The `germinationmetrics` Package: A Brief Introduction

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Contents

Overview

The package `germinationmetrics` is a collection of functions which implements various methods for describing the time-course of germination in terms of single-value germination indices as well as fitted curves.

The goal of this vignette is to introduce the users to these functions and get started in describing sequentially recorded germination count data. This document assumes a basic knowledge of `R` programming language.
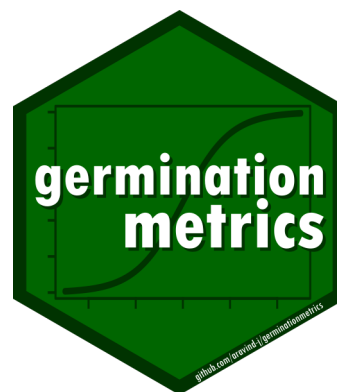
Installation

The package can be installed using the following functions:

```r
# Install from CRAN
install.packages('germinationmetrics', dependencies=TRUE)

# Install development version from Github
devtools::install_github("aravind-j/germinationmetrics")
```

Then the package can be loaded using the function

```r
library(germinationmetrics)
```

Version History

The current version of the package is 0.1.2. The previous versions are as follows.

Table 1. Version history of `germinationmetrics` R package.

Version	Date
0.1.0	2018-04-17
0.1.1	2018-07-26
0.1.1.1	2018-10-16

To know detailed history of changes use `news(package='germinationmetrics')`.

Germination count data

Typically in a germination test, the germination count data of a fixed number of seeds is recorded at regular intervals for a definite period of time or until all the seeds have germinated. These germination count data can be either partial or cumulative (Table 2).

Table 2 : A typical germination count data.

intervals	counts	cumulative.counts
1	0	0
2	0	0
3	0	0
4	0	0
5	4	4
6	17	21
7	10	31
8	7	38
9	1	39
10	0	39
11	1	40
12	0	40
13	0	40
14	0	40

The time-course of germination can be plotted as follows:

```
data <- data.frame(intervals = 1:14,
                   counts = c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0))

# Partial germination counts
x <- data$counts
# Cumulative germination counts
y <- cumsum(x)
# Time intervals of observations
int <- data$intervals

plot(int, cumsum(x))
```
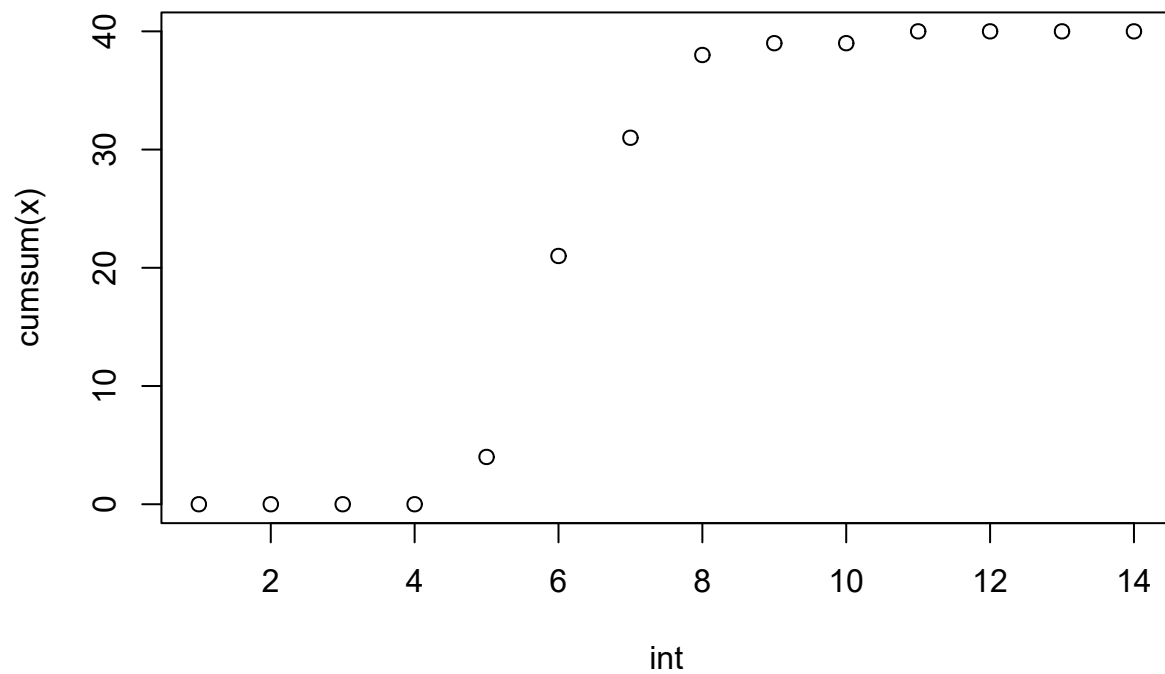
Single-value germination indices

The details about the single-value germination indices implemented in germinationmetrics are described in Table 3.

\begin{small}

Table 3 : Single-value germination indices implemented in `germinationmetrics`.

Germination index	function	Details	Unit	Measures	Reference
Germination percentage or Germinability (GP)	`GermPercent`	It is computed as follows: $$GP = \frac{N_g}{N_t} \times 100$$ Where, N_g is the number of germinated seeds and N_t is the total number of seeds.	Percentage (%)	Germination capacity	ISTA (2015)
Time for the first germination or Germination time lag (t_0)	`FirstGermTime`	It is the time for first germination to occur (e.g. First day of germination)	time	Germination time	Edwards (1932); Czabator (1962); Goloff and Bazzaz (1975); Labouriau (1983a); Ranal (1999); Quintanilla et al. (2000)
Time for the last germination (t_g)	`LastGermTime`	It is the time for last germination to occur (e.g. Last day of germination)	time	Germination time	Edwards (1932)
Time spread of germination or Germination distribution	`TimeSpreadGerm`	It is the difference between time for last germination (t_g) and time for first germination (t_0). $$Time\,spread\,of\,germination = t_g - t_0$$	time	Germination time	Al-Mudaris (1998); Schrader and Graves (2000); Kader (2005)
Peak period of germination or Modal time of germination	`PeakGermTime`	It is the time in which highest frequency of germinated seeds are observed and need not be unique.	time	Germination time	Ranal and Santana (2006)
Median germination time (t_{50}) (Coolbear)	`t50`	It is the time to reach 50% of final/maximum germination. With argument method specified as `"coolbear"`, it 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 $N_i < \frac{N+1}{2} < N_j$.	time	Germination time	Coolbear et al. (1984)

Germination index	function	Details	Unit	Measures	Reference
Median germination time (t_{50}) (Farooq)	`t50`	With argument method specified as `"farooq"`, it is computed according to the formula by (Coolbear et al., 1984) 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 $N_i < \frac{N}{2} < N_j$.	time	Germination time	Farooq et al. (2005)
Mean germination time or Mean length of incubation time ($\overline{T}$) or Germination resistance (GR) or Sprouting index (SI)	`MeanGermTime`	It is the average length of time required for maximum germination of a seed lot and is estimated according to the following formula. $$\overline{T} = \frac{\sum_{i=1}^{k} N_i T_i}{\sum_{i=1}^{k} N_i}$$ Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination. It is the inverse of mean germination rate ($\overline{V}$). $$\overline{T} = \frac{1}{\overline{V}}$$	time	Germination time	Edmond and Drapala (1958); Czabator (1962); Smith and Millet (1964); Gordon (1969); Gordon (1971); Ellis and Roberts (1980) Labouriau (1983a); Ranal and Santana (2006)
Variance of germination time (s_T^2)	`VarGermTime`	It is computed according to the following formula. $$s_T^2 = \frac{\sum_{i=1}^{k} N_i(T_i - \overline{T})^2}{\sum_{i=1}^{k} N_i - 1}$$ Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)

Germination index	function	Details	Unit	Measures	Reference
Standard error of germination time ($s_{\overline{T}}$)	`SEGermTime`	It signifies the accuracy of the calculation of the mean germination time. It is estimated according to the following formula: $$s_{\overline{T}} = \sqrt{\frac{s_T^2}{\sum_{i=1}^{k} N_i}}$$ Where, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Mean germination rate ($\overline{V}$)	`MeanGermRate`	It is computed according to the following formula: $$\overline{V} = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i}$$ Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination. It is the inverse of mean germination time ($\overline{T}$). $$\overline{V} = \frac{1}{\overline{T}}$$	time^{-1}	Germination rate	Labouriau and Valadares (1976); Labouriau (1983b); Ranal and Santana (2006)
Coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG)	`CVG`	It is estimated according to the following formula. $$CVG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i} \times 100$$ $$CVG = \overline{V} \times 100$$ Where, T_i is the time from the start of the experiment to the ith observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.	% day^{-1}	Germination rate	Kotowski (1926), Nichols and Heydecker (1968); Bewley and Black (1994); Labouriau (1983b); Scott et al. (1984)
Variance of germination rate (s_V^2)	`VarGermRate`	It is calculated according to the following formula. $$s_V^2 = \overline{V}^4 \times s_T^2$$ Where, s_T^2 is the variance of germination time.	time^{-2}	Germination rate	Labouriau (1983b); Ranal and Santana (2006)

Germination index	function	Details	Unit	Measures	Reference
Standard error of germination rate ($s_{\overline{V}}$)	`SEGermRate`	It is estimated according to the following formula. $$s_{\overline{V}} = \sqrt{\frac{s_V^2}{\sum_{i=1}^{k} N_i}}$$ Where, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.	time^{-1}	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Germination rate as the reciprocal of the median time (v_{50})	`GermRateRecip`	It is the reciprocal of the median germination time (t_{50}). $$v_{50} = \frac{1}{t_{50}}$$	time^{-1}	Germination rate	Went (1957); Labouriau (1983b); Ranal and Santana (2006)
Speed of germination or Germination rate Index or index of velocity of germination or Emergence rate index (Germination index according to AOSA)	`GermSpeed`	It is the rate of germination in terms of the total number of seeds that germinate in a time interval. It is estimated as follows: $$S = \frac{N_1}{T_1} + \frac{N_2}{T_2} + \frac{N_3}{T_3} + \cdots + \frac{N_n}{T_n}$$ Where, N_1, N_2, N_3, $\cdots$, N_n are the number of germinated seeds observed at time (days or hours) T_1, T_2, T_3, $\cdots$, T_n after sowing. (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time). Instead of germination counts, germination percentages may also be used for computation of speed of germination.	% time^{-1}	Mixed	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)
Speed of accumulated germination	`GermSpeedAccumulated`	It is estimated as follows: $$S_{accumulated} = \frac{N_1}{T_1} + \frac{N_1 + N_2}{T_2} + \frac{N_1 + N_2 + N_3}{T_3} + \cdots + \frac{N_1 + N_2 + \ldots}{T_i}$$ Where, N_1, N_2, N_3, $\cdots$, N_n are the number of germinated seeds observed at time (days or hours) T_1, T_2, T_3, $\cdots$, T_n after sowing. (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time). Instead of germination counts, germination percentages may also be used for computation of speed of germination.	% time^{-1}	Mixed	Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004)
Corrected germination rate index	`GermSpeedCorrected`	It is computed as follows: $$S_{corrected} = \frac{S}{FGP}$$ Where, FGP: the final germination percentage or germinability.	time^{-1}	Mixed	Evetts and Burnside (1972)

Germination index	function	Details	Unit	Measures	Reference
Weighted germination percentage (WGP)	WeightGermPercent	It is estimated as follows: $$WGP = \frac{\sum_{i=1}^{t}(t-i+1)N_i}{t \times N} \times 100$$ 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 t is the total number of time intervals.		Mixed	Reddy (1978)
Mean germination percentage per unit time ($\overline{GP}$)	MeanGermPercent	It is estimated as follows: $$\overline{G} = \frac{GP}{T_n}$$ Where, GP is the final germination percentage and T_n is the total number of intervals(e.g. days) required for final germination.		Mixed	Czabator (1962)
Number of seeds germinated per unit time $\overline{N}$	MeanGermNumber	It is estimated as follows: $$\overline{N} = \frac{N_g}{T_n}$$ Where, N_g is the number of germinated seeds and T_n is the total number of intervals (e.g. days) required for final germination.		Mixed	Khamassi et al. (2013)
Timson's index [$\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$] or Germination energy index (GEI)	TimsonsIndex	It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time and is estimated in terms of cumulative germination percentage (G_i) as follows: $$\sum n = \sum_{i=1}^{t} G_i$$ Where, G_i is the cumulative germination percentage in time interval i and t is the total number of time intervals. It also estimated in terms of partial germination percentage as follows: $$\sum n = \sum_{i=1}^{t} g_i(t-j)$$ Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to t) and t is the total number of time intervals and $j = i - 1$.		Mixed	Grose and Zimmer (1958); Timson (1965); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971)

Germination index	function	Details	Unit	Measures	Reference
Modified Timson's index (Labouriau)	TimsonsIndex	It is estimated as Timson's index T divided by the sum of partial germination percentages. $$T_{mod} = \frac{T}{\sum_{i=1}^{t} g_i}$$		Mixed	Ranal and Santana (2006)
Modified Timson's index (Khan and Unger)	TimsonsIndex	It is estimated as Timson's index (T) divided by the number of intervals (t). $$T_{mod} = \frac{T}{t}$$		Mixed	Khan and Ungar (1984)
George's index	GermRateGeorge	It is estimated as follows: $$GR = \sum_{i=1}^{t} N_i K_i$$ Where N_i is the number of seeds germinated by ith interval and K_i is the number of intervals(eg. days) until the end of the test.		Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968)
Peak value(PV) (Czabator) or Emergence Energy (EE)	PeakValue	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 computed as the maximum quotient obtained by dividing successive cumulative germination values by the relevant incubation time.		Mixed	Czabator (1962); Bonner (1967)
Germination value (GV) (Czabator)	GermValue	It is computed as follows: $$GV = PV \times MDG$$ Where, PV is the peak value and MDG is the mean daily germination percentage from the onset of germination. It can also be computed for other time intervals of successive germination counts, by replacing MDG with the mean germination percentage per unit time ($\overline{GP}$).		Mixed	Czabator (1962)

Germination index	function	Details	Unit	Measures	Reference
Germination value (GV) (Diavanshir and Pourbiek)	`GermValue`	It is computed as follows: $$GV = \frac{\sum DGS}{N} \times GP \times k$$ Where, DGS is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the 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 k is a constant. The value of k is decided on the basis of average daily speed of germination ($\frac{\sum DGS}{N}$). If it is less than 10, then k value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for k. GV value can be modified (GV_{mod}), to consider the entire duration from the beginning of the test instead of just from the onset of germination.		Mixed	Djavanshir and Pourbeik (1976); Brown and Mayer (1988)
Coefficient of uniformity of germination (CUG)	`CUGerm`	It is computed as follows: $$CV_T = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} (\overline{T} - T_i)^2 N_i}$$ Where, $\overline{T}$ is the the mean germination time, T_i is the time from the start of the experiment to the ith observation (day for the example); N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation), and k is the last time of germination.		Germinatin unifromity	Heydecker (1972); Bewley and Black (1994)
Coefficient of variation of the germination time (CV_T)	`CVGermTime`	It is estimated as follows: $$CV_T = \sqrt{\frac{s_T^2}{\overline{T}}}$$ Where, s_T^2 is the variance of germination time and $\overline{T}$ is the mean germination time.		Germinatin unifromity	Ranal and Santana (2006)
Synchronization index ($\overline{E}$) or Uncertainty of the germination process (U) or informational entropy (H)	`GermUncertainty`	It is estimated as follows: $$\overline{E} = -\sum_{i=1}^{k} f_i \log_2 f_i$$ Where, f_i is the relative frequency of germination ($f_i = \frac{N_i}{\sum_{i=1}^{k} N_i}$), N_i is the number of seeds germinated on the ith time and k is the last day of observation.	bit	Germination synchrony	Shannon (1948); Labouriau and Valadares (1976); Labouriau (1983b)

Germination index	function	Details	Unit	Measures	Reference
Synchrony of germination (Z index)	`GermSynchrony`	It is computed as follows: $$Z = \frac{\sum_{i=1}^{k} C_{N_i,2}}{C_{\Sigma N_i,2}}$$ 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 (estimated as $C_{N_i,2} = \frac{Ni(Ni-1)}{2}$) 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.		Germination synchrony	Primack (1985); Ranal and Santana (2006)

\end{small}

Examples

GermPercent()

```r
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)

# From partial germination counts
GermPercent(germ.counts = x, total.seeds = 50)
```

```
[1] 80
```

```r
# From cumulative germination counts
GermPercent(germ.counts = y, total.seeds = 50, partial = FALSE)
```

```
[1] 80
```

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

```
[1] 80
```

FirstGermTime(), LastGermTime(), PeakGermTime(), TimeSpreadGerm()

```r
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)
```

```
[1] 5
```

```r
LastGermTime(germ.counts = x, intervals = int)
```

```
[1] 11
```

```r
TimeSpreadGerm(germ.counts = x, intervals = int)
```

```
[1] 6
```

```r
PeakGermTime(germ.counts = x, intervals = int)
```

```
[1] 6
```

```r
# For multiple peak germination times
PeakGermTime(germ.counts = z, intervals = int)
```

```
Warning in PeakGermTime(germ.counts = z, intervals = int): Multiple peak
germination times exist.
```

```
[1] 5 6
```

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

```
[1] 5
```

```
LastGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 11
```
```
TimeSpreadGerm(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 6
```
```
PeakGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 6
```
```
# For multiple peak germination time
PeakGermTime(germ.counts = cumsum(z), intervals = int, partial = FALSE)
```

```
Warning in PeakGermTime(germ.counts = cumsum(z), intervals = int, partial =
FALSE): Multiple peak germination times exist.
```

```
[1] 5 6
```

```
t50()
```
```
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")
```

```
[1] 5.970588
```
```
t50(germ.counts = x, intervals = int, method = "farooq")
```

```
[1] 5.941176
```
```
# From cumulative germination counts
#-----------------------------------------------------------------------------
t50(germ.counts = y, intervals = int, partial = FALSE, method = "coolbear")
```

```
[1] 5.970588
```
```
t50(germ.counts = y, intervals = int, partial = FALSE, method = "farooq")
```

```
[1] 5.941176
```

```
MeanGermTime(), VarGermTime(), SEGermTime(), CVGermTime()
```
```
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)
```

```
[1] 6.7
```
```
VarGermTime(germ.counts = x, intervals = int)
```

```
[1] 1.446154
```

```r
SEGermTime(germ.counts = x, intervals = int)
```

```
[1] 0.1901416
```

```r
CVGermTime(germ.counts = x, intervals = int)
```

```
[1] 0.1794868
# From cumulative germination counts
#-----------------------------------------------------------------------------
MeanGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 6.7
```

```r
VarGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 19.04012
```

```r
SEGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.2394781
```

```r
CVGermTime(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.6512685
```

```r
MeanGermRate(), CVG(), VarGermRate(), SEGermRate(), GermRateRecip()
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)
```

```
[1] 0.1492537
```

```r
CVG(germ.counts = x, intervals = int)
```

```
[1] 14.92537
```

```r
VarGermRate(germ.counts = x, intervals = int)
```

```
[1] 0.0007176543
```

```r
SEGermRate(germ.counts = x, intervals = int)
```

```
[1] 0.004235724
```

```r
GermRateRecip(germ.counts = x, intervals = int, method = "coolbear")
```

```
[1] 0.1674877
```

```r
GermRateRecip(germ.counts = x, intervals = int, method = "farooq")
```

```
[1] 0.1683168
# From cumulative germination counts
#-----------------------------------------------------------------------------
MeanGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.1492537
```
```
CVG(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 14.92537
```
```
VarGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.009448666
```
```
SEGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.005334776
```
```
GermRateRecip(germ.counts = y, intervals = int,
              method = "coolbear", partial = FALSE)
```

```
[1] 0.1674877
```
```
GermRateRecip(germ.counts = y, intervals = int,
              method = "farooq", partial = FALSE)
```

```
[1] 0.1683168
```

```
GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()
```
```
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)
```

```
[1] 6.138925
```
```
GermSpeedAccumulated(germ.counts = x, intervals = int)
```

```
[1] 34.61567
```
```
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "normal")
```

```
[1] 0.07673656
```
```
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "accumulated")
```

```
[1] 0.4326958
```
```
# From partial germination counts (with percentages instead of counts)
#-------------------------------------------------------------------------
GermSpeed(germ.counts = x, intervals = int,
          percent = TRUE, total.seeds = 50)
```

```
[1] 12.27785
```
```
GermSpeedAccumulated(germ.counts = x, intervals = int,
                     percent = TRUE, total.seeds = 50)
```

```
[1] 69.23134
```

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

```
[1] 6.138925
```

```r
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 34.61567
```

```r
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "normal")
```

```
[1] 0.07673656
```

```r
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "accumulated")
```

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

```r
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE,
                     percent = TRUE, total.seeds = 50)
```

```
[1] 69.23134
```

```r
GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()
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)
```

```
[1] 6.138925
```

```r
GermSpeedAccumulated(germ.counts = x, intervals = int)
```

```
[1] 34.61567
```

```r
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "normal")
```

```
[1] 0.07673656
```

```r
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50,
                   method = "accumulated")
```

```
[1] 0.4326958
```

```r
# From partial germination counts (with percentages instead of counts)
#-------------------------------------------------------------------------
```

```r
GermSpeed(germ.counts = x, intervals = int,
          percent = TRUE, total.seeds = 50)
```

```
[1] 12.27785
```

```r
GermSpeedAccumulated(germ.counts = x, intervals = int,
                     percent = TRUE, total.seeds = 50)
```

```
[1] 69.23134
```

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

```
[1] 6.138925
```

```r
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 34.61567
```

```r
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "normal")
```

```
[1] 0.07673656
```

```r
GermSpeedCorrected(germ.counts = y, intervals = int,
                   partial = FALSE, total.seeds = 50, method = "accumulated")
```

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

```r
GermSpeedAccumulated(germ.counts = y, intervals = int, partial = FALSE,
                     percent = TRUE, total.seeds = 50)
```

```
[1] 69.23134
```

WeightGermPercent()

```r
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)
```

```
[1] 47.42857
```

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

```
[1] 47.42857
```

MeanGermPercent(), MeanGermNumber()

```r
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)
```

```
[1] 5.714286
```

```r
MeanGermNumber(germ.counts = x, intervals = int)
```

```
[1] 2.857143
```

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

```
[1] 5.714286
```

```r
MeanGermNumber(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 2.857143
```

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

```
[1] 5.714286
```

TimsonsIndex(), GermRateGeorge()

```r
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)
```

```
[1] 664
```

```r
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "none")
```

```
[1] 664
```

```r
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "labouriau")
```

```
[1] 8.3
```

```r
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             modification = "khanungar")
```

```
[1] 47.42857
```

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

```
[1] 344
```

```
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "none")
```

```
[1] 344
```

```
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "labouriau")
```

```
[1] 4.410256
```

```
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
             max = 10, modification = "khanungar")
```

```
[1] 24.57143
```

```
# Wihout max specified
GermRateGeorge(germ.counts = x, intervals = int)
```

```
[1] 332
```

```
# With max specified
GermRateGeorge(germ.counts = x, intervals = int, max = 10)
```

```
[1] 172
```

```
GermRateGeorge(germ.counts = x, intervals = int, max = 14)
```

```
[1] 332
```

```
# From cumulative germination counts
#---------------------------------------------------------------------------
```

```
# Wihout max specified
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE)
```

```
[1] 332
```

```
# With max specified
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE, max = 10)
```

```
[1] 172
```

```
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE, max = 14)
```

```
[1] 332
```

PeakValue(), GermValue()

```
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)
```

```
[1] 9.5
```

```
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "czabator")
```

```
$`Germination Value`
[1] 38.95
```

```
[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
17           0        17                    160                    80.0
18           2        18                    162                    81.0
19           0        19                    162                    81.0
20           2        20                    164                    82.0
        DGS
3   5.666667
4   9.250000
5   9.500000
6   8.750000
7   7.785714
8   7.125000
9   6.500000
10  6.100000
11  5.909091
12  5.708333
13  5.538462
14  5.357143
15  5.200000
16  5.000000
17  4.705882
18  4.500000
19  4.263158
20  4.100000
```

```
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "dp", k = 10)
```

```
$`Germination Value`
```

```
[1] 53.36595

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
17           0        17                    160                    80.0
18           2        18                    162                    81.0
19           0        19                    162                    81.0
20           2        20                    164                    82.0
        DGS SumDGSbyN        GV
3  5.666667  5.666667  9.633333
4  9.250000  7.458333 27.595833
5  9.500000  8.138889 38.659722
6  8.750000  8.291667 43.531250
7  7.785714  8.190476 44.638095
8  7.125000  8.012897 45.673512
9  6.500000  7.796769 45.611097
10 6.100000  7.584673 46.266503
11 5.909091  7.398497 48.090230
12 5.708333  7.229481 49.521942
13 5.538462  7.075752 50.945411
14 5.357143  6.932534 51.994006
15 5.200000  6.799262 53.034246
16 5.000000  6.670744 53.365948
17 4.705882  6.539753 52.318022
18 4.500000  6.412268 51.939373
19 4.263158  6.285850 50.915385
20 4.100000  6.164414 50.548194


$testend
[1] 16
```

```r
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "czabator", from.onset = FALSE)
```

```
$`Germination Value`
[1] 38.95

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
1            0         1                      0                     0.0
2            0         2                      0                     0.0
```

3	34	3	34	17.0
4	40	4	74	37.0
5	21	5	95	47.5
6	10	6	105	52.5
7	4	7	109	54.5
8	5	8	114	57.0
9	3	9	117	58.5
10	5	10	122	61.0
11	8	11	130	65.0
12	7	12	137	68.5
13	7	13	144	72.0
14	6	14	150	75.0
15	6	15	156	78.0
16	4	16	160	80.0
17	0	17	160	80.0
18	2	18	162	81.0
19	0	19	162	81.0
20	2	20	164	82.0

```
      DGS
1  0.000000
2  0.000000
3  5.666667
4  9.250000
5  9.500000
6  8.750000
7  7.785714
8  7.125000
9  6.500000
10 6.100000
11 5.909091
12 5.708333
13 5.538462
14 5.357143
15 5.200000
16 5.000000
17 4.705882
18 4.500000
19 4.263158
20 4.100000
```

```
GermValue(germ.counts = x, intervals = int, total.seeds = 200,
          method = "dp", k = 10, from.onset = FALSE)
```

```
$`Germination Value`
[1] 46.6952
```

```
[[2]]
  germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
1           0         1                      0                     0.0
2           0         2                      0                     0.0
3          34         3                     34                    17.0
4          40         4                     74                    37.0
5          21         5                     95                    47.5
6          10         6                    105                    52.5
7           4         7                    109                    54.5
```

8	5	8	114	57.0
9	3	9	117	58.5
10	5	10	122	61.0
11	8	11	130	65.0
12	7	12	137	68.5
13	7	13	144	72.0
14	6	14	150	75.0
15	6	15	156	78.0
16	4	16	160	80.0
17	0	17	160	80.0
18	2	18	162	81.0
19	0	19	162	81.0
20	2	20	164	82.0

```
         DGS SumDGSbyN         GV
1   0.000000  0.000000  0.000000
2   0.000000  0.000000  0.000000
3   5.666667  1.888889  3.211111
4   9.250000  3.729167 13.797917
5   9.500000  4.883333 23.195833
6   8.750000  5.527778 29.020833
7   7.785714  5.850340 31.884354
8   7.125000  6.009673 34.255134
9   6.500000  6.064153 35.475298
10 6.100000  6.067738 37.013202
11 5.909091  6.053316 39.346552
12 5.708333  6.024567 41.268285
13 5.538462  5.987174 43.107655
14 5.357143  5.942172 44.566291
15 5.200000  5.892694 45.963013
16 5.000000  5.836901 46.695205
17 4.705882  5.770370 46.162961
18 4.500000  5.699794 46.168331
19 4.263158  5.624182 45.555871
20 4.100000  5.547972 45.493374


$testend
[1] 16
```

```
# From cumulative germination counts
#------------------------------------------------------------------------------
PeakValue(germ.counts = y, interval = int, total.seeds = 200,
          partial = FALSE)
```

```
[1] 9.5
```

```
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "czabator")
```

```
$`Germination Value`
[1] 38.95


[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
3           34         3                     34                    17.0
4           40         4                     74                    37.0
```

```
5               21           5                       95                       47.5
6               10           6                      105                       52.5
7                4           7                      109                       54.5
8                5           8                      114                       57.0
9                3           9                      117                       58.5
10               5          10                      122                       61.0
11               8          11                      130                       65.0
12               7          12                      137                       68.5
13               7          13                      144                       72.0
14               6          14                      150                       75.0
15               6          15                      156                       78.0
16               4          16                      160                       80.0
17               0          17                      160                       80.0
18               2          18                      162                       81.0
19               0          19                      162                       81.0
20               2          20                      164                       82.0
        DGS
3  5.666667
4  9.250000
5  9.500000
6  8.750000
7  7.785714
8  7.125000
9  6.500000
10 6.100000
11 5.909091
12 5.708333
13 5.538462
14 5.357143
15 5.200000
16 5.000000
17 4.705882
18 4.500000
19 4.263158
20 4.100000
```

```r
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "dp", k = 10)
```

```
$`Germination Value`
[1] 53.36595

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
```

```
14             6          14              150              75.0
15             6          15              156              78.0
16             4          16              160              80.0
17             0          17              160              80.0
18             2          18              162              81.0
19             0          19              162              81.0
20             2          20              164              82.0
        DGS SumDGSbyN        GV
3  5.666667  5.666667  9.633333
4  9.250000  7.458333 27.595833
5  9.500000  8.138889 38.659722
6  8.750000  8.291667 43.531250
7  7.785714  8.190476 44.638095
8  7.125000  8.012897 45.673512
9  6.500000  7.796769 45.611097
10 6.100000  7.584673 46.266503
11 5.909091  7.398497 48.090230
12 5.708333  7.229481 49.521942
13 5.538462  7.075752 50.945411
14 5.357143  6.932534 51.994006
15 5.200000  6.799262 53.034246
16 5.000000  6.670744 53.365948
17 4.705882  6.539753 52.318022
18 4.500000  6.412268 51.939373
19 4.263158  6.285850 50.915385
20 4.100000  6.164414 50.548194


$testend
[1] 16
```

```r
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "czabator", from.onset = FALSE)
```

```
$`Germination Value`
[1] 38.95


[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
1            0         1                      0                     0.0
2            0         2                      0                     0.0
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
17           0        17                    160                    80.0
```

```
18              2      18                162                 81.0
19              0      19                162                 81.0
20              2      20                164                 82.0
        DGS
1   0.000000
2   0.000000
3   5.666667
4   9.250000
5   9.500000
6   8.750000
7   7.785714
8   7.125000
9   6.500000
10  6.100000
11  5.909091
12  5.708333
13  5.538462
14  5.357143
15  5.200000
16  5.000000
17  4.705882
18  4.500000
19  4.263158
20  4.100000
```

```
GermValue(germ.counts = y, intervals = int, total.seeds = 200,
          partial = FALSE, method = "dp", k = 10, from.onset = FALSE)
```

```
$`Germination Value`
[1] 46.6952


[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent
1            0         1                      0                     0.0
2            0         2                      0                     0.0
3           34         3                     34                    17.0
4           40         4                     74                    37.0
5           21         5                     95                    47.5
6           10         6                    105                    52.5
7            4         7                    109                    54.5
8            5         8                    114                    57.0
9            3         9                    117                    58.5
10           5        10                    122                    61.0
11           8        11                    130                    65.0
12           7        12                    137                    68.5
13           7        13                    144                    72.0
14           6        14                    150                    75.0
15           6        15                    156                    78.0
16           4        16                    160                    80.0
17           0        17                    160                    80.0
18           2        18                    162                    81.0
19           0        19                    162                    81.0
20           2        20                    164                    82.0
        DGS SumDGSbyN        GV
1  0.000000  0.000000  0.000000
```

```
2  0.000000  0.000000  0.000000
3  5.666667  1.888889  3.211111
4  9.250000  3.729167 13.797917
5  9.500000  4.883333 23.195833
6  8.750000  5.527778 29.020833
7  7.785714  5.850340 31.884354
8  7.125000  6.009673 34.255134
9  6.500000  6.064153 35.475298
10 6.100000  6.067738 37.013202
11 5.909091  6.053316 39.346552
12 5.708333  6.024567 41.268285
13 5.538462  5.987174 43.107655
14 5.357143  5.942172 44.566291
15 5.200000  5.892694 45.963013
16 5.000000  5.836901 46.695205
17 4.705882  5.770370 46.162961
18 4.500000  5.699794 46.168331
19 4.263158  5.624182 45.555871
20 4.100000  5.547972 45.493374


$testend
[1] 16
```

CUGerm()

```
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)
```

```
[1] 0.7092199
```

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

```
[1] 0.05267935
```

GermSynchrony(), GermUncertainty()

```
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)
```

```
[1] 0.2666667
```

```
GermUncertainty(germ.counts = x, intervals = int)
```

```
[1] 2.062987
```

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

```
[1] 0.2666667
```

```
GermUncertainty(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 2.062987
```

Curve fitting

Several mathematical functions have been used to fit the cumulative germination count data and describe the germination process such as Richard's, Weibull, logistic, log-logistic, gaussian, four-parameter hill function etc. Currently `germinationmetrics` implements the four-parameter hill function to fit the count data and computed various associated metrics.

Four-parameter hill function

The four-parameter hill function defined as follows (El-Kassaby et al., 2008):

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

Where, y is the cumulative germination percentage at time x, y_0 is the intercept on the y axis, a is the asymptote, b is a mathematical parameter controlling the shape and steepness of the germination curve and c is the "half-maximal activation level".

The details of various parameters that are computed from this function are given in Table 4.

Table 4 Germination parameters estimated from the four-parameter hill function.

Germination parameters	Details	Unit	Measures
y intercept (y_0)	The intercept on the y axis.		
Asymptote (a)	It is the maximum cumulative germination percentage, which is equivalent to germination capacity.	%	Germination capacity
Shape and steepness (b)	Mathematical parameter controlling the shape and steepness of the germination curve. The larger the b, the steeper the rise toward the asymptote a, and the shorter the time between germination onset and maximum germination.		Germination rate
Half-maximal activation level (c)	Time required for 50% of viable seeds to germinate.	time	Germination time
lag	It is the time at germination onset and is computed by solving four-parameter hill function after setting y to 0 as follows: $$lag = b\sqrt{\frac{-y_0 c^b}{a + y_0}}$$	time	Germination time
D_{lag-50}	The duration between the time at germination onset (*lag*) and that at 50% germination (c).	time	Germination time

Germination parameters	Details	Unit	Measures
$t_{50_{total}}$	Time required for 50% of total seeds to germinate.	time	Germination time
$t_{50_{germinated}}$	Time required for 50% of viable/germinated seeds to germinate	time	Germination time
$t_{x_{total}}$	Time required for x% of total seeds to germinate.	time	Germination time
$t_{x_{germinated}}$	Time required for x% of viable/germinated seeds to germinate	time	Germination time
Uniformity ($U_{t_{max}-t_{min}}$)	It is the time interval between the percentages of viable seeds specified in the arguments `umin` and `umin` to germinate.	time	Germination time
Time at maximum germination rate ($TMGR$)	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, $TMGR$ can be estimated as follows: $$TMGR = b\sqrt{\frac{c^b(b-1)}{b+1}}$$ It represents the point in time when the instantaneous rate of germination starts to decline.	time	Germination time
Area under the curve (AUC)	It is obtained by integration of the fitted curve between time 0 and time specified in the argument `tmax`.		Mixed
MGT	Calculated by integration of the fitted curve and proper normalisation.	time	Germination time
Skewness	It is computed as follows: $$\frac{MGT}{t_{50_{germinated}}}$$		

Examples

```
FourPHFfit()
```

```r
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)
```

```
$data
```

```
     gp csgp intervals
1    0    0         1
2    0    0         2
3    0    0         3
4    0    0         4
5    8    8         5
6   34   42         6
7   20   62         7
8   14   76         8
9    2   78         9
10   0   78        10
11   2   80        11
12   0   80        12
13   0   80        13
14   0   80        14


$Parameters
  term   estimate  std.error statistic      p.value
1    a  80.000000 1.24158595  64.43372 1.973240e-14
2    b   9.881947 0.70779379  13.96162 6.952322e-08
3    c   6.034954 0.04952654 121.85294 3.399385e-17
4   y0   0.000000 0.91607007   0.00000 1.000000e+00


$Fit
     sigma isConv      finTol    logLik      AIC      BIC deviance
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723
  df.residual
1          10


$a
[1] 80


$b
[1] 9.881947


$c
[1] 6.034954


$y0
[1] 0


$lag
[1] 0


$Dlag50
[1] 6.034954


$t50.total
[1] 6.355122


$txp.total
[1] 4.956266 6.744598


$t50.Germinated
```

```
[1] 6.034954

$txp.Germinated
[1] 4.831809 6.287724

$Uniformity
          90          10 uniformity
    7.537688    4.831809    2.705880

$TMGR
[1] 5.912195

$AUC
[1] 1108.975

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. Relative error in the sum of squares is at most `ftol'. "

$isConv
[1] TRUE

attr(,"class")
[1] "FourPHFfit"
```

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

```
$data
    gp csgp intervals
1    0    0         1
2    0    0         2
3    0    0         3
4    0    0         4
5    8    8         5
6   34   42         6
7   20   62         7
8   14   76         8
9    2   78         9
10   0   78        10
11   2   80        11
12   0   80        12
13   0   80        13
14   0   80        14


$Parameters
   term   estimate std.error statistic      p.value
1     a 80.000000 1.2415867  64.43368 1.973252e-14
```

```
2     b  9.881927 0.7077918   13.96163 6.952270e-08
3     c  6.034953 0.0495266 121.85275 3.399437e-17
4    y0  0.000000 0.9160705    0.00000 1.000000e+00

$Fit
     sigma isConv       finTol    logLik      AIC      BIC deviance
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723
  df.residual
1          10

$a
[1] 80

$b
[1] 9.881927

$c
[1] 6.034953

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034953

$t50.total
[1] 6.355121

$txp.total
[1] 4.956263 6.744599

$t50.Germinated
[1] 6.034953

$txp.Germinated
[1] 4.831806 6.287723

$Uniformity
        90           10 uniformity
  7.537691    4.831806   2.705885

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
```

```
[1] 1.098973

$msg
[1] "#1. Relative error in the sum of squares is at most `ftol'. "

$isConv
[1] TRUE

attr(,"class")
[1] "FourPHFfit"
```

```r
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)
```

```r
plot(fit2)
```
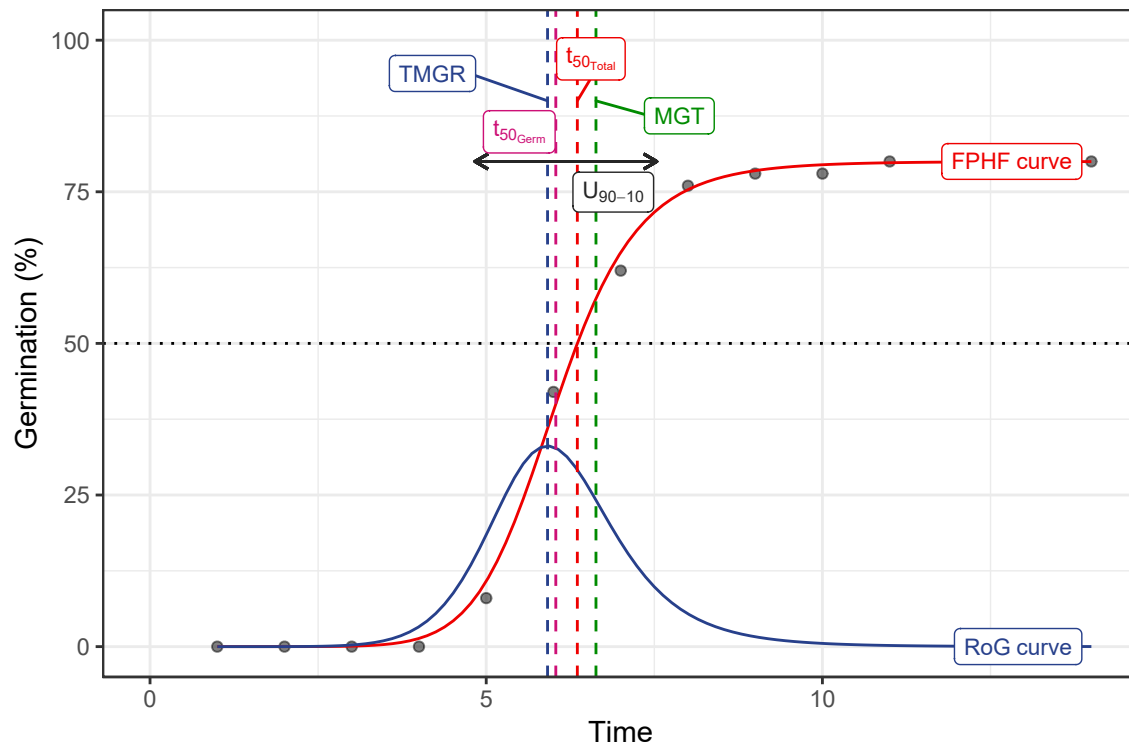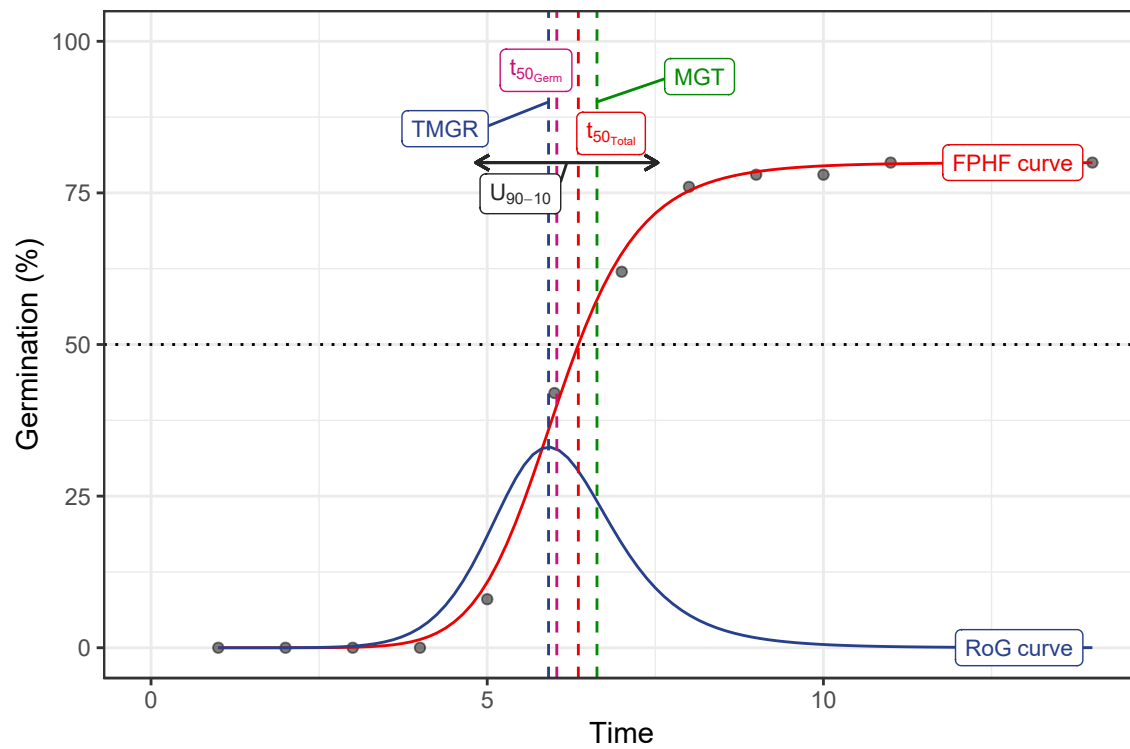


```r
# No labels
plot(fit1, plotlabels = FALSE)
```
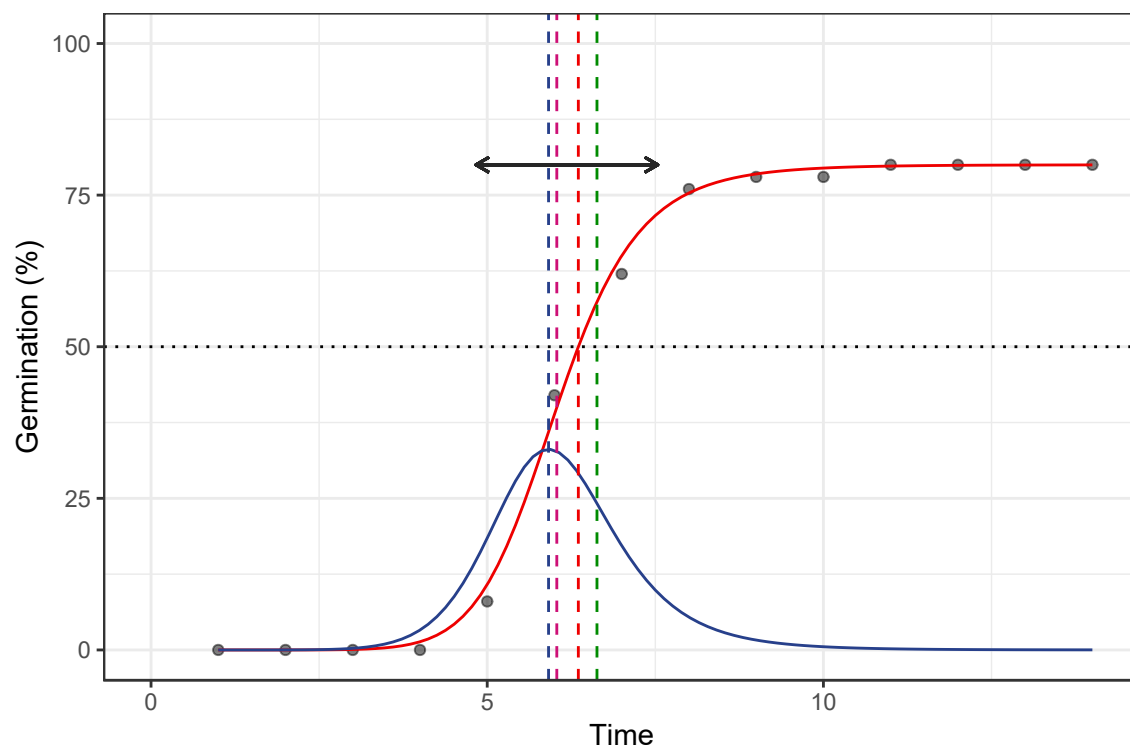
```r
plot(fit2, plotlabels = FALSE)
```
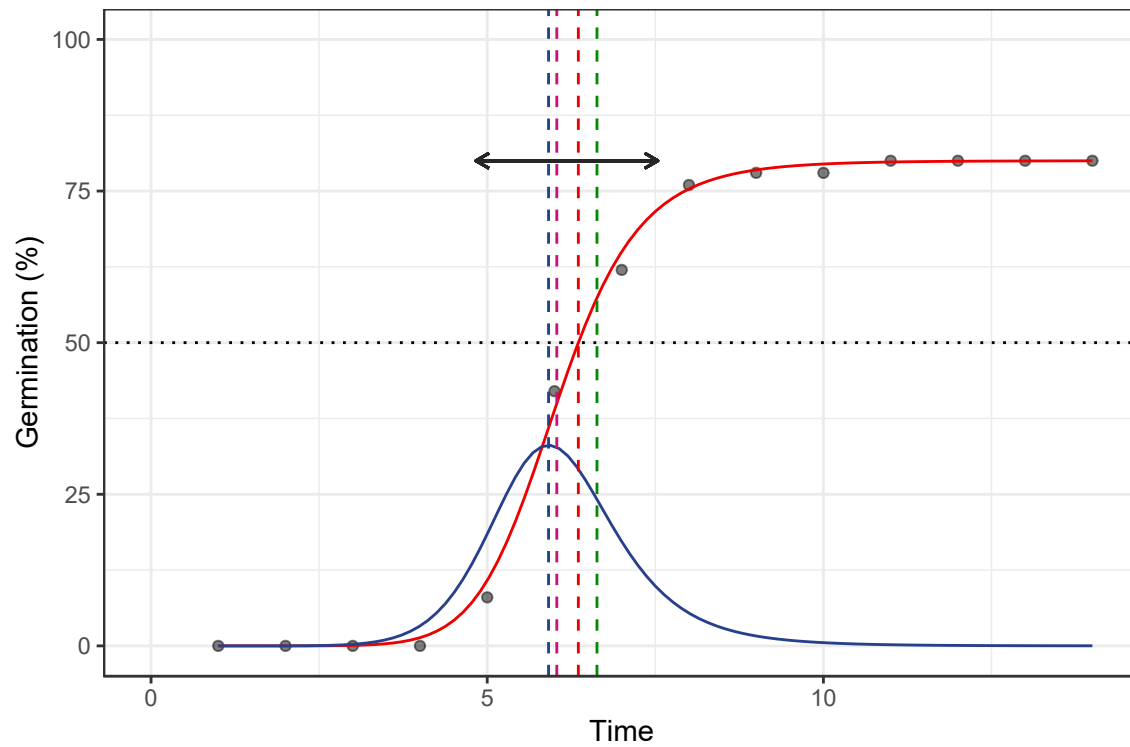


```r
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```
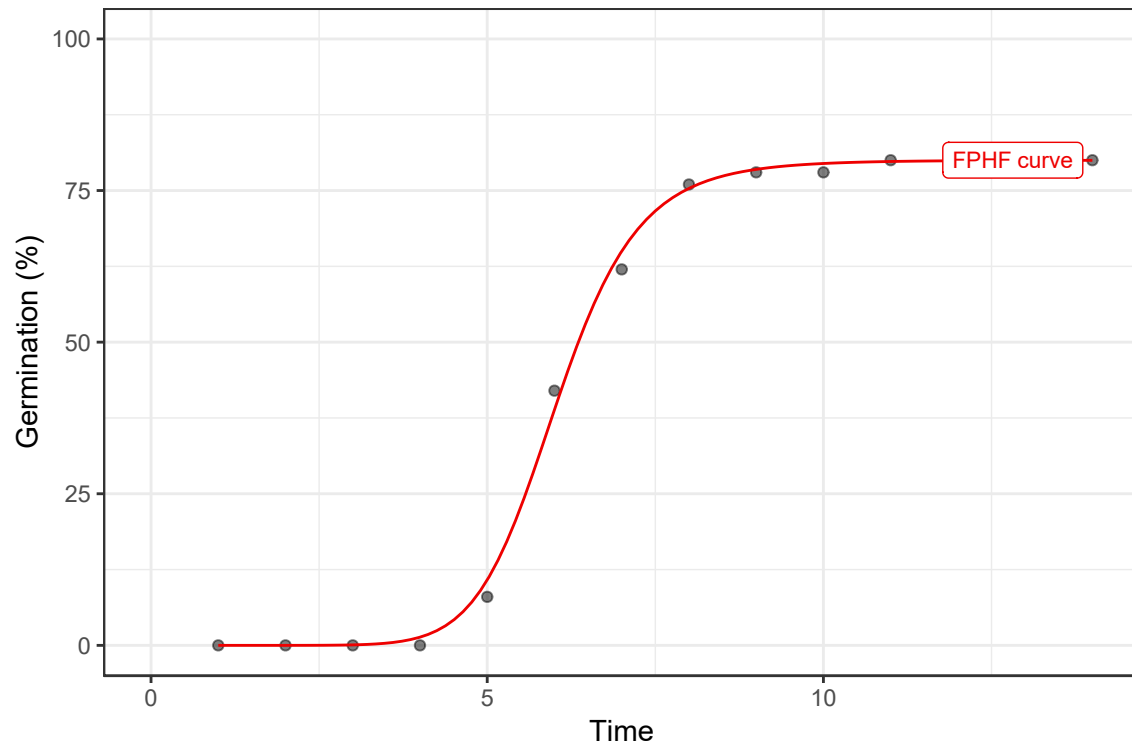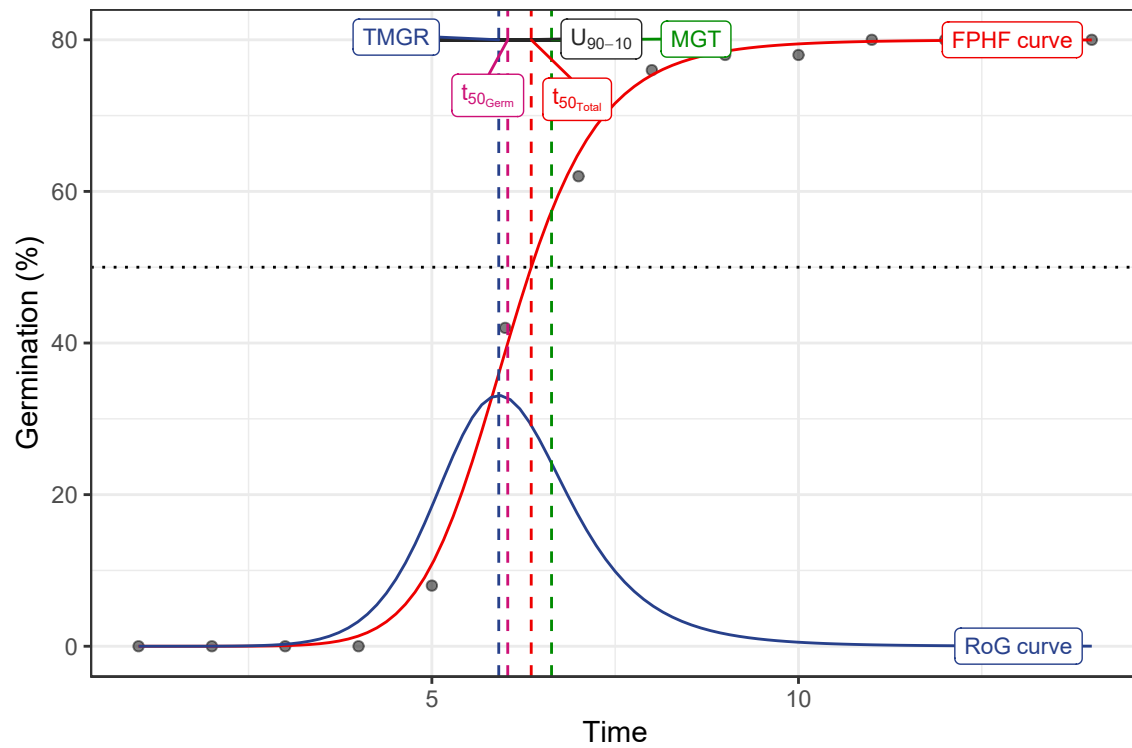
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```
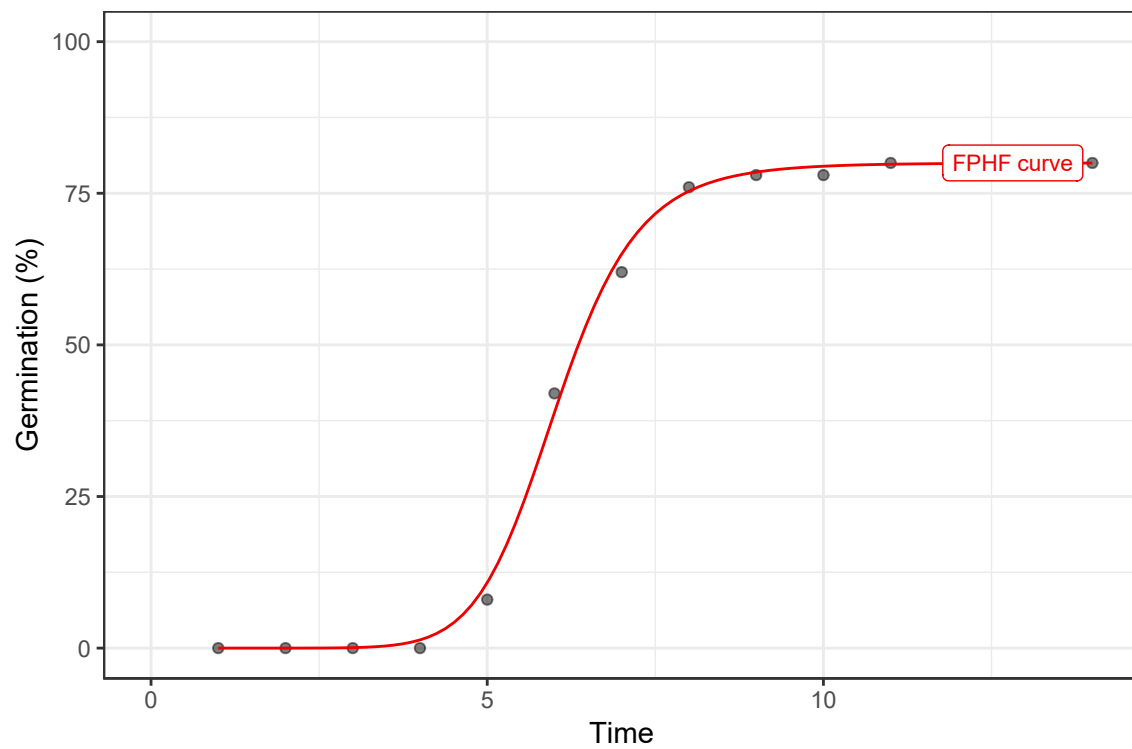


```
# Without y axis limits adjustment
plot(fit1, limits = FALSE)
```
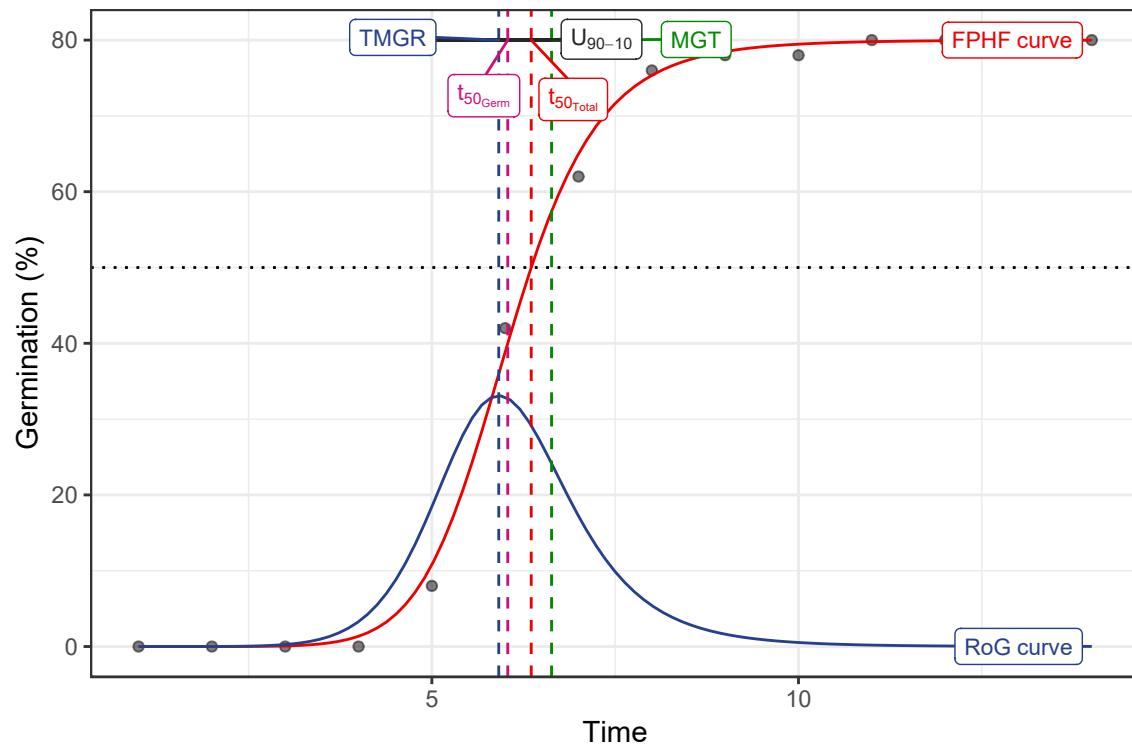
```r
plot(fit2, limits = FALSE)
```

Wrapper function

`germination.indices()`

```r
data(gcdata)

counts.per.intervals <- c("Day1", "Day2", "Day3", "Day4", "Day5",
                          "Day6", "Day7", "Day8", "Day9", "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)
```

	Genotype	Rep	Day1	Day2	Day3	Day4	Day5	Day6	Day7	Day8	Day9	Day10	Day11
1	G1	1	0	0	0	0	4	17	10	7	1	0	1
2	G2	1	0	0	0	1	3	15	13	6	2	1	0
3	G3	1	0	0	0	2	3	18	9	8	2	1	1
4	G4	1	0	0	0	0	4	19	12	6	2	1	1
5	G5	1	0	0	0	0	5	20	12	8	1	0	0
6	G1	2	0	0	0	0	3	21	11	7	1	1	1
7	G2	2	0	0	0	0	4	18	11	7	1	0	1
8	G3	2	0	0	0	1	3	14	12	6	2	1	0
9	G4	2	0	0	0	1	3	19	10	8	1	1	1
10	G5	2	0	0	0	0	4	18	13	6	2	1	0
11	G1	3	0	0	0	0	5	21	11	8	1	0	0
12	G2	3	0	0	0	0	3	20	10	7	1	1	1
13	G3	3	0	0	0	0	4	19	12	8	1	1	0
14	G4	3	0	0	0	0	3	21	11	6	1	0	1
15	G5	3	0	0	0	0	4	17	10	8	1	1	1

	Day12	Day13	Day14	Total Seeds	GermPercent	FirstGermTime	LastGermTime
1	0	0	0	50	80.00000	5	11
2	1	0	0	51	82.35294	4	12
3	1	0	0	48	93.75000	4	12
4	1	0	0	51	90.19608	5	12
5	1	1	0	50	96.00000	5	13
6	1	0	0	49	93.87755	5	12
7	0	0	0	48	87.50000	5	11
8	1	0	0	47	85.10638	4	12
9	1	0	0	52	86.53846	4	12
10	1	0	0	50	90.00000	5	12
11	1	1	0	51	94.11765	5	13
12	1	0	0	51	86.27451	5	12
13	1	1	0	49	95.91837	5	13
14	1	0	0	48	91.66667	5	12
15	0	0	0	48	87.50000	5	11

	PeakGermTime	TimeSpreadGerm	t50_Coolbear	t50_Farooq	MeanGermTime
1	6	6	5.970588	5.941176	6.700000
2	6	8	6.192308	6.153846	6.857143
3	6	8	6.000000	5.972222	6.866667
4	6	7	6.041667	6.000000	6.891304
5	6	8	5.975000	5.950000	6.812500
6	6	7	5.976190	5.952381	6.869565
7	6	6	5.972222	5.944444	6.690476
8	6	8	6.208333	6.166667	6.875000
9	6	8	6.000000	5.973684	6.866667

10	6	7	6.076923	6.038462	6.822222
11	6	8	5.928571	5.904762	6.791667
12	6	7	5.975000	5.950000	6.886364
13	6	8	6.083333	6.041667	6.936170
14	6	7	5.928571	5.904762	6.772727
15	6	6	6.050000	6.000000	6.809524

	VarGermTime	SEGermTime	CVGermTime	MeanGermRate	VarGermRate	SEGermRate
1	1.446154	0.1901416	0.1794868	0.1492537	0.0007176543	0.004235724
2	2.027875	0.2197333	0.2076717	0.1458333	0.0009172090	0.004673148
3	2.572727	0.2391061	0.2335882	0.1456311	0.0011572039	0.005071059
4	2.187923	0.2180907	0.2146419	0.1451104	0.0009701218	0.004592342
5	2.368351	0.2221275	0.2259002	0.1467890	0.0010995627	0.004786184
6	2.071498	0.2122088	0.2095140	0.1455696	0.0009301809	0.004496813
7	1.389663	0.1818989	0.1761967	0.1494662	0.0006935558	0.004063648
8	2.112179	0.2297923	0.2113940	0.1454545	0.0009454531	0.004861721
9	2.300000	0.2260777	0.2208604	0.1456311	0.0010345321	0.004794747
10	1.831313	0.2017321	0.1983606	0.1465798	0.0008453940	0.004334343
11	2.381206	0.2227295	0.2272072	0.1472393	0.0011191581	0.004828643
12	2.149577	0.2210295	0.2129053	0.1452145	0.0009558577	0.004660905
13	2.539315	0.2324392	0.2297410	0.1441718	0.0010970785	0.004831366
14	1.900634	0.2078370	0.2035568	0.1476510	0.0009033254	0.004531018
15	1.670151	0.1994129	0.1897847	0.1468531	0.0007767634	0.004300508

	CVG	GermRateRecip_Coolbear	GermRateRecip_Farooq	GermSpeed_Count
1	14.92537	0.1674877	0.1683168	6.138925
2	14.58333	0.1614907	0.1625000	6.362698
3	14.56311	0.1666667	0.1674419	6.882179
4	14.51104	0.1655172	0.1666667	6.927417
5	14.67890	0.1673640	0.1680672	7.318987
6	14.55696	0.1673307	0.1680000	6.931782
7	14.94662	0.1674419	0.1682243	6.448449
8	14.54545	0.1610738	0.1621622	6.053175
9	14.56311	0.1666667	0.1674009	6.830592
10	14.65798	0.1645570	0.1656051	6.812698
11	14.72393	0.1686747	0.1693548	7.342796
12	14.52145	0.1673640	0.1680672	6.622258
13	14.41718	0.1643836	0.1655172	7.052320
14	14.76510	0.1686747	0.1693548	6.706782
15	14.68531	0.1652893	0.1666667	6.363925

	GermSpeed_Percent	GermSpeedAccumulated_Count
1	12.27785	34.61567
2	12.47588	35.54058
3	14.33787	38.29725
4	13.58317	38.68453
5	14.63797	41.00786
6	14.14649	38.77620
7	13.43427	36.38546
8	12.87909	33.77079
9	13.13575	38.11511
10	13.62540	38.19527
11	14.39764	41.17452
12	12.98482	37.00640
13	14.39249	39.29399
14	13.97246	37.69490
15	13.25818	35.69697

	GermSpeedAccumulated_Percent	GermSpeedCorrected_Normal
1	69.23134	0.07673656
2	69.68741	0.07726134
3	79.78594	0.07340991
4	75.85202	0.07680397
5	82.01571	0.07623944
6	79.13509	0.07383855
7	75.80304	0.07369656
8	71.85275	0.07112480
9	73.29829	0.07893128
10	76.39054	0.07569665
11	80.73436	0.07801721
12	72.56158	0.07675799
13	80.19182	0.07352419
14	78.53103	0.07316490
15	74.36868	0.07273057

	GermSpeedCorrected_Accumulated	WeightGermPercent	MeanGermPercent
1	0.4326958	47.42857	5.714286
2	0.4315642	47.89916	5.882353
3	0.4085040	54.46429	6.696429
4	0.4288937	52.24090	6.442577
5	0.4271652	56.14286	6.857143
6	0.4130508	54.51895	6.705539
7	0.4158338	51.93452	6.250000
8	0.3968068	49.39210	6.079027
9	0.4404413	50.27473	6.181319
10	0.4243919	52.57143	6.428571
11	0.4374793	55.18207	6.722689
12	0.4289379	50.00000	6.162465
13	0.4096608	55.24781	6.851312
14	0.4112171	53.86905	6.547619
15	0.4079653	51.19048	6.250000

	MeanGermNumber	TimsonsIndex	TimsonsIndex_Labouriau
1	2.857143	8.000000	1.00
2	3.000000	9.803922	1.25
3	3.214286	14.583333	1.40
4	3.285714	7.843137	1.00
5	3.428571	10.000000	1.00
6	3.285714	6.122449	1.00
7	3.000000	8.333333	1.00
8	2.857143	10.638298	1.25
9	3.214286	9.615385	1.25
10	3.214286	8.000000	1.00
11	3.428571	9.803922	1.00
12	3.142857	5.882353	1.00
13	3.357143	8.163265	1.00
14	3.142857	6.250000	1.00
15	3.000000	8.333333	1.00

	TimsonsIndex_KhanUngar	GermRateGeorge	PeakValue	GermValue_Czabator
1	0.5714286	4	9.500000	54.28571
2	0.7002801	5	9.313725	54.78662
3	1.0416667	7	10.416667	69.75446
4	0.5602241	4	10.049020	64.74158
5	0.7142857	5	11.250000	77.14286

```
6                0.4373178        3 10.714286          71.84506
7                0.5952381        4 10.416667          65.10417
8                0.7598784        5  9.574468          58.20345
9                0.6868132        5  9.855769          60.92165
10               0.5714286        4 10.250000          65.89286
11               0.7002801        5 11.029412          74.14731
12               0.4201681        3  9.803922          60.41632
13               0.5830904        4 10.969388          75.15470
14               0.4464286        3 10.677083          69.90947
15               0.5952381        4 10.156250          63.47656
   GermValue_DP GermValue_Czabator_mod GermValue_DP_mod     CUGerm
1      57.93890                54.28571         39.56076 0.7092199
2      52.58713                54.78662         40.99260 0.5051546
3      68.62289                69.75446         53.42809 0.3975265
4      70.43331                64.74158         48.86825 0.4672113
5      80.16914                77.14286         56.23935 0.4312184
6      76.51983                71.84506         53.06435 0.4934701
7      69.41325                65.10417         47.37690 0.7371500
8      56.00669                58.20345         43.67948 0.4855842
9      58.13477                60.92165         45.30801 0.4446640
10     70.91875                65.89286         49.10820 0.5584666
11     77.39782                74.14731         54.27520 0.4288905
12     64.44988                60.41632         44.71582 0.4760266
13     78.16335                75.15470         54.94192 0.4023679
14     74.40140                69.90947         51.41913 0.5383760
15     67.62031                63.47656         46.48043 0.6133519
   GermSynchrony GermUncertainty
1      0.2666667        2.062987
2      0.2346109        2.321514
3      0.2242424        2.462012
4      0.2502415        2.279215
5      0.2606383        2.146051
6      0.2792271        2.160545
7      0.2729384        2.040796
8      0.2256410        2.357249
9      0.2494949        2.321080
10     0.2555556        2.187983
11     0.2686170        2.128670
12     0.2737844        2.185245
13     0.2506938        2.241181
14     0.2991543        2.037680
15     0.2497096        2.185028
```

Citing germinationmetrics

To cite the R package 'germinationmetrics' in publications use:

  Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and
  Kalyani Srinivasan (2018). germinationmetrics: Seed Germination
  Indices and Curve Fitting. R package version 0.1.2.9000,
  https://github.com/aravind-j/germinationmetricshttps://cran.r-project.org/package=germinationmetrics.

A BibTeX entry for LaTeX users is

```
@Manual{,
    title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
    author = {J. Aravind and S. {Vimala Devi} and J. Radhamani and Sherry Rachel Jacob and {Kalyani Sri
    year = {2018},
    note = {R package version 0.1.2.9000},
    note = {https://github.com/aravind-j/germinationmetrics},
    note = {https://cran.r-project.org/package=germinationmetrics},
}
```

This free and open-source software implements academic research by
the authors and co-workers. If you use it, please support the
project by citing the package.

Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2018-10-27 r75507)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows >= 8 x64 (build 9200)

Matrix products: default

locale:
[1] LC_COLLATE=English_India.1252  LC_CTYPE=English_India.1252
[3] LC_MONETARY=English_India.1252 LC_NUMERIC=C
[5] LC_TIME=English_India.1252

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] germinationmetrics_0.1.2.9000 readxl_1.1.0

loaded via a namespace (and not attached):
 [1] httr_1.3.1         pkgload_1.0.2      tidyr_0.8.2
 [4] jsonlite_1.5       Rdpack_0.10-3     assertthat_0.2.0
 [7] xmlparsedata_1.0.2 highr_0.7         pander_0.6.3
[10] cellranger_1.1.0   yaml_2.2.0        remotes_2.0.2
[13] ggrepel_0.8.0      sessioninfo_1.1.1 pillar_1.3.0
[16] backports_1.1.2    lattice_0.20-38   glue_1.3.0
[19] goodpractice_1.0.2 digest_0.6.18     colorspace_1.3-2
[22] htmltools_0.3.6    plyr_1.8.4        clisymbols_1.2.0
[25] XML_3.98-1.16      pkgconfig_2.0.2   devtools_2.0.1
[28] bibtex_0.4.2       rcmdcheck_1.3.2   broom_0.5.0
[31] purrr_0.2.5        scales_1.0.0      processx_3.2.0
[34] tibble_1.4.2       ggplot2_3.1.0     usethis_1.4.0
[37] withr_2.1.2        lazyeval_0.2.1    cli_1.0.1
[40] magrittr_1.5       crayon_1.3.4      memoise_1.1.0
[43] evaluate_0.12      ps_1.2.1          fs_1.2.6
[46] MASS_7.3-51.1      nlme_3.1-137      xml2_1.2.0
[49] pkgbuild_1.0.2     praise_1.0.0      tools_3.6.0
[52] hunspell_2.9       data.table_1.11.8 prettyunits_1.0.2
```

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[55] cyclocomp_1.1.0    minpack.lm_1.2-1   gbRd_0.4-11
[58] stringr_1.3.1      xopen_1.0.0        munsell_0.5.0
[61] bindrcpp_0.2.2     callr_3.0.0        pkgdown_1.2.0.9000
[64] rex_1.1.2          compiler_3.6.0     covr_3.2.1
[67] tinytex_0.9        rlang_0.3.0.1      debugme_1.1.0
[70] grid_3.6.0         RCurl_1.95-4.11    rstudioapi_0.8
[73] bitops_1.0-6       base64enc_0.1-3    labeling_0.3
[76] rmarkdown_1.10     testthat_2.0.1     gtable_0.2.0
[79] roxygen2_6.1.1     curl_3.2           R6_2.3.0
[82] knitr_1.20         dplyr_0.7.8        commonmark_1.7
[85] bindr_0.1.1        rprojroot_1.3-2    lintr_1.0.3
[88] desc_1.2.0         stringi_1.2.4      whoami_1.2.0
[91] Rcpp_1.0.0         tidyselect_0.2.5   xfun_0.4
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