

Package ‘GerminaR’

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Type Package

Title Germination Indexes for Seed Germination Variables for Ecophysiological Studies

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BugReports <https://github.com/Flavjack/GerminaR/issues>

Description Different types of seed indexes, rates and visualization techniques are used to provide a robust approach for germination data analysis. The package aims to make available germination seed indexes and graphical functions to analyze germination seed data.

Imports agricolae, assertthat, DT, dplyr, tibble, ggplot2, gtools, gsheets, magrittr, readxl, shiny, shinydashboard, tidyr

Depends R (>= 3.2.3)

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

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LazyData true

RoxygenNote 6.0.1

NeedsCompilation no

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R topics documented:

dtsm	2
evalDays	3
evalFactor	3
fplot	4
GerminaQuant	5
ger_ASG	5
ger_boxp	6
ger_cumsum	7
ger_CVG	7
ger_getdata	8
ger_GRP	8
ger_GRS	9
ger_GSP	10
ger_intime	10
ger_leq	11
ger_linereg	12
ger_MGR	13
ger_MGT	14
ger_SDG	15
ger_summary	15
ger_SYN	16
ger_testcomp	17
ger UNC	17
ger_VGT	18
prosopis	19
rep_row	20
starts_with	20
stat_sm	21
Index	22

dtsm

Mean Comparison Table Summary

Description

Function using resulting output from mean comparison test from agricolae package optimized for graphs.

Usage

```
dtsm(meanComp)
```

Arguments

meanComp Object list with the result from mean comparison test

Value

Table with complete data for graphics

evalDays	<i>Select Evaluation Days</i>
----------	-------------------------------

Description

Give matrix with the evaluation days

Usage

```
evalDays(evalName, data)
```

Arguments

evalName	Prefix of the evaluation variable
data	Data with germination values

Value

Evaluation columns

Examples

```
## Not run:  
library(GerminaR)  
dt <- prosopis  
dm <- evalDays(evalName = "D", data = dt)  
dm  
  
## End(Not run)
```

evalFactor	<i>Select Factors of germination matrix</i>
------------	---------------------------------------------

Description

Give matrix with the factor

Usage

```
evalFactor(evalName, data)
```

Arguments

evalName	Prefix of the evaluation variable
data	Data with germination values

Value

Factor columnsl

Examples

```
## Not run:
library(GerminaR)
dt <- prosopis
dm <- evalFactor(evalName = "D", data = dt)
dm

## End(Not run)
```

fplot

Plot line or bar graphic

Description

Function use the dtsm funtion for plot the results

Usage

```
fplot(data, type = "bar", x, y, z, ylab = NULL, xlab = NULL, lgl = NULL,
      lgd = "top", sig = NULL, erb = FALSE, lmt = NULL, brk = NULL,
      xbl = NULL, zbl = NULL, color = TRUE, font = 1)
```

Arguments

data	Output dtsm fuction
type	Type of graphic. "bar" or "line"
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)
sig	Significance of the result (letters)

erb	Show the error bar.
lmt	limits of the y axis
brk	break of the y axis
xb1	axis brakes labels in strign with doble space
zb1	legend label in strign with doble space
color	colored figure (TRUE), otherwise black & white (FALSE)
font	letter size in plot

Value

Line o bar plot

GerminaQuant	<i>@description GermiQuant App allows make the calculation for the germination variables 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 variables, statistical analysis and easy way to plot the results.</i>
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Description

@description GermiQuant App allows make the calculation for the germination variables 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 variables, statistical analysis and easy way to plot the results.

Usage

GerminaQuant()

ger_ASG	<i>ArcSin of Germination Percentage</i>
---------	-----------------------------------------

Description

This function calculates the arcsin of germination percentage for normalization.

Usage

ger_ASG(SeedN, evalName, data)

Arguments

SeedN	Name of the colum 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)
dt <- prosopis
gas <- ger_ASG(SeedN = "seeds", evalName = "D", data = dt)
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_cumsum	<i>Cumulative sum of germination matrix</i>
------------	---------------------------------------------

Description

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

Usage

```
ger_cumsum(SeedN, evalName, method = "percentage", data)
```

Arguments

SeedN	Name of the colonn with the seed numbers
evalName	Prefix of the evalaution variable
method	Type of cummulative germination. "percentage" or "relative"
data	Data with the germination avaliation process

Value

Data frame with the cumulative sum

Examples

```
library(GerminaR)
dt <- prosopis
gcs <- ger_cumsum(SeedN = "seeds", evalName = "D", method = "percentage", data = dt)
head(gcs, 10)
```

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)
dt <- prosopis
cvg <- ger_CVG(evalName = "D", data = dt)
cvg
```

ger_getdata	<i>Import google spreadsheet or xlsx file</i>
-------------	-----------------------------------------------

Description

function to import information from google spreadsheet or xlsx file.

Usage

```
ger_getdata(dir, sheet = 1)
```

Arguments

dir	local file directory for xlsx document or url from google spreadsheet
sheet	if is a xlsx file, you can choose the sheet number

Value

data frame

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 colum 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

Germinated Seed Number

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 germianated

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)
dt <- prosopis
gsp <- ger_GSP(evalName = "D", data = dt)
gsp
```

ger_intime	<i>Cumulative sum of germination by period of time for line graphic</i>
------------	-------------------------------------------------------------------------

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 wich will be graph in time
SeedN	Name of the colonn with the seed numbers
evalName	Prefix of the evalaution variable
method	Type of cummulative germination. "percentage" or "relative"
data	Data with the germination avaliation process

Details

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

Value

Data frame with the germination by period

Examples

```
library(GerminaR)
dt <- prosopis
grt <- ger_intime(Factor = "nacl", SeedN = "seeds",
                 evalName = "D", method = "percentage", data = dt)
head(grt, 10)
```

ger_leq	<i>Regresion line equation</i>
---------	--------------------------------

Description

Construc the regression line equation

Usage

```
ger_leq(x, y, data)
```

Arguments

x	variable in the x axis
y	variable in the y axis
data	dataframe with the information

Value

regression equation

 ger_linereg

Plot line regression

Description

Function plot linea regression

Usage

```
ger_linereg(data, x, y, z = NULL, ylab = NULL, xlab = NULL, lgl = NULL,
  lgd = "top", xbrk = NULL, ybrk = NULL, zbl = NULL, color = TRUE,
  font = 1, rlx = NULL, rly = NULL)
```

Arguments

data	Output dtsm fuction
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)
xbrk	brakes for x axis
ybrk	brakes for y axis
zbl	legend label in strign with doble space
color	colored figure (TRUE), otherwise black & white (FALSE)
font	letter size in plot
rlx	regression line position in axis x.
rly	regression line position in axis y.

Value

Line regression plot

ger_MGR	<i>Mean Germination Rate</i>
---------	------------------------------

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)
dt <- prosopis
mgr <- ger_MGR(evalName = "D", data = dt)
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)
dt <- prosopis
mgt <- ger_MGT(evalName = "D", data = dt)
mgt
```

ger_SDG	<i>Standard deviation of the Mean Germination Time</i>
---------	--------------------------------------------------------

Description

This function calculates the standard desviation 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 desviation of germination

Examples

```
library(GerminaR)
dt <- prosopis
sdg <- ger_SDG(evalName = "D", data = dt)
sdg
```

ger_summary	<i>Summary of Germination Variables</i>
-------------	-----------------------------------------

Description

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

Usage

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

Arguments

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

Value

Data frame with the summary values of germination variables.

Examples

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

ger_testcomp	<i>Multiple comparison test</i>
--------------	---------------------------------

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

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: [s.n.]. LABOURIAU, L. G.; VALADARES, M. E. B. The germination of seeds. OEA, Washington, DC, 1983.

Examples

```
library(GerminaR)
dt <- prosopis
unc <- ger UNC(evalName = "D", data = dt)
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)
dt <- prosopis
vgt <- ger_VGT(evalName = "D", data = dt)
vgt
```

prosopis	<i>Germination under different osmotic potentials and temperatures.</i>
----------	-------------------------------------------------------------------------

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

```
GerminaR
```

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 sequance for the data matrix
Nrow	Number of rows for the data matrix

Value

Data Matrix with day of the germination

starts_with	<i>Select colum according the initial letters of the words</i>
-------------	----------------------------------------------------------------

Description

Select colum according the initial letters of the words

Usage

```
starts_with(vars, match, ignore.case = TRUE)
```

Arguments

vars	vars
match	match
ignore.case	case

Details

<https://github.com/hadley/dplyr/blob/50309db8f04cbcc87e4568a4bfa1f0c718e824c9/R/select-utils.R>

Value

Matrix with the select colum

Author(s)

Hadley Wickham

stat_sm	<i>Descriptive Statistics for a model</i>
---------	-------------------------------------------

Description

Function to summary descriptive statistics from a model

Usage

```
stat_sm(modelo, data)
```

Arguments

modelo	an object containing the results returned by a model fitting function
data	data set used for the model

Value

data frame

Index

dtsm, 2

evalDays, 3

evalFactor, 3

fplot, 4

ger_ASG, 5

ger_boxp, 6

ger_cumsum, 7

ger_CVG, 7

ger_getdata, 8

ger_GRP, 8

ger_GRS, 9

ger_GSP, 10

ger_intime, 10

ger_leq, 11

ger_linereg, 12

ger_MGR, 13

ger_MGT, 14

ger_SDG, 15

ger_summary, 15

ger_SYN, 16

ger_testcomp, 17

ger UNC, 17

ger_VGT, 18

GerminaQuant, 5

GerminaR (prosopis), 19

prosopis, 19

rep_row, 20

starts_with, 20

stat_sm, 21