Package 'germinationmetrics'

August 20, 2022

Title Seed Germination Indices and Curve Fitting

Version 0.1.7

Description Provides functions to compute various germination indices such as
germinability, median germination time, mean germination time, mean
germination rate, speed of germination, Timson's index, germination value,
coefficient of uniformity of germination, uncertainty of germination
process, synchrony of germination etc. from germination count data. Includes
functions for fitting cumulative seed germination curves using
four-parameter hill function and computation of associated parameters. See
the vignette for more, including full list of citations for the methods
implemented.

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Encoding UTF-8

LazyData true

Depends R (>= 3.5.0)

VignetteBuilder knitr

RoxygenNote 7.2.1

Imports broom,
data.table,
ggplot2,
ggrepel,
mathjaxr,
minpack.lm,
plyr,
Rdpack,
utils,
stats

Suggests knitr,
rmarkdown,
reshape2,
pander,
XML,
httr,
RCurl

RdMacros mathjaxr,
Rdpack

URL https://github.com/aravind-j/germinationmetrics,

https://aravind-j.github.io/germinationmetrics/

https://CRAN.R-project.org/package=germinationmetrics

https://doi.org/10.5281/zenodo.1219630

BugReports https://github.com/aravind-j/germinationmetrics/issues

R topics documented:

CUGerm   *Coefficient of uniformity of germination*

Description

Compute the Coefficient of uniformity of germination (CUG).

Usage

```
CUGerm(germ.counts, intervals, partial = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

CUG is computed as follows (Heydecker 1972; Bewley and Black 1994).

$$CUG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} (\overline{T} - T_i)^2 N_i}$$

Where, $\overline{T}$ is the the mean germination time, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.

Value

The value of the coefficient of uniformity of germination as time^{-2}.

References

Bewley JD, Black M (1994). *Seeds: Physiology of Development and Germination.*. Plenum Publishing Corporation, New York, USA. ISBN 0-306-44748-7.

Heydecker W (1972). *Seed Ecology. Proceedings of the Nineteenth Easter School in Agricultural Science, University of Nottingham, 1972*. Pennsylvania State University Press, University Park, USA.

See Also

GermSynchrony, MeanGermTime

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
CUGerm(germ.counts = x, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------------
CUGerm(germ.counts = y, intervals = int, partial = FALSE)
```

EmergenceRateIndex   *Emergence Rate Index or Germination Rate Index*

Description

Compute the Emergence rate index or Germination rate index according to

- Shmueli and Goldberg (1971) and it's modification by de Santana and Ranal (2004) (Ranal and de Santana 2006);
- Bilbro and Wanjura (1982); and
- Fakorede and Ayoola (1980), Fakorede and Ojo (1981), and Fakorede and Agbana (1983).

Usage

```
EmergenceRateIndex(
  germ.counts,
  intervals,
  partial = TRUE,
  total.seeds = NULL,
  method = c("shmueligoldberg", "sgsantanaranal", "bilbrowanjura", "fakorede")
)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.
total.seeds	Total number of seeds.
method	The method to be used. Either `"shmueligoldberg"`, `"sgsantanaranal"`, `"bilbrowanjura"` or `"fakorede"`. Default is `"shmueligoldberg"` (see **Details**).

Value

The value of the Emergence rate index with the units according to `method` as follows.

shmueligoldberg	count
sgsantanaranal	no unit
bilbrowanjura	$\text{count}\,time^{-1}$
fakorede	$time\,\text{count}^{-1}$

Details

Several germination indices are referred to as Emergence rate Index (ERI).

Shmueli and Goldberg (1971): With argument `method` specified as `"shmueligoldberg"` ERI is estimated as follows.

$$ERI = \sum_{i=i_0}^{k-1} N_i(k-i)$$

Where, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), i_0 is the time interval when emergence/germination started, and k is the total number of time intervals.

A modification for the same was suggested by de Santana and Ranal (2004) (Ranal and de Santana 2006) and is estimated by dividing Emergence rate index (ERI) by total number of emerged seedlings (or germinated seeds) as follows with argument `method` specified as `"sgsantanaranal"`).

$$ERI_{mod} = \frac{\sum_{i=i_0}^{k-1} N_i(k-i)}{N_g} = \frac{ERI}{N_g}$$

Where, N_g is the total number of germinated seeds at the end of the test, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), i_0 is the time interval when emergence/germination started, and k is the total number of time intervals.

Bilbro and Wanjura (1982): With argument `method` specified as `"bilbrowanjura"` ERI is the estimated as follows.

$$ERI = \frac{\sum_{i=1}^{k} N_i}{\overline{T}} = \frac{N_g}{\overline{T}}$$

Where, N_g is the total number of germinated seeds at the end of the test, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and $\overline{T}$ is the mean germination time or mean emergence time.

Fakorede and Ayoola (1980); Fakorede and Ojo (1981); Fakorede and Agbana (1983): With argument `method` specified as `"fakorede"` ERI is the estimated as follows.

$$ERI = \frac{\overline{T}}{FGP/100}$$

Where, $\overline{T}$ is the Mean germination time and FGP is the final germination time.

Others: Apart from the above the above, the name Emergence rate index (ERI) has also been used to for the mathematical expressions for Speed of germination (`GermSpeed`) (Allan et al. 1962; Erbach 1982), Timson's index (`TimsonsIndex`) (Chaudhary and Ghildyal 1970), and George's index (`GermRateGeorge`) (Chopra and Chaudhary 1980).

References

Allan RE, Vogel OA, Peterson CJ (1962). "Seedling emergence rate of fall-sown wheat and its association with plant height and coleoptile length." *Agronomy Journal*, **54**(4), 347.

Bilbro JD, Wanjura DF (1982). "Soil crusts and cotton emergence relationships." *Transactions of the ASAE*, **25**(6), 1484–1487.

Chaudhary TN, Ghildyal BP (1970). "Effect of temperature associated with levels of bulk density on rice seedling emergence." *Plant and Soil*, **33**(1), 87–90.

Chopra UK, Chaudhary TN (1980). "Effect of soil temperature alteration by soil covers on seedling emergence of wheat (*Triticum aestivum* L.) sown on two dates." *Plant and Soil*, **57**(1), 125–129.

Erbach DC (1982). "Tillage for continuous corn and corn-soybean rotation." *Transactions of the ASAE*, **25**(4), 906–0911.

Fakorede MAB, Agbana SB (1983). "Heterotic effects and association of seedling vigour with mature characteristics and grain yield in some tropical maize cultivars." *Maydica*, **28**, 327–338.

Fakorede MAB, Ayoola AO (1980). "Relation between seedling vigor and selection for yield improvement in maize." *Maydica*, **25**(3), 135–147.

Fakorede MAB, Ojo DK (1981). "Variability for seedling vigour in maize." *Experimental Agriculture*, **17**(2), 195–201.

Ranal MA, de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), 1–11.

Shmueli M, Goldberg D (1971). "Emergence, early growth, and salinity of five vegetable crops germinated by sprinkle and trickle irrigation in an arid zone." *HortScience*, **6**, 563–565.

de Santana DG, Ranal MA (2004). *Analise Da Germinacao: Um Enfoque Estatistico*. Universidade de Brasilia, Brasilia.

See Also

[GermSpeed](), [TimsonsIndex](), [GermRateGeorge]()

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
EmergenceRateIndex(germ.counts = x, intervals = int)
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "shmueligoldberg")
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "sgsantanaranal")
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "bilbrowanjura")
EmergenceRateIndex(germ.counts = x, intervals = int,
                   total.seeds = 50, method = "fakorede")

# From cumulative germination counts
#----------------------------------------------------------------------------
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,)
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "shmueligoldberg")
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "sgsantanaranal")
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "bilbrowanjura")
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   total.seeds = 50, method = "fakorede")
```

FirstGermTime   *Time for first, last and peak germination*

Description

Compute the following metrics:

FirstGermTime Time of first germination or Germination time lag (t_0) (Edwards 1932; Czabator 1962; Goloff and Bazzaz 1975; Labouriau 1983; Ranal 1999; Quintanilla et al. 2000).

LastGermTime Time of last germination (t_g) (Edwards 1932; Labouriau 1983; Ranal and de Santana 2006).

TimeSpreadGerm Time spread of germination (Al-Mudaris 1998; Kader 2005) or Germination distribution (Schrader and Graves 2000).

PeakGermTime Peak time of germination or Modal time of germination (t_{peak}) (Ranal and de Santana 2006).

Usage

```
FirstGermTime(germ.counts, intervals, partial = TRUE)

LastGermTime(germ.counts, intervals, partial = TRUE)

PeakGermTime(germ.counts, intervals, partial = TRUE)

TimeSpreadGerm(germ.counts, intervals, partial = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

Time of first germination indicates time of germination of the faster seeds in a seedlot.

Lower value of time of first germination indicates faster initiation of germination and lower value of time of last germination indicates faster termination of germination.

$$t_0 = \min\{T_i : N_i \neq 0\}$$

$$t_g = \max\{T_i : N_i \neq 0\}$$

Where, T_i is the time from the start of the experiment to the ith interval and N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval).

Time spread of germination ($t_g - t_0$) indicates difference between faster and slower germinating members of a sample.

Peak time of germination is the time in which highest frequency of germinated seeds are observed. Multiple peak times of germination are possible and if detected are indicated by a warning message.

$$t_{peak} = \{T_i : N_i = N_{max}\}$$

Where, N_{max} is the maximum number of seeds germinated per interval.

Value

For `FirstGermTime`, the time of first germination value in the same unit of time as specified in the argument `intervals`.

For `LastGermTime`, the time of last germination value in the same unit of time as specified in the argument `intervals`.

For `TimeSpreadGerm`, the time spread of germination value in the same unit of time as specified in the argument `intervals`.

For `PeakGermTime`, the time(s) of peak germination value(s) as a numeric vector in the same unit of time as specified in the argument `intervals`.

References

Al-Mudaris MA (1998). "Notes on various parameters recording the speed of seed germination." *Der Tropenlandwirt-Journal of Agriculture in the Tropics and Subtropics*, **99**(2), 147–154.

Czabator FJ (1962). "Germination value: An index combining speed and completeness of pine seed germination." *Forest Science*, **8**(4), 386–396.

Edwards TI (1932). "Temperature relations of seed germination." *The Quarterly Review of Biology*, **7**(4), 428–443.

Goloff AA, Bazzaz FA (1975). "A germination model for natural seed populations." *Journal of Theoretical Biology*, **52**(2), 259–283.

Kader MA (2005). "A comparison of seed germination calculation formulae and the associated interpretation of resulting data." *Journal and Proceedings of the Royal Society of New South Wales*, **138**, 65–75.

Labouriau LG (1983). *A Germinacao Das Sementes*. Organizacao dos Estados Americanos. Programa Regional de Desenvolvimento Cientifico e Tecnologico. Serie de Biologia. Monografia 24.

Quintanilla LG, Pajaron S, Pangua E, Amigo J (2000). "Effect of temperature on germination in northernmost populations of *Culcita macrocarpa* and *Woodwardia radicans*." *Plant Biology*, **2**(6), 612–617.

Ranal MA (1999). "Effects of temperature on spore germination in some fern species from semideciduous mesophytic forest." *American Fern Journal*, **89**(2), 149.

Ranal MA, de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), 1–11.

Schrader JA, Graves WR (2000). "Seed germination and seedling growth of *Alnus maritima* from its three disjunct populations." *Journal of the American Society for Horticultural Science*, **125**(1), 128–134.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
z <- c(0, 0, 0, 0, 11, 11, 9, 7, 1, 0, 1, 0, 0, 0)
int <- 1:length(x)
```

```
# From partial germination counts
#---------------------------------------------------------------------------
FirstGermTime(germ.counts = x, intervals = int)
LastGermTime(germ.counts = x, intervals = int)
TimeSpreadGerm(germ.counts = x, intervals = int)
PeakGermTime(germ.counts = x, intervals = int)
# For multiple peak germination times
PeakGermTime(germ.counts = z, intervals = int)

# From cumulative germination counts
#---------------------------------------------------------------------------
FirstGermTime(germ.counts = y, intervals = int, partial = FALSE)
LastGermTime(germ.counts = y, intervals = int, partial = FALSE)
TimeSpreadGerm(germ.counts = y, intervals = int, partial = FALSE)
PeakGermTime(germ.counts = y, intervals = int, partial = FALSE)
# For multiple peak germination time
PeakGermTime(germ.counts = cumsum(z), intervals = int, partial = FALSE)
```

FourPHFfit	*Fit four-parameter hill function*

Description

Fit a four-parameter hill function (El-Kassaby et al. 2008) to cumulative germination count data and compute the associated parameters.

Usage

```
FourPHFfit(
  germ.counts,
  intervals,
  total.seeds,
  partial = TRUE,
  fix.y0 = TRUE,
  fix.a = TRUE,
  tmax,
  xp = c(10, 60),
  umin = 10,
  umax = 90,
  tries = 3
)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
total.seeds	Total number of seeds.
partial	logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

fix.y0	Force the intercept of the y axis through 0.
fix.a	Fix a as the actual maximum germination percentage at the end of the experiment.
tmax	The time up to which AUC is to be computed.
xp	Germination percentage value(s) for which the corresponding time is to be computed as a numeric vector. Default is `c(10, 60)`.
umin	The minimum germination percentage value for computing uniformity. Default is `10`. Seed `Details`.
umax	The maximum germination percentage value for computing uniformity. Default is `90`. Seed `Details`.
tries	The number of tries to be attempted to fit the curve. Default is 3.

Details

The cumulative germination count data of a seed lot can be modelled to fit a four-parameter hill function defined as follows (El-Kassaby et al. 2008).

$$y = y_0 + \frac{ax^b}{c^b + x^b}$$

Where, y is the cumulative germination percentage at time x, y_0 is the intercept on the y axis, a is the asymptote, or maximum cumulative germination percentage, which is equivalent to germination capacity, b is a mathematical parameter controlling the shape and steepness of the germination curve (the larger the b parameter, the steeper the rise toward the asymptote a, and the shorter the time between germination onset and maximum germination), and c is the "half-maximal activation level" which represents the time required for 50% of viable seeds to germinate (c is equivalent to the germination speed).

Once this function is fitted to the curve, `FourPHFfit` computes the time to 50% germination of total seeds (`t50.total`) or viable seeds (`t50.Germinated`). Similarly the time at any percentage of germination (in terms of both total and viable seeds) as specified in argument xp can be computed.

The time at germination onset (lag) can be computed as follows.

$$lag = b\sqrt{\frac{-y_0 c^b}{a + y_0}}$$

The value D_{lag-50} is defined as the duration between the time at germination onset (lag) and that at 50% germination (c).

The time interval between the percentages of viable seeds specified in the arguments umin and umin to germinate is computed as uniformity ($U_{t_{max}-t_{min}}$).

$$U_{t_{max}-t_{min}} = t_{max} - t_{min}$$

The partial derivative of the four-parameter hill function gives the instantaneous rate of germination (s) as follows.

$$s = \frac{\partial y}{\partial x} = \frac{abc^b x^{b-1}}{(c^b + x^b)^2}$$

From this function for instantaneous rate of germination, the time at maximum germination rate ($TMGR$) can be estimated as follows.

$$TMGR = b\sqrt{\frac{c^b(b-1)}{b+1}}$$

TMGR represents the point in time when the instantaneous rate of germination starts to decline.

The area under the curve (AUC) is obtained by integration of the fitted curve between time 0 and time specified in the argument 'tmax'.

Integration of the fitted curve gives the value of mean germination time (MGT) and the skewness of the germination curve is computed as the ratio of MGT and the time for 50% of viable seeds to germinate (t_{50}).

$$Skewness = \frac{MGT}{t_{50}}$$

If final germination percentage is less than 10%, a warning is given, as the results may not be informative.

Value

A list with the following components:

data	A data frame with the data used for computing the model.
Parameters	A data frame of parameter estimates, standard errors and p value.
Fit	A one-row data frame with estimates of model fitness such as log likelyhoods, Akaike Information Criterion, Bayesian Information Criterion, deviance and residual degrees of freedom.
a	The asymptote or the maximum cumulative germination percentage.
b	The mathematical parameter controlling the shape and steepness of the germination curve.
c	The half-maximal activation level.
y0	The intercept on the y axis.
lag	Time at germination onset.
Dlag50	duration between the time at germination onset (lag) and that at 50% germination.
t50.total	time required for 50% of total seeds to germinate.
txp.total	time required for x% (as specified in argument xp) of total seeds to germinate.
t50.Germinated	time required for 50% of viable/germinated seeds to germinate.
txp.Germinated	time required for x% (as specified in argument xp) of viable/germinated seeds to germinate.
Uniformity	Time interval between umin% and umax% of viable seeds to germinate.
TMGR	Time at maximum germination rate.
AUC	The estimate of area under the curve.
MGT	Mean germination time.
Skewness	Skewness of mean germination time.
msg	The message from nls.lm.
isConv	Logical value indicating whether convergence was achieved.

References

El-Kassaby YA, Moss I, Kolotelo D, Stoehr M (2008). "Seed germination: Mathematical representation and parameters extraction." *Forest Science*, **54**(2), 220–227.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

# From partial germination counts
#-----------------------------------------------------------------------------
FourPHFfit(germ.counts = x, intervals = int, total.seeds = 50, tmax = 20)

# From cumulative germination counts
#-----------------------------------------------------------------------------
FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, tmax = 20,
partial = FALSE)
```

FourPHFfit.bulk   *Fit four-parameter hill function for multiple samples*

Description

Fit four-parameter hill function from a data frame of germination counts recorded at specific time intervals for multiple samples in batch.

Usage

```
FourPHFfit.bulk(
  data,
  total.seeds.col,
  counts.intervals.cols,
  intervals,
  partial = TRUE,
  fix.y0 = TRUE,
  fix.a = TRUE,
  tmax,
  xp = c(10, 60),
  umin = 10,
  umax = 90,
  tries = 3
)
```

Arguments

data   A data frame with the germination count data. It should possess columns with

- Partial or cumulative germination counts per time interval (to be indicated by the argument `counts.intervals.cols` and
- Total number of seeds tested (to be indicated by the argument `total.seeds.col`).

```
total.seeds.col
```
        The name of the column in `data` with the total number of seeds tested.

```
counts.intervals.cols
```
        The names of columns in `data` with the germination counts (partial or cumulative, as indicated by the argument `partial`) per time interval (indicated by the argument `intervals`).

`intervals`   The time intervals.

`partial`   logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

`fix.y0`   Force the intercept of the y axis through 0.

`fix.a`   Fix a as the actual maximum germination percentage at the end of the experiment.

`tmax`   The time up to which AUC is to be computed.

`xp`   Germination percentage value(s) for which the corresponding time is to be computed as a numeric vector. Default is `c(10, 60)`.

`umin`   The minimum germination percentage value for computing uniformity. Default is `10`. Seed `Details`.

`umax`   The maximum germination percentage value for computing uniformity. Default is `90`. Seed `Details`.

`tries`   The number of tries to be attempted to fit the curve. Default is 3.

Value

A data frame with the original data along with the various parameters of the respective fitted four-parameter hill function.

References

El-Kassaby YA, Moss I, Kolotelo D, Stoehr M (2008). "Seed germination: Mathematical representation and parameters extraction." *Forest Science*, **54**(2), 220–227.

See Also

This function is a wrapper around the [FourPHFfit](#) function for fitting four-parameter hill curve.

Examples

```
data(gcdata)

counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
                          "Day11", "Day12", "Day13", "Day14")

FourPHFfit.bulk(gcdata, total.seeds.col = "Total Seeds",
                  counts.intervals.cols = counts.per.intervals,
                  intervals = 1:14, partial = TRUE,
                  fix.y0 = TRUE, fix.a = TRUE, xp = c(10, 60),
                  tmax = 20, tries = 3, umax = 90, umin = 10)
```

---

gcdata   *Germination count data*

Description

An example germination count dataset. It includes germination count data over 14 days from five genotypes (G1 to G5) in three replications

Usage

```
gcdata
```

Format

A data frame with 17 columns:

Genotype The genotype.

Rep Replication.

Day01 Number of seeds that germinated (germination counts) on Day 1.

Day02 Number of seeds that germinated (germination counts) on Day 2.

Day03 Number of seeds that germinated (germination counts) on Day 3.

Day04 Number of seeds that germinated (germination counts) on Day 4.

Day05 Number of seeds that germinated (germination counts) on Day 5.

Day06 Number of seeds that germinated (germination counts) on Day 6.

Day07 Number of seeds that germinated (germination counts) on Day 7.

Day08 Number of seeds that germinated (germination counts) on Day 8.

Day09 Number of seeds that germinated (germination counts) on Day 9.

Day10 Number of seeds that germinated (germination counts) on Day 10.

Day11 Number of seeds that germinated (germination counts) on Day 11.

Day12 Number of seeds that germinated (germination counts) on Day 12.

Day13 Number of seeds that germinated (germination counts) on Day 13.

Day14 Number of seeds that germinated (germination counts) on Day 14.

Total Seeds Total number of seeds tested.

Examples

```
data(gcdata)
library(ggplot2)
library(reshape2)

# Plot partial germination counts over time
#-----------------------------------------------------------------------------
# Convert wide-from to long-form
gcdatamelt <- melt(gcdata[, !names(gcdata) %in% c("Total Seeds")],
                   id.vars = c("Genotype", "Rep"))

ggplot(gcdatamelt, aes(x = variable, y = value,
```

```
                              group = interaction(Genotype, Rep),
                              colour = Genotype)) +
  geom_point(alpha = 0.7) +
  geom_line(alpha = 0.7) +
  ylab("Germination count (Partial)") +
  xlab("Intervals") +
  theme_bw()

# Plot partial germination counts over time
#----------------------------------------------------------------------------

# Convert wide-from to long-form
# Compute cumulative germination counts
gcdata2 <- gcdata
gcdata2[, !names(gcdata2) %in% c("Genotype", "Rep", "Total Seeds")] <-
  t(apply(gcdata2[, !names(gcdata2) %in% c("Genotype", "Rep", "Total Seeds")], 1, cumsum))


gcdatamelt2 <- melt(gcdata2[, !names(gcdata2) %in% c("Total Seeds")],
                    id.vars = c("Genotype", "Rep"))

ggplot(gcdatamelt2, aes(x = variable, y = value,
                        group = interaction(Genotype, Rep),
                        colour = Genotype)) +
  geom_point(alpha = 0.7) +
  geom_line(alpha = 0.7) +
  ylab("Germination count (Cumulative)") +
  xlab("Intervals") +
  theme_bw()

# Compute germination indices
#----------------------------------------------------------------------------

counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
                          "Day11", "Day12", "Day13", "Day14")
germination.indices(gcdata, total.seeds.col = "Total Seeds",
                    counts.intervals.cols = counts.per.intervals,
                    intervals = 1:14, partial = TRUE, max.int = 5)
```

---

germination.indices   *Germination Indices*

Description

Compute germination indices from a data frame of germination counts recorded at specific time intervals for multiple samples in batch.

Usage

```
germination.indices(
  data,
```

```
    total.seeds.col,
    counts.intervals.cols,
    intervals,
    partial = TRUE,
    PeakGermPercent = TRUE,
    FirstGermTime = TRUE,
    LastGermTime = TRUE,
    PeakGermTime = TRUE,
    TimeSpreadGerm = TRUE,
    t50 = TRUE,
    MeanGermTime = TRUE,
    VarGermTime = TRUE,
    SEGermTime = TRUE,
    CVGermTime = TRUE,
    MeanGermRate = TRUE,
    CVG = TRUE,
    VarGermRate = TRUE,
    SEGermRate = TRUE,
    GermRateRecip = TRUE,
    GermSpeed = TRUE,
    GermSpeedAccumulated = TRUE,
    GermSpeedCorrected = TRUE,
    WeightGermPercent = TRUE,
    MeanGermPercent = TRUE,
    MeanGermNumber = TRUE,
    TimsonsIndex = TRUE,
    GermRateGeorge = TRUE,
    max.int,
    GermIndex = TRUE,
    EmergenceRateIndex = TRUE,
    PeakValue = TRUE,
    GermValue = TRUE,
    gv.k = 10,
    CUGerm = TRUE,
    GermSynchrony = TRUE,
    GermUncertainty = TRUE
)
```

Arguments

data
: A data frame with the germination count data. It should possess columns with

    - Partial or cumulative germination counts per time interval (to be indicated by the argument `counts.intervals.cols` and
    - Total number of seeds tested (to be indicated by the argument `total.seeds.col`).

total.seeds.col
: The name of the column in `data` with the total number of seeds tested.

counts.intervals.cols
: The names of columns in `data` with the germination counts (partial or cumulative, as indicated by the argument `partial`) per time interval (indicated by the argument `intervals`).

intervals
: The time intervals at which germination counts (in the columns specified in argument `counts.intervals.cols`) were recorded.

partial	logical. If TRUE, germination counts in counts.intervals.cols is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.
PeakGermPercent	
	logical. If TRUE, then the Peak germination percentage (Vallance 1950; Roh et al. 2004) is computed. Default is TRUE.
FirstGermTime	logical. If TRUE, the Time of first germination or Germination time lag (t_0) (Edwards 1932; Czabator 1962; Goloff and Bazzaz 1975; Labouriau 1983; Ranal 1999; Quintanilla et al. 2000) is computed. Default is TRUE.
LastGermTime	logical. If TRUE, the Time of last germination (t_g) (Edwards 1932; Labouriau 1983; Ranal and de Santana 2006). is computed. Default is TRUE.
PeakGermTime	logical. If TRUE, the Peak time of germination or Modal time of germination (Ranal and de Santana 2006) is computed. Default is TRUE.
TimeSpreadGerm	logical. If TRUE, the Time spread of germination (Al-Mudaris 1998; Kader 2005) or Germination distribution (Schrader and Graves 2000). is computed. Default is TRUE.
t50	logical. If TRUE, the Median germination time (t_{50}) (Coolbear et al. 1984; Farooq et al. 2005) is computed. Default is TRUE.
MeanGermTime	logical. If TRUE, the Mean germination time ($\overline{T}$) or Mean length of incubation time (Edmond and Drapala 1958; Czabator 1962; Ellis and Roberts 1980; Labouriau 1983; Ranal and de Santana 2006). or Sprouting index (SI) (Smith and Millet 1964) or Germination Resistance (GR) Gordon (1969, 1971) is computed. Default is TRUE.
VarGermTime	logical. If TRUE, the Variance of germination time (s_T^2) (Labouriau 1983; Ranal and de Santana 2006) is computed. Default is TRUE.
SEGermTime	logical. If TRUE, the Standard error of germination time ($s_{\overline{T}}$) (Labouriau 1983; Ranal and de Santana 2006). is computed. Default is TRUE.
CVGermTime	logical. If TRUE, the Coefficient of variation of the germination time (CV_T) (Ranal and de Santana 2006) is computed. Default is TRUE.
MeanGermRate	logical. If TRUE, the Mean germination rate ($\overline{V}$) (Labouriau and Valadares 1976; Labouriau 1983; Ranal and de Santana 2006). is computed. Default is TRUE.
CVG	logical. If TRUE, the Coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG) (Kotowski 1926; Nichols and Heydecker 1968; Labouriau 1983; Scott et al. 1984; Bewley and Black 1994). is computed. Default is TRUE.
VarGermRate	logical. If TRUE, the Variance of germination rate (s_V^2) (Labouriau 1983; Ranal and de Santana 2006) is computed. Default is TRUE.
SEGermRate	logical. If TRUE, the Standard error of germination rate ($s_{\overline{V}}$) (Labouriau 1983; Ranal and de Santana 2006) is computed. Default is TRUE.
GermRateRecip	logical. If TRUE, the Germination rate as reciprocal of median time (v_{50}) (Went 1957; Labouriau 1983; Ranal and de Santana 2006) is computed.
GermSpeed	logical. If TRUE, the Speed of germination or Germination rate index or Index of velocity of germination or Germination index or Emergence rate index (Throneberry and Smith 1955; Maguire 1962; Allan et al. 1962; Kendrick and Frankland 1969; Bouton et al. 1976; AOSA 1983; Khandakar and Bradbeer 1983; Bradbeer 1988; Wardle et al. 1991) considering both counts and percentages is computed.

GermSpeedAccumulated

> logical. If TRUE, the Speed of accumulated germination (Bradbeer 1988; Wardle et al. 1991; Haugland and Brandsaeter 1996; de Santana and Ranal 2004) considering both counts and percentages is computed.

GermSpeedCorrected

> logical. If TRUE, the Corrected speed of germination or Corrected germination rate index and the Corrected speed of accumulated germination (Evetts and Burnside 1972) is computed.

WeightGermPercent

> logical. If TRUE, the Weighted germination percentage WGP or Weighted germination index WGI (Reddy 1978; Reddy et al. 1985) is computed.

MeanGermPercent

> logical. If TRUE, the Mean/average germination percentage per unit time $(\overline{GP})$ (Czabator 1962) is computed.

MeanGermNumber   logical. If TRUE, the Number of seeds germinated per unit time $(\overline{N})$ (Khamassi et al. 2013) is computed.

TimsonsIndex   logical. If TRUE, the Timson's index or Timson's germination velocity index (Grose and Zimmer 1958; Timson 1965; Brown and Mayer 1988; Baskin and Baskin 1998) and it's modifications by Labouriau (Ranal and de Santana 2006) and (Khan and Ungar 1984) is computed.

GermRateGeorge   logical. If TRUE, the George's index George (1961) is computed.

max.int   The maximum interval value up to which Timson's index/George's germination rate is to be computed.

GermIndex   logical. If TRUE, the Germination index according to Melville et al. (1980) and its modification by de Santana and Ranal (2004) (Ranal and de Santana 2006) are computed.

EmergenceRateIndex

> logical. If TRUE, the Emergence rate index or Germination rate index are computed according to
>
> - Shmueli and Goldberg (1971) and it's modification by de Santana and Ranal (2004) (Ranal and de Santana 2006);
> - Bilbro and Wanjura (1982); and
> - Fakorede and Ayoola (1980), Fakorede and Ojo (1981), and Fakorede and Agbana (1983).

PeakValue   logical. If TRUE, the Peak value (PV) or Emergence Energy (EE) (Czabator 1962; Bonner 1967) is computed.

GermValue   logical. If TRUE, the Germination value (Czabator 1962; Djavanshir and Pourbeik 1976) and its modification considering duration from start of test instead of from onset of germination (Brown and Mayer 1988) is computed.

gv.k   The k Constant for computation of germination value. Default is 10.

CUGerm   logical. If TRUE, the Coefficient of uniformity of germination (CUG) (Heydecker 1972; Bewley and Black 1994) is computed.

GermSynchrony   logical. If TRUE, the Synchrony of germination (Z index) (Primack 1985; Ranal and de Santana 2006) is computed.

GermUncertainty

> logical. If TRUE, the Synchronization index $(\overline{E})$ or Uncertainty of the germination process (U) or Informational entropy (H) (Shannon 1948; Labouriau and Valadares 1976; Labouriau 1983) is computed.

Value

A data frame with the original data along with the various single-value germination indices specified in the function arguments.

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See Also

This function is a wrapper around the different functions for computation of single-value germination indices in germinationmetrics (PeakGermPercent, FirstGermTime, LastGermTime, PeakGermTime, TimeSpreadGerm, t50, MeanGermTime, VarGermTime, SEGermTime, CVGermTime, MeanGermRate, CVG, VarGermRate, SEGermRate, GermRateRecip, GermSpeed, GermSpeedAccumulated, GermSpeedCorrected, WeightGermPercent, MeanGermPercent, MeanGermPercent, TimsonsIndex, GermRateGeorge, GermIndex, EmergenceRateIndex, GermValue, PeakValue, CUGerm, GermSynchrony, GermUncertainty)

Examples

```
data(gcdata)

counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
                          "Day11", "Day12", "Day13", "Day14")
germination.indices(gcdata, total.seeds.col = "Total Seeds",
                    counts.intervals.cols = counts.per.intervals,
                    intervals = 1:14, partial = TRUE, max.int = 5)
```

GermIndex   *Germination Index*

Description

Compute the Germination index according to Melville et al. (1980) and its modification by de Santana and Ranal (2004) (Ranal and de Santana 2006).

Usage

```
GermIndex(
  germ.counts,
  intervals,
  partial = TRUE,
  total.seeds,
  modification = c("none", "santanaranal")
)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument partial.
intervals	The time intervals.
partial	logical. If TRUE, germ.counts is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.
total.seeds	Total number of seeds.
modification	The modification to be applied. Either "none" or "santanaranal". Default is "none" (see **Details**).

Details

Germination index (GI) is computed as follows (Melville et al. 1980).

$$GI = \sum_{i=1}^{k} \frac{|(T_k - T_i)\, N_i|}{N_t}$$

Where, T_i is the time from the start of the experiment to the ith interval (day for the example), N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), N_t is the total number of seeds used in the test, and k is the total number of time intervals.

A modified germination index (GI_{mod}) was proposed by (de Santana and Ranal 2004) where total number of seeds tested (N_t) is replaced by the total number of germinated seeds (N_g) in the expression of Melville et al. (1980) to remove the effect of sample size (Ranal and de Santana 2006). It is computed as follows (Specified by the argument modification = "santanaranal").

$$GI_{mod} = \sum_{i=1}^{k} \frac{|(T_k - T_i)\, N_i|}{N_g}$$

The term Germination index (GI) has also been used to describe the mathematical expression for Speed of germination (GermSpeed) by AOSA (1983).

Value

The value of the Germination index in the same unit of time as specified in the argument `intervals`.

References

AOSA (1983). *Seed Vigor Testing Handbook*. Association of Official Seed Analysts, Ithaca, NY, USA.

Melville AH, Galletta GJ, Draper AD, Ng TJ (1980). "Seed germination and early seedling vigor in progenies of inbred strawberry selections." *HortScience*, **15**(6, I), 749–750.

Ranal MA, de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), 1–11.

de Santana DG, Ranal MA (2004). *Analise Da Germinacao: Um Enfoque Estatistico*. Universidade de Brasilia, Brasilia.

See Also

GermSpeed

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------
GermIndex(germ.counts = x, intervals = int, total.seeds = 50)
GermIndex(germ.counts = x, intervals = int, total.seeds = 50,
          modification = "none")
GermIndex(germ.counts = x, intervals = int, total.seeds = 50,
          modification = "santanaranal")

# From cumulative germination counts
#----------------------------------------------------------------------
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50)
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50,
          modification = "none")
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50,
          modification = "santanaranal")
```

GermPercent *Germination percentage*

Description

Compute the following metrics:

GermPercent Germination percentage or Final germination percentage or Germinability (ISTA 2015).

PeakGermPercent Peak germination percentage (Vallance 1950; Roh et al. 2004).

Usage

```
GermPercent(germinated.seeds, germ.counts, total.seeds, partial = TRUE)

PeakGermPercent(germ.counts, intervals, total.seeds, partial = TRUE)
```

Arguments

germinated.seeds
        Number of germinated seeds

germ.counts Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.

total.seeds Total number of seeds.

partial logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

intervals The time intervals.

Details

Germination percentage is computed as follows (ISTA 2015).

$$GP = \frac{N_g}{N_t} \times 100$$

Where, N_g is the number of germinated seeds and N_t is the total number of seeds.

The value of N_g can be either specified using the argument `germinated.seeds` or is computed from the `germ.counts` argument.

Peak germination percentage is computed as follows (Vallance 1950; Roh et al. 2004).

$$PGP = \frac{N_{max}}{N_t} \times 100$$

Where, N_{max} is the maximum number of seeds germinated per interval.

Value

The germination percentage (%) value.

References

ISTA (2015). "Chapter 5: The germination test." *International Rules for Seed Testing. International Seed Testing Association, Zurich, Switzerland.*, **2015**, i–5–56.

Roh M, Bentz J, Wang P, Li E, Koshioka M (2004). "Maturity and temperature stratification affect the germination of *Styrax japonicus* seeds." *The Journal of Horticultural Science and Biotechnology*, **79**(4), 645–651.

Vallance KB (1950). "Studies on the germination of the seeds of *Striga hermonthica* I. The influence of moisture-treatment, stimulant-dilution, and after-ripening on germination." *Annals of Botany*, **14**(55), 347–363.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
z <- c(0, 0, 0, 0, 11, 11, 9, 7, 1, 0, 1, 0, 0, 0)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
GermPercent(germ.counts = x, total.seeds = 50)
PeakGermPercent(germ.counts = x, intervals = int, total.seeds = 50)
# For multiple peak germination times
PeakGermPercent(germ.counts = z, intervals = int, total.seeds = 50)

# From cumulative germination counts
#----------------------------------------------------------------------------
GermPercent(germ.counts = y, total.seeds = 50, partial = FALSE)
PeakGermPercent(germ.counts = y, intervals = int, total.seeds = 50,
                partial = FALSE)
# For multiple peak germination times
PeakGermPercent(germ.counts = cumsum(z), intervals = int, total.seeds = 50,
                partial = FALSE)

# From number of germinated seeds
#----------------------------------------------------------------------------
GermPercent(germinated.seeds = 40, total.seeds = 50)
```

GermSpeed   *Speed of germination*

Description

Compute the following metrics:

GermSpeed Speed of germination or Germination rate index or Index of velocity of germination or Germination index or Emergence rate index (Throneberry and Smith 1955; Maguire 1962; Allan et al. 1962; Kendrick and Frankland 1969; Bouton et al. 1976; Erbach 1982; AOSA 1983; Khandakar and Bradbeer 1983; Hsu and Nelson 1986; Bradbeer 1988; Wardle et al. 1991).

GermSpeedAccumulated Speed of accumulated germination (Bradbeer 1988; Wardle et al. 1991; Haugland and Brandsaeter 1996; de Santana and Ranal 2004).

GermSpeedCorrected Corrected speed of germination or Corrected germination rate index (Evetts and Burnside 1972).

Usage

```
GermSpeed(
  germ.counts,
  intervals,
  partial = TRUE,
  percent = FALSE,
  total.seeds = NULL
)

GermSpeedAccumulated(
  germ.counts,
  intervals,
  partial = TRUE,
  percent = FALSE,
  total.seeds = NULL
)

GermSpeedCorrected(
  germ.counts,
  intervals,
  partial = TRUE,
  total.seeds,
  method = c("normal", "accumulated")
)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument partial.
intervals	The time intervals.
partial	logical. If TRUE, germ.counts is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.
percent	logical. If TRUE, germination percentage is used instead of counts for computation. Default is FALSE.
total.seeds	Total number of seeds. Mandatory for computation when percent = TRUE.
method	The method for computing germination speed in GermSpeedCorrected. Either "normal" (GermSpeed) or "accumulated" (GermSpeedAccumulated).

Details

GermSpeed computes the speed of germination according to the following formula (Throneberry and Smith 1955; Maguire 1962; Allan et al. 1962; Kendrick and Frankland 1969; Bouton et al. 1976; Erbach 1982; AOSA 1983; Khandakar and Bradbeer 1983; Hsu and Nelson 1986; Bradbeer 1988; Wardle et al. 1991).

$$S = \frac{N_1}{T_1} + \frac{N_2}{T_2} + \frac{N_3}{T_3} + \cdots + \frac{N_k}{T_k}$$

Where, N_1, N_2, N_3, $\cdots$, N_k are the number of germinated seeds observed at time (days or hours) T_1, T_2, T_3, $\cdots$, T_k after sowing (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time) and k is the total number of time intervals.

It is the same as Emergence Rate Index (ERI) described by Allan et al. (1962), Erbach (1982) and Hsu and Nelson (1986) as well as Germination Index (GI) according to AOSA (1983).

The formula can also be described as follows.

$$S = \sum_{i=1}^{k} \frac{N_i}{T_i}$$

Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.

`GermSpeedAccumulated` computes the speed of accumulated germination as follows (Bradbeer 1988; Wardle et al. 1991; Haugland and Brandsaeter 1996; de Santana and Ranal 2004).

$$S_{accumulated} = \frac{N_1}{T_1} + \frac{N_1 + N_2}{T_2} + \frac{N_1 + N_2 + N_3}{T_3} + \cdots + \frac{N_1 + N_2 + \cdots + N_k}{T_k}$$

Where, N_1, N_2, N_3, $\cdots$, N_k are the number of germinated seeds observed at time (days or hours) T_1, T_2, T_3, $\cdots$, T_k after sowing (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time), and k is the total number of time intervals.

The formula can also be described as follows.

$$S_{accumulated} = \sum_{i=1}^{k} \frac{\sum_{j=1}^{i} N_j}{T_i}$$

Where, T_i is the time from the start of the experiment to the ith interval, $\sum_{j=1}^{i} N_j$ is the cumuative/accumulated number of seeds germinated in the ith time interval, and k is the total number of time intervals.

Speed of germination expresses the rate of germination in terms of the total number of seeds that germinate in a time interval. Higher values indicate greater and faster germination. This is useful for comparisons only when samples or treatments possess similar germinabilities. This is overcome by either using the corrected speed of germination or by using germination percentages instead of counts for computing speed.

`GermSpeedCorrected` computes the corrected speed of germination as follows (Evetts and Burnside 1972).

$$S_{corrected} = \frac{S}{FGP}$$

Where, S is the germination speed (either standard or accumulated as specified by the argument `method = "normal"` or `method = "accumulated"` respectively) computed with germination percentage instead of counts and FGP is the final germination percentage or germinability.

With `percent = TRUE`, germination percentage is used instead of counts for computation in `GermSpeed` and `GermSpeedAccumulated`. In case of `GermSpeedCorrected`, germination percentage is always used for the numerator.

Value

For `GermSpeed`, the value of germination speed as count time^{-1} or $\% \text{ time}^{-1}$.

For `GermSpeedAccumulated`, the value of accumulated germination speed as count time^{-1} or $\% \text{ time}^{-1}$.

For `GermSpeedCorrected`, the corrected speed of germination as time^{-1}.

References

AOSA (1983). *Seed Vigor Testing Handbook*. Association of Official Seed Analysts, Ithaca, NY, USA.

Allan RE, Vogel OA, Peterson CJ (1962). "Seedling emergence rate of fall-sown wheat and its association with plant height and coleoptile length." *Agronomy Journal*, **54**(4), 347.

Bouton JH, Dudeck AE, Smith RL (1976). "Germination in freshly harvested seed of centipede-grass." *Agronomy Journal*, **68**(6), 991.

Bradbeer JW (1988). *Seed Dormancy and Germination*. Blackie, Glasgow and London.

Erbach DC (1982). "Tillage for continuous corn and corn-soybean rotation." *Transactions of the ASAE*, **25**(4), 906–0911.

Evetts LL, Burnside OC (1972). "Germination and seedling development of common milkweed and other species." *Weed Science*, **20**(4), 371–378.

Haugland E, Brandsaeter LO (1996). "Experiments on bioassay sensitivity in the study of allelopathy." *Journal of Chemical Ecology*, **22**(10), 1845–1859.

Hsu FH, Nelson CJ (1986). "Planting date effects on seedling development of perennial warm-season forage grasses. I. Field emergence." *Agronomy Journal*, **78**(1), 33–38.

Kendrick RE, Frankland B (1969). "Photocontrol of germination in *Amaranthus caudatus*." *Planta*, **85**(4), 326–339.

Khandakar AL, Bradbeer JW (1983). *Jute seed quality*. Bangladesh Agricultural Research Council, Dhaka.

Maguire JD (1962). "Speed of germination - Aid in selection and evaluation for seedling emergence and vigor." *Crop Science*, **2**(2), 176–177.

Throneberry GO, Smith FG (1955). "Relation of respiratory and enzymatic activity to corn seed viability." *Plant Physiology*, **30**(4), 337–343.

Wardle DA, Ahmed M, Nicholson KS (1991). "Allelopathic influence of nodding thistle (*Carduus nutans* L.) seeds on germination and radicle growth of pasture plants." *New Zealand Journal of Agricultural Research*, **34**(2), 185–191.

de Santana DG, Ranal MA (2004). *Analise Da Germinacao: Um Enfoque Estatistico*. Universidade de Brasilia, Brasilia.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#-----------------------------------------------------------------------------
GermSpeed(germ.counts = x, intervals = int)
GermSpeedAccumulated(germ.counts = x, intervals = int)
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "normal")
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "accumulated")

# From partial germination counts (with percentages instead of counts)
#-----------------------------------------------------------------------------
GermSpeed(germ.counts = x, intervals = int,
          percent = TRUE, total.seeds = 50)
GermSpeedAccumulated(germ.counts = x, intervals = int,
                     percent = TRUE, total.seeds = 50)

# From cumulative germination counts
#-----------------------------------------------------------------------------
GermSpeed(germ.counts = y, intervals = int, partial = FALSE)
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE)
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "normal")
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "accumulated")

# From cumulative germination counts (with percentages instead of counts)
#-----------------------------------------------------------------------------
GermSpeed(germ.counts = y, intervals = int, partial = FALSE,
          percent = TRUE, total.seeds = 50)
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE,
                     percent = TRUE, total.seeds = 50)
```

GermSynchrony   *Synchrony and uncertainty of germination*

Description

Compute the following metrics:

GermSynchrony Synchrony of germination (Z index) (Primack 1985; Ranal and de Santana 2006).

GermUncertainty Synchronization index ($\overline{E}$) or Uncertainty of the germination process (U) or Informational entropy (H) (Shannon 1948; Labouriau and Valadares 1976; Labouriau 1983).

Usage

```
GermSynchrony(germ.counts, intervals, partial = TRUE)

GermUncertainty(germ.counts, intervals, partial = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

`GermSynchrony` computes the value of synchrony of germination (Z index) as follows (Primack 1985; Ranal and de Santana 2006).

$$Z = \frac{\sum_{i=1}^{k} C_{N_i,2}}{C_{\Sigma N_i,2}}$$

Where, $C_{N_i,2}$ is the partial combination of the two germinated seeds from among N_i, the number of seeds germinated on the ith time interval (estimated as $C_{N_i,2} = \frac{N_i(N_i-1)}{2}$), and $C_{\Sigma N_i,2}$ is the partial combination of the two germinated seeds from among the total number of seeds germinated at the final count, assuming that all seeds that germinated did so simultaneously.

`GermUncertainty` computes the value of synchronization index ($\overline{E}$) or uncertainty of the germination process (U) or informational entropy (H) as follows (Shannon 1948; Labouriau and Valadares 1976; Labouriau 1983).

$$\overline{E} = -\sum_{i=1}^{k} f_i \log_2 f_i$$

Where, f_i is the relative frequency of germination (estimated as $f_i = \frac{N_i}{\sum_{i=1}^{k} N_i}$), N_i is the number of seeds germinated on the ith time interval, and k is the total number of time intervals.

Value

For `GermUncertainty`, the value of uncertainty of germination process in bit.

For `GermSynchrony`, the value of synchrony of germination.

References

Labouriau LG (1983). "Uma nova linha de pesquisa na fisiologia da germinacao das sementes." *Anais do XXXIV Congresso Nacional de Botanica. SBB, Porto Alegre*, 11–50.

Labouriau LG, Valadares MEB (1976). "On the germination of seeds of *Calotropis procera* (Ait.) Ait. f." *Anais da Academia Brasileira de Ciencias*, **48**(263-284).

Primack RB (1985). "Longevity of individual flowers." *Annual Review of Ecology and Systematics*, **16**(1), 15–37.

Ranal MA, de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), 1–11.

Shannon CE (1948). "A mathematical theory of communication." *Bell System Technical Journal*, **27**(3), 379–423.

See Also

CUGerm

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
GermSynchrony(germ.counts = x, intervals = int)
GermUncertainty(germ.counts = x, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------------
GermSynchrony(germ.counts = y, intervals = int, partial = FALSE)
GermUncertainty(germ.counts = y, intervals = int, partial = FALSE)
```

GermValue   *Peak value and germination value*

Description

Compute the Peak value (PV) or Emergence Energy (EE) (Czabator 1962; Bonner 1967) and Germination value (GV) (Czabator 1962; Djavanshir and Pourbeik 1976; Brown and Mayer 1988).

Usage

```
PeakValue(germ.counts, intervals, total.seeds, partial = TRUE)

GermValue(
  germ.counts,
  intervals,
  total.seeds,
  partial = TRUE,
  method = c("czabator", "dp"),
  from.onset = TRUE,
  k = 10
)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
total.seeds	Total number of seeds.
partial	logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.
method	The method for computing germination value. Either `"czabator"` or `"dp"`.

from.onset	logical. If TRUE, duration is considered only from the onset of germination. If FALSE, full duration of germination test is considered. Default is TRUE.
k	Constant (See **Details**). Default is 10.

Details

Peak value (PV) is the maximum quotient obtained by dividing successive cumulative germination values by the relevant incubation time (Czabator 1962).

$$PV = \max\left(\frac{G_1}{T_1}, \frac{G_2}{T_2}, \cdots \frac{G_k}{T_k}\right)$$

Where, T_i is the time from the start of the experiment to the ith interval, G_i is the cumulative germination percentage in the ith time interval, and k is the total number of time intervals.

It represents the mean daily germination of the most vigorous component of the seed lot, and is a mathematical expression of the break, or shoulder, of a typical sigmoid germination curve (Djavanshir and Pourbeik 1976). It is the accumulated number of seeds germinated at the point on the germination curve at which the rate of germination starts to decrease. It is also described as Emergence energy (Bonner 1967).

For daily germination counts, germination value (GV) is computed as follows (Czabator 1962) (Specified by the argument method = "czabator").

$$GV = PV \times MDG$$

Where, PV is the peak value, and MDG is the mean daily germination percentage from the onset of germination.

Germination value (GV) can also be computed for other time intervals of successive germination counts, by replacing MDG with the mean germination percentage per unit time ($\overline{GP}$).

A new estimation of germination value was given by Djavanshir and Pourbeik (1976) as follows (Specified by the argument method = "dp").

$$GV = \frac{\sum DGS}{N} \times GP \times c$$

Where, DGS is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the onset of germination, N is the frequency or number of DGS calculated during the test, GP is the germination percentage expressed over 100, and c is a constant. The value of c is decided on the basis of average daily speed of germination ($\frac{\sum DGS}{N}$). If it is less than 10, then c value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for c.

For both methods of computing GV, only the duration from the onset of germination is considered by default. Alternatively, modified GV (GV_{mod}), where the entire duration from the beginning of the test is considered can be obtained by using the argument from.onset = FALSE (Brown and Mayer 1988).

Value

A list with the following components:

Germination Value

        The germination value.

Calculations	The data frame of calculations.
testend	The end of test value (Only for method dp).

References

Bonner FT (1967). "Ideal sowing depth for sweetgum seed." *Tree Planters' Notes*, **18**(1), 1–1.

Brown RF, Mayer DG (1988). "Representing cumulative germination. 1. A critical analysis of single-value germination indices." *Annals of Botany*, **61**(2), 117–125.

Czabator FJ (1962). "Germination value: An index combining speed and completeness of pine seed germination." *Forest Science*, **8**(4), 386–396.

Djavanshir K, Pourbeik H (1976). "Germination value-A new formula." *Silvae Genetica*, **25**(2), 79–83.

Examples

```
x <- c(0, 0, 34, 40, 21, 10, 4, 5, 3, 5, 8, 7, 7, 6, 6, 4, 0, 2, 0, 2)
y <- c(0, 0, 34, 74, 95, 105, 109, 114, 117, 122, 130, 137, 144, 150,
      156, 160, 160, 162, 162, 164)
int <- 1:length(x)
total.seeds = 200

# From partial germination counts
#-----------------------------------------------------------------------------
PeakValue(germ.counts = x, intervals = int, total.seeds = 200)
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "czabator")
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "dp", k = 10)
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "czabator", from.onset = FALSE)
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "dp", k = 10, from.onset = FALSE)

# From cumulative germination counts
#-----------------------------------------------------------------------------
PeakValue(germ.counts = y, interval = int, total.seeds = 200,
          partial = FALSE)
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "czabator")
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "dp", k = 10)
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "czabator", from.onset = FALSE)
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "dp", k = 10, from.onset = FALSE)
```

MeanGermPercent   *Mean germination percentage and number of seeds per time interval*

Description

Compute the following metrics:

MeanGermPercent Mean/average germination percentage per unit time ($\overline{GP}$) (Czabator 1962).
MeanGermNumber Number of seeds germinated per unit time ($\overline{N}$) (Khamassi et al. 2013).

Usage

```
MeanGermPercent(
  germinated.seeds,
  germ.counts,
  total.seeds,
  intervals,
  partial = TRUE
)

MeanGermNumber(germ.counts, intervals, partial = TRUE)
```

Arguments

germinated.seeds

Number of germinated seeds

germ.counts   Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.

total.seeds   Total number of seeds.

intervals   The time intervals.

partial   logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

Mean germination percentage per unit time ($\overline{GP}$) is computed as follows (Czabator 1962).

$$\overline{GP} = \frac{GP}{T_k}$$

Where, GP is the final germination percentage, T_k is the time at the kth time interval, and k is the total number of time intervals required for final germination.

Mean number of seeds germinated per unit time ($\overline{N}$) is computed as follows (Khamassi et al. 2013).

$$\overline{N} = \frac{N_g}{T_k}$$

Where, N_g is the number of germinated seeds at the end of the germination test, T_k is the time at the kth time interval, and k is the total number of time intervals required for final germination.

Value

The value of mean germination percentage as $\%\ \text{time}^{-1}$ or mean number of seeds per time interval as $\text{count}\ \text{time}^{-1}$.

References

Czabator FJ (1962). "Germination value: An index combining speed and completeness of pine seed germination." *Forest Science*, **8**(4), 386–396.

Khamassi K, Harbaoui K, Jaime ATdS, Jeddi FB (2013). "Optimal germination temperature assessed by indices and models in field bean (*Vicia faba* L. var. *minor*)." *Agriculturae Conspectus Scientificus*, **78**(2), 131–136.

See Also

GermPercent

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
MeanGermPercent(germ.counts = x, total.seeds = 50, intervals = int)
MeanGermNumber(germ.counts = x, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------------
MeanGermPercent(germ.counts = y, total.seeds = 50, intervals = int, partial = FALSE)
MeanGermNumber(germ.counts = y, intervals = int, partial = FALSE)

# From number of germinated seeds
#----------------------------------------------------------------------------
MeanGermPercent(germinated.seeds = 40, total.seeds = 50, intervals = int)
```

MeanGermRate   *Germination rate*

Description

Compute the following metrics:

MeanGermRate Mean germination rate ($\overline{V}$) (Labouriau and Valadares 1976; Labouriau 1983; Ranal and de Santana 2006).

VarGermRate Variance of germination rate (s_V^2) (Labouriau 1983; Ranal and de Santana 2006).

SEGermRate Standard error of germination rate ($s_{\overline{V}}$) (Labouriau 1983; Ranal and de Santana 2006).

CVG Coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG) (Kotowski 1926; Nichols and Heydecker 1968; Labouriau 1983; Scott et al. 1984; Bewley and Black 1994).

GermRateRecip Germination rate as reciprocal of median time (v_{50}) (Went 1957; Labouriau 1983; Ranal and de Santana 2006).

Usage

```
MeanGermRate(germ.counts, intervals, partial = TRUE)

CVG(germ.counts, intervals, partial = TRUE)

VarGermRate(germ.counts, intervals, partial = TRUE)

SEGermRate(germ.counts, intervals, partial = TRUE)
```

```
GermRateRecip(
  germ.counts,
  intervals,
  partial = TRUE,
  method = c("coolbear", "farooq")
)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If TRUE, germ.counts is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.
method	The method for computing median germination time. Either "coolbear" or "farooq".

Details

`MeanGermRate` computes the mean germination rate ($\overline{V}$) according to the following formula (Labouriau and Valadares 1976; Labouriau 1983; Ranal and de Santana 2006).

$$\overline{V} = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i}$$

Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.

It is the inverse of mean germination time ($\overline{T}$).

$$\overline{V} = \frac{1}{\overline{T}}$$

`VarGermRate` computes the variance of germination rate (s_V^2) according to the following formula (Labouriau 1983; Ranal and de Santana 2006).

$$s_V^2 = \overline{V}^4 \times s_T^2$$

Where, s_T^2 is the variance of germination time.

`SEGermRate` computes the standard error of germination time ($s_{\overline{V}}$) according to the following formula (Labouriau 1983; Ranal and de Santana 2006).

$$s_{\overline{V}} = \sqrt{\frac{s_V^2}{\sum_{i=1}^{k} N_i}}$$

Where, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.

`CVG` computes the coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG) according to the following formula (Kotowski 1926; Nichols and Heydecker 1968; Labouriau 1983; Scott et al. 1984; Bewley and Black 1994).

$$CVG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i} \times 100$$

$$CVG = \overline{V} \times 100$$

Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.

`GermRateRecip` computes the germination rate (v_{50}) as the reciprocal of the median germination time (t_{50}) (Went 1957; Labouriau 1983; Ranal and de Santana 2006) according to the methods of Coolbear et al. (1984) (Specified by the argument `method = "coolbear"`) or Farooq et al. (2005) (Specified by the argument `method = "farooq"`) as follows.

$$v_{50} = \frac{1}{t_{50}}$$

Value

For `MeanGermRate`, the mean germination rate value as time^{-1}.

For `VarGermTime`, the variance of germination rate value as time^{-2}.

For `SEGermTime`, the standard error of germination rate as time^{-1}.

For `CVG`, the value of Coefficient of of velocity/rate of germination or Kotowski's coefficient of velocity as $\% \ \text{time}^{-1}$.

For `GermRateRecip`, the value of germination rate as time^{-1}.

References

Bewley JD, Black M (1994). *Seeds: Physiology of Development and Germination..* Plenum Publishing Corporation, New York, USA. ISBN 0-306-44748-7.

Coolbear P, Francis A, Grierson D (1984). "The effect of low temperature pre-sowing treatment on the germination performance and membrane integrity of artificially aged tomato seeds." *Journal of Experimental Botany*, **35**(11), 1609–1617.

Farooq M, Basra SMA, Ahmad N, Hafeez K (2005). "Thermal hardening: A new seed vigor enhancement tool in rice." *Journal of Integrative Plant Biology*, **47**(2), 187–193.

Kotowski F (1926). "Temperature relations to germination of vegetable seeds." *Proceedings of the American Society for Horticultural Science*, **23**, 176–184.

Labouriau LG (1983). "Uma nova linha de pesquisa na fisiologia da germinacao das sementes." *Anais do XXXIV Congresso Nacional de Botanica. SBB, Porto Alegre*, 11–50.

Labouriau LG, Valadares MEB (1976). "On the germination of seeds of *Calotropis procera* (Ait.) Ait. f." *Anais da Academia Brasileira de Ciencias*, **48**(263-284).

Nichols MA, Heydecker W (1968). "Two approaches to the study of germination data." *Proceedings of the International Seed Testing Association*, **33**(3), 531–540.

Ranal MA, de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), 1–11.

Scott SJ, Jones RA, Williams WA (1984). "Review of data analysis methods for seed germination." *Crop Science*, **24**(6), 1192–1199.

Went FW (1957). *The experimental control of plant growth*, volume 17. Chronica Botanica Co., Waltham, Mass., USA and The Ronald Press Co., New York, USA.

See Also

MeanGermTime, t50

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#-----------------------------------------------------------------------
MeanGermRate(germ.counts = x, intervals = int)
CVG(germ.counts = x, intervals = int)
VarGermRate(germ.counts = x, intervals = int)
SEGermRate(germ.counts = x, intervals = int)
GermRateRecip(germ.counts = x, intervals = int, method = "coolbear")
GermRateRecip(germ.counts = x, intervals = int, method = "farooq")

# From cumulative germination counts
#-----------------------------------------------------------------------
MeanGermRate(germ.counts = y, intervals = int, partial = FALSE)
CVG(germ.counts = y, intervals = int, partial = FALSE)
VarGermRate(germ.counts = y, intervals = int, partial = FALSE)
SEGermRate(germ.counts = y, intervals = int, partial = FALSE)
GermRateRecip(germ.counts = y, intervals = int,
              method = "coolbear", partial = FALSE)
GermRateRecip(germ.counts = y, intervals = int,
              method = "farooq", partial = FALSE)
```

MeanGermTime   *Germination time*

Description

Compute the following metrics:

MeanGermTime Mean germination time ($\overline{T}$) or Mean length of incubation time (Edmond and Drapala 1958; Czabator 1962; Mock and Eberhart 1972; Ellis and Roberts 1980; Labouriau 1983; Ranal and de Santana 2006).

VarGermTime Variance of germination time (s_T^2) (Labouriau 1983; Ranal and de Santana 2006).

SEGermTime   Standard error of germination time ($s_{\overline{T}}$) (Labouriau 1983; Ranal and de Santana 2006).

CVGermTime   Coefficient of variation of the germination time (CV_T) (Gomes 1960; Ranal and de Santana 2006).

Usage

```
MeanGermTime(germ.counts, intervals, partial = TRUE)

VarGermTime(germ.counts, intervals, partial = TRUE)

SEGermTime(germ.counts, intervals, partial = TRUE)

CVGermTime(germ.counts, intervals, partial = TRUE)
```

Arguments

germ.counts   Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.

intervals   The time intervals.

partial   logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

`MeanGermTime` computes the mean germination time according to the following formula (Edmond and Drapala 1958; Czabator 1962; Smith and Millet 1964; Ellis and Roberts 1980; Labouriau 1983; Ranal and de Santana 2006).

$$\overline{T} = \frac{\sum_{i=1}^{k} N_i T_i}{\sum_{i=1}^{k} N_i}$$

Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.

It is the same as Sprouting Index (SI) or Emergence Index (EI) described by Smith and Millet (1964) and Mock and Eberhart (1972) as well as Germination Resistance (GR) described by Gordon (1969, 1971).

It is the inverse of mean germination rate ($\overline{V}$).

$$\overline{T} = \frac{1}{\overline{V}}$$

It indicates the average length of time required for maximum germination of a seed lot. Lower the $\overline{T}$, faster the sample has germinated and reflects seed vigor.

`VarGermTime` computes the variance of germination time according to the following formula (Labouriau 1983; Ranal and de Santana 2006).

$$s_T^2 = \frac{\sum_{i=1}^{k} N_i (T_i - \overline{T})^2}{\sum_{i=1}^{k} N_i - 1}$$

Where, T_i is the time from the start of the experiment to the ith interval, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.

`SEGermTime` computes the standard error of germination time ($s_{\overline{T}}$) according to the following formula (Labouriau 1983; Ranal and de Santana 2006).

$$s_{\overline{T}} = \sqrt{\frac{s_T^2}{\sum_{i=1}^{k} N_i}}$$

Where, N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.

It signifies the accuracy of the calculation of the mean germination time.

`CVGermTime` computes the coefficient of variation of germination time (CV_T) according to the following formula (Gomes 1960; Ranal and de Santana 2006).

$$CV_T = \frac{\sqrt{s_T^2}}{\overline{T}}$$

This indicates the uniformity of germination and permits comparisons irrespective of the magnitude of mean germination time ($\overline{T}$).

Value

For `MeanGermTime`, the mean germination time value in the same unit of time as specified in the argument `intervals`.

For `VarGermTime`, the variance of germination time value as time^2.

For `SEGermTime`, the standard error of germination time in the same unit of time specified in the argument `intervals`.

For `CVGermTime`, the value of coefficient of variation of the germination time.

References

Czabator FJ (1962). "Germination value: An index combining speed and completeness of pine seed germination." *Forest Science*, **8**(4), 386–396.

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Gordon AG (1969). "Some observations on the germination energy tests for cereals." *Proceedings of the Association of Official Seed Analysts*, **59**, 58–72.

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Labouriau LG (1983). *A Germinacao Das Sementes*. Organizacao dos Estados Americanos. Programa Regional de Desenvolvimento Cientifico e Tecnologico. Serie de Biologia. Monografia 24.

Mock JJ, Eberhart SA (1972). "Cold tolerance in adapted maize populations." *Crop Science*, **12**(4), 466–469.

Ranal MA, de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), 1–11.

Smith PG, Millet AH (1964). "Germinating and sprouting responses of the tomato at low temperatures." *Proceedings of the American Society for Horticultural Science*, **84**, 480–484.

See Also

MeanGermRate

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
MeanGermTime(germ.counts = x, intervals = int)
VarGermTime(germ.counts = x, intervals = int)
SEGermTime(germ.counts = x, intervals = int)
CVGermTime(germ.counts = x, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------------
MeanGermTime(germ.counts = y, intervals = int, partial = FALSE)
VarGermTime(germ.counts = y, intervals = int, partial = FALSE)
SEGermTime(germ.counts = y, intervals = int, partial = FALSE)
CVGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

---

plot.FourPHFfit	*Plot the four-parameter hill function fitted cumulative germination curve from a* FourPHFfit *object*

Description

plot.FourPHFfit plots the four-parameter hill function fitted cumulative germination curve (FPHF curve) from a FourPHFfit object as an object of class ggplot. Further, the rate of germination curve (RoG curve) is plotted and different parameters annotated as specified in the different arguments.

Usage

```
## S3 method for class 'FourPHFfit'
plot(
  x,
  rog = TRUE,
```

```
      t50.total = TRUE,
      t50.germ = TRUE,
      tmgr = TRUE,
      mgt = TRUE,
      uniformity = TRUE,
      limits = TRUE,
      plotlabels = TRUE,
      ...
    )
```

Arguments

x	An object of class FourPHFfit obtained as output from the [FourPHFfit](#) function.
rog	If TRUE, plots the Rate of Germination curve (RoG). Default is TRUE.
t50.total	If TRUE, highlights the time required for 50% of total seeds to germinate ($t_{50_{Total}}$) as a vertical line. Default is TRUE.
t50.germ	If TRUE, highlights the time required for 50% of viable/germinated seeds to germinate ($t_{50_{Germ}}$) as a vertical line. Default is TRUE.
tmgr	If TRUE, highlights the Time at Maximum Germination Rate (TMGR) as a vertical line. Default is TRUE.
mgt	If TRUE, highlights the Mean Germination Time (MGT) as a vertical line. Default is TRUE.
uniformity	If TRUE, highlights the uniformity value ($U_{t_{max}-t_{min}}$) as a horizontal line. Default is TRUE.
limits	logical. If TRUE, set the limits of y axis (germination percentage) between 0 and 100 in the germination curve plot. If FALSE, limits are set according to the data. Default is TRUE.
plotlabels	logical. If TRUE, adds labels to the germination curve plot. Default is TRUE.
...	Default plot arguments.

Value

The plot of the cumulative germination curve as an object of class ggplot.

See Also

[FourPHFfit](#)

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

# From partial germination counts
#----------------------------------------------------------------------------
fit1 <- FourPHFfit(germ.counts = x, intervals = int,
                   total.seeds = 50, tmax = 20)
```

```
# From cumulative germination counts
#-----------------------------------------------------------------------
fit2 <- FourPHFfit(germ.counts = y, intervals = int,
                   total.seeds = 50, tmax = 20, partial = FALSE)

# Default plots
plot(fit1)
plot(fit2)

# No labels
plot(fit1, plotlabels = FALSE)
plot(fit2, plotlabels = FALSE)

# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)

# Without y axis limits adjustment
plot(fit1, limits = FALSE)
plot(fit2, limits = FALSE)
```

---

plot.FourPHFfit.bulk   *Plot the multiple four-parameter hill function fitted cumulative germination curves from a* FourPHFfit.bulk *object*

Description

plot.FourPHFfit plots multiple four-parameter hill function fitted cumulative germination curves (FPHF curves) or the rate of germination curves (RoG curves) from a FourPHFfit.bulk object as an object of class ggplot. Further, either one of the parameters such as time required for 50% of total seeds to germinate ($t_{50_{Total}}$), time required for 50% of viable/germinated seeds to germinate ($t_{50_{Germ}}$), Time at Maximum Germination Rate (TMGR), Mean Germination Time (MGT), or uniformity value ($U_{t_{max}-t_{min}}$) can also be annotated in the plot as specified in the annotate argument.

Usage

```
## S3 method for class 'FourPHFfit.bulk'
plot(
  x,
  rog = FALSE,
  annotate = c("none", "t50.total", "t50.germ", "tmgr", "mgt", "uniformity"),
  limits = TRUE,
  group.col,
  show.points = FALSE,
  ...
)
```

Arguments

x	An data frame object of class `FourPHFfit.bulk` obtained as output from the `FourPHFfit.bulk` function.
rog	If TRUE, plots the Rate of Germination curves (RoG) instead of the Four-Parameter Hill Function fitted cumulative germination curves (FPHF). Default is FALSE.
annotate	The parameter to be annotated in the plot. Either `"t50.total"` ($t_{50_{Total}}$), `"t50.germ"` ($t_{50_{Germ}}$), `"tmgr"` (TMGR), `"mgt"` (MGT), or `"uniformity"` ($U_{t_{max}-t_{min}}$). All the parameters are annotated as vertical lines, except for ($U_{t_{max}-t_{min}}$), which is annotated as horizontal lines.
limits	logical. If TRUE, set the limits of y axis (germination percentage) between 0 and 100 in the germination curve plot. If FALSE, limits are set according to the data. Default is TRUE.
group.col	The names of the column in data frame x according to which grouping has to be done.
show.points	logical. If TRUE, shows the original data points (only for the FPHF curve). Default is TRUE.
...	Default plot arguments.

Value

The plot of the cumulative germination curve as an object of class `ggplot`.

See Also

`FourPHFfit.bulk`

Examples

```
data(gcdata)

counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
                          "Day11", "Day12", "Day13", "Day14")

fits <- FourPHFfit.bulk(gcdata, total.seeds.col = "Total Seeds",
                   counts.intervals.cols = counts.per.intervals,
                   intervals = 1:14, partial = TRUE,
                   fix.y0 = TRUE, fix.a = TRUE, xp = c(10, 60),
                   tmax = 20, tries = 3, umax = 90, umin = 10)

# Plot FPHF curves
plot(fits, group.col = "Genotype")

# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")

# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)

# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```

```
plot(fits, group.col = "Genotype", annotate = "tmgr")
plot(fits, group.col = "Genotype", annotate = "mgt")
plot(fits, group.col = "Genotype", annotate = "uniformity")

# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "tmgr")
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")



# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

# 'Dark2' palette from RColorBrewer
curvesplot + scale_colour_brewer(palette = "Dark2")

# Manual colours
curvesplot +
  scale_colour_manual(values = c("Coral", "Brown", "Blue",
                                 "Aquamarine", "Red"))
```

---

t50   *Median germination time*

Description

Compute the median germination time (t_{50}). Median germination time is the time to reach 50% of final/maximum germination.

Usage

```
t50(germ.counts, intervals, partial = TRUE, method = c("coolbear", "farooq"))
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If TRUE, germ.counts is considered as partial and if FALSE, it is considered as cumulative. Default is TRUE.
method	The method for computing median germination time. Either "coolbear" or "farooq".

Details

With argument `method` specified as `"coolbear"`, median germination time is computed according to the formula by Coolbear et al. (1984) as follows.

$$t_{50} = T_i + \frac{(\frac{N+1}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$

Where, t_{50} is the median germination time, N is the final number of germinated seeds, and N_i and N_j are the total number of seeds germinated in adjacent counts at time T_i and T_j respectively, when $N_i < \frac{N+1}{2} < N_j$.

Similarly with argument `method` specified as `"farooq"`, median germination time is computed according to the formula by by Farooq et al. (2005) as follows.

$$t_{50} = T_i + \frac{(\frac{N}{2} - N_i)(T_j - T_i)}{N_j - N_i}$$

Where, t_{50} is the median germination time, N is the final number of germinated seeds, and N_i and N_j are the total number of seeds germinated in adjacent counts at time T_i and T_j respectively, when $N_i < \frac{N}{2} < N_j$.

Value

The median germination time (t_{50}) value in the same unit of time as specified in the argument `intervals`.

References

Coolbear P, Francis A, Grierson D (1984). "The effect of low temperature pre-sowing treatment on the germination performance and membrane integrity of artificially aged tomato seeds." *Journal of Experimental Botany*, **35**(11), 1609–1617.

Farooq M, Basra SMA, Ahmad N, Hafeez K (2005). "Thermal hardening: A new seed vigor enhancement tool in rice." *Journal of Integrative Plant Biology*, **47**(2), 187–193.

See Also

MeanGermRate

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------------
t50(germ.counts = x, intervals = int, method = "coolbear")
t50(germ.counts = x, intervals = int, method = "farooq")

# From cumulative germination counts
#----------------------------------------------------------------------------
t50(germ.counts = y, intervals = int, partial = FALSE, method = "coolbear")
t50(germ.counts = y, intervals = int, partial = FALSE, method = "farooq")
```

TimsonsIndex   *Timson's index*

Description

Compute George's index (George 1961; Tucker and Wright 1965; Nichols and Heydecker 1968; Chopra and Chaudhary 1980), Timson's index or Timson's germination velocity index (Grose and Zimmer 1958; Timson 1965; Lyon and Coffelt 1966; Chaudhary and Ghildyal 1970; Negm and Smith 1978; Brown and Mayer 1988; Baskin and Baskin 1998) and it's modifications by Labouriau (Ranal and de Santana 2006) and (Khan and Ungar 1984).

Usage

```
TimsonsIndex(
  germ.counts,
  intervals,
  partial = TRUE,
  total.seeds,
  max,
  modification = c("none", "labouriau", "khanungar")
)

GermRateGeorge(germ.counts, intervals, partial = TRUE, max)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
intervals	The time intervals.
partial	logical. If `TRUE`, germ.counts is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.
total.seeds	Total number of seeds.
max	The maximum interval value up to which Timson's index/George's germination rate is to be computed.
modification	The modification to be applied. Either `"none"`, `"labouriau"` or `"khanungar"`. Default is `"none"` (see **Details**).

Details

Timson's index (Timson 1965) is computed as follows (Grose and Zimmer 1958; Brown and Mayer 1988; Baskin and Baskin 1998).

$$\Sigma k = \sum_{i=1}^{k} G_i$$

Where, G_i is the cumulative germination percentage in time interval i and k is the total number of time intervals.

For example ten summation ($\Sigma 10$) is expressed as follows.

$$\Sigma 10 = G_1 + G_2 + \cdots + G_{10}$$

Where $G_1, G_2, \cdots G_{10}$ are the cumulative germination percentage at day 1, 2, 3, $\cdots$, 10 respectively.

Similarly $\Sigma 5$ or $\Sigma 20$ can be estimated. For $\Sigma 10$, the value can range from 0 (no germination) to 1,000 (100% germination after 24 hours).

It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time. It combines onset, rate and total percentage of germination and estimates the area under the cumulative germination percentage curve. It is same as the indices for area under time course curve of germination described by Lyon and Coffelt (1966) as well as Negm and Smith (1978). It is also described as Emergence Rate Index (ERI) by Chaudhary and Ghildyal (1970).

Goodchild and Walker (1971), described the same in terms of partial germination percentage as follows.

$$\Sigma k = \sum_{i=1}^{k} g_i(k - j)$$

Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to k), k is the total number of time intervals, and $j = i - 1$.

Timson's index is equivalent to the Germination Energy Index GEI proposed by Grose and Zimmer (1958).

As Timson's index is useful for comparison only when samples have similar germinabilities or final germination percentage, the following modification was suggested by Labouriau (Ranal and de Santana 2006) (Specified by the argument `modification = "labouriau"`).

$$\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}$$

Here Timson's index (Σk) is divided by the sum of partial germination percentages.

Similarly another modification was proposed by (Khan and Ungar 1984), where Timson's index (Σk) is divided by the total time period of germination (T_k) (Specified by the argument `modification = "khanungar"`).

$$\Sigma k_{mod} = \frac{\Sigma k}{T_k}$$

Timson's index is similar to the Germination Rate (GR) proposed by George (1961) as follows (Tucker and Wright 1965; Nichols and Heydecker 1968).

$$GR = \sum_{i=1}^{k} N_i K_i$$

Where N_i is the number of seeds germinated by ith interval, K_i is the number of intervals(e.g. days) until the end of the test, and k is the total number of time intervals.

This index uses number of seeds germinated instead of germination percentage. It is also described as Emergence Rate Index (ERI) by Chopra and Chaudhary (1980).

So germination rate (GR) can also be described in terms of partial (N_i) and cumulative ($\sum_{j=1}^{i} N_j$) number of seeds germinated in each time interval (i) as follows.

$$GR = \sum_{i=1}^{k} \sum_{j=1}^{i} N_j$$

$$GR = \sum_{i=1}^{k} N_i(k - j)$$

Value

For `TimsonsIndex`, the value of Timson's index (%) if `modification = "none"`. If `modification = "labouriau"`, then value with no unit and if `modification = "khanungar"`, then value as % time^{-1}.

For `GermRateGeorge` The value of George's germination rate as *counttime*.

References

Baskin CC, Baskin JM (1998). *Seeds: Ecology, Biogeography, and Evolution of Dormancy and Germination*. Academic Press, San Diego. ISBN 0-12-080260-0.

Brown RF, Mayer DG (1988). "Representing cumulative germination. 1. A critical analysis of single-value germination indices." *Annals of Botany*, **61**(2), 117–125.

Chaudhary TN, Ghildyal BP (1970). "Effect of temperature associated with levels of bulk density on rice seedling emergence." *Plant and Soil*, **33**(1), 87–90.

Chopra UK, Chaudhary TN (1980). "Effect of soil temperature alteration by soil covers on seedling emergence of wheat (*Triticum aestivum* L.) sown on two dates." *Plant and Soil*, **57**(1), 125–129.

George DW (1961). "Influence of germination temperature on the expression of post-harvest dormancy in wheat." *Crop Science Abstracts; Western Society of Crop Science Annual Meeting, 1961*, 15.

Goodchild NA, Walker MG (1971). "A method of measuring seed germination in physiological studies." *Annals of Botany*, **35**(141), 615–621.

Grose RJ, Zimmer WJ (1958). "Some laboratory germination responses of the seeds of river red gum, *Eucalyptus camaldulensis* Dehn. Syn. *Eucalyptus rostrata* Schlecht." *Australian Journal of Botany*, **6**(2), 129.

Khan MA, Ungar IA (1984). "The effect of salinity and temperature on the germination of polymorphic seeds and growth of *Atriplex triangularis* Willd." *American Journal of Botany*, **71**(4), 481–489.

Lyon JL, Coffelt RJ (1966). "Rapid method for determining numerical indexes for time-course curves." *Nature*, **211**(5046), 330–330.

Negm FB, Smith OE (1978). "Effects of ethylene and carbon dioxide on the germination of osmotically inhibited lettuce seed." *Plant Physiology*, **62**(4), 473–476.

Nichols MA, Heydecker W (1968). "Two approaches to the study of germination data." *Proceedings of the International Seed Testing Association*, **33**(3), 531–540.

Ranal MA, de Santana DG (2006). "How and why to measure the germination process?" *Brazilian Journal of Botany*, **29**(1), 1–11.

Timson J (1965). "New method of recording germination data." *Nature*, **207**(4993), 216.

Tucker H, Wright LN (1965). "Estimating rapidity of germination." *Crop Science*, **5**(5), 398–399.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#-------------------------------------------------------------------------------
# Wihout max specified
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50)
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "none")
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "labouriau")
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "khanungar")
GermRateGeorge(germ.counts = x, intervals = int)


# With max specified
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50, max = 10)
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "none")
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "labouriau")
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "khanungar")
GermRateGeorge(germ.counts = x, intervals = int, max = 10)
GermRateGeorge(germ.counts = x, intervals = int, max = 14)


# From cumulative germination counts
#-------------------------------------------------------------------------------
# Wihout max specified
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50)
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "none")
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "labouriau")
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "khanungar")
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,)

# With max specified
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50, max = 10)
```

```
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             max = 10, modification = "none")
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             max = 10, modification = "labouriau")
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             max = 10, modification = "khanungar")
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 10)
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 14)
```

WeightGermPercent   *Weighted germination percentage*

Description

Compute the Weighted germination percentage WGP or Weighted germination index WGI (Reddy 1978; Reddy et al. 1985).

Usage

```
WeightGermPercent(germ.counts, total.seeds, intervals, partial = TRUE)
```

Arguments

germ.counts	Germination counts at each time interval. Can be partial or cumulative as specified in the argument `partial`.
total.seeds	Total number of seeds tested.
intervals	The time intervals.
partial	logical. If `TRUE`, `germ.counts` is considered as partial and if `FALSE`, it is considered as cumulative. Default is `TRUE`.

Details

Weighted germination percentage was calculated by giving maximum weight to the seeds that germinate first and decreasing weight to the seeds that germinate subsequently. It is computed as follows (Reddy 1978; Reddy et al. 1985).

$$WGP = \frac{\sum_{i=1}^{k}(k - i + 1)N_i}{k \times N} \times 100$$

Where, N_i is the number of seeds that germinated in the time interval i (not cumulative, but partial count), N is the total number of seeds tested, and k is the total number of time intervals.

Value

The weighted germination percentage (%) value.

References

Reddy LV (1978). *Effect of temperature on seed dormancy and alpha-amylase activity during kernel maturation and germination in wheat (Triticum aestivum L.) cultivars.* Ph.D. Thesis, Oregon State University.

Reddy LV, Metzger RJ, Ching TM (1985). "Effect of temperature on seed dormancy of wheat." *Crop Science*, **25**(3), 455.

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)

# From partial germination counts
#----------------------------------------------------------------------
WeightGermPercent(germ.counts = x, total.seeds = 50, intervals = int)

# From cumulative germination counts
#----------------------------------------------------------------------
WeightGermPercent(germ.counts = y, total.seeds = 50, intervals = int,
                  partial = FALSE)
```

Index