Package ‘AnimalAPD’

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Title Compare Activity Patterns with Activity Probability Density (APD)

Version 1.0.0

Description Calculation and analyses of Activity Probability Density (APD) for comparing animal activity patterns with automated Bayesian model selection using ‘STAN’. See Campbell et al. (in press) "A new approach to comparing animal temporal activity: a more informative, robust, and flexible method that controls for nested data, quantifies relationship asymmetries, and allows linear modelling of temporal behaviour."

Imports brms, circular, overlap, graphics, stats, loo, ggplot2, gridExtra, activityGCMM

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**APDraw**

-Calculate Raw APD Values-

Description

Calculates raw APD values, uncorrected for hierarchical data structure

Usage

`APDraw(focal, contingent, adjust = 1)`

Arguments

- **focal**: Vector of observations in radians of one species/group/individual/etc. for which predictions on another will be made
- **contingent**: Vector of observations in radians of a species/group/individual/etc. from which predictions will be made
- **adjust**: Smoothing of predicted line; recommended to use default value for observed values and higher value for estimations from circular models; default=1

Value

Numeric vector of raw APD values, without correction for nested data structure

Examples

```r
data(wolfexample)
data(boarexample)
APDraw(focal=wolfexample$Radians, contingent=boarexample$Radians)
```
Description

Calculation of animal activity probability density controlling for nested data with random intercepts using Bayesian GLMMs with 'STAN' and brm. The function can automatically select the statistical distribution that is most appropriate for the dataset (weibull, frechet, gamma, lognormal, inverse gaussian) using loo and automatically ensures that MCMC chains converge and that a specified minimum effective sample size from the posterior distribution is achieved. An APD activity curve plot is provided.

Package: AnimalAPD Version: 1.0.0 Date: 2020-11-08

Usage

APDRE(
  focal,
  contingent,
  RE1,
  RE2 = NULL,
  weibullGLMM = TRUE,
  frechetGLMM = TRUE,
  gammaGLMM = TRUE,
  lognormalGLMM = FALSE,
  invgaussianGLMM = TRUE,
  cores = 1,
  iter = 5000,
  burnin = iter/2,
  center = "pi",
  Reloo = TRUE,
  adapt_delta = 0.95,
  adjust = 1,
  minESS = 1000,
  col = "deeppink3",
  histcol = "deeppink",
  linecol = "black",
  xlimCV = NULL,
  min = TRUE,
  max = TRUE,
  points = TRUE,
  mean = TRUE,
  HDI = TRUE,
  rawmean = FALSE,
  ... )
Arguments

- **focal**
  Vector of observations in radians of one species/group/individual/etc. for which predictions on another will be made

- **contingent**
  Vector of observations in radians or output from generalized circular mixture model of activity curves from link[GCM][GCMM][activityGCMM] of a species/group/individual/etc. from which predictions will be made

- **RE1**
  Vector identifying a random intercept for observations of the focal to control for hierarchical data (e.g. camera trap IDs)

- **RE2**
  Optional vector identifying levels of a second random effect, for data with additional hierarchical levels (e.g. study sites, sampling periods, data collection seasons); default is NULL

- **weibullGLMM**
  Specifies whether to run a weibull GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned

- **frechetGLMM**
  Specifies whether to run a frechet GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned

- **gammaGLMM**
  Specifies whether to run a Gamma GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned

- **lognormalGLMM**
  Specifies whether to run a lognormal GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned

- **invgaussianGLMM**
  Specifies whether to run a inverse.gaussian GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned

- **cores**
  Number of cores to use when running MCMC chains in parallel; default=1

- **iter**
  Number of MCMC iterations per chain; default=5000

- **burnin**
  Number of MCMC iterations discarded as burnin; default=iter/2

- **center**
  Value to use as center of graph; default=pi

- **Reloo**
  Whether to use reloo when running leave-one-out cross-validation of models (loo)

- **adapt_delta**
  Value to use for adapt_delta with brms; default=0.95

- **adjust**
  Smoothing of predicted line; recommended to use default value for observed values and higher value for estimations from circular models

- **minESS**
  Desired minimum effective sample size; default=1000

- **col**
  Specifies colour of points for the focal in the graph

- **histcol**
  Specifies colour of the histogram plot of the posterior distribution

- **linecol**
  Specifies colour of HDI line in histogram plot of the posterior distribution

- **xlimCV**
  A vector of two values indicating the x axis limits for the histCV graph

- **min**
  Whether to include minimum APD on the graph; default=TRUE; default=TRUE

- **max**
  Whether to include maximum APD on the graph; default=TRUE; default=TRUE

- **points**
  Whether to include datapoints for observations of the focal on the graph; default=TRUE
mean  Whether to include the estimated mean APD from the GLMM on the graph; default=TRUE

HDI  Whether to include the estimated 95% highest density interval of mean APD from the GLMM on the graph; default=TRUE

rawmean  Whether to include the raw mean, not correcting for random effects, on the graph; default=FALSE

...  Additional parameters

Value

Prints graph of activity curve and APD estimates from best-fitting GLMM and prints summary of analysis. Returns object of class APD is returned, containing a list of analysis results and details:

data  List of data used in analysis

output  Matrix with summary output from selected model

distribution  Name of distribution of selected model

model  An object of class brmsfit containing output from the selected model, including the posterior samples and other information. See brm

CVposterior  Numeric vector of posterior samples for the calculated family-specific population coefficient of variation (CV)

allmodels  List of objects of class brmsfit containing output from all models from the analysis.

rawvalues  Numeric vector of the raw, uncorrected APD values

rawsummary  List of summary stats of raw APD values

Author(s)

Liz AD Campbell

See Also

GCMM brm loo

Examples

data(wolfexample)
data(boarexample)
APDRE(focal=wolfexample$Radians, contingent=boarexample$Radians, RE1=wolfexample$SamplingPeriod, weibullGLMM=TRUE, frechetGLMM=FALSE, gammaGLMM=FALSE, lognormalGLMM=FALSE, invgaussianGLMM=FALSE, min=TRUE, max=TRUE, points=TRUE, mean=TRUE, HDI=TRUE, rawmean=FALSE)
**Description**

Calculates estimated relationships between activity probability density (APD) of the focal and contingent(s) using Bayesian GLMMs with 'STAN' using `brm`, with the option to automatically select the statistical distribution that best fits the dataset (weibull, frechet, gamma, lognormal, inverse gaussian) by `loo`. The function automatically ensures that MCMC chains reach convergence and that the specified minimum effective sample size from the posterior distribution is achieved.

Package: AnimalAPD Version: 1.0.0 Date: 2020-11-10

**Usage**

```r
APDREcorr(
  focal,
  cont1,
  cont2 = NULL,
  cont3 = NULL,
  cont4 = NULL,
  RE1,
  RE2 = NULL,
  weibullGLMM = TRUE,
  frechetGLMM = TRUE,
  gammaGLMM = TRUE,
  lognormalGLMM = FALSE,
  invgaussianGLMM = TRUE,
  cores = 1,
  iter = 5000,
  minESS = 1000,
  burnin = iter/2,
  thin = 1,
  adapt_delta = 0.95,
  center = "pi",
  adjust = 1,
  Reloo = TRUE,
  plothist = TRUE,
  ploteffects = TRUE,
  histcol = "cyan4",
  effectcol = "cyan4",
  linecol = "red"
)
```
Arguments

focal Vector of observations in radians of one species/group/individual/etc. for which predictions on another will be made.

cont1 Vector of observations in radians, or output from generalized circular mixture model of activity curves from GCMM, of a species/group/individual/etc. from which predictions will be made.

cont2 Optional vector of observations in radians, or output from generalized circular mixture model of activity curves from GCMM, of additional species/group/individual/etc. from which predictions will be made.

cont3 Optional vector of observations in radians, or output from generalized circular mixture model of activity curves from GCMM, of additional species/group/individual/etc. from which predictions will be made.

cont4 Optional vector of observations in radians, or output from generalized circular mixture model of activity curves from GCMM, of additional species/group/individual/etc. from which predictions will be made.

RE1 Vector identifying a random intercept for observations of the focal to control for hierarchical data (e.g. camera trap IDs).

RE2 Optional vector identifying levels of a second random effect, for data with additional hierarchical levels (e.g. study sites, sampling periods, data collection seasons); default is NULL.

weibullGLMM Specifies whether to run a weibull GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned.

frechetGLMM Specifies whether to run a frechet GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned.

gammaGLMM Specifies whether to run a Gamma GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned.

lognormalGLMM Specifies whether to run a lognormal GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned.

invgaussianGLMM Specifies whether to run a inverse.gaussian GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned.

cores Number of cores to use when running MCMC chains in parallel; default=1.

iter Number of MCMC iterations per chain; burnin is iter/2; default=5000.

minESS Desired minimum effective sample size; default=1000.

burnin Number of MCMC iterations to be discarded as the burn-in; default=iter/2.

thin Thinning rate for saving MCMC draws; default=1.

adapt_delta Value to use for adapt_delta with brms; default=0.95; see also brms.

center Value to use as center of graph; default=pi.

adjust Smoothing of predicted line; recommended to use default value for observed values and higher value for estimations from circular models.

Reloo Whether to use reloo when running leave-one-out cross-validation of models (loo); see also brms and loo.
plothist  Whether to plot histograms of samples from the posterior distribution for the
    correlation parameters; default=TRUE
ploteffects Whether to plot predicted effects; default=TRUE
histcol Colour for histogram bars
effectcol Colour for predicted effect plot 95% HDI
linecol Colour for histogram lines for the 95% HDI and 0

Value
Prints results of best-fitting model and posterior samples and/or predicted effects of parameter es-
   timates if plothist=TRUE and ploteffects=TRUE, and returns object of class APD with list of
analysis results and information.
data List of data used in analysis
model Object of class brmsfit containing results and information for best-fitting model.
distribution Character vector of statistical distribution of best-fitting model
allmodels List of output for all tested models; object of class brmsfit

Author(s)
Liz AD Campbell

See Also
GCMM brm loo

Examples
data(wolfexample)
data(boarexample)
APDREcorr(focal=wolfexample$Radians, cont1=boarexample$Radians,  
    RE1=wolfexample$SamplingPeriod)

boarexample      Camera Trap Observations of wild boar

Description
Example dataset with boar observation times in radians and the sampling period during which each 
observation was recorded

Usage
boarexample
exampleAPDRE

Format

Dataframe with 2 columns and 35 rows Radians Time of observations, in radians from 0 to 2pi
SamplingPeriod Variable identifying camera trap sampling period

Source

\ Campbell L.A.D. 2017

Examples

## Not run: APDRE(focal=wolfexample$Radians, contingent=boarexample$Radians, RE1=wolfexample$SamplingPeriod,
weibullGLMM=FALSE, frechetGLMM=FALSE, gammaGLMM=FALSE,
lognormalGLMM=FALSE, infegaussianGLMM=FALSE,
mean=FALSE, HDI=FALSE, rawmean=TRUE)
## End(Not run)

exampleAPDREcorr

Executable Example of APDREcorr Function

Description

Example of APDREcorr function using data included in the package

Usage

eexampleAPDREcorr()

Value

Prints message with example code for using the APDREcorr function using data included in the package
plotAPDavg  
*Plot APDavg Posterior Samples*

**Description**

Plot histogram of samples from posterior distribution for estimated APDavg from `APDRE` function.

**Usage**

```r
plotAPDavg(model, histcol = "deeppink", linecol = "black")
```

**Arguments**

- `model`  
  Output from `APDRE` function, an object of class APD
- `histcol`  
  Colour for histogram
- `linecol`  
  Colour for 95% HDI line

**Value**

Histogram plot of samples from posterior distribution for estimated APDavg.

**Examples**

```r
data(wolfexample)
data(boarexample)
WolfBoarAPD <- APDRE(focal = wolfexample$Radians, contingent = boarexample$Radians,
  RE1 = wolfexample$SamplingPeriod)
plotAPDavg(WolfBoarAPD)
```

---

plotAPDcorr  
*Plot APDcorr Posterior Samples and Predicted Effects*

**Description**

Plot histogram of posterior distribution samples and/or predicted effects of parameter estimated from `APDREcorr` function.

**Examples**

```r
data(wolfexample)
data(boarexample)
WolfBoarAPDcorr <- APDREcorr(focal = wolfexample$Radians, contingent = boarexample$Radians,
  RE1 = wolfexample$SamplingPeriod)
plotAPDcorr(WolfBoarAPDcorr)
```
plotAPDcorr

Usage

plotAPDcorr(
  model,
  hist = TRUE,
  effects = TRUE,
  histcol = c("cyan4", "cyan4", "cyan4", "cyan4"),
  linecol = "red",
  effectcol = c("cyan4", "cyan4", "cyan4", "cyan4"),
  yname = "Focal",
  xname = c("C1", "C2", "C3", "C4")
)

Arguments

model Object of class APD of model output from APDREcorr function
hist Logical argument for whether to plot histogram of posterior distribution samples; default=TRUE
effects Logical argument for whether to plot predicted effects; default=TRUE
histcol Colour for posterior distribution histogram
linecol Colour for 95% HDI line on posterior distribution histogram
effectcol Colour for 95% HDI ribbon in line plot of predicted effects
yname Character vector of name of focal, to be used in the y axis labels
xname Character vector of name(s) of contingent(s), to be used in the x axis labels

Value

Histogram plot(s) of samples from posterior distribution for estimated relationship between focal and contingent(s), if plothist=TRUE
Plot of predicted effects (mean and 95% highest density interval) for relationship between focal APD and contingent(s) APD, if ploteffects=TRUE

Examples

data(wolfexample)
data(boarexample)
WolfBoarAPDc<-APDREcorr(focal=wolfexample$Radians, cont1=boarexample$Radians,
  RE1=wolfexample$SamplingPeriod)
plotAPDcorr(WolfBoarAPDc, yname="Wolf", xname="Boar")
plotAPDcv  

Plot APDcv Posterior Samples

Description
Plot histogram of samples from posterior distribution for estimated APD family-specific population coefficient of variation (CV) from `APDRE` function

Usage
plotAPDcv(model, histcol = "deeppink", linecol = "black")

Arguments
- model: Output from `APDRE` function, an object of class APD
- histcol: Colour for histogram
- linecol: Colour for 95% HDI line

Value
Histogram plot of samples from posterior distribution for estimated APDavg

Examples
```r
data(wolfexample)
data(boarexample)
WolfBoarAPD<-APDRE(focal=wolfexample$Radians, contingent=boarexample$Radians,
RE1=wolfexample$SamplingPeriod)
plotAPDcv(WolfBoarAPD)
```

wolfexample  

Camera Trap Observations of African golden wolves

Description
Example dataset with wolf observation times in radians and the sampling period during which each observation was recorded

Usage
wolfexample

Format
Dataframe with 2 columns and 30 rows Radians Time of observations, in radians from 0 to 2pi SamplingPeriod variable identifying camera trap sampling period
Source

\ Campbell L.A.D. 2017
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