Package ‘GerminaR’

June 11, 2021

Type Package

Title Indice}s and Graphics for Assess Seed Germination Process


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Suggests knitr, markdown, gsheet, inti

VignetteBuilder knitr

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### Description

Function use the `dtsm` function for plot the results.

### Usage

```r
fplot(
  data,
  type = "bar",
  x,
  y,
  group = NULL,
  xlab = NULL,
  ylab = NULL,
  glab = NULL,
  ylimits = NULL,
  xrotation = NULL,
  xtext = NULL,
```

---

**Plot line or bar graphic**
Arguments

data Output from ger_testcomp function
type Type of graphic. "bar" or "line"
x Axis x variable
y Axis y variable
group Group variable
xlab Title for the axis x
ylab Title for the axis y
glab Title for the legend
ylimits limits of the y axis
xrotation Rotation in x axis c(angle, h, v)
xtext Text labels in x axis
gtext Text labels in groups
legend the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)
sig Column with the significance
sigsize Font size in significance letters
error Show the error bar ("ste" or "std").
color colored figure c(TRUE, FALSE) or vector with the color.
opt Add new layer to the plot

Value

Line or bar plot

Examples

## Not run:

library(GerminaR)

smr <- ger_summary(SeedN = "seeds"
                   , evalName = "D"
                   , gtext = NULL,
                   legend = "top",
                   sig = NULL,
                   sigsize = 3,
                   error = NULL,
                   color = TRUE,
                   opt = NULL)
GerminaQuant

Description

GerminaQuant for R app allows make the calculation for the germination indices incredibly easy in a interactive applications build in base a GerminaR R package and Shiny. GermiQuant app is live!. Outputs change instantly as users modify inputs, without requiring a reload the app. The principal features of the application allow calculate the principal germination indices, statistical analysis and easy way to plot the results.

Usage

GerminaQuant(dependencies = FALSE)

Arguments

dependencies | Install package dependencies for run the app

Source

**ger_ASG**  
*ArcSin of Germination Percentage*

**Description**
This function calculates the arcsin of germination percentage for normalization.

**Usage**
\[
\text{ger\_ASG}(\text{SeedN}, \text{evalName}, \text{data})
\]

**Arguments**
- **SeedN**: Name of the column with the number of seeds sown.
- **evalName**: Prefix of the names of the periods of evaluation.
- **data**: The name of the data frame containing the data.

**Value**
It returns an vector with the ArcSin of Germination values.

**Examples**
```r
library(GerminaR)
dfr <- prosopis
gas <- ger_ASG(SeedN = "seeds", evalName = "D", data = dfr)
gas
```

---

**ger_boxp**  
*Boxplot graphic*

**Description**
Function use the raw data for made a boxplot graphic.

**Usage**
\[
\text{ger\_boxp}(\text{data}, \text{x}, \text{y}, \text{group} = \text{NULL}, \text{xlab} = \text{NULL}, \text{ylab} = \text{NULL}, \text{glab} = \text{NULL})
\]
ylimits = NULL,
xrotation = NULL,
legend = "top",
xtext = NULL,
gtext = NULL,
opt = NULL
)

Arguments

- **data**: raw data
- **x**: Axis x variable
- **y**: Axis y variable
- **group**: Group variable
- **xlab**: Title for the axis x
- **ylab**: Title for the axis y
- **glab**: Title for the legend
- **ylimits**: Limits and break of the y axis c(init, end, brakes)
- **xrotation**: Rotation in x axis c(angle, h, v)
- **legend**: the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)
- **xtext**: Text labels in x axis
- **gtext**: Text labels in groups
- **opt**: Add news layer to the plot

Value

boxplot

Examples

```r
## Not run:
library(GerminaR)
fb <- ger_summary(SeedN = "seeds", evalName = "D", data = prosopis)
ger_boxp(data = fb
  , x = "nacl"
  , y = "grp"
  , group = "temp"
)

## End(Not run)
```
---

**ger_CVG**

*Coefficient of Variance of the Mean Germination Time*

**Description**

This function calculates the coefficient of variation of the mean germination time.

**Usage**

```r
ger_CVG(evalName, data)
```

**Arguments**

- `evalName` Prefix of the names of the periods of evaluation.
- `data` The name of the data frame containing the data.

**Value**

It returns an vector with the values of Coefficient of Variance of germination.

**Examples**

```r
library(GerminaR)
dfr <- prosopis
cvg <- ger_CVG(evalName = "D", data = dfr)
cvg
```

---

**ger_GRP**

*Germination Seed Percentage*

**Description**

This function calculates the germination percentage related at total seed sown for experimental unit.

**Usage**

```r
ger_GRP(SeedN, evalName, data)
```

**Arguments**

- `SeedN` Name of the column with the number of seeds sown.
- `evalName` Prefix of the names of the periods of evaluation.
- `data` The name of the data frame containing the data.
Details

According Gouvea Labouriau (1983), the germinability of a sample of is the percentage of seeds in which the seed germination process comes to an end, in experimental conditions by the seminal intrauterine growth resulting protrusion (or emergence) of a living embryo.

Value

It returns an vector with the percentage of seed germinated.

References


Examples

```r
library(GerminaR)
dt <- prosopis
gp <- ger_GRP(SeedN = "seeds", evalName = "D", data = dt)
gp
```

```
<table>
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<tr>
<th>ger_GRS</th>
<th>Germinated Seed Number</th>
</tr>
</thead>
</table>
```

Description

This function calculates the number of seed germinated.

Usage

```
ger_GRS(evalName, data)
```

Arguments

- `evalName`: Prefix of the names of the periods of evaluation.
- `data`: The name of the data frame containing the data.

Value

Number of seed germinated

Examples

```r
library(GerminaR)
dt <- prosopis
grs <- ger_GRS(evalName = "D", data = dt)
grs
```
**Germination Speed**

Description

This function calculates the Germination Speed according at the time lapse of the evaluations.

Usage

\[
g_{\text{GSP}}(\text{evalName}, \text{data})
\]

Arguments

- `evalName`: Prefix of the names of the periods of evaluation.
- `data`: The name of the data frame containing the data.

Value

It returns a vector with the Germination Speed.

Examples

```r
library(GerminaR)
dfr <- prosopis
gsp <- ger_GSP(evalName = "D", data = dfr)
gsp
```

---

**Cumulative sum of germination by period of time for line graphic**

Description

This function makes a data table with the cumulative sum of values of germination by days.

Usage

\[
g_{\text{intime}}(\text{Factor}, \text{SeedN}, \text{evalName}, \text{method = "percentage"}, \text{data})
\]

Arguments

- `Factor`: Factor which will be graph in time
- `SeedN`: Name of the column with the seed numbers
- `evalName`: Prefix of the evaluation variable
- `method`: Type of cumulative germination. "percentage" or "relative"
- `data`: Data with the germination evaluation process
Details

Need a summary by factor before use it with function SummaryBy.

Value

Data frame with the germination by period

Examples

```r
## Not run:
library(GerminaR)
data <- prosopis
grt <- ger_intime(Factor = "temp",
  SeedN = "seeds",
  evalName = "D",
  method = "rel",
  data = data)
head(grt, 10)
fplot(data = grt,
  type = "line",
  x = "evaluation",
  y = "mean",
  groups = "temp",
  sig = NULL)
## End(Not run)
```
Details

The average speed of germination is defined as the reciprocal of the average time germination (RANAL; SANTANA, 2006).

Value

It returns an vector with the values of Mean Germination Rate

References


Examples

library(GerminaR)
dfr <- prosopis
mgr <- ger_MGR(evalName = "D", data = dfr)
mgr

---

ger_MGT  Mean Germination Time

Description

This function calculates the mean germination time of germination according at the time lapse of the evaluations.

Usage

ger_MGT(evalName, data)

Arguments

evalName  Prefix of the names of the periods of evaluation.
data  The name of the data frame containing the data.

Details

It was proposed by Haberlandt in 1875. It is calculated as the weighted average germination time. The number of germinated seeds at the intervals established for the collection of data is used as weight. It is expressed in terms of the same units of time used in the germination count (CZABATOR, 1962).

Value

It returns an vector with the values of Mean Germination Time.
References


Examples

```r
library(GerminaR)
dfr <- prosopis
mgt <- ger_MGT(evalName = "D", data = dfr)
mgt
```

---

### ger_SDG

*Standard deviation of the Mean Germination Time*

**Description**

This function calculates the standard deviation of the mean germination time.

**Usage**

```r
ger_SDG(evalName, data)
```

**Arguments**

- `evalName`: Prefix of the names of the periods of evaluation.
- `data`: The name of the data frame containing the data.

**Value**

It returns a vector with the values of Standard deviation of germination.

**Examples**

```r
library(GerminaR)
dfr <- prosopis
sdg <- ger_SDG(evalName = "D", data = dfr)
sdg
```
**ger_summary**  

*Summary of Germination indices*

**Description**

This function makes a data table with the result of germination indices for each experimental unit.

**Usage**

```r
ger_summary(SeedN, evalName, data)
```

**Arguments**

- `SeedN` Name of the column with the seed numbers
- `evalName` Prefix of the evaluation variable
- `data` The name of the data frame containing the data.

**Value**

Data frame with the summary values of germination variables.

**Examples**

```r
library(GerminaR)
fb <- prosopis
smr <- ger_summary(SeedN = "seeds", evalName = "D", data = fb)
smr
```

**ger_SYN**  

*Germination Synchronization Index*

**Description**

This function calculates the germination synchronization of the germination process.

**Usage**

```r
ger_SYN(evalName, data)
```

**Arguments**

- `evalName` Prefix of the names of the periods of evaluation.
- `data` The name of the data frame containing the data.
Details

The Synchory Index $Z$ has been proposed to assess the degree of overlap between flowering individuals in a population. By adopting the idea expressed by PRIMACK, R.B. (1980) the synchrony of one seed with other included in the same replication. $Z = 1$ when germination of all the seeds occurs at the same time and $Z = 0$ when at least two seeds can germinate one each time. $Z$ produces a number if and only if there are two seeds finishing the seed germination process at the same time. Thus, the value of $Z$ assessments is the grade of overlap between seed germination.

Value

It returns an vector with the values of Germination synchrony

References


Examples

```r
library(GerminaR)
dfr <- prosopis
syn <- ger_SYN(evalName = "D", data = dfr)
syn
```

```
  ger_testcomp          Multiple comparison test
```

Description

Function analysis of variance for summary data.

Usage

```r
ger_testcomp(aov, comp, type = "snk", sig = 0.05)
```

Arguments

- `aov`: lm o aov result function.
- `comp`: treatments will be compared.
- `type`: method for made comparison analysis: c("snk", "tukey", "duncan").
- `sig`: significance level. Default 0.05

Value

Table with complete data for graphics
Examples

```r
## Not run:
library(GerminaR)
library(dplyr)
data <- prosopis %>% mutate(across(c(nacl, temp, rep), as.factor))
smr <- ger_summary(SeedN = "seeds", evalName = "D", data = data)
aov <- aov(grp ~ nacl*temp, smr)
mc <- ger_testcomp(aov = aov
  , comp <- c("nacl", "temp")
)
## End(Not run)
```

g**er** _UNC_  

Germination Uncertainty

Description

This function calculates the germination uncertainty in the germination process.

Usage

```
ger_UNC(evalName, data)
```

Arguments

- **evalName**: Prefix of the names of the periods of evaluation.
- **data**: The name of the data frame containing the data.

Details

The uncertainty index $u$ is an adaptation of Shannon index measures the degree of uncertainty in predicting the informational entropy or uncertainty associated with the distribution of the relative frequency of germination (Gouveia Laboriau 1983; Laboriau; Valadares, 1983). Low values of $u$ indicate frequencies with short peaks, i.e. the more concentrated the germination in time. Just a germinated seed changes the value of $u$. This means that $u$ measures the degree of germination scattering.

Value

It returns an vector with the values of Germination Uncertainty.
References


Examples

library(GerminaR)
dfr <- prosopis
unc <- ger_UNC(evalName = "D", data = dfr)
unc

---

**ger_VGT**

*Variance of the Mean Germination Time*

Description

This function calculates the variance of the mean germination time.

Usage

`ger_VGT(evalName, data)`

Arguments

- `evalName`: Prefix of the names of the periods of evaluation.
- `data`: The name of the data frame containing the data.

Value

It returns an vector with the values of Variance of Germination

Examples

library(GerminaR)
dfr <- prosopis
vgt <- ger_VGT(evalName = "D", data = dfr)
vgt
osmp

Osmotic potential calculator

Description
Function to calculate the grams of salt or PEG-6000 needed for determined osmotic potential

Usage
osmp(type = "salt", vol, pres, temp, mw, ki)

Arguments
- type: Salt or PEG-6000 c("salt", "peg6000"). Default: "salt".
- vol: volume (liters)
- pres: Pressure (Mpa) in negative values. 1 bar = 0.1 Mpa
- temp: Temperature (centigrade)
- mw: Molecular weight
- ki: Salt dissociation constant (NaCl = 1.8)

Value
Numeric value (grams)

prosopis

Germination under different osmotic potentials and temperatures.

Description
Dataset containing information from germination experiment with Prosopis juliflor under different osmotic potentials and temperatures.

- rep a numeric vector, repetitions or replications.
- nacl a numeric vector, NaCl osmotic potentials levels in Mpa to be evaluated.
- temp a numeric vector, temperature levels in centigrades to be evaluated.
- seeds a numeric vector, number of seed used for experimental unit.
- D0-D10 numeric vectors, ten evaluations days performed in the germination experiment.

Usage
prosopis
Format

A data frame with 15 columns and 80 rows.

Source

LEV-UFRPE

References


---

rep_row

Repeated Rows in a data matrix

Description

This function made a data table with the evaluation days of germination

Usage

rep_row(Rseq, Nrow)

Arguments

- `Rseq`: Row sequence for the data matrix
- `Nrow`: Number of rows for the data matrix

Value

Data Matrix with day of the germination

---

textcolor

Colourise text for display in the terminal.

Description

If R is not currently running in a system that supports terminal colours the text will be returned unchanged.

Usage

textcolor(text, fg = "red", bg = NULL)
Arguments

text character vector
fg foreground colour, defaults to white
bg background colour, defaults to transparent

Details

Allowed colours are: black, blue, brown, cyan, dark gray, green, light blue, light cyan, light gray,
light green, light purple, light red, purple, red, white, yellow

Author(s)

testthat package

Examples

print(textcolor("Red", "red"))
cat(textcolor("Red", "red"), "\n")
cat(textcolor("White on red", "white", "red"), "\n")

webTable

Description

Web table

Usage

webTable(
  data,
  caption = NULL,
  digits = 3,
  rnames = FALSE,
  buttons = NULL,
  file_name = NULL,
  scrolly = NULL
)
Arguments

- `data`  Dataset.
- `caption`  Title for the table.
- `digits`  Digits number in the table exported.
- `rnames`  Row names.
- `buttons`  Buttons: "excel", "copy" or "none". Default c("excel", "copy")
- `file_name`  Excel file name
- `scroll_y`  Windows height to show the table
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