

Package ‘GerminaR’

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Type Package

Title Indices and Graphics for Assess Seed Germination Process

Version 2.0.0

Description

A collection of different indices and visualization techniques for evaluate the seed germination process in ecophysiological studies (Lozano-Isla et al. 2019) <doi:10.1111/1440-1703.1275>.

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URL <https://flavjack.github.io/germinquant/>

BugReports <https://github.com/flavjack/germinar/issues>

Imports agricolae, shiny, dplyr, tidyr, ggplot2, tibble, purrr, gtools

Depends R (>= 3.5.0)

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

NeedsCompilation no

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fplot	<i>Plot line or bar graphic</i>
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Description

Function use the dtsm function for plot the results

Usage

```
fplot(  
  data,  
  type = "bar",  
  x,  
  y,  
  groups,  
  xlab = NULL,  
  ylab = NULL,  
  glab = NULL,  
  legend = "top",  
  sig = NULL,  
  error = "ste",  
  limits = NULL,  
  brakes = NULL,
```

```

    xbrks = NULL,
    gbrks = NULL,
    color = TRUE
  )

```

Arguments

<code>data</code>	Output from <code>ger_testcomp</code> function
<code>type</code>	Type of graphic. "bar" or "line"
<code>x</code>	Axis x variable
<code>y</code>	Axis y variable
<code>groups</code>	Group variable
<code>xlab</code>	Title for the axis x
<code>ylab</code>	Title for the axis y
<code>glab</code>	Title for the legend
<code>legend</code>	the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)
<code>sig</code>	Column with the significance
<code>error</code>	Show the error bar ("ste" or "std").
<code>limits</code>	limits of the y axis
<code>brakes</code>	break of the y axis
<code>xbrks</code>	axis brakes labels in string with double space
<code>gbrks</code>	legend label in string with double space
<code>color</code>	colored figure (TRUE), otherwise black & white (FALSE)

Value

Line o bar plot

Examples

```

## 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")
  )

```

```

data <- mc$table

fplot(data = data
      , type = "line"
      , x = "temp"
      , y = "grp"
      , groups = "nacl"
      , limits = c(0,150)
      , brakes = 20
      , color = FALSE
      )

## End(Not run)

```

GerminaQuant

GerminaQuant for R

Description

GermiQuant 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()
```

Source

Lozano-Isla, F., Benites Alfaro, O., & Pompelli, M. F. (2016). GerminaQuant for R (Patent No. BR 51 2016 001327-3). <https://flavjack.shinyapps.io/germinaquant/>

ger_ASG

ArcSin of Germination Percentage

Description

This function calculates the arcsin of germination percentage for normalization.

Usage

```
ger_ASG(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.

Value

It returns an vector with the ArcSin of Germination values

Examples

```
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

```
ger_boxp(
  data,
  x,
  y,
  z,
  ylab = NULL,
  xlab = NULL,
  lgl = NULL,
  lgd = "top",
  brk = NULL,
  font = 1
)
```

Arguments

data	raw data
x	Axis x variable
y	Axis y variable
z	Group variable
ylab	Title for the axis y

xlab	Title for the axis x
lgl	Title for the legend
lgd	the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)
brk	break of the y axis
font	letter size in plot

Value

boxplot

ger_CVG	<i>Coefficient of Variance of the Mean Germination Time</i>
---------	---

Description

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

Usage

```
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

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

ger_GRP	<i>Germination Seed Percentage</i>
---------	------------------------------------

Description

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

Usage

```
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

LABOURIAU, L. G.; VALADARES, M. E. B. The germination of seeds. OEA, Washington, DC, 1983.

Examples

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

ger_GRS	<i>Germinated Seed Number</i>
---------	-------------------------------

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

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

ger_GSP	<i>Germination Speed</i>
---------	--------------------------

Description

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

Usage

```
ger_GSP(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 Germination Speed

Examples

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

ger_intime

*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

```
ger_intime(Factor, SeedN, evalName, method = "percentage", 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

```
## 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)
```

ger_MGR

Mean Germination Rate

Description

This function calculates the mean germination rate of the germination.

Usage

```
ger_MGR(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 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

RANAL, M. A.; SANTANA, D. G. DE. How and why to measure the germination process? Revista Brasileira de Botanica, v. 29, n. 1, p. 1-11, mar. 2006.

Examples

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

ger_MGT	<i>Mean Germination Time</i>
---------	------------------------------

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

CZABATOR, F. J. Germination value: an index combining speed and completeness of pine seed germination. Forest Science, v. 8, n. 4, p. 386-396, 1962.

Examples

```
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

```
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 an vector with the values of Standard deviation of germination

Examples

```
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

```
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

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

ger_SYN

Germination Synchronization Index

Description

This function calculates the germination synchronization of the germination process.

Usage

```
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 Synchrony 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

RANAL, M. A.; SANTANA, D. G. DE. How and why to measure the germination process? Revista Brasileira de Botanica, v. 29, n. 1, p. 1-11, mar. 2006.

Examples

```
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

```
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

```
## 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)
```

ger_UNC	<i>Germination Uncertainty</i>
---------	--------------------------------

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 (GOUVEA LABOURIAU 1983; LABOURIAU; 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

GOUVEA LABOURIAU, L. L. G. L. A germinacao das sementes. Washington. LABOURIAU, L. G.; VALADARES, M. E. B. The germination of seeds. OEA, Washington, DC, 1983.

Examples

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

ger_VGT	<i>Variance of the Mean Germination Time</i>
---------	--

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	<i>Osmotic potential calculator</i>
------	-------------------------------------

Description

Function to calculate the grams of salt or PEG-6000 needed for determinated 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

MIRANDA, R. D. Q.; CORREIA, R. M.; DE ALMEIDA-CORTEZ, J. S.; POMPELLI, M. F. Germination of Prosopis juliflora (Sw.) D.C. seeds at different osmotic potentials and temperatures. Plant Species Biology, v. 29, n. 3, p. E9-E20, set. 2014.

rep_row	<i>Repeated Rows in a data matrix</i>
---------	---------------------------------------

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

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