# Package 'GerminaR'

March 28, 2020

**Type** Package

**Title** Indices and Graphics for Assess Seed Germination Process

**Version** 1.4.2

**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>.

**Date** 2020-03-23

**URL** https://flavjack.github.io/germinaquant/

**BugReports** https://github.com/flavjack/germinar/issues

**Imports** agricolae, dplyr, ggplot2, magrittr, readxl, tibble, tidyr, assertthat, DT, purrr, gtools, gsheet, shiny, shinydashboard

**Depends** R (>= 3.5.0)

**Suggests** testthat, knitr, rmarkdown

**VignetteBuilder** knitr

**License** MIT + file LICENSE

**LazyData** true

**RoxygenNote** 7.1.0

**NeedsCompilation** no

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**Repository** CRAN

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# R **topics documented:**

---

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 | *Select Evaluation Days* |
|---|---|

---

## Description

Give matrix with the evaluation days

## Usage

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

## Arguments

| | |
|---|---|
| evalName | Prefix of the evalaution variable |
| data | Data with germination values |

## Value

Evalution colums

## Examples

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

## End(Not run)
```

---

evalFactor                  *Select Factors of germination matrix*

---

### Description

Give matrix with the factor

### Usage

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

### Arguments

| | |
|---|---|
| evalName | Prefix of the evalaution variable |
| data | Data with germination values |

### Value

Factor columsl

### 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 |
| xbl | axis brakes labels in strign with doble space |
| zbl | 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 | *@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.* |
|---|---|

## Description

@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()
```

| 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 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)
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_cumsum                    *Cumulative sum of germination matrix*

---

### 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                    *Coefficient of Variance of the Mean Germination Time*

---

### 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_getdata | *Import google spreadsheet or xlsx file* |
|---|---|

---

### 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 | *Germination Seed Percentage* |
|---|---|

---

### 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 *Germination Speed*

---

### 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 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                         *Regresion line equation*

---

## 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                          *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                          *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

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 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)
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 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 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**

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 analisis 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 comparision analysis: c("snk", "tukey", "duncan"). |
| sig | significance level. Default 0.05 |

### Value

Table with complete data for graphics

---

ger_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 (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)
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
```

---

metamorphosis                   *Transform dataframe based in a dictionary*

---

## Description

Transform all fieldbook data frame according to data dictionary

## Usage

```
metamorphosis(fieldbook, dictionary, from, to, index, colnames)
```

## Arguments

| | |
|---|---|
| fieldbook | data frame with the original information |
| dictionary | data frame with at least 3 columns (original names, new names and variable type) |
| from | Column name of a data frame with the original names of the variables |
| to | Column name of a data frame with the new names for the variables |
| index | Column name of a data frame with the type and level of the variables |
| colnames | Character vector with the column names |

## Value

List with original fieldbook, variables and new fieldbook

---

osmp                            *Osmotic potential calculator*

---

## 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)

---

| plot_gr | *Plot line or bar graphic* |
|---|---|

---

## Description

Function for present the results in line or bar plot

## Usage

```
plot_gr(
  data,
  type = "bar",
  x,
  y,
  group,
  x_lab = NULL,
  y_lab = NULL,
  g_lab = NULL,
  lgd = "top",
  sig = NULL,
  erb = FALSE,
  y_lmt = NULL,
  y_brk = NULL,
  x_brk = NULL,
  g_brk = NULL,
  color = TRUE,
  ang = 0,
  font = 1.5
)
```

## Arguments

| | |
|---|---|
| `data` | Output dtsm fuction |
| `type` | Type of graphic. "bar" or "line" |
| `x` | Axis x variable |
| `y` | Axis y variable |
| `group` | Group variable |
| `x_lab` | Title for the axis x |
| `y_lab` | Title for the axis y |
| `g_lab` | 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. |
| `y_lmt` | limits of the y axis |
| `y_brk` | break of the y axis |
| `x_brk` | axis brakes labels in strign with doble space |
| `g_brk` | legend label in strign with doble space |
| `color` | colored figure (TRUE), otherwise black & white (FALSE) |
| `ang` | x text label angle |
| `font` | letter size in plot |

## Value

Line o bar plot

---

| 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 evelauted.
- `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 | *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 sequance for the data matrix |
| Nrow | Number of rows for the data matrix |

## Value

Data Matrix with day of the germination

---

stat_sm                      *Descriptive Statistics for a model*

---

### 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

---

web_table                     *HTML tables for markdown documents*

---

### Description

Export tables with download, pasta and copy buttons

### Usage

```
web_table(data, caption = NULL, digits = 3, rnames = FALSE, buttons = NULL)
```

### Arguments

| | |
|---|---|
| data | dataset |
| caption | Title for the table |
| digits | digits number in the table exported |
| rnames | row names |
| buttons | "excel", "copy" or "none". Default c("excel", "copy") |

### Value

table in markdown format for html documents

# Index