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 0.1.4. 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
0.1.2	2018-10-31

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.

```r
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))
```
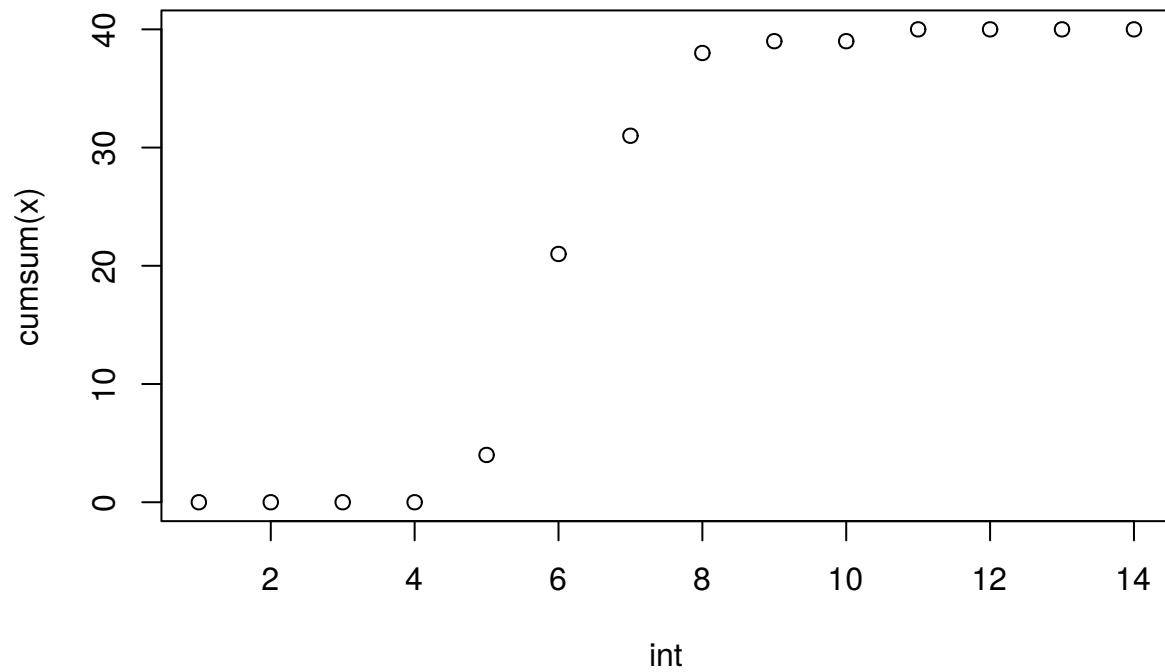
Single-value germination indices

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

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

Germination index	Function	Details	Unit	Measures	Reference
Germination percentage or Final 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 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 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) or Emergence index (EI)	`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 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 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); Mock and Eberhart (1972); 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 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.	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 interval (not the accumulated number, but the number corresponding to the ith interval) and k is the total number of time intervals.	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 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 $(\overline{T})$. $$\overline{V} = \frac{1}{\overline{T}}$$	time^{-1}	Germination rate	Labouriau and Valadares (1976); Labouriau (1983b); Ranal and Santana (2006)
Coefficient of velocity of germination (CVG) or Coefficient of rate of germination (CRG) or Kotowski's coefficient of velocity	`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 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.	% 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. $$s_{\overline{V}} = \sqrt{\dfrac{s_V^2}{\sum_{i=1}^{k} N_i}}$$ 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.	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 (Allan, Vogel and Peterson; Erbach; Hsu and Nelson) or Germination index (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. $$S = \sum_{i=1}^{k} \frac{N_i}{T_i}$$ 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. 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); Erbach (1982); AOSA (1983); Khandakar and Bradbeer (1983); Hsu and Nelson (1986); Bradbeer (1988); Wardle et al. (1991)

Germination index	Function	Details	Unit	Measures	Reference
Speed of accumulated germination	`GermSpeedAccumula`	It is the rate of germination in terms of the accumulated/cumulative total number of seeds that germinate in a time interval. It is estimated 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 interval, and k is the total number of time intervals. 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	`GermSpeedCorrecte`	It is computed as follows. $$S_{corrected} = \frac{S}{FGP}$$ Where, FGP is the final germination percentage or germinability.	time^{-1}	Mixed	Evetts and Burnside (1972)
Weighted germination percentage (WGP)	`WeightGermPercent`	It is estimated as follows. $$WGP = \frac{\sum_{i=1}^{k}(k-i+1)N_i}{k \times N} \times 100$$ 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.		Mixed	Reddy et al. (1985); Reddy (1978)
Mean germination percentage per unit time ($\overline{GP}$)	`MeanGermPercent`	It is estimated as follows. $$\overline{GP} = \frac{GP}{T_k}$$ 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.		Mixed	Czabator (1962)
Number of seeds germinated per unit time $\overline{N}$	`MeanGermNumber`	It is estimated as follows. $$\overline{N} = \frac{N_g}{T_k}$$ 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.		Mixed	Khamassi et al. (2013)

Germination index	Function	Details	Unit	Measures	Reference
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. $$\Sigma k = \sum_{i=1}^{k} G_i$$ Where, G_i is the cumulative germination percentage in time interval i, and k is the total number of time intervals. It also estimated 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 $j = i - 1$.		Mixed	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); Goodchild and Walker (1971)
Modified Timson's index (Σk_{mod}) (Labouriau)	`TimsonsIndex`	It is estimated as Timson's index Σk divided by the sum of partial germination percentages. $$\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}$$		Mixed	Ranal and Santana (2006)
Modified Timson's index (Σk_{mod}) (Khan and Unger)	`TimsonsIndex`	It is estimated as Timson's index (Σk) divided by the total time period of germination (T_k). $$\Sigma k_{mod} = \frac{\Sigma k}{T_k}$$		Mixed	Khan and Ungar (1984)
George's index (GR)	`GermRateGeorge`	It is estimated as follows. $$GR = \sum_{i=1}^{k} N_i K_i$$ 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, and and k is the total number of time intervals.		Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968)

Germination index	Function	Details	Unit	Measures	Reference
Germination Index (GI) (Melville)	`GermIndex`	It is estimated as follows. $$GI = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i)\, N_i \rvert}{N_t}$$ 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.		Mixed	Melville et al. (1980)
Germination Index (GI_{mod}) (Melville; Santana and Ranal)	`GermIndex`	It is estimated as follows. $$GI_{mod} = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i)\, N_i \rvert}{N_g}$$ 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_g is the total number of germinated seeds at the end of the test, and k is the total number of time intervals.		Mixed	Melville et al. (1980); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (ERI) or Germination Rate Index (Shmueli and Goldberg)	`EmergenceRateInde`	It 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.		Mixed	Shmueli and Goldberg (1971)

Germination index	Function	Details	Unit	Measures	Reference
Modified Emergence Rate Index (ERI_{mod}) or Modified Germination Rate Index (Shmueli and Goldberg; Santana and Ranal)	EmergenceRateInde	It is estimated by dividing Emergence rate index (ERI) by total number of emerged seedlings (or germinated seeds). $$ERI_{mod} = \frac{\sum_{i=i_0}^{k-1} N_i(k-i)}{N_g} = \frac{ERI}{N_g}$$ 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.		Mixed	Shmueli and Goldberg (1971); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (ERI) or Germination Rate Index (Bilbro & Wanjura)	EmergenceRateInde	It 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.		Mixed	Bilbro and Wanjura (1982)
Emergence Rate Index (ERI) or Germination Rate Index (Fakorede)	EmergenceRateInde	It is estimated as follows. $$ERI = \frac{\overline{T}}{FGP/100}$$ Where, $\overline{T}$ is the Mean germination time and FGP is the final germination time.		Mixed	Fakorede and Ayoola (1980); Fakorede and Ojo (1981); Fakorede and Agbana (1983)
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. $$PV = \max\left(\frac{G_1}{T_1}, \frac{G_2}{T_2}, \cdots \frac{G_k}{T_k}\right)$$ 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.	% time^{-1}	Mixed	Czabator (1962); Bonner (1967)

Germination index	Function	Details	Unit	Measures	Reference
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 ($\overline{GP}$). 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	Czabator (1962); Brown and Mayer (1988)
Germination value (GV) (Diavanshir and Pourbiek)	`GermValue`	It is computed as follows. $$GV = \frac{\sum DGS}{N} \times GP \times c$$ Where, DGS is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the 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. 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. $$CUG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} (\overline{T} - T_i)^2 N_i}$$ Where, $\overline{T}$ is the the mean germination time, T_i is the time from the start of the experiment to the ith interval (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), and k is the total number of time intervals.	Germination 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.	Germination unifromity	Gomes (1960); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
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 interval, and k is the total number of time intervals.	bit	Germination synchrony	Shannon (1948); Labouriau and Valadares (1976); Labouriau (1983b)
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 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.		Germination synchrony	Primack (1985); Ranal and Santana (2006)

Examples

```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)
```

GermPercent()

```
[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
```

```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)
```

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

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
```

```
# 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
```

```
# 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 germi
```

```
[1] 5 6
```

```
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()
```

```
[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
```

```
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)
```

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

```
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
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)
```

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

```
[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
```

```
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)
```

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

```
[1] 6.138925
```

```
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)
#------------------------------------------------------------------------
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
```

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

```
[1] 69.23134
```

```
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)
```

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

```
[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
```

```
# 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
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)
```

```
WeightGermPercent()
```

```
[1] 47.42857
```

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

```
[1] 47.42857
```

```
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)
```

MeanGermPercent(), MeanGermNumber()

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

```
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(), GermRateGeorge()

```
[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
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

```r
GermRateGeorge(germ.counts = x, intervals = int, max = 10)
```

```
[1] 172
```

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

```
[1] 332
```

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

```
[1] 664
```

```
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "none")
```

```
[1] 664
```

```
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "labouriau")
```

```
[1] 8.3
```

```
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             modification = "khanungar")
```

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

```r
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
             total.seeds = 50,
             max = 10, modification = "khanungar")
```

```
[1] 24.57143
```

```r
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 10)
```

```
[1] 172
```

```r
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 14)
```

```
[1] 332
```

```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
#-------------------------------------------------------------------------------
GermIndex(germ.counts = x, intervals = int, total.seeds = 50)
```

```r
GermIndex()
```

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```
[1] 5.84
```

```
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50,
          modification = "none")
```

```
[1] 5.84
```

```
GermIndex(germ.counts = y, intervals = int, partial = FALSE,
          total.seeds = 50,
          modification = "santanaranal")
```

```
[1] 7.3
```

```
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()
```

```
[1] 292
```

```
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "melville")
```

```
[1] 292
```

```
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "melvillesantanaranal")
```

```
[1] 7.3
```

```
EmergenceRateIndex(germ.counts = x, intervals = int,
                   method = "bilbrowanjura")
```

```
[1] 5.970149
```

```
EmergenceRateIndex(germ.counts = x, intervals = int,
                   total.seeds = 50, method = "fakorede")
```

```
[1] 8.375
```

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

```
[1] 292
```

```
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "melville")
```

```
[1] 292
```

```
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "melvillesantanaranal")
```

```
[1] 7.3
```

```
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   method = "bilbrowanjura")
```

```
[1] 5.970149
```

```
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                   total.seeds = 50, method = "fakorede")
```

```
[1] 8.375
```

```
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)
```

```
PeakValue(), GermValue()
```

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

```r
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      DGS SumDGSbyN         GV
3           34        3                      34                   17.0 5.666667  5.666667  9.633333
4           40        4                      74                   37.0 9.250000  7.458333 27.595833
5           21        5                      95                   47.5 9.500000  8.138889 38.659722
6           10        6                     105                   52.5 8.750000  8.291667 43.531250
7            4        7                     109                   54.5 7.785714  8.190476 44.638095
8            5        8                     114                   57.0 7.125000  8.012897 45.673512
9            3        9                     117                   58.5 6.500000  7.796769 45.611097
10           5       10                     122                   61.0 6.100000  7.584673 46.266503
11           8       11                     130                   65.0 5.909091  7.398497 48.090230
12           7       12                     137                   68.5 5.708333  7.229481 49.521942
13           7       13                     144                   72.0 5.538462  7.075752 50.945411
14           6       14                     150                   75.0 5.357143  6.932534 51.994006
15           6       15                     156                   78.0 5.200000  6.799262 53.034246
16           4       16                     160                   80.0 5.000000  6.670744 53.365948
17           0       17                     160                   80.0 4.705882  6.539753 52.318022
18           2       18                     162                   81.0 4.500000  6.412268 51.939373
19           0       19                     162                   81.0 4.263158  6.285850 50.915385
20           2       20                     164                   82.0 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      DGS
1            0         1                      0                     0.0 0.000000
2            0         2                      0                     0.0 0.000000
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
```

```r
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      DGS SumDGSbyN        GV
1            0         1                      0                     0.0 0.000000  0.000000  0.000000
2            0         2                      0                     0.0 0.000000  0.000000  0.000000
3           34         3                     34                    17.0 5.666667  1.888889  3.211111
4           40         4                     74                    37.0 9.250000  3.729167 13.797917
5           21         5                     95                    47.5 9.500000  4.883333 23.195833
6           10         6                    105                    52.5 8.750000  5.527778 29.020833
7            4         7                    109                    54.5 7.785714  5.850340 31.884354
8            5         8                    114                    57.0 7.125000  6.009673 34.255134
9            3         9                    117                    58.5 6.500000  6.064153 35.475298
10           5        10                    122                    61.0 6.100000  6.067738 37.013202
11           8        11                    130                    65.0 5.909091  6.053316 39.346552
12           7        12                    137                    68.5 5.708333  6.024567 41.268285
13           7        13                    144                    72.0 5.538462  5.987174 43.107655
14           6        14                    150                    75.0 5.357143  5.942172 44.566291
15           6        15                    156                    78.0 5.200000  5.892694 45.963013
16           4        16                    160                    80.0 5.000000  5.836901 46.695205
17           0        17                    160                    80.0 4.705882  5.770370 46.162961
18           2        18                    162                    81.0 4.500000  5.699794 46.168331
19           0        19                    162                    81.0 4.263158  5.624182 45.555871
20           2        20                    164                    82.0 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      DGS
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
```

```
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      DGS SumDGSbyN        GV
3           34         3                     34                    17.0 5.666667  5.666667  9.633333
4           40         4                     74                    37.0 9.250000  7.458333 27.595833
5           21         5                     95                    47.5 9.500000  8.138889 38.659722
6           10         6                    105                    52.5 8.750000  8.291667 43.531250
7            4         7                    109                    54.5 7.785714  8.190476 44.638095
8            5         8                    114                    57.0 7.125000  8.012897 45.673512
```

```
9            3        9              117              58.5 6.500000  7.796769 45.611097
10           5        10             122              61.0 6.100000  7.584673 46.266503
11           8        11             130              65.0 5.909091  7.398497 48.090230
12           7        12             137              68.5 5.708333  7.229481 49.521942
13           7        13             144              72.0 5.538462  7.075752 50.945411
14           6        14             150              75.0 5.357143  6.932534 51.994006
15           6        15             156              78.0 5.200000  6.799262 53.034246
16           4        16             160              80.0 5.000000  6.670744 53.365948
17           0        17             160              80.0 4.705882  6.539753 52.318022
18           2        18             162              81.0 4.500000  6.412268 51.939373
19           0        19             162              81.0 4.263158  6.285850 50.915385
20           2        20             164              82.0 4.100000  6.164414 50.548194

$testend
[1] 16
```

```
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      DGS
1           0        1                1                      0.0 0.000000
2           0        2                0                      0.0 0.000000
3          34        3               34                     17.0 5.666667
4          40        4               74                     37.0 9.250000
5          21        5               95                     47.5 9.500000
6          10        6              105                     52.5 8.750000
7           4        7              109                     54.5 7.785714
8           5        8              114                     57.0 7.125000
9           3        9              117                     58.5 6.500000
10          5        10             122                     61.0 6.100000
11          8        11             130                     65.0 5.909091
12          7        12             137                     68.5 5.708333
13          7        13             144                     72.0 5.538462
14          6        14             150                     75.0 5.357143
15          6        15             156                     78.0 5.200000
16          4        16             160                     80.0 5.000000
17          0        17             160                     80.0 4.705882
18          2        18             162                     81.0 4.500000
19          0        19             162                     81.0 4.263158
20          2        20             164                     82.0 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      DGS SumDGSbyN        GV
```

```
1              0          1                    0              0.0 0.000000  0.000000   0.000000
2              0          2                    0              0.0 0.000000  0.000000   0.000000
3             34          3                   34             17.0 5.666667  1.888889   3.211111
4             40          4                   74             37.0 9.250000  3.729167 13.797917
5             21          5                   95             47.5 9.500000  4.883333 23.195833
6             10          6                  105             52.5 8.750000  5.527778 29.020833
7              4          7                  109             54.5 7.785714  5.850340 31.884354
8              5          8                  114             57.0 7.125000  6.009673 34.255134
9              3          9                  117             58.5 6.500000  6.064153 35.475298
10             5         10                  122             61.0 6.100000  6.067738 37.013202
11             8         11                  130             65.0 5.909091  6.053316 39.346552
12             7         12                  137             68.5 5.708333  6.024567 41.268285
13             7         13                  144             72.0 5.538462  5.987174 43.107655
14             6         14                  150             75.0 5.357143  5.942172 44.566291
15             6         15                  156             78.0 5.200000  5.892694 45.963013
16             4         16                  160             80.0 5.000000  5.836901 46.695205
17             0         17                  160             80.0 4.705882  5.770370 46.162961
18             2         18                  162             81.0 4.500000  5.699794 46.168331
19             0         19                  162             81.0 4.263158  5.624182 45.555871
20             2         20                  164             82.0 4.100000  5.547972 45.493374

$testend
[1] 16
```

```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
#----------------------------------------------------------------------------
CUGerm(germ.counts = x, intervals = int)
```

```
CUGerm()
```

```
[1] 0.7092199
```

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

```
[1] 0.05267935
```

```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
#----------------------------------------------------------------------------
GermSynchrony(germ.counts = x, intervals = int)
```

```
GermSynchrony(), GermUncertainty()
```

```
[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
```

Non-linear regression analysis

Several mathematical functions have been used to fit the cumulative germination count data and describe the germination process by non-linear regression analysis. They include functions 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

Germination parameters	Details	Unit	Measures
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
$t_{50_{total}}$	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

```
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)
```

FourPHFfit()

```
$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 1.24158597  64.43372 1.973240e-14
2    b  9.881947 0.70779381  13.96162 6.952324e-08
3    c  6.034954 0.04952654 121.85294 3.399384e-17
4   y0  0.000000 0.91607007   0.00000 1.000000e+00

$Fit
     sigma isConv       finTol   logLik      AIC      BIC deviance df.residual
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723          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
      10       60
4.956266 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10       60
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 df.residual
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723          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
      10        60
4.956263 6.744599


$t50.Germinated
[1] 6.034953
```

```
$txp.Germinated
      10       60
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"
```
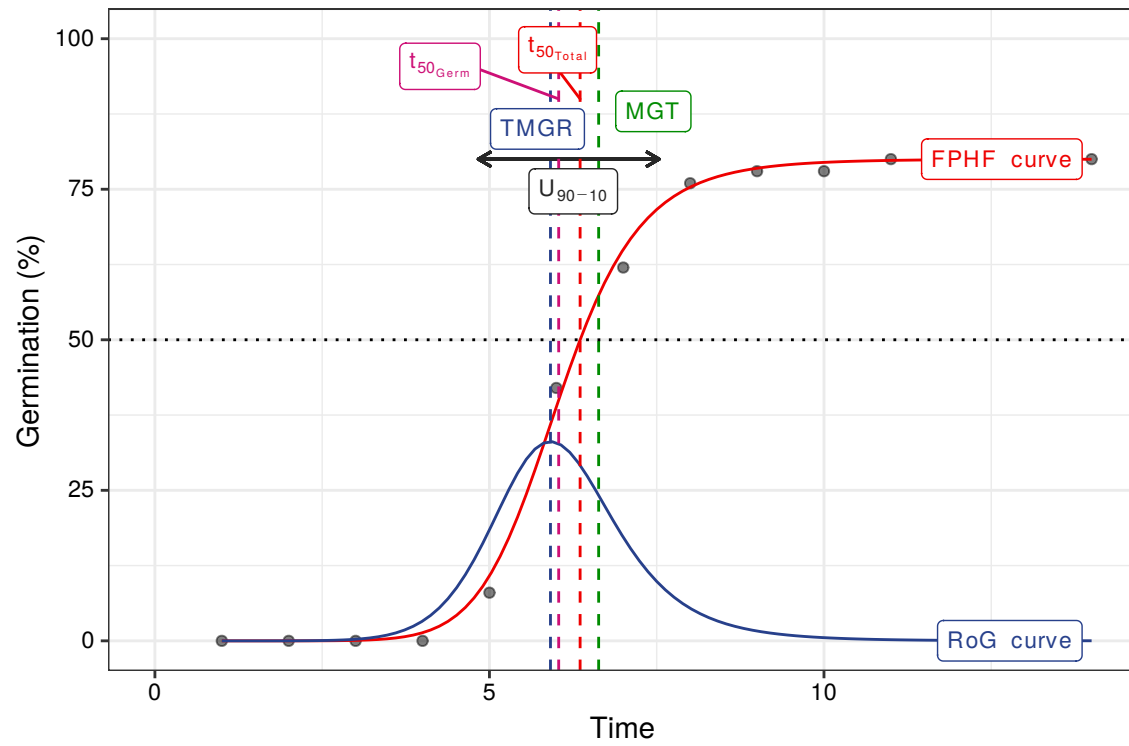
```r
## No test:
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

# 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)
```
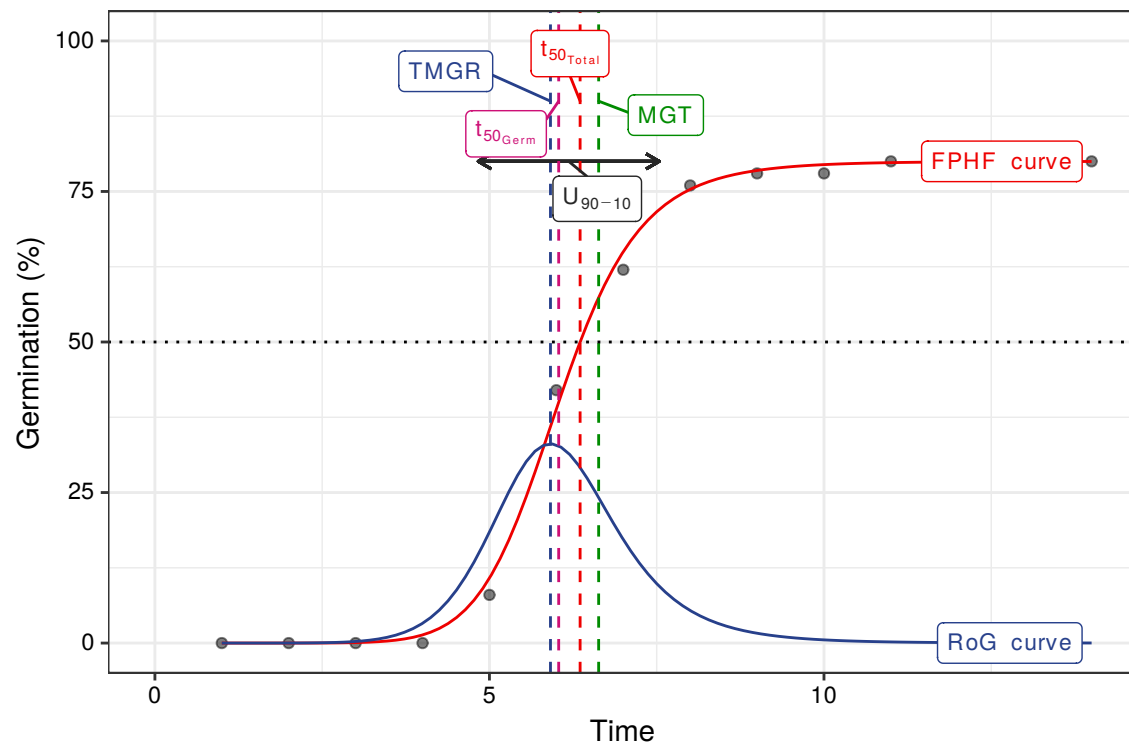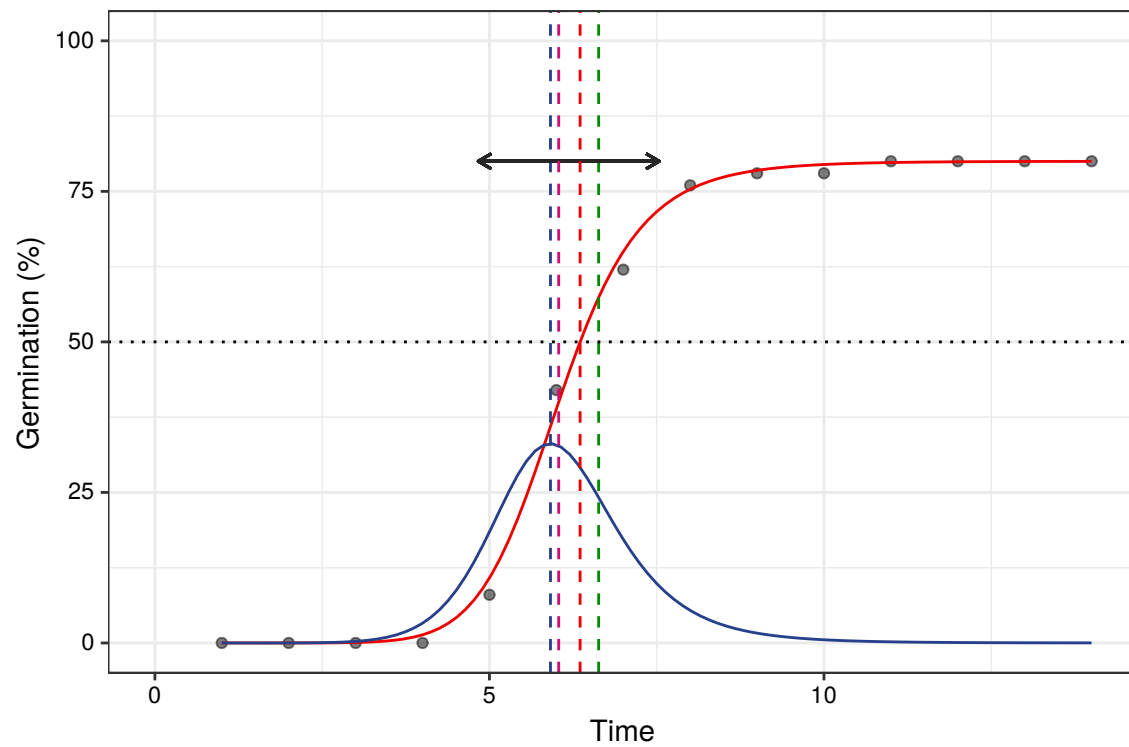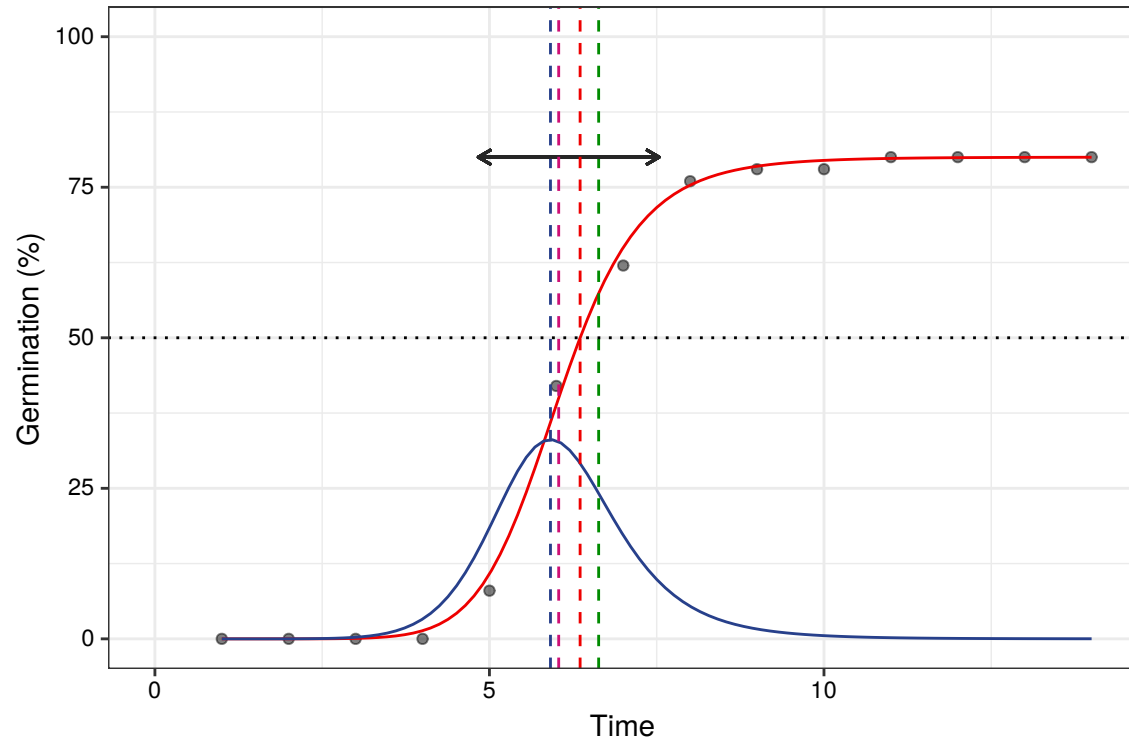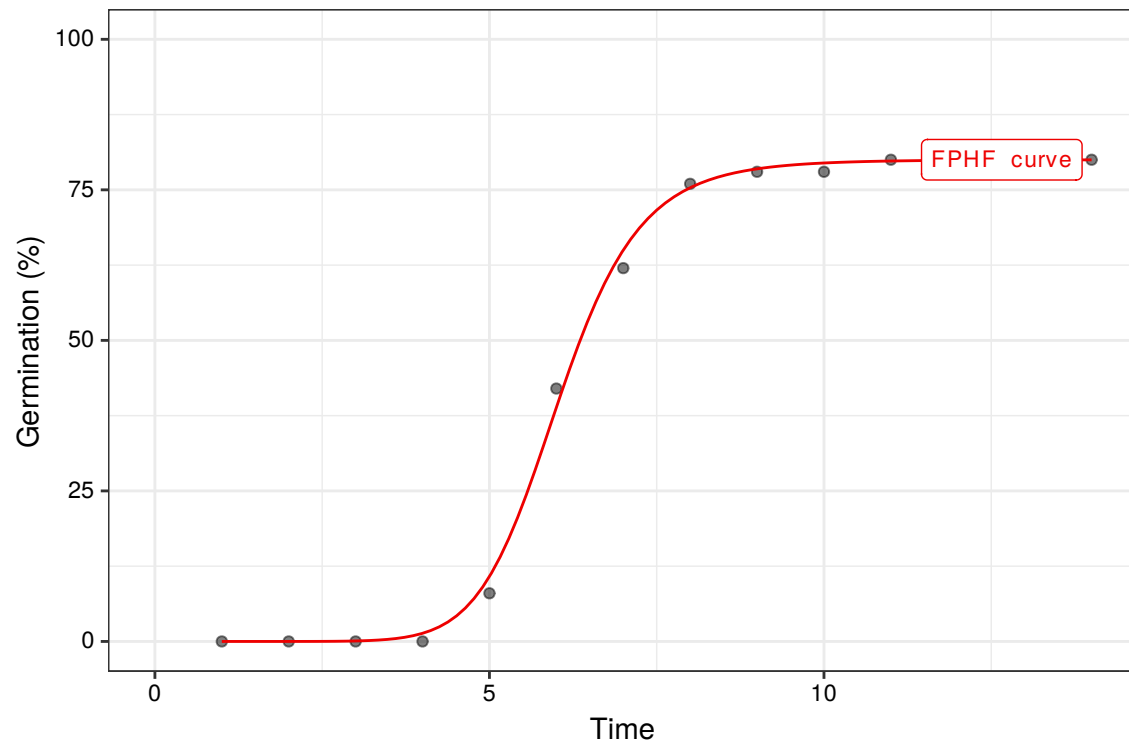
```r
plot(fit2)
```

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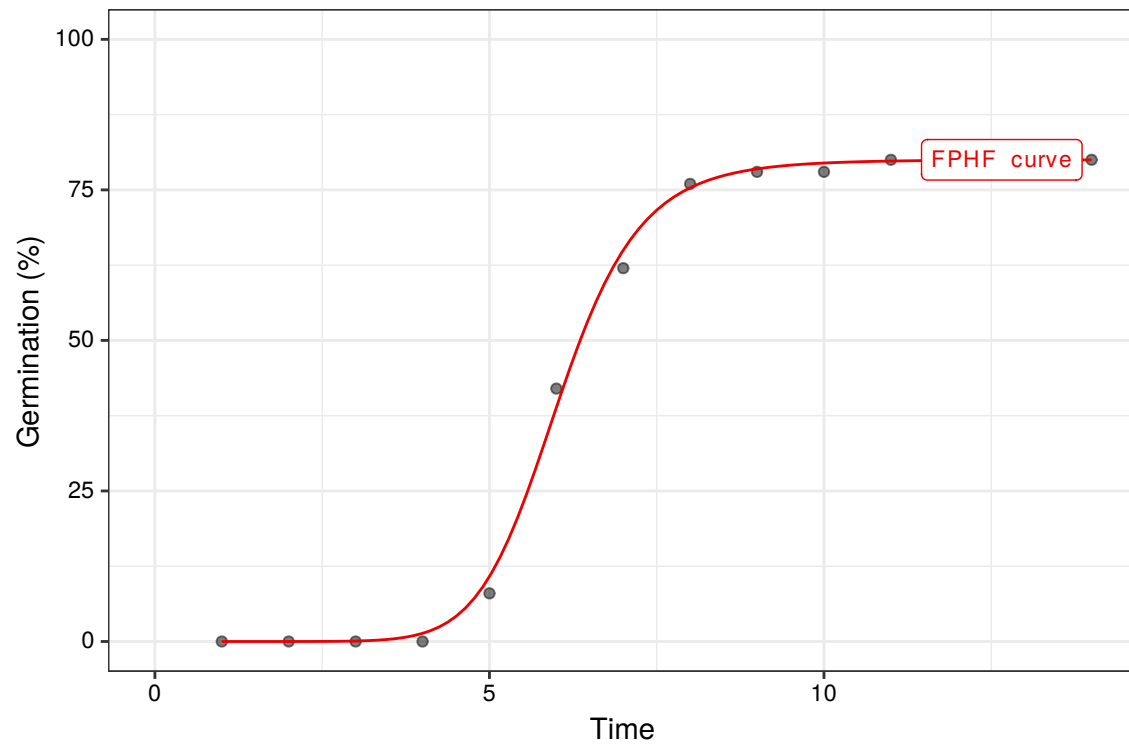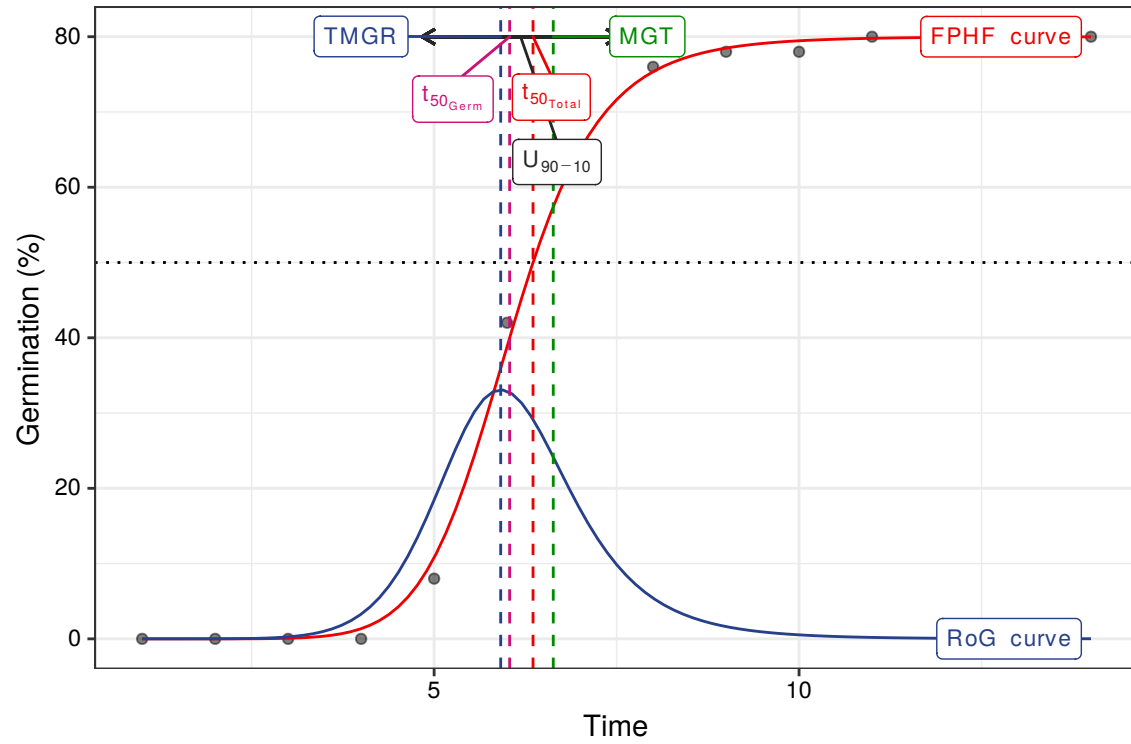


```
plot(fit2, plotlabels = FALSE)
```

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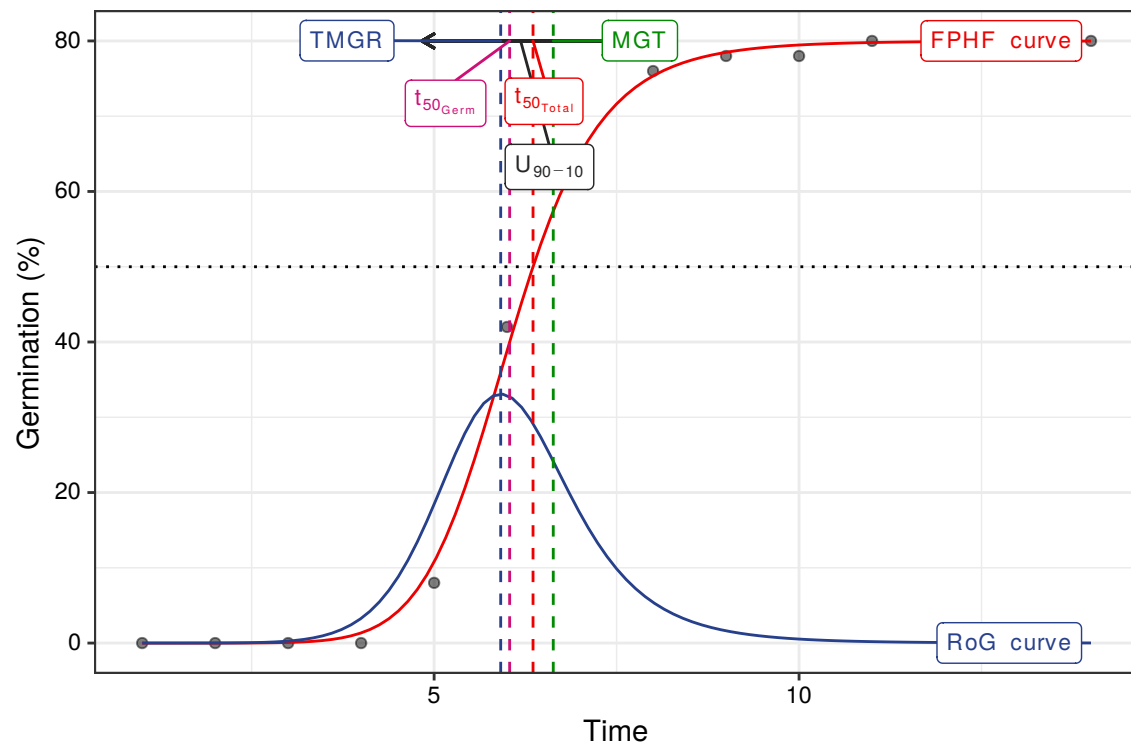
```r
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



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

```
plot(fit2, limits = FALSE)
```

```
## End(No test)
```

Wrapper functions

Wrapper functions `germination.indices()` and `FourPHFfit.bulk()` are available in the package for computing results for multiple samples in batch from a data frame of germination counts recorded at specific time intervals.

`germination.indices()`   This wrapper function can be used to compute several germination indices simultaneously for multiple samples in batch.

```
## No test:
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)
```

	Genotype	Rep	Day01	Day02	Day03	Day04	Day05	Day06	Day07	Day08	Day09	Day10	Day11	Day12	Day13	Day14	Tota
1	G1	1	0	0	0	0	4	17	10	7	1	0	1	0	0	0	
2	G2	1	0	0	0	1	3	15	13	6	2	1	0	1	0	0	
3	G3	1	0	0	0	2	3	18	9	8	2	1	1	1	0	0	
4	G4	1	0	0	0	0	4	19	12	6	2	1	1	1	0	0	
5	G5	1	0	0	0	0	5	20	12	8	1	0	0	1	1	0	
6	G1	2	0	0	0	0	3	21	11	7	1	1	1	1	0	0	
7	G2	2	0	0	0	0	4	18	11	7	1	0	1	0	0	0	
8	G3	2	0	0	0	1	3	14	12	6	2	1	0	1	0	0	
9	G4	2	0	0	0	1	3	19	10	8	1	1	1	1	0	0	
10	G5	2	0	0	0	0	4	18	13	6	2	1	0	1	0	0	
11	G1	3	0	0	0	0	5	21	11	8	1	0	0	1	1	0	
12	G2	3	0	0	0	0	3	20	10	7	1	1	1	1	0	0	
13	G3	3	0	0	0	0	4	19	12	8	1	1	0	1	1	0	
14	G4	3	0	0	0	0	3	21	11	6	1	0	1	1	0	0	
15	G5	3	0	0	0	0	4	17	10	8	1	1	1	0	0	0	

	LastGermTime	PeakGermTime	TimeSpreadGerm	t50_Coolbear	t50_Farooq	MeanGermTime	VarGermTime	SEGermTime
1	11	6	6	5.970588	5.941176	6.700000	1.446154	0.1901416
2	12	6	8	6.192308	6.153846	6.857143	2.027875	0.2197333
3	12	6	8	6.000000	5.972222	6.866667	2.572727	0.2391061
4	12	6	7	6.041667	6.000000	6.891304	2.187923	0.2180907
5	13	6	8	5.975000	5.950000	6.812500	2.368351	0.2221275
6	12	6	7	5.976190	5.952381	6.869565	2.071498	0.2122088
7	11	6	6	5.972222	5.944444	6.690476	1.389663	0.1818989
8	12	6	8	6.208333	6.166667	6.875000	2.112179	0.2297923
9	12	6	8	6.000000	5.973684	6.866667	2.300000	0.2260777
10	12	6	7	6.076923	6.038462	6.822222	1.831313	0.2017321
11	13	6	8	5.928571	5.904762	6.791667	2.381206	0.2227295
12	12	6	7	5.975000	5.950000	6.886364	2.149577	0.2210295
13	13	6	8	6.083333	6.041667	6.936170	2.539315	0.2324392

14	12	6	7	5.928571	5.904762	6.772727	1.900634	0.2078370
15	11	6	6	6.050000	6.000000	6.809524	1.670151	0.1994129

	SEGermRate	CVG	GermRateRecip_Coolbear	GermRateRecip_Farooq	GermSpeed_Count	GermSpeed_Percent
1	0.004235724	14.92537	0.1674877	0.1683168	6.138925	12.27785
2	0.004673148	14.58333	0.1614907	0.1625000	6.362698	12.47588
3	0.005071059	14.56311	0.1666667	0.1674419	6.882179	14.33787
4	0.004592342	14.51104	0.1655172	0.1666667	6.927417	13.58317
5	0.004786184	14.67890	0.1673640	0.1680672	7.318987	14.63797
6	0.004496813	14.55696	0.1673307	0.1680000	6.931782	14.14649
7	0.004063648	14.94662	0.1674419	0.1682243	6.448449	13.43427
8	0.004861721	14.54545	0.1610738	0.1621622	6.053175	12.87909
9	0.004794747	14.56311	0.1666667	0.1674009	6.830592	13.13575
10	0.004334343	14.65798	0.1645570	0.1656051	6.812698	13.62540
11	0.004828643	14.72393	0.1686747	0.1693548	7.342796	14.39764
12	0.004660905	14.52145	0.1673640	0.1680672	6.622258	12.98482
13	0.004831366	14.41718	0.1643836	0.1655172	7.052320	14.39249
14	0.004531018	14.76510	0.1686747	0.1693548	6.706782	13.97246
15	0.004300508	14.68531	0.1652893	0.1666667	6.363925	13.25818

	GermSpeedAccumulated_Percent	GermSpeedCorrected_Normal	GermSpeedCorrected_Accumulated	WeightGermPerc
1	69.23134	0.07673656	0.4326958	47.428
2	69.68741	0.07726134	0.4315642	47.899
3	79.78594	0.07340991	0.4085040	54.464
4	75.85202	0.07680397	0.4288937	52.240
5	82.01571	0.07623944	0.4271652	56.141
6	79.13509	0.07383855	0.4130508	54.518
7	75.80304	0.07369656	0.4158338	51.934
8	71.85275	0.07112480	0.3968068	49.391
9	73.29829	0.07893128	0.4404413	50.274
10	76.39054	0.07569665	0.4243919	52.571
11	80.73436	0.07801721	0.4374793	55.181
12	72.56158	0.07675799	0.4289379	50.000
13	80.19182	0.07352419	0.4096608	55.247
14	78.53103	0.07316490	0.4112171	53.869
15	74.36868	0.07273057	0.4079653	51.190

	TimsonsIndex	TimsonsIndex_Labouriau	TimsonsIndex_KhanUngar	GermRateGeorge	GermIndex	GermIndex_mod	Eme
1	8.000000	1.00	0.5714286	4	5.840000	7.300000	
2	9.803922	1.25	0.7002801	5	5.882353	7.142857	
3	14.583333	1.40	1.0416667	7	6.687500	7.133333	
4	7.843137	1.00	0.5602241	4	6.411765	7.108696	
5	10.000000	1.00	0.7142857	5	6.900000	7.187500	
6	6.122449	1.00	0.4373178	3	6.693878	7.130435	
7	8.333333	1.00	0.5952381	4	6.395833	7.309524	
8	10.638298	1.25	0.7598784	5	6.063830	7.125000	
9	9.615385	1.25	0.6868132	5	6.173077	7.133333	
10	8.000000	1.00	0.5714286	4	6.460000	7.177778	
11	9.803922	1.00	0.7002801	5	6.784314	7.208333	
12	5.882353	1.00	0.4201681	3	6.137255	7.113636	
13	8.163265	1.00	0.5830904	4	6.775510	7.063830	
14	6.250000	1.00	0.4464286	3	6.625000	7.227273	
15	8.333333	1.00	0.5952381	4	6.291667	7.190476	

	EmergenceRateIndex_Melville_mod	EmergenceRateIndex_BilbroWanjura	EmergenceRateIndex_Fakorede	PeakValu
1	7.300000	5.970149	8.375000	9.5000
2	7.142857	6.125000	8.326531	9.3137
3	7.133333	6.553398	7.324444	10.4166

```
4                         7.108696                    6.675079                    7.640359 10.04901
5                         7.187500                    7.045872                    7.096354 11.25000
6                         7.130435                    6.696203                    7.317580 10.71428
7                         7.309524                    6.277580                    7.646259 10.41660
8                         7.125000                    5.818182                    8.078125  9.57440
9                         7.133333                    6.553398                    7.934815  9.85570
10                        7.177778                    6.596091                    7.580247 10.25000
11                        7.208333                    7.067485                    7.216146 11.02941
12                        7.113636                    6.389439                    7.981921  9.80392
13                        7.063830                    6.776074                    7.231326 10.96938
14                        7.227273                    6.496644                    7.388430 10.67708
15                        7.190476                    6.167832                    7.782313 10.15625
   GermValue_Czabator_mod GermValue_DP_mod   CUGerm GermSynchrony GermUncertainty
1              54.28571         39.56076 0.7092199     0.2666667        2.062987
2              54.78662         40.99260 0.5051546     0.2346109        2.321514
3              69.75446         53.42809 0.3975265     0.2242424        2.462012
4              64.74158         48.86825 0.4672113     0.2502415        2.279215
5              77.14286         56.23935 0.4312184     0.2606383        2.146051
6              71.84506         53.06435 0.4934701     0.2792271        2.160545
7              65.10417         47.37690 0.7371500     0.2729384        2.040796
8              58.20345         43.67948 0.4855842     0.2256410        2.357249
9              60.92165         45.30801 0.4446640     0.2494949        2.321080
10             65.89286         49.10820 0.5584666     0.2555556        2.187983
11             74.14731         54.27520 0.4288905     0.2686170        2.128670
12             60.41632         44.71582 0.4760266     0.2737844        2.185245
13             75.15470         54.94192 0.4023679     0.2506938        2.241181
14             69.90947         51.41913 0.5383760     0.2991543        2.037680
15             63.47656         46.48043 0.6133519     0.2497096        2.185028
```

```
## End(No test)
```

FourPHFfit.bulk()   This wrapper function can be used to fit the four-parameter hill function for multiple samples in batch.

```r
## No test:
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)
```

```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14 To
1:       G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2:       G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3:       G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4:       G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
5:       G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
```

```
 6:       G1   2     0    0    0    0    3   21   11    7    1    1    1    1    0    0
 7:       G2   2     0    0    0    0    4   18   11    7    1    0    1    0    0    0
 8:       G3   2     0    0    0    1    3   14   12    6    2    1    0    1    0    0
 9:       G4   2     0    0    0    1    3   19   10    8    1    1    1    1    0    0
10:       G5   2     0    0    0    0    4   18   13    6    2    1    0    1    0    0
11:       G1   3     0    0    0    0    5   21   11    8    1    0    0    1    1    0
12:       G2   3     0    0    0    0    3   20   10    7    1    1    1    1    0    0
13:       G3   3     0    0    0    0    4   19   12    8    1    1    0    1    1    0
14:       G4   3     0    0    0    0    3   21   11    6    1    0    1    1    0    0
15:       G5   3     0    0    0    0    4   17   10    8    1    1    1    0    0    0
    y0 lag   Dlag50 t50.total t50.Germinated     TMGR      AUC      MGT Skewness
 1:  0   0 6.034954  6.355122        6.034954 5.912195 1108.975 6.632252 1.098973
 2:  0   0 6.175193  6.473490        6.175193 6.031282 1128.559 6.784407 1.098655
 3:  0   0 6.138110  6.244190        6.138110 5.938179 1283.693 6.772742 1.103392
 4:  0   0 6.125172  6.276793        6.125172 5.972686 1239.887 6.739665 1.100323
 5:  0   0 6.049641  6.103433        6.049641 5.914289 1328.328 6.654980 1.100062
 6:  0   0 6.097412  6.182276        6.097412 5.961877 1294.463 6.702470 1.099232
 7:  0   0 6.029851  6.202812        6.029851 5.914057 1213.908 6.622417 1.098272
 8:  0   0 6.189774  6.439510        6.189774 6.036193 1164.346 6.804000 1.099232
 9:  0   0 6.125121  6.352172        6.125121 5.961631 1188.793 6.745241 1.101242
10:  0   0 6.109503  6.253042        6.109503 5.978115 1240.227 6.711899 1.098600
11:  0   0 6.018759  6.099434        6.018759 5.883558 1305.200 6.624247 1.100600
12:  0   0 6.108449  6.326181        6.108449 5.964079 1188.021 6.718636 1.099892
13:  0   0 6.149011  6.207500        6.149011 5.998270 1316.407 6.762272 1.099733
14:  0   0 6.015907  6.122385        6.015907 5.905179 1273.386 6.604963 1.097916
15:  0   0 6.121580  6.317392        6.121580 5.976088 1203.664 6.732267 1.099760
                                                  msg isConv txp.total_10 txp.total_60 Unifo
 1: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.956266     6.744598
 2: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.983236     6.872603
 3: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.673022     6.608437     8
 4: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.850876     6.614967
 5: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.814126     6.386788
 6: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.868635     6.477594
 7: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.930423     6.510495
 8: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.940058     6.823299
 9: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.836659     6.733275
10: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.920629     6.566505
11: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.798630     6.391288
12: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.893597     6.684521
13: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.841310     6.509952
14: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.915143     6.397486
15: #1. Relative error in the sum of squares is at most 'ftol'.   TRUE     4.892505     6.667247
```

```
## End(No test)
```

Citing germinationmetrics

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

Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan (2020). germination
Germination Indices and Curve Fitting. R package version 0.1.4,
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 = {2020},
  note = {R package version 0.1.4},
  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 us
the project by citing the package.

Session Info

```r
sessionInfo()
```

```
R version 4.0.1 (2020-06-06)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 18.04.4 LTS

Matrix products: default
BLAS:   /usr/lib/x86_64-linux-gnu/atlas/libblas.so.3.10.3
LAPACK: /usr/lib/x86_64-linux-gnu/atlas/liblapack.so.3.10.3

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C              LC_TIME=en_IN.UTF-8       LC_COLLATE=en_US.U
 [6] LC_MESSAGES=en_US.UTF-8    LC_PAPER=en_IN.UTF-8      LC_NAME=C                 LC_ADDRESS=C
[11] LC_MEASUREMENT=en_IN.UTF-8 LC_IDENTIFICATION=C

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

other attached packages:
[1] germinationmetrics_0.1.4

loaded via a namespace (and not attached):
 [1] whoami_1.3.0       nlme_3.1-147      bitops_1.0-6      fs_1.4.1          xopen_1.0.0        use
 [8] covr_3.5.0         httr_1.4.1        rprojroot_1.3-2   hunspell_3.0      tools_4.0.1        bac
[15] lazyeval_0.2.2     colorspace_1.4-1  withr_2.2.0       tidyselect_1.1.0  prettyunits_1.1.1  pro
[22] compiler_4.0.1     cli_2.0.2         xml2_1.3.2        desc_1.2.0        labeling_0.3       sca
[29] goodpractice_1.0.2 pkgdown_1.5.1     stringr_1.4.0     digest_0.6.25     rmarkdown_2.2      lin
[36] htmltools_0.4.0    bibtex_0.4.2.2    sessioninfo_1.1.1 highr_0.8         rlang_0.4.6        rst
[43] farver_2.0.3       jsonlite_1.6.1    dplyr_1.0.0       RCurl_1.98-1.2    magrittr_1.5       Rcp
[50] fansi_0.4.1        lifecycle_0.2.0   stringi_1.4.6     yaml_2.2.1        mathjaxr_0.8-3     gbR
[57] pkgbuild_1.0.8     plyr_1.8.6        grid_4.0.1        ggrepel_0.8.2     crayon_1.3.4       lat
[64] knitr_1.28         ps_1.3.3          pillar_1.4.4      clisymbols_1.2.0  pkgload_1.1.0      XML
[71] packrat_0.5.0      praise_1.0.0      evaluate_0.14     rex_1.2.0         data.table_1.12.8  rem
[78] Rdpack_0.11-1      testthat_2.3.2    gtable_0.3.0      purrr_0.3.4       rcmdcheck_1.3.3    tid
[85] ggplot2_3.3.1      xfun_0.14         broom_0.5.6       roxygen2_7.1.0    cyclocomp_1.1.0    min
```

[92] memoise_1.1.0   ellipsis_0.3.1   xmlparsedata_1.0.3

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