage may occur.
The midpoint of the size bin at which the stage may occur, in terms of a second size variable.

The width of the size bin corresponding to the stage, in terms of a second size variable.

The half-width of the size bin of a third size variable, as input.

The minimum size at which the stage may occur, in terms of a third size variable.

The maximum size at which the stage may occur, in terms of a third size variable.

The midpoint of the size bin at which the stage may occur, in terms of a third size variable.

The width of the size bin corresponding to the stage, in terms of a third size variable.

An integer denoting the size classification group that the stage falls within.

A text field for stage descriptions.

Notes

If an IPM or function-based matrix with automated size classification is desired, then two stages that occur within the dataset and represent the lower and upper size limits of the IPM must be marked with \textit{ipm} in the stagenames vector. These stages should have all characteristics other than size equal, and the size input for whichever size will be classified automatically must include the minimum in one stage and the maximum in the other. The actual characteristics of the first stage encountered in the inputs will be used as the template for the creation of these sizes. Note that \textit{ipm} refers to size classification with the primary size variable. To automate size classification with the secondary size variable, use \textit{ipmb}, and to automate size classification with the tertiary size variable, use \textit{ipmc}. To nest automated size classifications, use \textit{ipmab} for the primary and secondary size variables, \textit{ipmac} for the primary and tertiary size variables, \textit{ipmbc} for the secondary and tertiary size variables, and \textit{ipmabc} for all three size variables. The primary size variable can also be set with \textit{ipma}.

If two or more groups of stages, each with its own characteristics, are to be developed for an IPM or function-based MPM, then an even number of stages with two stages marking the minimum and maximum size of each group should be marked with the same code as given above, with all other characteristics equal within each group.

Stage classification groups set with the \textit{group} variable create zones within function-based matrices in which survival transitions are estimated. These groups should not be set if transitions are possible between all stages regardless of group. To denote specific transitions as estimable between stage groups, use the \textit{supplemental()} function.

Examples

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagenamevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repcvector <- c(0, 0, 0, 0, 0, 1, 0)
```
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
    repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
    immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
    propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
    patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
    juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
    fecacol = "Intactseed88", deadacol = "Dead1988",
    nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
    censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
    stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
    stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
    eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
    eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
    eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
    givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
    multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
    type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
    stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
    stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
    yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
ehrlen3mean$A[[1]]

data(cypdata)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
    repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
sf_distrib

Test Overdispersion and Zero Inflation in Size and Fecundity Distributions

Description

Function sf_distrib takes a historically formatted vertical data as input and tests whether size and fecundity data are dispersed according to a Poisson distribution (where mean = variance), and whether the number of 0s exceeds expectations.

Usage

sf_distrib(
  data,
  sizea = NA,
  sizeb = NA,
  sizec = NA,
  obs3 = NA,
  fec = NA,
)
Arguments

data A historical vertical data file, which is a data frame of class hfvdata.

sizea A vector holding the name or column number of the variables corresponding to primary size in occasions *t+1* and *t*. Input only if sizea is to be tested.

sizeb A vector holding the name or column number of the variables corresponding to secondary size in occasions *t+1* and *t*. Input only if sizeb is to be tested.

sizec A vector holding the name or column number of the variables corresponding to tertiary size in occasions *t+1* and *t*. Input only if sizec is to be tested.

obs3 The name or column number of the variable corresponding to observation status in occasion *t+1*. This should be used if observation status will be used as a vital rate to absorb states of size = 0.

fec The name or column number of the variable corresponding to fecundity. The name of the variable should correspond to the proper occasion, either occasion *t* or occasion *t*-1. Input only if fec is to be tested.

repst The name or column number of the variable corresponding to reproductive status in occasion *t*. If not provided, then fecundity will be tested without subsetting to only reproductive individuals.

zisizea A logical value indicating whether to conduct a test of zero inflation in primary size. Defaults to TRUE.

zisizeb A logical value indicating whether to conduct a test of zero inflation in secondary size. Defaults to TRUE.

zisizec A logical value indicating whether to conduct a test of zero inflation in tertiary size. Defaults to TRUE.

zifec A logical value indicating whether to conduct a test of zero inflation in fecundity. Defaults to TRUE.

fectime An integer indicating whether to treat fecundity as occurring in time *t* (2) or time *t+1* (3). Defaults to 2.

Value

Produces text describing the degree and significance of difference from expected dispersion, and the degree and significance of zero inflation. The tests are chi-squared score tests based on the expectations of mean = variance, and 0s as abundant as predicted by the value of lambda estimated from the dataset. See van der Broek (1995) for more details.
Notes

This function subsets the data in the same way as `modelsearch()` before testing underlying distributions, making the output much more appropriate than a simple analysis of size and fecundity variables in data.

The specific test used for overdispersion is a chi-squared test of the dispersion parameter estimated using a generalized linear model predicting the response given size in occasion *t*, under a quasi-Poisson distribution.

The specific test used for zero-inflation is the chi-squared test presented in van der Broek (1995).

Examples

# Lathyrux example
data(lathyrus)

sizevector <- c(0, 4.6, 1, 2, 3, 4, 5, 6, 7, 8, 9, 1, 2, 3, 4, 5, 6, 7, 8, 9)
stagevector <- c("Sd", "Sdl", "Dorm", "Sz1nr", "Sz2nr", "Sz3nr", "Sz4nr", 
              "Sz5nr", "Sz6nr", "Sz7nr", "Sz8nr", "Sz9nr", "Sz1r", "Sz2r", "Sz3r", 
              "Sz4r", "Sz5r", "Sz6r", "Sz7r", "Sz8r", "Sz9r")
repsvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 4.6, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)
lathframeln <- sf_create(sizes = sizevector, stagenames = stagevector,
                   repstatus = repsvector, obsstatus = obsvector, matstatus = matvector,
                   immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                   propstatus = propvector)
lathvertln <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
              patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
               juvcol = "Seedling1988", sizeacol = "lnVol88", repstracol = "Intactseed88",
               fecacol = "Intactseed88", deadacol = "Dead1988",
               nonobssacol = "Dormant1988", stageassign = lathframeln, stagesize = "sizea",
               censorcol = "Missing1988", censorkeep = NA, NAas0 = TRUE, censor = TRUE)
lathvertln$feca2 <- round(lathvertln$feca2)
lathvertln$feca1 <- round(lathvertln$feca1)
lathvertln$feca3 <- round(lathvertln$feca3)

# The following will only test fecundity, since size is Gaussian.
# Zero-inflation will not be assessed in this example, since 0 values in
# fecundity have been excluded in the life history model.
sf_distrib(lathvertln, sizea = c("sizea3", "sizea2"), fec = c("feca3", "feca2"),
       repst = c("repstatus3", "repstatus2"), zifec = FALSE)
# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repsvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repsvector, obsstatus = obsvector, matstatus = matvector, propstatus = propvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004, patchidcol = "patch", individcol = "plantid", blocksize = 4, sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04", repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04", stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE, NRasRep = TRUE)
sf_distrib(cypraw_v1, sizea = c("size3added", "size2added"), fec = c("feca3", "feca2"), repst = c("repstatus3", "repstatus2"), zisizea = TRUE)

---

**slambda3**

**Estimate Stochastic Population Growth Rate**

**Description**

Function slambda3() estimates the stochastic population growth rate, \( \lambda \), defined as the long-term arithmetic mean of the log population growth rate estimated per simulated occasion (as given in equation 2 in Tuljapurkar, Horvitz, and Pascarella 2003). This term is estimated via projection of randomly sampled matrices, similarly to the procedure outlined in Box 7.4 of Morris and Doak (2002). Can handle both lefkoMat objects and lists of full A matrices.

**Usage**

slambda3(mpm, times = 10000L, dense_only = FALSE, tweights = NULL)
Arguments

- **npm**: A matrix projection model of class `lefkoMat`, or a list of full matrix projection matrices.
- **times**: Number of occasions to iterate. Defaults to 10,000.
- **dense_only**: A logical value indicating whether to force matrices to be run in dense format. Defaults to `FALSE`, and should only be used if errors occur when running under default conditions.
- **tweights**: Numeric vector denoting the probabilistic weightings of annual matrices. Defaults to equal weighting among occasions.

Value

A data frame with the following variables:

- **pop**: The identity of the population.
- **patch**: The identity of the patch.
- **a**: Estimate of stochastic growth rate, estimated as the arithmetic mean of the log population growth rate across simulated occasions.
- **var**: The estimated variance of a.
- **sd**: The standard deviation of a.
- **se**: The standard error of a.

Notes

Stochastic growth rate is estimated both at the patch level and at the population level. Population level estimates will be noted at the end of the data frame with 0 entries for patch designation.

Weightings given in `tweights` do not need to sum to 1. Final weightings used will be based on the proportion per element of the sum of elements in the user-supplied vector.

Examples

```r
# Lathyrus example
data(lathyrus)
sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagenamevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 0, 1)
obsvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 1, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagenamevector,
  repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
  immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
```
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl"),
stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep"),
stage1 = c("Sd", "rep", "Sd", "rep", "all", "all"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
type = c(1, 1, 1, 1, 3, 3), type_t12 = c(1, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe,
year = c(1989, 1990), stages = c("stage3", "stage2", "stage1"),
supplement = lathsupp3, yearcol = "year2", individcol = "individ")

slambda3(ehrlen3)

# Cypripedium example
data(cypdata)
sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg",
"XLg")
reppvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypraw_v1, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)
cypsupp3r <- supplemental(stage3 = c("SD", "SD", "P1", "P1", "P2", "P3", "SL",
"D", "XSm", "Sm", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "SD", "SD", "P1", "P2", "P3"),
stage1 = c("SD", "P1", "P2", "P3", "SL"),
stagframe = cypraw_v1, NAas0 = TRUE)
cypmain_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypmain_v1, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)
stablestage3

Estimate Stable Stage Distribution

Description

stablestage3() is a generic function that returns the stable stage distribution for a population projection matrix or set of matrices. This function is made to handle very large and sparse matrices supplied as lefkoMat objects or as individual matrices, and can be used with large historical matrices, IPMs, age x stage matrices, as well as ahistorical matrices.

Usage

stablestage3(mats, ...)

Arguments

mats A lefkoMat object, or population projection matrix, for which the stable stage distribution is desired.

... Other parameters.

Value

The value returned depends on the class of the mats argument. See related functions for details.
See Also

`stablestage3.lefkoMat()`
`stablestage3.matrix()`

Examples

```r
# Lathyrus deterministic example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sd", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = reppvector, obsstatus = obsvector, matstatus = matvector,
                        immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                          patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                          juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                          fecacol = "Intactseed88", deadacol = "Dead1988",
                          nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                          censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sd", "Sd", "mat"),
                            stage2 = c("SD", "SD", "SD", "SD"),
                            stage1 = c("SD", "SD", "SD", "SD"),
                            eststage3 = c(NA, NA, NA, NA, NA, NA),
                            eststage2 = c(NA, NA, NA, NA, NA, NA),
                            eststage1 = c(NA, NA, NA, NA, NA, NA),
                            givenrate = c(0.345, 0.345, 0.054, 0.054),
                            multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
                            type = c(1, 1, 1, 1, 1),
                            stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
                   stages = c("stages", "stages", "stages"),
                   supplement = lathsupp3, yearcol = "year2", indivicol = "individ")

ehrlen3mean <- lmean(ehrlen3)
stablestage3(ehrlen3mean)

# Cypripedium stochastic example
rm(list=ls(all=TRUE))
data(cypdata)
```
stablestage3.lefkoMat <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, propstatus = propvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004, patchidcol = "patch", individcol = "plantid", blocksize = 4, sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04", repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04", stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE, NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Lg", "XLg"), stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"), eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA), eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", NA, NA), givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA), multiplier = c(NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5), type = c(1, 1, 1, 1, 1, 1, 1, 3, 3), stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw, year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"), size = c("size3added", "size2added"), supplement = cypsupp2r, yearcol = "year2", patchcol = "patchid", individcol = "individ")

stablestage3(cypmatrix2r, stochastic = TRUE)

stablestage3.lefkoMat  Estimate Stable Stage Distribution of Matrices in lefkoMat Object

Description

stablestage3.lefkoMat() returns the deterministic stable stage distributions of all A matrices in an object of class lefkoMat, as well as the long-run projected mean stage distribution in stochastic
analysis. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as ahistorical matrices.

Usage

```r
## S3 method for class 'lefkoMat'
stablestage3(
  mats,
  stochastic = FALSE,
  times = 10000,
  tweights = NA,
  seed = NA,
  sparse = "auto",
  ...
)
```

Arguments

- `mats`: An object of class `lefkoMat`.
- `stochastic`: A logical value indicating whether to use deterministic (FALSE) or stochastic (TRUE) analysis. Defaults to FALSE.
- `times`: An integer variable indicating number of occasions to project if using stochastic analysis. Defaults to 10000.
- `tweights`: An optional vector indicating the probability weighting to use for each matrix in stochastic simulations. If not given, then defaults to equal weighting.
- `seed`: A number to use as a random number seed.
- `sparse`: A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
- `...`: Other parameters.

Value

This function returns the stable stage distributions (and long-run mean stage distributions in stochastic analysis) corresponding to the matrices in a lefkoMat object.

The output depends on whether the lefkoMat object used as input is ahistorical or historical, and whether the analysis is deterministic or stochastic. If deterministic and ahistorical, then a single data frame is output, which includes the number of the matrix within the A element of the input lefkoMat object, followed by the stage id (numeric and assigned through `sf_create()`), the stage name, and the estimated proportion of the stable stage distribution (ss_prop). If stochastic and ahistorical, then a single data frame is output starting with the number of the population-patch (matrix_set), a string concatenating the names of the population and the patch (poppatch), the assigned stage id number (stage_id), and the stage name (stage), and the long-run average stage distribution (ss_prop).

If a historical matrix is used as input, then two data frames are output into a list object. The hist element describes the historical stage-pair distribution, while the ahist element describes the stage distribution. If deterministic, then hist contains a data frame including the matrix number (matrix), the numeric stage designations for stages in occasions t and t-1, (stage_id_2 and
stage_id_1, respectively), followed by the respective stage names (stage_2 and stage_1), and ending with the estimated stable stage-pair distribution. The associated ahist element is as before. If stochastic, then the hist element contains a single data frame with the number of the population-patch (matrix_set), a string concatenating the names of the population and the patch (poppatch), the assigned stage id numbers in times t and t-1 (stage_id_2 and stage_id_2, respectively), and the associated stage names (stage_2 and stage_1, respectively), and the long-run average stage distribution (ss_prop). The associated ahist element is as before in the ahistorical, stochastic case.

In addition to the data frames noted above, stochastic analysis will result in the additional output of a list of matrices containing the actual projected stage distributions across all projected occasions, in the order of population-patch combinations in the lefkoMat input.

Notes

In stochastic analysis, the projected mean distribution is the arithmetic mean across the final 1000 projected occasions if the simulation is at least 2000 projected occasions long. If between 500 and 2000 projected occasions long, then only the final 200 are used, and if fewer than 500 occasions are used, then all are used. Note that because stage distributions in stochastic simulations can change greatly in the initial portion of the run, we encourage a minimum of 2000 projected occasions per simulation, with 10000 preferred.

See Also

stablestage3()
stablestage3.matrix()

Examples

# Lathyrus deterministic example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagenamevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagenamevector,
                      repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                      immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                      propstatus = propvector)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                         patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                         juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                         fecacol = "Intactseed88", deadacol = "Dead1988",
                         nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                         ...)
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "Sdl"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1),
type_t12 = c(1, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
stablestage3(ehrlen3mean)

# Cypripedium stochastic example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
revector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = revector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstlyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
restracol = "Inf.04", restrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagemap = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cyssupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "SD", "P1"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1),
type_t12 = c(1, 2, 1, 2, 1, 1, 1, 1),
stageframe = cyprawframe, historical = TRUE)
stablestage3.matrix

eststage2 = c(NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, NA, NA),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
  year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
  size = c("size3added", "size2added"), supplement = cypsupp2r,
  yearcol = "year2", patchcol = "patchid", individcol = "individ")

stablestage3(cypmatrix2r, stochastic = TRUE)

stablestage3.matrix

---

Estimate Stable Stage Distribution of a Single Population Projection Matrix

---

Description

`stablestage3.matrix()` returns the stable stage distribution for a population projection matrix. This function can handle large and sparse matrices, and so can be used with large historical matrices, IPMs, age x stage matrices, as well as smaller ahistorical matrices.

Usage

```r
# S3 method for class 'matrix'
stablestage3(mats, sparse = "auto", ...)
```

Arguments

- `mats`: A population projection matrix of class `matrix`.
- `sparse`: A text string indicating whether to use sparse matrix encoding ("yes") or dense matrix encoding ("no"). Defaults to "auto".
- `...`: Other parameters.

Value

This function returns the stable stage distribution corresponding to the input matrix.

See Also

- `stablestage3()`
- `stablestage3.lefkoMat()`
Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 1, 0)
obsvvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 0)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                        immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                        patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                        juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                        fecacol = "Intactseed88", deadacol = "Dead1988",
                        nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                        censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
                        stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
                        stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
                        eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
                        eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
                        eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
                        givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
                        multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
                        type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
                        stageframe = lathframe, historical = TRUE)

ehr3len3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
                    stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
                    yearcol = "year2", individcol = "individ")

ehr3len3mean <- lmean(ehrlen3)
stablestage3(ehrlen3mean$A[[1]])

# Cypripedium stochastic example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
reppvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)


cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info
cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", "rep", NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
stageframe = cypframe_raw, historical = FALSE)

cymatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

stablestage3(cymatrix2r$A[[1]])

start_input

Create a Starting Vector for Population Projection

Description

Function `start_input()` creates a data frame summarizing the non-zero elements of the start vector for use in population projection analysis via function `projection3()`.

Usage

`start_input(mpm, stage2, stage1 = NA, age2 = NA, value = 1)`
Arguments

mpm  The `lefkoMat` object to be used in projection analysis.

stage2  A vector showing the name or number of a stage in occasion $t$ that should be set to a positive number of individuals in the start vector. Abbreviations for groups of stages are also usable (see Notes). This input is required and has no default input.

stage1  A vector showing the name or number of a stage in occasion $t-1$ that should be set to a positive number of individuals in the start vector. Abbreviations for groups of stages are also usable (see Notes). This is only used for historical MPMs, since the rows of hMPMs correspond to stage-pairs in times $t$ and $t-1$ together. Only required for historical MPMs, and will result in errors if otherwise used.

age2  A vector showing the age of each respective stage in occasion $t$ that should be set to a positive number of individuals in the start vector. Only used for age-by-stage MPMs. Defaults to NA.

value  A vector showing the values, in order, of the number of individuals set for the stage or stage-pair in question. Defaults to 1.

Value

A list of class `lefkoStart`, with 4 objects, which can be used as input in function `projection3()`. The last three include the `ahstages`, `hstages`, and `agestages` objects from the `lefkoMat` object supplied in `mpm`. The first element in the list is a data frame with the following variables:

- `stage2`: Stage at occasion $t$.
- `stage_id_2`: The stage number associated with `stage2`.
- `stage1`: Stage at occasion $t-1$, if historical. Otherwise NA.
- `stage_id_1`: The stage number associated with `stage1`.
- `age2`: The age of individuals in `stage2` and, if applicable, `stage1`. Only used in age-by-stage MPMs.
- `row_num`: A number indicating the respective starting vector element.
- `value`: Number of individuals in corresponding stage or stage-pair.

Notes

Entries in `stage2`, and `stage1` can include abbreviations for groups of stages. Use `rep` if all reproductive stages are to be used, `nrep` if all mature but non-reproductive stages are to be used, `mat` if all mature stages are to be used, `immat` if all immature stages are to be used, `prop` if all propagule stages are to be used, `npr` if all non-propagule stages are to be used, and leave empty or use `all` if all stages in stageframe are to be used.

See Also

`density_input()`, `projection3()`
Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)
lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)
ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")
ehrlen3mean <- lmean(ehrlen3)
e3m_sv <- start_input(ehrlen3mean, stage2 = "Sd", stage1 = "Sd", value = 1000)
Description

Function `subset_lM()` creates a new `lefkoMat` object from a subset of matrices in another `lefkoMat` object.

Usage

```
subset_lM(lM, mat_num = NA, pop = NA, patch = NA, year = NA)
```

Arguments

- `lM` The `lefkoMat` object to select matrices from.
- `mat_num` Either a single integer corresponding to the matrix to select within the `labels` element of `lM`, or a vector of such integers.
- `pop` The population designation for matrices to select. Only used if `mat_num` is not given.
- `patch` The patch designation for matrices to select. Only used if `mat_num` is not given.
- `year` The time *t* designation for matrices to select. Only used if `mat_num` is not given.

Value

A `lefkoMat` object composed of the matrices specified in the options.

Notes

If `mat_num` is not provided, then at least one of `pop`, `patch`, or `year` must be provided. If at least two of `pop`, `patch`, and `year` are provided, then function `subset_lM()` will identify matrices as the intersection of provided inputs.

See Also

- `create_lM()`
- `add_lM()`
- `delete_lM()`

Examples

```
sizevector <- c(1, 1, 2, 3) # These sizes are not from the original paper
stagevector <- c("Sdl", "Veg", "SmFlo", "LFlo")
repvector <- c(0, 0, 1, 1)
obsvector <- c(1, 1, 1, 1)
matvector <- c(0, 1, 1, 1)
immvector <- c(1, 0, 0, 0)
propvector <- c(0, 0, 0, 0)
```
indataset <- c(1, 1, 1, 1)
binvec <- c(0.5, 0.5, 0.5, 0.5)

anthframe <- sf_create(sizes = sizevector, stagenames = stagevector,
    reppstatus = repvector, obsstatus = obsvector, matstatus = matvector,
    immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
    propstatus = propvector)

# POPN C 2003-2004
XC3 <- matrix(c(0, 0, 1.74, 1.74,
    0.208333333, 0, 0, 0.057142857,
    0.041666667, 0.076923077, 0, 0,
    0.083333333, 0.076923077, 0.066666667, 0.028571429), 4, 4, byrow = TRUE)

# 2004-2005
XC4 <- matrix(c(0, 0, 0.3, 0.6,
    0.32183908, 0.142857143, 0, 0,
    0.16091954, 0.285714286, 0, 0,
    0.252873563, 0.285714286, 0.5, 0.6), 4, 4, byrow = TRUE)

# 2005-2006
XC5 <- matrix(c(0, 0, 0.50625, 0.675,
    0, 0, 0.035714286,
    0.1, 0.068965517, 0.0625, 0.107142857,
    0.3, 0.137931034, 0, 0.071428571), 4, 4, byrow = TRUE)

# POPN E 2003-2004
XE3 <- matrix(c(0, 0, 2.44, 6.569230769,
    0.196428571, 0, 0, 0,
    0.125, 0.5, 0, 0,
    0.160714286, 0.5, 0.133333333, 0.076923077), 4, 4, byrow = TRUE)

XE4 <- matrix(c(0, 0, 0.45, 0.646153846,
    0.065577377, 0.0090909091, 0.125, 0,
    0.032786885, 0, 0.125, 0.076923077,
    0.049180328, 0, 0.125, 0.230769231), 4, 4, byrow = TRUE)

XE5 <- matrix(c(0, 0, 2.85, 3.99,
    0.083333333, 0, 0, 0,
    0, 0, 0, 0,
    0.416666667, 0.1, 0, 0.1), 4, 4, byrow = TRUE)

# POPN F 2003-2004
XF3 <- matrix(c(0, 0, 1.815, 7.058333333,
    0.075949367, 0, 0.05, 0.083333333,
    0.139240506, 0, 0.25,
    0.075949367, 0, 0.083333333), 4, 4, byrow = TRUE)

XF4 <- matrix(c(0, 0, 1.233333333, 7.4,
    0.223880597, 0, 0.111111111, 0.142857143,
    0.134328358, 0.272727273, 0.166666667, 0.142857143,
    0.119402985, 0.363636364, 0.055555556, 0.142857143), 4, 4, byrow = TRUE)
```r
XF5 <- matrix(c(0, 0, 1.06, 3.372727273,
0.073170732, 0.025, 0.033333333, 0,
0.036585366, 0.15, 0.1, 0.136363636,
0.06097561, 0.225, 0.166666667, 0.272727273), 4, 4, byrow = TRUE)

# POPN G 2003-2004
XG3 <- matrix(c(0, 0, 0.245454545, 2.1,
0, 0, 0.045454545, 0,
0.125, 0, 0.090909091, 0,
0.125, 0, 0.090909091, 0.333333333), 4, 4, byrow = TRUE)

XG4 <- matrix(c(0, 0, 1.1, 1.54,
0.111111111, 0, 0, 0,
0, 0, 0, 0,
0.111111111, 0, 0, 0), 4, 4, byrow = TRUE)

XG5 <- matrix(c(0, 0, 0, 1.5,
0, 0, 0, 0,
0.090909091, 0, 0, 0,
0.545454545, 0.5, 0, 0.5), 4, 4, byrow = TRUE)

# POPN L 2003-2004
XL3 <- matrix(c(0, 0, 1.785365854, 1.856521739,
0.128571429, 0, 0, 0.010869565,
0.028571429, 0, 0, 0,
0.014285714, 0, 0, 0.02173913), 4, 4, byrow = TRUE)

XL4 <- matrix(c(0, 0, 14.25, 16.625,
0.131443299, 0.057142857, 0, 0.25,
0.144329897, 0, 0, 0,
0.092783505, 0.2, 0, 0.25), 4, 4, byrow = TRUE)

XL5 <- matrix(c(0, 0, 0.594642857, 1.765909091,
0, 0, 0.017857143, 0,
0.021052632, 0.018518519, 0.035714286, 0.045454545,
0.021052632, 0.018518519, 0.035714286, 0.068181818), 4, 4, byrow = TRUE)

# POPN O 2003-2004
XO3 <- matrix(c(0, 0, 11.5, 2.775862069,
0.6, 0.285714286, 0.333333333, 0.24137931,
0.04, 0.142857143, 0, 0,
0.16, 0.285714286, 0, 0.172413793), 4, 4, byrow = TRUE)

XO4 <- matrix(c(0, 0, 3.78, 1.225,
0.28358209, 0.171052632, 0, 0.166666667,
0.084577114, 0.026315789, 0, 0.055555556,
0.139303483, 0.447368421, 0, 0.385555556), 4, 4, byrow = TRUE)

XO5 <- matrix(c(0, 0, 1.542857143, 1.035616438,
0.12684127, 0.105263158, 0.047619048, 0.054794521,
0.095238095, 0.157894737, 0.19047619, 0.082191781,
0.111111111, 0.223684211, 0, 0.356164384), 4, 4, byrow = TRUE)
```
# POPN Q 2003-2004
XQ3 <- matrix(c(0, 0, 0.15, 0.175,
                0, 0, 0, 0,
                0, 0, 0, 0,
                1, 0, 0, 0), 4, 4, byrow = TRUE)

XQ4 <- matrix(c(0, 0, 0, 0.25,
                0, 0, 0, 0,
                0, 0, 0, 0,
                1, 0.666666667, 0, 1), 4, 4, byrow = TRUE)

XQ5 <- matrix(c(0, 0, 0, 1.428571429,
                0, 0, 0.142857143, 0,
                0, 0, 0, 0.25,
                0, 0, 0.571428571, 0), 4, 4, byrow = TRUE)

# POPN R 2003-2004
XR3 <- matrix(c(0, 0, 0.7, 0.6125,
                0.25, 0, 0, 0.125,
                0, 0, 0, 0,
                0.25, 0.166666667, 0, 0.25), 4, 4, byrow = TRUE)

XR4 <- matrix(c(0, 0, 0, 0.6,
                0.285714286, 0, 0, 0,
                0.285714286, 0.333333333, 0, 0,
                0.285714286, 0.333333333, 0, 1), 4, 4, byrow = TRUE)

XR5 <- matrix(c(0, 0, 0.7, 0.6125,
                0, 0, 0, 0,
                0, 0, 0, 0,
                0.333333333, 0, 0.333333333, 0.625), 4, 4, byrow = TRUE)

# POPN S 2003-2004
XS3 <- matrix(c(0, 0, 2.1, 0.816666667,
                0.166666667, 0, 0, 0,
                0, 0, 0, 0,
                0, 0, 0.166666667), 4, 4, byrow = TRUE)

XS4 <- matrix(c(0, 0, 0, 7,
                0.333333333, 0.5, 0, 0,
                0, 0, 0, 0,
                0.333333333, 0, 0, 1), 4, 4, byrow = TRUE)

XS5 <- matrix(c(0, 0, 0, 1.4,
                0, 0, 0, 0,
                0, 0, 0.2,
                0.111111111, 0.75, 0, 0.2), 4, 4, byrow = TRUE)

mats_list <- list(XC3, XC4, XC5, XE3, XE4, XE5, XF3, XF4, XF5, XG3, XG4, XG5,
                   XL3, XL4, XL5, XQ3, XQ4, XQ5, XR3, XR4, XR5, XS3, XS4, XS5)

yr_ord <- c(1, 2, 3, 1, 2, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3)
pch_ord <- c(1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4, 5, 5, 5, 6, 6, 6, 7, 7, 7, 8, 8, 9, 9, 9)

anth_lefkoMat <- create_lM(mats_list, anthframe, hstages = NA, historical = FALSE, poporder = 1, patchorder = pch_ord, yearorder = yr_ord)

smaller_anth_lM <- subset_lM(anth_lefkoMat, patch = c(1, 2, 3), year = c(1, 2))

smaller_anth_lM

summary.lefkoCondMat  
Summary of Class "lefkoCondMat"

Description

This function provides basic information summarizing the characteristics of conditional matrices derived from a lefkoCondMat object.

Usage

## S3 method for class 'lefkoCondMat'
summary(object, ...)

Arguments

object  
An object of class lefkoCondMat.

...  
Other parameters.

Value

A text summary of the object shown on the console, showing the number of historical matrices, as well as the number of conditional matrices nested within each historical matrix.

Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 0)
obsvvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1)
immvvector <- c(1, 1, 0, 0, 0, 0)
propvvector <- c(1, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)
lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
feacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 1, 1), type_t12 = c(1, 2, 1, 2, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrلن3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")
lathcondmats <- cond_hmpm(ehrlen3)
summary(lathcondmats)

# Cypripedium example
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg",
"XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0) 
obsvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
matvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
immvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binvec)
cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
...
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

cypsupp3r <- supplemental(stage3 = c("SD", "SD", "P1", "P2", "P3", "SL",
"D", "XSm", "Sm", "D", "XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL",
"SL", "SL", "rep", "rep"),
stage1 = c("SD", "rep", "SD", "rep", "SD", "P1", "P2", "P3", "P3",
"SL", "SL", "mat", "mat"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA),
givenrate = c(0.1, 0.1, 0.2, 0.2, 0.2, 0.2, 0.2, 0.25, NA, NA, NA, NA, NA, NA,
NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 3, 3),
type_t12 = c(1, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1),
stageframe = cypframe_raw, historical = TRUE)

cypmatrix3r <- rlefko3(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added", "size1added"),
supplement = cypsupp3r, yearcol = "year2", patchcol = "patchid",
indivcol = "individ")

cypcondmats <- cond_hmpm(cypmatrix3r)

summary(cypcondmats)

---

**summary.lefkoElas**

*Summarize lefkoElas Objects*

**Description**

Function `summary.lefkoElas()` summarizes `lefkoElas` objects. Particularly, it breaks down elasticity values by the kind of ahistorical and, if applicable, historical transition.

**Usage**

```r
# S3 method for class 'lefkoElas'
summary(object, ...)  
```

**Arguments**

- `object`  
  A `lefkoElas` object.
- `...`  
  Other parameters.
Value

A list composed of 2 data frames. The first, hist, is a data frame showing the summed elasticities for all 16 kinds of historical transition per matrix, with each column corresponding to each elasticity matrix in order. The second, ahist, is a data frame showing the summed elasticities for all 4 kinds of ahistorical transition per matrix, with each column corresponding to each elasticity matrix in order.

Examples

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = reppvector, obsstatus = obsvector, matstatus = matvector,
                        immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)
lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                        patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                        juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                        fecacol = "Intactseed88", deadacol = "Dead1988",
                        nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                        censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
                           stage2 = c("Sd", "Sd", "Sdl", "Sd", "Sdl"),
                           stage1 = c("Sd", "rep", "Sd", "rep", "npr", "Sd"),
                           eststage3 = c(NA, NA, NA, NA, NA, "mat"),
                           eststage2 = c(NA, NA, NA, NA, NA, "Sdl"),
                           eststage1 = c(NA, NA, NA, NA, NA, "NotAlive"),
                           givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
                           multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
                           type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1),
                           stageframe = lathframe, historical = TRUE)

lathsupp2 <- supplemental(stage3 = c("Sd", "Sdl", "Sd", "Sdl"),
                           stage2 = c("Sd", "Sdl", "rep", "rep"),
                           givenrate = c(0.345, 0.054, NA, NA),
                           multiplier = c(NA, NA, 0.345, 0.054),
                           type = c(1, 1, 3, 3), stageframe = lathframe, historical = FALSE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all")
```
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
        yearcol = "year2", indivcol = "individ")

ehrlen2 <- rlefko2(data = lathvert, stageframe = lathframe, year = "all",
                  stages = c("stage3", "stage2"), supplement = lathsupp2,
                  yearcol = "year2", indivcol = "individ")

ehrlen3elas <- elasticity3(ehrlen3)
ehrlen2elas <- elasticity3(ehrlen2)

summary(ehrlen3elas)
summary(ehrlen2elas)

summary.lefkoLTRE

Summarize lefkoLTRE Objects

Description

Function summary.lefkoLTRE() summarizes lefkoLTRE objects. Particularly, it breaks down
LTRE contributions by the kind of ahistorical and, if applicable, historical transition.

Usage

## S3 method for class 'lefkoLTRE'
summary(object, ...)

Arguments

object       A lefkoLTRE object.
...
Other parameters.

Value

A list composed of 2 (if deterministic) or 4 (if stochastic) data frames. If deterministic, then
hist_det is a data frame showing the summed LTRE contributions for all 16 kinds of historical
transition per matrix, with each column corresponding to each A matrix in order, followed by all
summed positive and all summed negative contributions. Object ahist_det is a data frame show-
ing the summed LTRE contributions for all 4 kinds of ahistorical transition per matrix, with order
as before, followed by summed positive and summed negative contributions. If stochastic, then
hist_mean and hist_sd are the summed LTRE contributions for the mean vital rates and variabil-
ity in vital rates, respectively, according to all 16 historical transition types, followed by summed
positive and negative contributions, and ahist_mean and ahist_sd are the equivalent ahistorical
versions.
Examples

# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = reppvector, obsstatus = obsvector, matstatus = matvector,
imstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sdl", "Sd1", "Sd", "Sdl1", "mat"),
stage2 = c("Sd", "Sdl", "Sdl", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA, NA),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA),
type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

lathsupp2 <- supplemental(stage3 = c("Sd", "Sdl", "Sd1", "Sdl"),
stage2 = c("Sd", "Sdl", "rep", "rep"),
givenrate = c(0.345, 0.054, NA, NA),
multiplier = c(NA, NA, 0.345, 0.054),
type = c(1, 1, 3, 3), stageframe = lathframe, historical = FALSE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")

ehrlen2 <- rlefko2(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2"), supplement = lathsupp2,
yearcol = "year2", individcol = "individ")

ehrlenltre <- ltre3(ehrlen3)
Summary of Class "lefkoMat"

Description

A function to simplify the viewing of basic information describing the matrices produced through functions `fleko3()`, `fleko2()`, `rleko3()`, `rleko2()`, and `afleko2()`.

Usage

```r
## S3 method for class 'lefkoMat'
summary(object, colsums = TRUE, ...)
```

Arguments

- **object**: An object of class `lefkoMat`.
- **colsums**: A logical value indicating whether column sums should be shown for U matrices, allowing users to check stage survival probabilities. Defaults to `TRUE`.
- **...**: Other parameters.

Value

A summary of the object, showing the number of each type of matrix, the number of annual matrices, the number of estimated (non-zero) elements across all matrices and per matrix, the number of unique transitions in the dataset, the number of individuals, and summaries of the column sums of the survival-transition matrices.

Examples

```r
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8.0, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
reppvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
immvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1.0, 1.0, 2.5, 4.5, 7.0)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
...)
```
binhalfwidth = bivec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,  
patchidcol = "plantid", individcol = "plantid", blocksize = 4,  
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",  
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",  
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,  
NRasRep = TRUE)

# Here we use supplemental() to provide overwrite and reproductive info  
cypraw_suppl2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",  
"XSm", "Sm", "SD", "P1"),  
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",  
"rep"),  
eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA),  
eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA),  
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA, NA),  
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),  
type =c(1, 1, 1, 1, 1, 1, 1, 1, 3, 3),  
stageframe = cypframe_raw, historical = FALSE)

cypraw_matrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,  
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),  
size = c("size3added", "size2added"), supplement = cypraw_suppl2r,  
yearcol = "year2", patchcol = "patchid", indivcol = "individ")

summary(cypraw_matrix2r)

summary.liefkoMod  

Summary of Class "liefkoMod"

Description
A function to summarize objects of class liefkoMod. This function shows the best-fit models,  
summarizes the numbers of models in the model tables, shows the criterion used to determine the best-fit  
models, and provides some basic quality control information.

Usage
```r
## S3 method for class 'liefkoMod'
summary(object, ...)  
```

Arguments

- **object**: An R object of class liefkoMod resulting from `modelsearch()`.
- **...**: Other parameters.
Value

A summary of the object, showing the best-fit models for all vital rates, with constants of 0 or 1 used for unestimated models. This is followed by a summary of the number of models tested per vital rate, and a table showing the names of the parameters used to model vital rates and represent tested factors. At the end is a section describing the numbers of individuals and of individual transitions used to estimate each vital rate best-fit model, along with the accuracy of each binomial model.

Examples

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 4.6, 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 1, 2, 3, 4, 5, 6, 7, 8, 9)
stagevector <- c("Sd", "Sdl", "Dorm", "Sz1nr", "Sz2nr", "Sz3nr", "Sz4nr", 
                   "Sz5nr", "Sz6nr", "Sz7nr", "Sz8nr", "Sz9nr", "Sz1r", "Sz2r", "Sz3r", 
                   "Sz4r", "Sz5r", "Sz6r", "Sz7r", "Sz8r", "Sz9r")
repgvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
obsvector <- c(0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 4.6, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 
                   0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)
lathframeln <- sf_create(sizes = sizevector, stagenames = stagevector,
                         repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                         immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                         propstatus = propvector)

lathvertln <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                         patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                         juvcol = "Seedling1988", sizeacol = "lnVol88", repstracol = "Intactseed88",
                         fecacol = "Intactseed88", deadacol = "Dead1988",
                         nonobsacol = "Dormant1988", stageassign = lathframeln,
                         stagesize = "sizea", censorcol = "Missing1988", censorkeep = NA,
                         NAas0 = TRUE, censor = TRUE)

lathvertln$feca2 <- round(lathvertln$feca2)
lathvertln$feca1 <- round(lathvertln$feca1)
lathvertln$feca3 <- round(lathvertln$feca3)
lathmodelsln2 <- modelsearch(lathvertln, historical = FALSE,
                              approach = "mixed", suite = "main",
                              vitalrates = c("surv", "obs", "size", "reps", "fec"), juvestimate = "Sdl",
                              bestfit = "AICc&k", sizedist = "gaussian", fecdist = "poisson",
                              indiv = "individ", patch = "patchid", year = "year2",
                              year.as.random = TRUE, patch.as.random = TRUE, show.model.tables = TRUE,
                              quiet = TRUE)
```
summary.lefkoProj

**Summary lefkoProj Objects**

**Description**

Function `summary.lefkoProj()` summarizes `lefkoProj` objects. Particularly, it breaks down the data frames provided in the projection element in ways meaningful for those running simulations.

**Usage**

```r
# S3 method for class 'lefkoProj'
summary(object, threshold = 1, milepost = c(0, 0.25, 0.5, 0.75, 1), ...)
```

**Arguments**

- `object`: A `lefkoProj` object.
- `threshold`: A threshold population size to be searched for in projections. Defaults to 1.
- `milepost`: A numeric vector indicating at which points in the projection to assess detailed results. Can be input as integer values, in which case each number must be between 1 and the total number of occasions projected in each projection, or decimals between 0 and 1, which would then be translated into the corresponding projection steps of the total. Defaults to `c(0, 0.25, 0.50, 0.75, 1.00)`.
- `...`: Other parameters.

**Value**

Apart from a statement of the results, we have the following item in the output:

- `milepost_sums`: A data frame showing the number of replicates at each of the milepost times that is above the threshold population/patch size.

**Examples**

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvector <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
```
summary.lefkoProj

```
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                          repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                          immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
                          propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                          patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
                          juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
                          fecacol = "Intactseed88", deadacol = "Dead1988",
                          nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
                          censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathrepm <- matrix(0, 7, 7)
lathrepm[1, 6] <- 0.345
lathrepm[2, 6] <- 0.054

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl"),
                          stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep"),
                          stage1 = c("Sd", "rep", "Sd", "rep", "all", "all"),
                          givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
                          multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
                          type = c(1, 1, 1, 1, 3, 3), type_t12 = c(1, 2, 1, 2, 1, 1),
                          stageframe = lathframe, historical = TRUE)

ehrler3 <- rlefko3(data = lathvert, stageframe = lathframe,
                    year = c(1989, 1990), stages = c("stage3", "stage2", "stage1"),
                    repmatrix = lathrepm, supplement = lathsupp3, yearcol = "year2",
                    indivcol = "individ")

lathproj <- projection3(ehrler3, nreps = 5, stochastic = TRUE)
summary(lathproj)
```

```
# Cypripedium example
rm(list = ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XS", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 0, 0, 1, 1, 1, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 0.5, 1, 1, 1, 2.5, 7)

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
                          repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                          propstatus = propvector, immstatus = immvector, indataset = indataset,
                          binhalfwidth = binvec)
supplemental

create a data frame of supplemental data for MPM development

Description

Function supplemental() provides all necessary supplemental data for matrix estimation, particularly bringing together data on proxy rates, data to overwrite existing rates, identified reproductive transitions complete, and fecundity multipliers.

Usage

supplemental()
stage3,  
stage2,  
stage1 = NA,  
eststage3 = NA,  
eststage2 = NA,  
eststage1 = NA,  
givenrate = NA,  
multiplier = 1,  
type = NA,  
type_t12 = NA,  
stageframe,  
historical = TRUE  
)

Arguments

stage3          The name of the stage in occasion \( t+1 \) in the transition to be replaced. Abbreviations for groups of stages are also usable (see Notes).

stage2          The name of the stage in occasion \( t \) in the transition to be replaced. Abbreviations for groups of stages are also usable (see Notes).

stage1          The name of the stage in occasion \( t-1 \) in the transition to be replaced. Only needed if a historical matrix is to be produced. Abbreviations for groups of stages are also usable (see Notes).

eststage3       The name of the stage to replace stage3 in a proxy transition. Only needed if a transition will be replaced by another estimated transition.

eststage2       The name of the stage to replace stage2 in a proxy transition. Only needed if a transition will be replaced by another estimated transition.

eststage1       The name of the stage to replace stage1 in a proxy historical transition. Only needed if a transition will be replaced by another estimated transition, and the matrix to be estimated is historical. Stage NotAlive is also possible for raw hMPMs as a means of handling the prior stage for individuals entering the population in occasion \( t \).

givenrate       A fixed rate or probability to replace for the transition described by stage3, stage2, and stage1.

multiplier      A vector of numeric multipliers for fecundity or for proxy transitions. Defaults to 1.

type            A vector denoting the kind of transition between occasions \( t \) and \( t+1 \) to be replaced. This should be entered as 1, S, or s for the replacement of a survival transition; 2, F, or f for the replacement of a fecundity transition; or 3, R, or r for a fecundity multiplier. If empty or not provided, then defaults to 1 for survival transition.

type_t12        An optional vector denoting the kind of transition between occasions \( t-1 \) and \( t \). Only necessary if a historical MPM in deVries format is desired. This should be entered as 1, S, or s for a survival transition; or 2, F, or f for a fecundity transitions. Defaults to 1 for survival transition, with impacts only on the construction of deVries-format hMPMs.
stageframe The stageframe being used to produce the MPMs in the study.

historical A logical value indicating whether the MPMs intended will be historical or ahistorical. Defaults to TRUE.

Value

A data frame of class lefkoSD. This object can be used as input in flefko3(), flefko2(), rlefko3(), rlefko2(), and afllefko2().

Variables in this object include the following:

- **stage3**: Stage at occasion $t+1$ in the transition to be replaced.
- **stage2**: Stage at occasion $t$ in the transition to be replaced.
- **stage1**: Stage at occasion $t-1$ in the transition to be replaced.
- **eststage3**: Stage at occasion $t+1$ in the transition to replace the transition designated by stage3, stage2, and stage1.
- **eststage2**: Stage at occasion $t$ in the transition to replace the transition designated by stage3, stage2, and stage1.
- **eststage1**: Stage at occasion $t-1$ in the transition to replace the transition designated by stage3, stage2, and stage1.
- **givenrate**: A constant to be used as the value of the transition.
- **multiplier**: A multiplier for proxy transitions or for fecundity.
- **convtype**: Designates whether the transition from occasion $t$ to occasion $t+1$ is a survival transition probability (1), a fecundity rate (2), or a fecundity multiplier (3).
- **convtype_t12**: Designates whether the transition from occasion $t-1$ to occasion $t$ is a survival transition probability (1), a fecundity rate (2).

Notes

Negative values are not allowed in givenrate and multiplier input.

Fecundity multiplier data supplied via the supplemental() function acts in the same way as non-zero entries supplied via a reproductive matrix, but gets priority in all matrix creations. Thus, in cases where fecundity multipliers are provided for the same function via the reproductive matrix and function supplemental(), the latter is used.

Entries in stage3, stage2, and stage1 can include abbreviations for groups of stages. Use rep if all reproductive stages are to be used, nrep if all mature but non-reproductive stages are to be used, mat if all mature stages are to be used, immat if all immature stages are to be used, prop if all propagule stages are to be used, npr if all non-propagule stages are to be used, and leave empty or use all if all stages in stageframe are to be used. Also use groupX to denote all stages in group X (e.g. group1 will use all stages in the respective stageframe’s group 1).

Examples

```r
# Lathyrus example
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
```
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 0, 1, 0)
obsvector <- c(0, 0, 0, 0, 0, 0, 0)
matvector <- c(0, 1, 1, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET", blocksize = 9,
juvcol = "Seedling1988", sizeacol = "Volume88", repstracol = "FCODE88",
fecacol = "Intactseed88", deadacol = "Dead1988",
nonobsacol = "Dormant1988", stageassign = lathframe, stagesize = "sizea",
censorcol = "Missing1988", censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
type = c(1, 1, 1, 1, 1, 1, 1),
type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
ehrlen3mean$A[[1]]

# Cypripedium example
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
matvector <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
immvector <- c(0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
binvec <- c(0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
verticalize3

Create Historical Vertical Data Frame from Horizontal Data Frame

Description

Function `verticalize3()` returns a vertically formatted demographic data frame organized to create historical projection matrices, given a horizontally formatted input data frame. It also handles stage assignments if given an appropriate stageframe.

Usage

```r
data, noyears, firstyear = 1, popidcol = 0, patchidcol = 0
```

```r
cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
propstatus = propvector, immstatus = immvector, indataset = indataset,
binhalfwidth = binevec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
patchidcol = "patch", individcol = "plantid", blocksize = 4,
sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
NRasRep = TRUE)

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
"XSm", "Sm", "SD", "P1"),
stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
"rep"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA, NA, NA),
givenrate = c(0.10, 0.20, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA),
multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA),
type = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 3),
stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
size = c("size3added", "size2added"), supplement = cypsupp2r,
yearcol = "year2", patchcol = "patchid", individcol = "individ")

cyp2mean <- lmean(cypmatrix2r)
cyp2mean
```
individcol = 0,
blocksize = NA,
xcol = 0,
ycol = 0,
juvcol = 0,
sizeacol,
sizebcol = 0,
sizeccol = 0,
repstracol = 0,
repstrbcoll = 0,
fecacol = 0,
fecbcol = 0,
indcovacol = 0,
indcovbcol = 0,
indcovccol = 0,
aliveacol = 0,
deadacl = 0,
obscoll = 0,
nonobsacoll = 0,
censorcoll = 0,
repstrrel = 1,
fecrel = 1,
stagecoll = 0,
stageassign = NA,
stagesize = NA,
censorkeep = 0,
censorRepeatt = FALSE,
censor = FALSE,
coordsRepeatt = FALSE,
spacing = NA,
NAas0 = FALSE,
NRasRep = FALSE,
reduce = TRUE,
a2check = FALSE
)

Arguments

data                   The horizontal data file. A valid data frame is required as input.
noyears                The number of years or observation occasions in the dataset. A valid integer is
                        required as input.
firstyear              The first year or occasion of observation. Defaults to 1.
popidcol               A variable name or column number corresponding to the identity of the population for each individual.
patchidcol             A variable name or column number corresponding to the identity of the patch or subpopulation for each individual, if patches have been designated within populations.
individcol  A variable name or column number corresponding to the identity of each individual.

blocksize  The number of variables corresponding to each occasion in the input dataset designated in data, if a set pattern of variables is used for each observation occasion in the data frame used as input. If such a pattern is not used, and all variable names are properly noted as character vectors in the other input variables, then this may be set to NA. Defaults to NA.

col      A variable name(s) or column number(s) corresponding to the X coordinate of each individual, or of each individual at each occasion, in Cartesian space. Can refer to the only instance, the first instance, or all instances of X variables. In the last case, the values should be entered as a vector.

cyol     A variable name(s) or column number(s) corresponding to the Y coordinate of each individual, or of each individual at each occasion, in Cartesian space. Can refer to the only instance, the first instance, or all instances of Y variables. In the last case, the values should be entered as a vector.

juvcol    A variable name(s) or column number(s) that marks individuals in immature stages within the dataset. This function assumes that immature individuals are identified in this variable marked with a number equal to or greater than 1, and that mature individuals are marked as 0 or NA. Can refer to the first instance, or all instances of these variables. In the latter case, the values should be entered as a vector.

sizeacol  A variable name(s) or column number(s) corresponding to the size entry associated with the first year or observation occasion in the dataset. Can refer to the first instance, or all instances of these variables. In the latter case, the values should be entered as a vector. This variable should refer to the first size variable in the stageframe, unless stagesize = "sizeadded".

sizebcol  A second variable name(s) or column number(s) corresponding to the size entry associated with the first year or observation occasion in the dataset. Can refer to the first instance, or all instances of these variables. In the latter case, the values should be entered as a vector. This variable should refer to the second size variable in the stageframe, unless stagesize = "sizeadded".

sizeccol  A third variable name(s) or column number(s) corresponding to the size entry associated with the first year or observation occasion in the dataset. Can refer to the first instance, or all instances of these variables. In the latter case, the values should be entered as a vector. This variable should refer to the third size variable in the stageframe, unless stagesize = "sizeadded".

repstracol A variable name(s) or column number(s) corresponding to the production of reproductive structures, such as flowers, associated with the first year or observation period in the input dataset. This can be binomial or count data, and is used to analyze the probability of reproduction. Can refer to the first instance, or all instances of these variables. In the latter case, the values should be entered as a vector.

repstrbcol A second variable name(s) or column number(s) corresponding to the production of reproductive structures, such as flowers, associated with the first year or observation period in the input dataset. This can be binomial or count data, and is used to analyze the probability of reproduction. Can refer to the first instance,
or all instances of these variables. In the latter case, the values should be entered as a vector.

**fecacol**
A variable name(s) or column number(s) denoting fecundity associated with the first year or observation occasion in the input dataset. This may represent egg counts, fruit counts, seed production, etc. Can refer to the first instance, or all instances of these variables. In the latter case, the values should be entered as a vector.

**fecbcol**
A second variable name(s) or column number(s) denoting fecundity associated with the first year or observation occasion in the input dataset. This may represent egg counts, fruit counts, seed production, etc. Can refer to the first instance, or all instances of these variables. In the latter case, the values should be entered as a vector.

**indcovacol**
A variable name(s) or column number(s) corresponding to an individual covariate to be used in analysis. Can refer to the only instance, the first instance, or all instances of these variables. In the last case, the values should be entered as a vector.

**indcovbcol**
A variable name(s) or column number(s) corresponding to an individual covariate to be used in analysis. Can refer to the only instance, the first instance, or all instances of these variables. In the last case, the values should be entered as a vector.

**indcovccol**
A second variable name(s) or column number(s) corresponding to an individual covariate to be used in analysis. Can refer to the only instance, the first instance, or all instances of these variables. In the last case, the values should be entered as a vector.

**aliveacol**
Variable name(s) or column number(s) providing information on whether an individual is alive at a given occasion. If used, living status must be designated as binomial (living = 1, dead = 0). Can refer to the first instance of a living status variable in the dataset, or a full vector of all living status variables in temporal order.

**deadacol**
Variable name(s) or column number(s) providing information on whether an individual is alive at a given occasion. If used, dead status must be designated as binomial (dead = 1, living = 0). Can refer to the first instance of a dead status variable in the dataset, or a full vector of all dead status variables in temporal order.

**obsacol**
A variable name(s) or column number(s) providing information on whether an individual is in an observable stage at a given occasion. If used, observation status must be designated as binomial (observed = 1, not observed = 0). Can refer to the first instance of an observation status variable in the dataset, or a full vector of all observation status variables in temporal order.

**nonobsacol**
A variable name(s) or column number(s) providing information on whether an individual is in an unobservable stage at a given occasion. If used, observation status must be designated as binomial (not observed = 1, observed = 0). Can refer to the first instance of a non-observation status variable in the dataset, or a full vector of all non-observation status variables in temporal order.

**censorcol**
A variable name(s) or column number(s) corresponding to the first entry of a censor variable, used to distinguish between entries to use and entries not to
use, or to designate entries with special issues that require further attention. Can refer to the first instance of a censor status variable in the dataset, or a full vector of all censor status variables in temporal order. Can also refer to a single censor status variable used for the entire individual, if singlecensor = TRUE.

repstrrel This is a scalar multiplier on variable repstrbcol to make it equivalent to repstracol. This can be useful if two reproductive status variables have related but unequal units, for example if repstracol refers to one-flowered stems while repstrbcol refers to two-flowered stems. Defaults to 1.

fecrel This is a scalar multiplier on variable fecbcol to make it equivalent to fecacol. This can be useful if two fecundity variables have related but unequal units. Defaults to 1.

stagecol Optional variable name(s) or column number(s) corresponding to life history stage at a given occasion. Can refer to the first instance of a stage identity variable in the dataset, or a full vector of all stage identity variables in temporal order.

stageassign The stageframe object identifying the life history model being operationalized. Note that if stagecol is provided, then this stageframe is not used for stage designation.

stagesize A variable name or column number describing which size variable to use in stage estimation. Defaults to NA, and can also take sizea, sizeb, sizec, sizeab, sizebc, sizeac, sizeabc, or sizeadded, depending on which size variable within the input dataset is chosen. Note that the variable(s) chosen should be presented in the order of the primary, secondary, and tertiary variables in the stageframe input with stageassign. For example, choosing sizeb assumes that this size is the primary variable in the stageframe.

censorkeep The value of the censor variable identifying data to be included in analysis. Defaults to 0, but may take any value including NA. Note that if NA is the value to keep, then this function will alter all NAs to 0 values, and all other values to 1, treating 0 as the new value to keep.

censorRepeat A logical value indicating whether the censor variable is a single column, or whether it repeats across occasion blocks. Defaults to FALSE.

censor A logical variable determining whether the output data should be censored using the variable defined in censorcol. Defaults to FALSE.

cordsRepeat A logical value indicating whether X and Y coordinates correspond to single X and Y columns. If TRUE, then each observation occasion has its own X and Y variables. Defaults to FALSE.

spacing The spacing at which density should be estimated, if density estimation is desired and X and Y coordinates are supplied. Given in the same units as those used in the X and Y coordinates given in xcol and ycol. Defaults to NA.

NAas0 If TRUE, then all NA entries for size and fecundity variables will be set to 0. This can help increase the sample size analyzed by modelsearch(), but should only be used when it is clear that this substitution is biologically realistic. Defaults to FALSE.

NRasRep If TRUE, then will treat non-reproductive but mature individuals as reproductive during stage assignment. This can be useful when a matrix is desired without
separation of reproductive and non-reproductive but mature stages of the same size. Only used if stageassign is set to a stageframe. Defaults to FALSE.

reduce A logical variable determining whether unused variables and some invariant state variables should be removed from the output dataset. Defaults to TRUE.

a2check A logical variable indicating whether to retain all data with living status at occasion $t$ equal to 0. Defaults to FALSE, and should be kept FALSE except to inspect potential errors in the dataset.

Value

If all inputs are properly formatted, then this function will output a historical vertical data frame (class hfvdata), meaning that the output data frame will have three consecutive occasions of size and reproductive data per individual per row. This data frame is in standard format for all functions used in lefko3, and so can be used without further modification.

Variables in this data frame include the following:

- rowid Unique identifier for the row of the data frame.
- popid Unique identifier for the population, if given.
- patchid Unique identifier for patch within population, if given.
- individ Unique identifier for the individual.
- year2 Year or time at occasion $t$.
- firstseen Occasion of first observation.
- lastseen Occasion of last observation.
- obsage Observed age in occasion $t$, assuming first observation corresponds to age = 0.
- obslifespan Observed lifespan, given as lastseen - firstseen + 1.
- xpos1,xpos2,xpos3 X position in Cartesian space in occasions $t-1$, $t$, and $t+1$, respectively, if provided.
- ypos1,ypos2,ypos3 Y position in Cartesian space in occasions $t-1$, $t$, and $t+1$, respectively, if provided.
- sizea1,sizea2,sizea3 Main size measurement in occasions $t-1$, $t$, and $t+1$, respectively.
- sizeb1,sizeb2,sizeb3 Secondary size measurement in occasions $t-1$, $t$, and $t+1$, respectively.
- sizec1,sizec2,sizec3 Tertiary measurement in occasions $t-1$, $t$, and $t+1$, respectively.
- size1added,size2added,size3added Sum of primary, secondary, and tertiary size measurements in occasions $t-1$, $t$, and $t+1$, respectively.
- repstra1,repstra2,repstra3 Main numbers of reproductive structures in occasions $t-1$, $t$, and $t+1$, respectively.
repstrb1, repstrb2, repstrb3
Secondary numbers of reproductive structures in occasions \(t-1\), \(t\), and \(t+1\), respectively.

repstr1added, repstr2added, repstr3added
Sum of primary and secondary reproductive structures in occasions \(t-1\), \(t\), and \(t+1\), respectively.

fec1, fec2, fec3
Main numbers of offspring in occasions \(t-1\), \(t\), and \(t+1\), respectively.

fecb1, fecb2, fecb3
Secondary numbers of offspring in occasions \(t-1\), \(t\), and \(t+1\), respectively.

feca1, feca2, feca3
Sum of primary and secondary fecundity in occasions \(t-1\), \(t\), and \(t+1\), respectively.

censor1, censor2, censor3
Censor state values in occasions \(t-1\), \(t\), and \(t+1\), respectively.

juvgiven1, juvgiven2, juvgiven3
Binomial variable indicating whether individual is juvenile in occasions \(t-1\), \(t\), and \(t+1\). Only given if juvcol is provided.

obsstatus1, obsstatus2, obsstatus3
Binomial observation state in occasions \(t-1\), \(t\), and \(t+1\), respectively.

repstatus1, repstatus2, repstatus3
Binomial reproductive state in occasions \(t-1\), \(t\), and \(t+1\), respectively.

fecstatus1, fecstatus2, fecstatus3
Binomial offspring production state in occasions \(t-1\), \(t\), and \(t+1\), respectively.

matstatus1, matstatus2, matstatus3
Binomial maturity state in occasions \(t-1\), \(t\), and \(t+1\), respectively.

alive1, alive2, alive3
Binomial state as alive in occasions \(t-1\), \(t\), and \(t+1\), respectively.

density
Radial density of individuals per unit designated in spacing. Only given if spacing is not NA.

Notes

In some datasets on species with unobserveable stages, observation status (obsstatus) might not be inferred properly if a single size variable is used that does not yield sizes greater than 0 in all cases in which individuals were observed. Such situations may arise, for example, in plants when leaf number is the dominant size variable used, but individuals occasionally occur with inflorescences but no leaves. In this instances, it helps to mark related variables as sizeb and sizec, because observation status will be interpreted in relation to all 3 size variables. Further analysis can then utilize only a single size variable, of the user’s choosing. Similar issues can arise in reproductive status (repstatus).

Juvenile designation should only be used when juveniles fall outside of the size classification scheme used in determining stages. If juveniles are to be size classified along the size spectrum that adults also fall on, then it is best to treat juveniles as mature but not reproductive.

Warnings that some individuals occur in state combinations that do not match any stages in the stageframe used to assign stages are common when first working with a dataset. Typically, these
situations can be identified as NoMatch entries in stage3, although such entries may crop up in stage1 and stage2, as well. In rare cases, these warnings will arise with no concurrent NoMatch entries, which indicates that the input dataset contained conflicting state data at once suggesting that the individual is in some stage but is also dead. The latter is removed if the conflict occurs in occasion $t$ or $t-1$, as only living entries are allowed in time $t$ and time $t-1$ may involve living entries as well as unliving entries immediately prior to birth.

Care should be taken to avoid variables with negative values indicating size, fecundity, or reproductive or observation status. Negative values can be interpreted in different ways, typically reflecting estimation through other algorithms rather than actual measured data. Variables holding negative values can conflict with data management algorithms in ways that are difficult to predict.

Unusual errors (e.g. "Error in .pfj...") may occur in cases where the variables are improperly passed, where seemingly numeric variables include text, or where the blocksize is improperly set.

Density estimation is performed as a count of individuals alive and within the radius specified in spacing of the respective individual at some point in time.

Examples

```r
# Lathyrus example using blocksize - when repeated patterns exist in variable
# order
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
reppvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 1, 1, 1, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1, 1)
immvctor <- c(1, 1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1, 1)
binvec <- c(0, 100, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
                        repstatus = repvector, obsstatus = obsvector,
                        matstatus = matvector, immstatus = immvector,
                        indataset = indataset, binhalfwidth = binvec,
                        propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
                         patchidcol = "SUBPLOT", individcol = "GENET",
                         blocksize = 9, juvcol = "Seedling1988", sizeacol = "Volume88",
                         fecacol = "Intactseed88", deadacol = "Dead1988",
                         nonobsacol = "Dormant1988", stageassign = lathframe,
                         stagesize = "sizea", censorcol = "Missing1988",
                         censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sdl", "Sd", "Sdl", "mat"),
                          stage2 = c("Sd", "Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
                          stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
                          eststage3 = c(NA, NA, NA, NA, NA, NA, "mat"),
                          eststage2 = c(NA, NA, NA, NA, NA, NA, "Sdl"),
                          eststage1 = c(NA, NA, NA, NA, NA, NA, "NotAlive"),
                          givenrate = c(0.345, 0.345, 0.054, 0.054, NA, NA, NA),
                          multiplier = c(NA, NA, NA, NA, 0.345, 0.054, NA))
```

verticalize3

type = c(1, 1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
yearcol = "year2", individcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
ehrlen3mean$A[[1]]

# Lathyrus example without blocksize - when no repeated patterns exist in
# variable order and all variables names are specified
data(lathyrus)

sizevector <- c(0, 100, 13, 127, 3730, 3800, 0)
stagevector <- c("Sd", "Sdl", "VSm", "Sm", "VLa", "Flo", "Dorm")
repvector <- c(0, 0, 0, 0, 1, 0)
obsvector <- c(0, 0, 0, 0, 1, 0)
matvector <- c(0, 0, 1, 1, 1, 1)
immvector <- c(1, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0)
indataset <- c(0, 1, 1, 1, 1, 1)
binvec <- c(0, 0, 11, 103, 3500, 3800, 0.5)

lathframe <- sf_create(sizes = sizevector, stagenames = stagevector,
repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
immstatus = immvector, indataset = indataset, binhalfwidth = binvec,
propstatus = propvector)

lathvert <- verticalize3(lathyrus, noyears = 4, firstyear = 1988,
patchidcol = "SUBPLOT", individcol = "GENET",
sizeacol = c("Volume88", "Volume89", "Volume90", "Volume91"),
repstracol = c("FCODE88", "FCODE89", "FCODE90", "FCODE91"),
feccol = c("Intactseed88", "Intactseed89", "Intactseed90", "Intactseed91"),
deadacol = c("Dead1988", "Dead1989", "Dead1990", "Dead1991"),
stageassign = lathframe, stagesize = "sizea",
censorkeep = NA, censor = TRUE)

lathsupp3 <- supplemental(stage3 = c("Sd", "Sd", "Sdl", "Sd", "Sdl", "mat"),
stage2 = c("Sd", "Sd", "Sd", "rep", "rep", "Sdl"),
stage1 = c("Sd", "rep", "Sd", "rep", "npr", "npr", "Sd"),
eststage3 = c(NA, NA, NA, NA, NA, NA, NA),
eststage2 = c(NA, NA, NA, NA, NA, NA, NA),
eststage1 = c(NA, NA, NA, NA, NA, NA, NA),
givencol = c(0.345, 0.345, 0.054, 0.054, NA, NA),
multiplier = c(NA, NA, NA, NA, 0.345, 0.054),
type = c(1, 1, 1, 3, 3, 1), type_t12 = c(1, 2, 1, 2, 1, 1),
stageframe = lathframe, historical = TRUE)

ehrlen3 <- rlefko3(data = lathvert, stageframe = lathframe, year = "all",

205
stages = c("stage3", "stage2", "stage1"), supplement = lathsupp3,
        yearcol = "year2", indivcol = "individ")

ehrlen3mean <- lmean(ehrlen3)
ehrlen3mean$A[[1]]

# Cypripedium example using blocksize
rm(list=ls(all=TRUE))
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XS\m", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0)
immvector <- c(0, 1, 1, 1, 1, 0, 0, 0, 0, 0)

binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)
cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector,
                          repstatus = repvector, obsstatus = obsvector, matstatus = matvector,
                          propstatus = propvector, immstatus = immvector, indataset = indataset,
                          binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004,
                           patchidcol = "patch", individcol = "plantid", blocksize = 4,
                           sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04",
                           repstracol = "Inf.04", repstrbcol = "Inf2.04", fecacol = "Pod.04",
                           stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE,
                           NRasRep = TRUE)

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D",
                                     "XS\m", "Sm"),
                          stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep",
                                     "rep"),
                          eststage3 = c(NA, NA, NA, NA, NA, "D", "XS\m", "Sm", NA, NA),
                          eststage2 = c(NA, NA, NA, NA, NA, "XS\m", "XS\m", "XS\m", NA, NA),
                          givenrate = c(0.10, 0.20, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA),
                          multiplier = c(NA, NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5),
                          type = c(1, 1, 1, 1, 1, 1, 1, 3, 3),
                          stageframe = cypframe_raw, historical = FALSE)

cymatrix2r <- rlefko2(data = cypraw_v1, stageframe = cypframe_raw,
                       year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"),
                       size = c("size3added", "size2added"), supplement = cybpsupp2r,
                       yearcol = "year2", patchcol = "patchid", indivcol = "individ")

cyp2mean <- lmean(cymatrix2r)
cyp2mean
# Cypripedium example using partial repeat patterns with blocksize and part
# explicit variable name cast
data(cypdata)

sizevector <- c(0, 0, 0, 0, 0, 0, 1, 2.5, 4.5, 8, 17.5)
stagevector <- c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Md", "Lg", "XLg")
repvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
obsvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
matvector <- c(0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1)
immvector <- c(0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0)
propvector <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
indataset <- c(0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1)

binvec <- c(0, 0, 0, 0, 0, 0.5, 0.5, 1, 1, 2.5, 7)

# Create the dataframe

cypframe_raw <- sf_create(sizes = sizevector, stagenames = stagevector, repstatus = repvector, obsstatus = obsvector, matstatus = matvector, propstatus = propvector, immstatus = immvector, indataset = indataset, binhalfwidth = binvec)

cypraw_v1 <- verticalize3(data = cypdata, noyears = 6, firstyear = 2004, patchidcol = "patch", individcol = "plantid", blocksize = 4, sizeacol = "Inf2.04", sizebcol = "Inf.04", sizeccol = "Veg.04", repstracol = c("Inf.04", "Inf.05", "Inf.06", "Inf.07", "Inf.08", "Inf.09"), repstrbcol = c("Inf2.04", "Inf2.05", "Inf2.06", "Inf2.07", "Inf2.08", "Inf2.09"), fecacol = "Pod.04", stageassign = cypframe_raw, stagesize = "sizeadded", NAas0 = TRUE, NRasRep = TRUE)

cypsupp2r <- supplemental(stage3 = c("SD", "P1", "P2", "P3", "SL", "D", "XSm", "Sm", "Lg"), stage2 = c("SD", "SD", "P1", "P2", "P3", "SL", "SL", "SL", "rep", "rep"), eststage3 = c(NA, NA, NA, NA, NA, "D", "XSm", "Sm", NA, NA), eststage2 = c(NA, NA, NA, NA, NA, "XSm", "XSm", "XSm", NA, NA), givenrate = c(0.10, 0.20, 0.20, 0.20, 0.20, 0.25, NA, NA, NA, NA), multiplier = c(NA, NA, NA, NA, NA, NA, NA, 0.5, 0.5), type = c(1, 1, 1, 1, 1, 1, 3, 3), stageframe = cypframe_raw, historical = FALSE)

cypmatrix2r <- rleko2(data = cypraw_v1, stageframe = cypframe_raw, year = "all", patch = "all", stages = c("stage3", "stage2", "stage1"), size = c("size3added", "size2added"), supplement = cypsupp2r, yearcol = "year2", patchcol = "patchid", individcol = "individ")

# Calculate the mean

cyp2mean <- lmean(cypmatrix2r)
cyp2mean
Index

* datasets
  cypdata, 25
cypvert, 28
lathyrus, 97
add_lM, 3, 20, 31, 178
aflefko2, 8, 120, 155, 157, 188, 195
cond_hmpm, 16
create_lM, 4, 18, 31, 178
cypdata, 25
cypvert, 28
delete_lM, 4, 20, 30, 178
density_input, 34, 122, 123, 176
dredge, 116
elasticity3, 37, 41, 44, 47
elasticity3.lefkoMat, 38, 40, 44, 47
elasticity3.list, 38, 41, 43, 47
elasticity3.matrix, 38, 41, 44, 46
flefko2, 48, 120, 155, 157, 158, 188, 195
flefko3, 58, 120, 155, 157, 158, 188, 195
glm, 116
glm.nb, 116
glmer, 116
glmmTMB, 116
historicalize3, 67, 111, 137, 142
image, 75, 77, 80, 82, 85, 87
image3, 75
image3.lefkoElas, 77
image3.lefkoMat, 75, 80
image3.lefkoSens, 82
image3.list, 84
image3.matrix, 75, 87
lambda3, 89, 92, 95

summary.lefkoMat. 19, 188
summary.lefkoMod. 189
summary.lefkoProj. 191
supplemental. 10, 50, 59, 135, 141, 159, 193

verticalize3. 111, 134, 137, 140, 142, 197
vglm. 116, 117

zeroinfl. 116, 117