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:

```
# 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

```
library(germinationmetrics)
```

Version History

The current version of the package is 0.1.8. 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
0.1.3	2019-01-19
0.1.4	2020-06-16
0.1.5	2021-02-17
0.1.6	2022-06-15
0.1.7	2022-08-28

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))
```
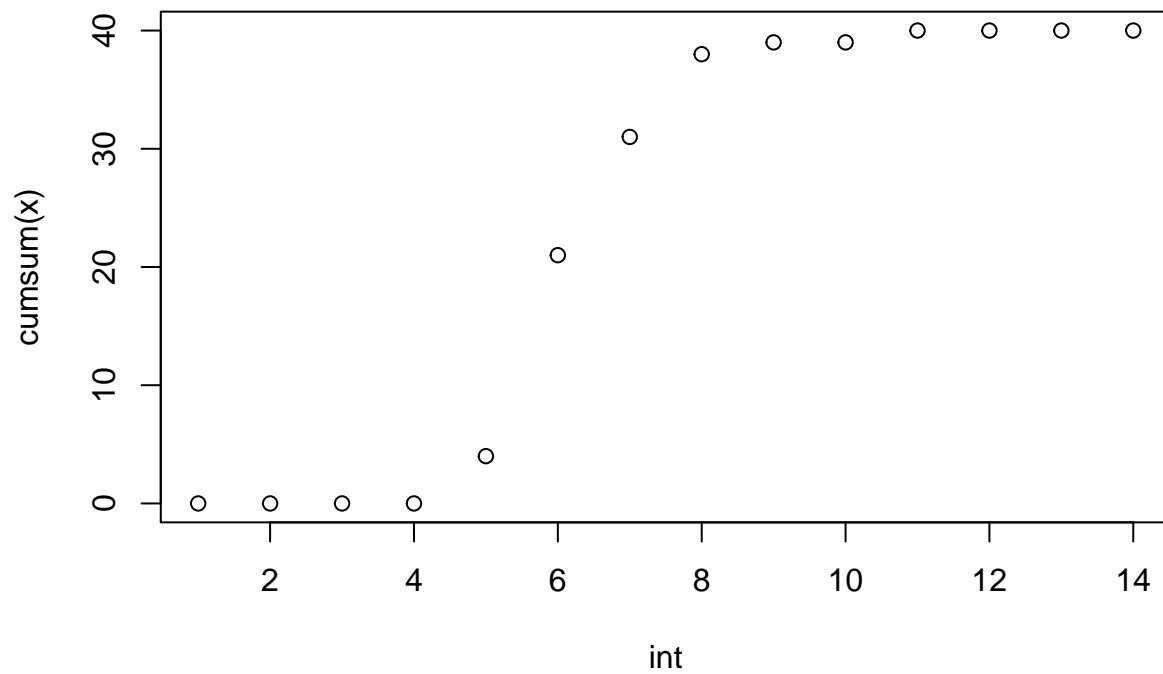

Single-value germination indices

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)
Peak germination percentage (PGP)	`PeakGermPercent`	It is computed as follows. $$PGP = \frac{N_{max}}{N_t} \times 100$$ Where, N_{max} is the maximum number of seeds germinated per interval.	Percentage (%)	Germination capacity	Vallance (1950); Roh et al. (2004)
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). $$t_0 = \min\{T_i : N_i \neq 0\}$$ Where, T_i is the time from the start of the experiment to the ith interval and N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval)	time	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) $$t_g = \max\{T_i : N_i \neq 0\}$$ Where, T_i is the time from the start of the experiment to the ith interval and N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval)	time	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 (t_{peak})	`PeakGermTime`	It is the time in which highest frequency of germinated seeds are observed and need not be unique. $$t_{peak} = \{T_i : N_i = N_{max}\}$$ 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 N_{max} is the maximum number of seeds germinated per interval.	time	Germination time	Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
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)
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)

Germination index	Function	Details	Unit	Measures	Reference
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^{-1}	Germination time	Labouriau (1983a); Ranal and Santana (2006)
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)

Germination index	Function	Details	Unit	Measures	Reference
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.	% time^{-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)
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 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 (S) 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} or count 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 ($S_{accumulated}$)	GermSpeedAccumulate	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 cumative/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} or count time^{-1}	Mixed	Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004)
Corrected speed of germination or Corrected germination rate index ($\hat{S}$)	GermSpeedCorrected	It is computed as follows. $$S_{corrected} = \frac{S}{FGP}$$ Where, S is the germination speed computed with germination percentage instead of counts and FGP is the final germination percentage or germinability. It can also be computed from speed of accumulated germination (computed with germination percentage). $$\hat{S}_{accumulated} = \frac{S_{accumulated}}{FGP}$$ Where, $S_{accumulated}$ is the speed of accumulated germination computed with germination percentage instead of counts and 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.	Percentage (%)	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.	% time^{-1}	Mixed	Czabator (1962)

Germination index	Function	Details	Unit	Measures	Reference
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.	count time[-1]	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. $$\Sigma k = \sum_{i=1}^{k} G_i$$ 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 $j = i - 1$.	Percentage (%)	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. $$\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}$$	no unit	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). $$\Sigma k_{mod} = \frac{\Sigma k}{T_k}$$	% time[-1]	Mixed	Khan and Ungar (1984)

Germination index	Function	Details	Unit	Measures	Reference
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.	count time	Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968);Chopra and Chaudhary (1980)
Germination Index (GI) (Melville)	`GermIndex`	It is estimated as follows. $$GI = \sum_{i=1}^{k} \frac{|(T_k - T_i)\,N_i|}{N_t}$$ Where, T_i is the time from the start of the experiment to the ith interval (day for the example), N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), N_t is the total number of seeds used in the test, and k is the total number of time intervals.	time	Mixed	Melville et al. (1980)
Germination Index (GI_{mod}) (Melville; Santana and Ranal)	`GermIndex`	It is estimated as follows. $$GI_{mod} = \sum_{i=1}^{k} \frac{|(T_k - T_i)\,N_i|}{N_g}$$ 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.	time	Mixed	Melville et al. (1980); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (ERI) or Germination Rate Index (Shmueli and Goldberg)	`EmergenceRateIndex`	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.	count	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)	EmergenceRateIndex	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.	no unit	Mixed	Shmueli and Goldberg (1971); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (ERI) or Germination Rate Index (Bilbro & Wanjura)	EmergenceRateIndex	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.	count time⁻¹	Mixed	Bilbro and Wanjura (1982)
Emergence Rate Index (ERI) or Germination Rate Index (Fakorede)	EmergenceRateIndex	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.	time count⁻¹	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.	$\%^2$ time^{-2}	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.	$\%^2$ time^{-1}	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.	time^{-2}	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.	no unit	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.	no unit	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)
z <- c(0, 0, 0, 0, 11, 11, 9, 7, 1, 0, 1, 0, 0, 0)
int <- 1:length(x)

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

```r
GermPercent()
```

```
[1] 80
```

```r
PeakGermPercent(germ.counts = x, intervals = int, total.seeds = 50)
```

```
[1] 34
```

```r
# For multiple peak germination times
PeakGermPercent(germ.counts = z, intervals = int, total.seeds = 50)
```

```
Warning in PeakGermPercent(germ.counts = z, intervals = int, total.seeds = 50): Multiple peak germinati
```

```
[1] 22
```

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

```
[1] 80
```

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

```
[1] 34
```

```r
# For multiple peak germination times
PeakGermPercent(germ.counts = cumsum(z), intervals = int, total.seeds = 50,
                partial = FALSE)
```

```
Warning in PeakGermPercent(germ.counts = cumsum(z), intervals = int, total.seeds = 50, : Multiple peak 
```

```
[1] 22
```

```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

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

[1] 11

```
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

```r
t50(germ.counts = x, intervals = int, method = "farooq")
```

```
[1] 5.941176
```

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

```
[1] 5.970588
```

```r
t50(germ.counts = y, intervals = int, partial = FALSE, method = "farooq")
```

```
[1] 5.941176
```

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

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

```
[1] 6.7
```

```r
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
```

```r
# 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] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

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

```
[1] 14.92537
VarGermRate(germ.counts = x, intervals = int)
```

```
[1] 0.0007176543
SEGermRate(germ.counts = x, intervals = int)
```

```
[1] 0.004235724
GermRateRecip(germ.counts = x, intervals = int, method = "coolbear")
```

```
[1] 0.1674877
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] 0.0007176543
SEGermRate(germ.counts = y, intervals = int, partial = FALSE)
```

```
[1] 0.004235724
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
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

```
# 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
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

```
# 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
```

```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
```

```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)
```

MeanGermPercent(), MeanGermNumber()

```
[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
```

```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
#----------------------------------------------------------------------
# Without max specified
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50)
```

```
TimsonsIndex(), GermRateGeorge()
```

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

```
# 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
```

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

```
[1] 172
```

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

```
[1] 332
```

```
# From cumulative germination counts
#----------------------------------------------------------------------
# Without 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
```
```
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
            total.seeds = 50,
            max = 10, modification = "khanungar")
```

```
[1] 24.57143
```
```
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 10)
```

```
[1] 172
```
```
GermRateGeorge(germ.counts = y, intervals = int, partial = FALSE,
               max = 14)
```

```
[1] 332
```

```
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)
```

```r
# 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
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```r
EmergenceRateIndex()
```

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

```
EmergenceRateIndex(germ.counts = x, intervals = int, total.seeds = 50,
                   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, total.seeds = 50,
                   partial = FALSE)
```

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
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] 0.7092199
```

```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
```

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

```
[1] 2.062987
```

```r
# 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".

this function can also be be reparameterized by substituting b with e^β to constraint b to positive values only.

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

Where, $b = e^\beta$ and $\beta = \log_e(b)$.

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

Germination parameters	Details	Unit	Measures
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
#----------------------------------------------------------------------------
```

30

```
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  bta 2.290709 0.05602634  40.88628 2.965932e-14
2    c 6.034954 0.03872162 155.85488 3.270089e-21
```

$Fit
```
    sigma isConv      finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.61522   TRUE 7.105427e-14 -25.49868 56.99736 58.91453 31.30723          12   14
```

$a
[1] 80

$b
[1] 9.881937

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034954

$t50.total
[1] 6.355121

$txp.total
```
      10       60
4.956264 6.744598
```

```
$t50.Germinated
[1] 6.034954

$txp.Germinated
      10        60
4.831807 6.287724

$Uniformity
         90          10 uniformity
  7.537690    4.831807    2.705882

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. success "

$isConv
[1] TRUE

$model
Nonlinear regression model
  model: csgp ~ FourPHF_fixa_fixy0(x = intervals, a = max(csgp), bta,      c)
   data: data
  bta      c
2.291 6.035
 residual sum-of-squares: 31.31

Algorithm: multifit/levenberg-marquardt, (scaling: levenberg, solver: qr)

Number of iterations to convergence: 9
Achieved convergence tolerance: 7.105e-14

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

```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  bta 2.290709 0.05602634  40.88628 2.965932e-14
2    c 6.034954 0.03872162 155.85488 3.270089e-21

$Fit
    sigma isConv       finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.61522   TRUE 7.105427e-14 -25.49868 56.99736 58.91453 31.30723          12   14

$a
[1] 80

$b
[1] 9.881937

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034954

$t50.total
[1] 6.355121

$txp.total
      10       60
4.956264 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10       60
4.831807 6.287724
```

```
$Uniformity
        90          10 uniformity
  7.537690    4.831807    2.705882


$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. success "

$isConv
[1] TRUE


$model
Nonlinear regression model
  model: csgp ~ FourPHF_fixa_fixy0(x = intervals, a = max(csgp), bta,      c)
   data: data
  bta       c
2.291 6.035
 residual sum-of-squares: 31.31

Algorithm: multifit/levenberg-marquardt, (scaling: levenberg, solver: qr)

Number of iterations to convergence: 9
Achieved convergence tolerance: 7.105e-14

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

```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)
```

Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.

Warning in geom_segment(aes(x = UfmMax, xend = UfmMin, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
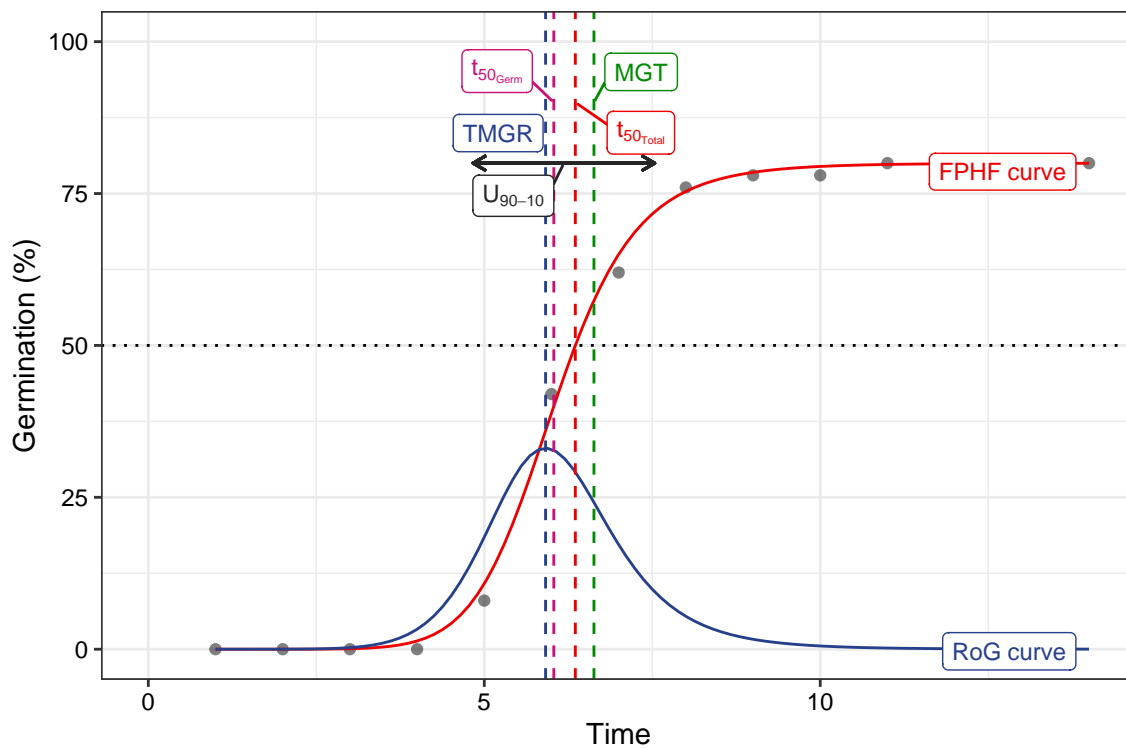

```
plot(fit2)
```

Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
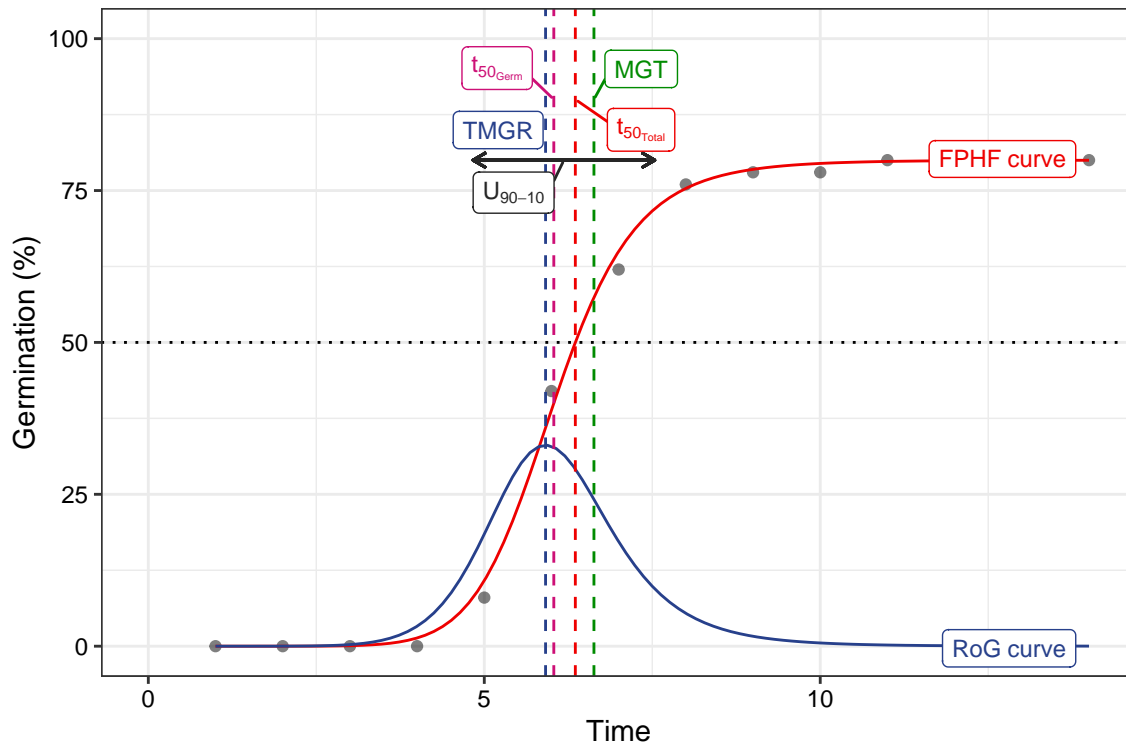
```
# No labels
plot(fit1, plotlabels = FALSE)
```

Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have l
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
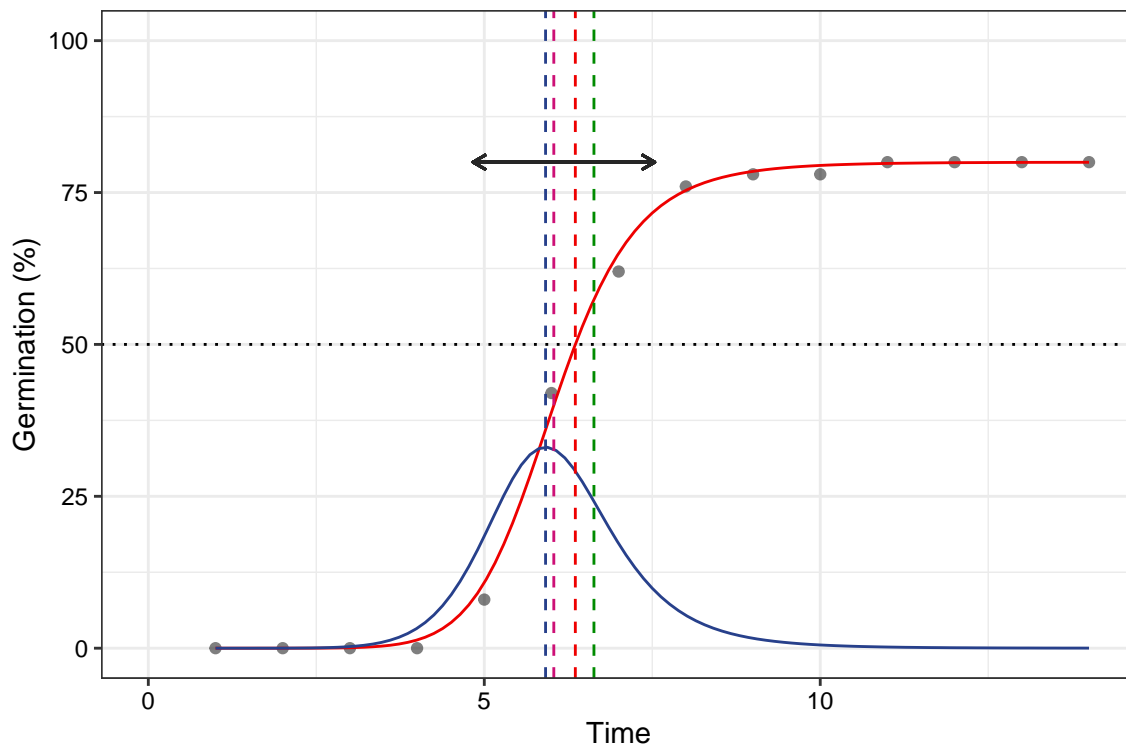
```
plot(fit2, plotlabels = FALSE)
```

Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
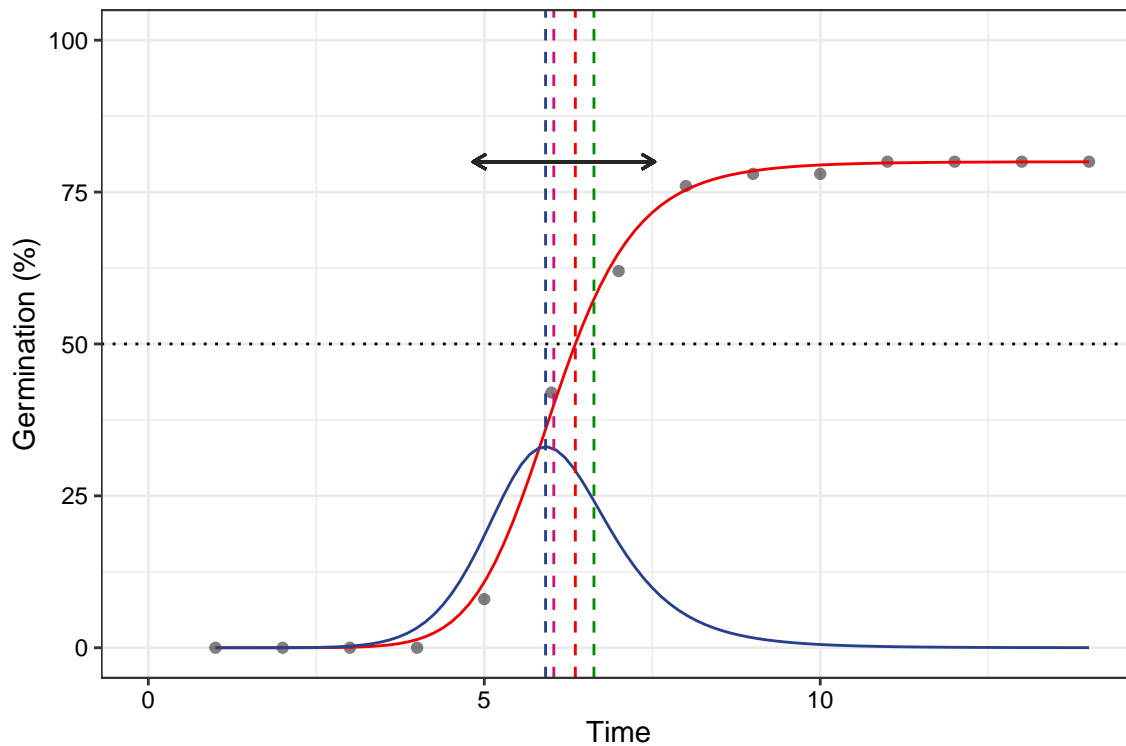

```
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```
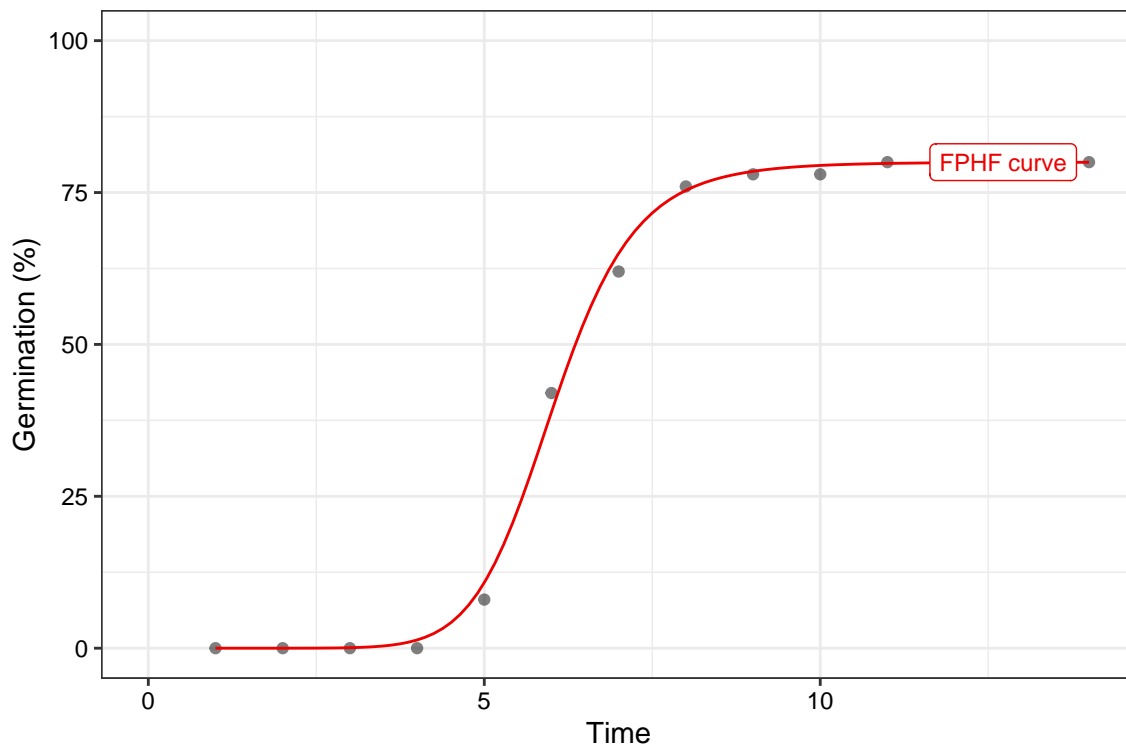
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```
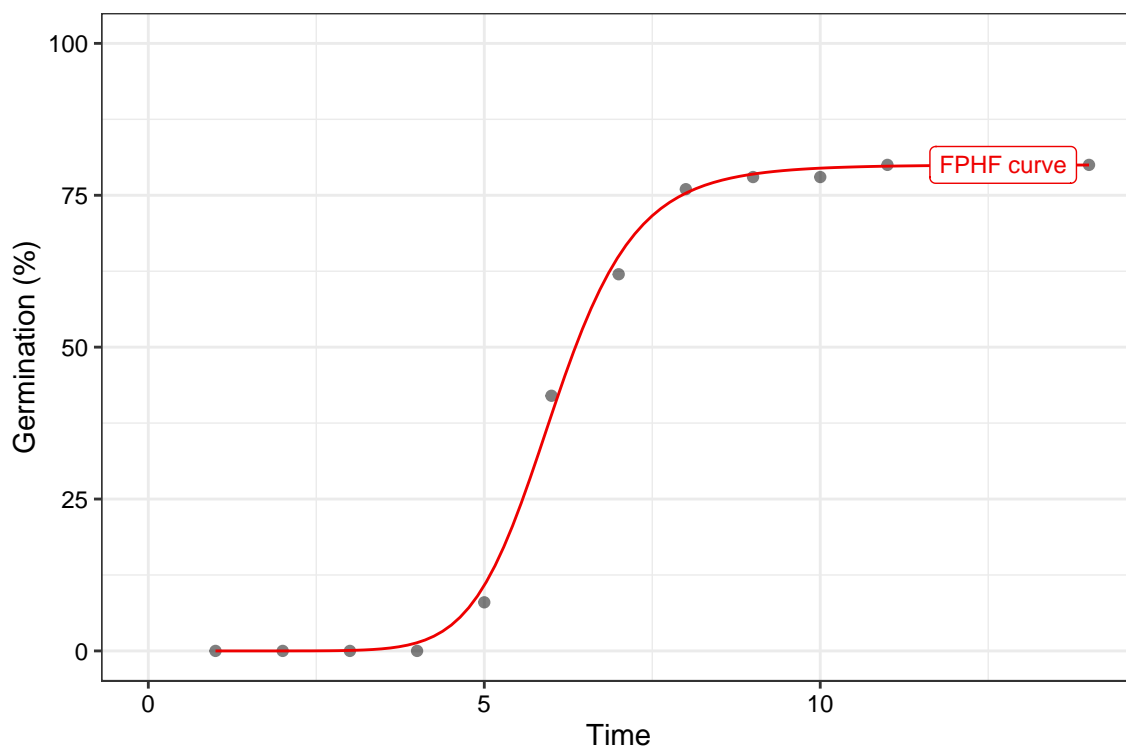


```
# Without y axis limits adjustment
plot(fit1, limits = FALSE)
```

```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
```

```
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
```
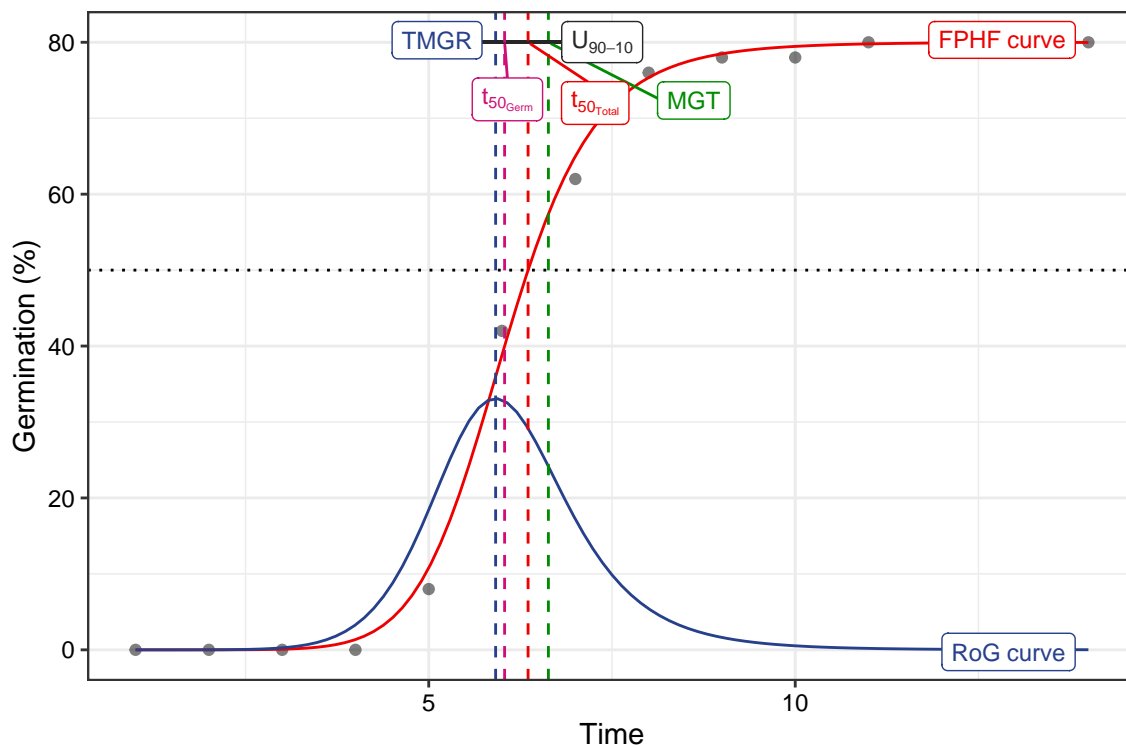


```
plot(fit2, limits = FALSE)
```

```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide this layer with data containing a single row.
```
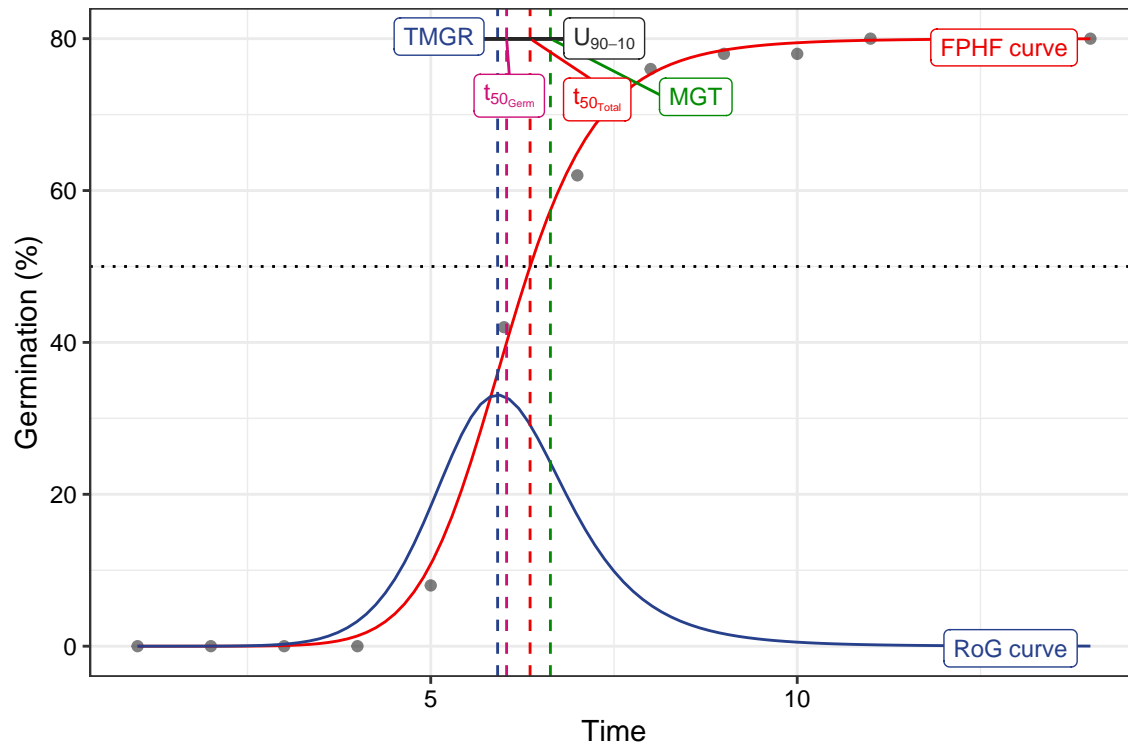
Wrapper functions

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.

```r
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

	FirstGermTime	LastGermTime	PeakGermTime	TimeSpreadGerm	t50_Coolbear	t50_Farooq	MeanGermTime	VarGermTi
1	5	11	6	6	5.970588	5.941176	6.700000	1.446
2	4	12	6	8	6.192308	6.153846	6.857143	2.0278
3	4	12	6	8	6.333333	5.972222	6.866667	2.5727
4	5	12	6	7	6.041667	6.225806	6.891304	2.1879
5	5	13	6	8	5.975000	5.950000	6.812500	2.3683
6	5	12	6	7	5.976190	5.952381	6.869565	2.0714
7	5	11	6	6	5.972222	5.944444	6.690476	1.3890
8	4	12	6	8	6.208333	6.166667	6.875000	2.112
9	4	12	6	8	6.310345	5.973684	6.866667	2.3000
10	5	12	6	7	6.076923	6.038462	6.822222	1.8313
11	5	13	6	8	5.928571	5.904762	6.791667	2.3812
12	5	12	6	7	5.975000	5.950000	6.886364	2.1495
13	5	13	6	8	6.083333	6.041667	6.936170	2.5393
14	5	12	6	7	5.928571	5.904762	6.772727	1.9000
15	5	11	6	6	6.050000	6.259259	6.809524	1.6701

	VarGermRate	SEGermRate	CVG	GermRateRecip_Coolbear	GermRateRecip_Farooq	GermSpeed_Count	GermSpe
1	0.0007176543	0.004235724	14.92537	0.1674877	0.1683168	6.138925	
2	0.0009172090	0.004673148	14.58333	0.1614907	0.1625000	6.362698	
3	0.0011572039	0.005071059	14.56311	0.1578947	0.1674419	6.882179	
4	0.0009701218	0.004592342	14.51104	0.1655172	0.1606218	6.927417	
5	0.0010995627	0.004786184	14.67890	0.1673640	0.1680672	7.318987	
6	0.0009301809	0.004496813	14.55696	0.1673307	0.1680000	6.931782	
7	0.0006935558	0.004063648	14.94662	0.1674419	0.1682243	6.448449	
8	0.0009454531	0.004861721	14.54545	0.1610738	0.1621622	6.053175	
9	0.0010345321	0.004794747	14.56311	0.1584699	0.1674009	6.830592	
10	0.0008453940	0.004334343	14.65798	0.1645570	0.1656051	6.812698	
11	0.0011191581	0.004828643	14.72393	0.1686747	0.1693548	7.342796	
12	0.0009558577	0.004660905	14.52145	0.1673640	0.1680672	6.622258	
13	0.0010970785	0.004831366	14.41718	0.1643836	0.1655172	7.052320	
14	0.0009033254	0.004531018	14.76510	0.1686747	0.1693548	6.706782	
15	0.0007767634	0.004300508	14.68531	0.1652893	0.1597633	6.363925	

	GermSpeedAccumulated_Percent	GermSpeedCorrected_Normal	GermSpeedCorrected_Accumulated	WeightGermPerc
1	69.23134	0.1534731	0.8653917	47.428
2	69.68741	0.1514928	0.8462043	47.899
3	79.78594	0.1529373	0.8510501	54.464
4	75.85202	0.1505960	0.8409680	52.240
5	82.01571	0.1524789	0.8543303	56.141
6	79.13509	0.1506909	0.8429608	54.518
7	75.80304	0.1535345	0.8663205	51.934
8	71.85275	0.1513294	0.8442698	49.391
9	73.29829	0.1517909	0.8470024	50.274
10	76.39054	0.1513933	0.8487837	52.571
11	80.73436	0.1529749	0.8578026	55.181
12	72.56158	0.1505059	0.8410547	50.000
13	80.19182	0.1500494	0.8360424	55.241
14	78.53103	0.1524269	0.8567022	53.869
15	74.36868	0.1515220	0.8499278	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_SG_mod	EmergenceRateIndex_BilbroWanjura	EmergenceRateIndex_Fakorede	PeakValue	Germ
1	7.300000	5.970149	8.375000	9.500000	
2	7.142857	6.125000	8.326531	9.313725	
3	7.133333	6.553398	7.324444	10.416667	
4	7.108696	6.675079	7.640359	10.049020	
5	7.187500	7.045872	7.096354	11.250000	
6	7.130435	6.696203	7.317580	10.714286	
7	7.309524	6.277580	7.646259	10.416667	
8	7.125000	5.818182	8.078125	9.574468	
9	7.133333	6.553398	7.934815	9.855769	
10	7.177778	6.596091	7.580247	10.250000	
11	7.208333	7.067485	7.216146	11.029412	
12	7.113636	6.389439	7.981921	9.803922	
13	7.063830	6.776074	7.231326	10.969388	
14	7.227273	6.496644	7.388430	10.677083	
15	7.190476	6.167832	7.782313	10.156250	

	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

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

```
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	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	

	lag	Dlag50	t50.total	t10.total	t60.total	t50.Germinated	t10.Germinated	t60.Germinated	Uniformity_9
1	0	6.034954	6.355121	4.956264	6.744598	6.034954	4.831807	6.287724	7.537690
2	0	6.175193	6.473490	4.983236	6.872603	6.175193	4.866755	6.452582	7.835407
3	0	6.138110	6.244191	4.673022	6.608438	6.138110	4.630062	6.465924	8.137342
4	0	6.125173	6.276794	4.850875	6.614968	6.125173	4.788597	6.409838	7.834810
5	0	6.049642	6.103433	4.814125	6.386789	6.049642	4.790946	6.315746	7.639028
6	0	6.097415	6.182279	4.868632	6.477599	6.097415	4.832471	6.364722	7.693469
7	0	6.029851	6.202812	4.930422	6.510495	6.029851	4.858476	6.275050	7.483643
8	0	6.189774	6.439510	4.940057	6.823299	6.189774	4.841105	6.476945	7.914163
9	0	6.125122	6.352172	4.836658	6.733276	6.125122	4.746573	6.420208	7.904041
10	0	6.109504	6.253043	4.920629	6.566506	6.109504	4.860681	6.372823	7.679177
11	0	6.018760	6.099435	4.798627	6.391291	6.018760	4.764246	6.284051	7.603611
12	0	6.108452	6.326184	4.893596	6.684526	6.108452	4.806013	6.384836	7.763854
13	0	6.149012	6.207501	4.841308	6.509954	6.149012	4.816393	6.432524	7.850345
14	0	6.015910	6.122389	4.915140	6.397491	6.015910	4.869398	6.255276	7.432371
15	0	6.121579	6.317392	4.892502	6.667247	6.121579	4.813083	6.399357	7.785800

	AUC	MGT	Skewness	msg	sigma	finTol	logLik	AIC	BIC	deviance
1	1108.976	6.632252	1.098973	#1. success	1.615220	7.105427e-14	-25.49868	56.99736	58.91453	31.30723
2	1128.559	6.784407	1.098655	#1. success	1.115372	2.309264e-14	-20.31471	46.62943	48.54660	14.92865
3	1283.693	6.772742	1.103392	#1. success	2.432704	9.947598e-14	-31.23213	68.46426	70.38143	71.01658
4	1239.887	6.739666	1.100323	#1. success	2.396582	5.684342e-14	-31.02269	68.04538	69.96256	68.92324
5	1328.328	6.654981	1.100062	#1. success	2.399662	1.094236e-12	-31.04067	68.08135	69.99852	69.10052
6	1294.463	6.702473	1.099232	#1. success	3.034962	1.563194e-13	-34.32887	74.65774	76.57491	110.53195
7	1213.908	6.622417	1.098272	#1. success	1.663019	1.421085e-13	-25.90697	57.81395	59.73112	33.18760
8	1164.346	6.804000	1.099232	#1. success	1.120704	4.327205e-12	-20.38149	46.76298	48.68015	15.07174
9	1188.793	6.745241	1.101242	#1. success	2.429960	7.958079e-13	-31.21633	68.43266	70.34984	70.85647
10	1240.227	6.711900	1.098600	#1. success	1.686656	8.142820e-12	-26.10456	58.20911	60.12629	34.13771
11	1305.200	6.624248	1.100600	#1. success	2.628113	1.989520e-13	-32.31381	70.62762	72.54479	82.88372
12	1188.021	6.718639	1.099892	#1. success	2.878146	1.151079e-12	-33.58613	73.17227	75.08944	99.40469
13	1316.407	6.762274	1.099733	#1. success	2.604588	2.984279e-13	-32.18793	70.37586	72.29303	81.40654

```
14 1273.385 6.604967 1.097916 #1. success   2.764756 9.805490e-13 -33.02342 72.04684 73.96401  91.72652
15 1203.664 6.732266 1.099760 #1. success   1.954008 8.739676e-13 -28.16444 62.32888 64.24606  45.81777
```

Multiple fitted curves generated in batch can also be plotted.

```
data(gcdata)

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

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

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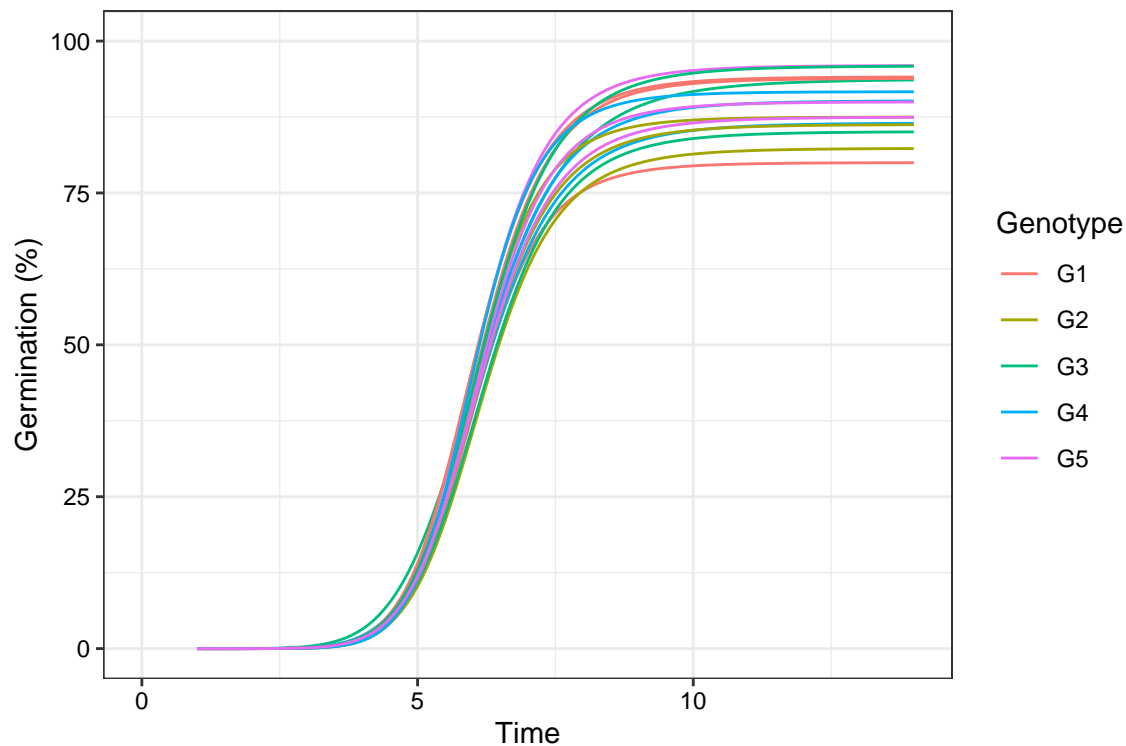


```
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```
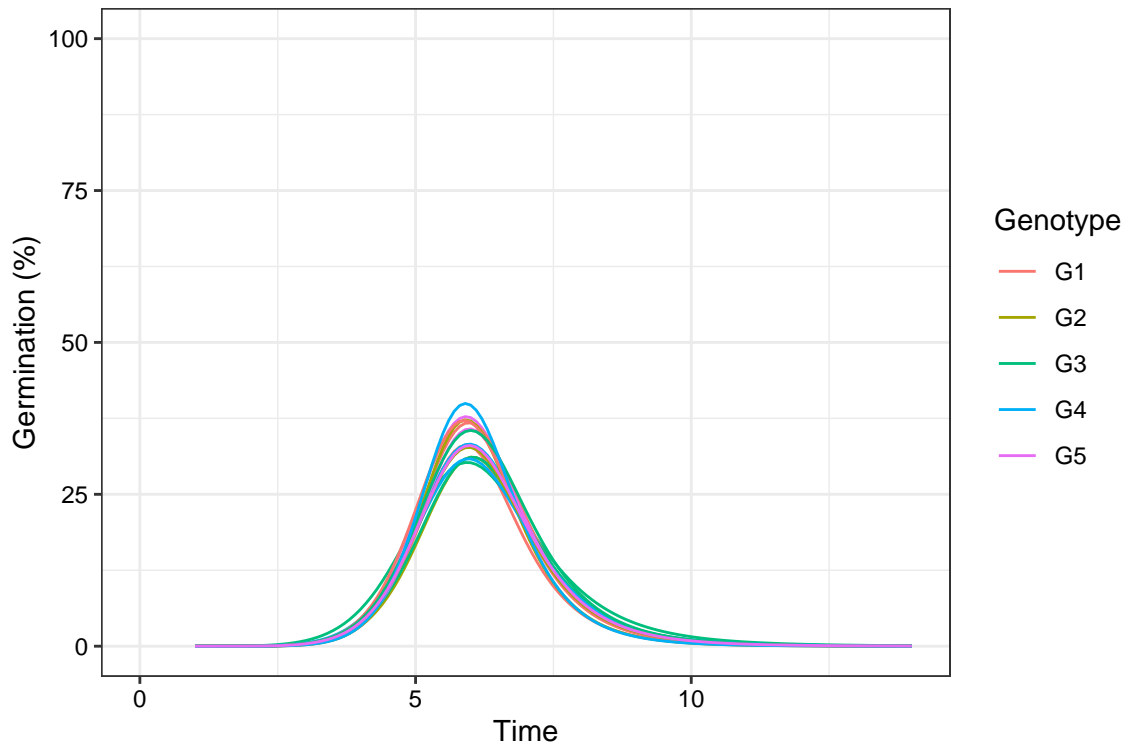
```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```
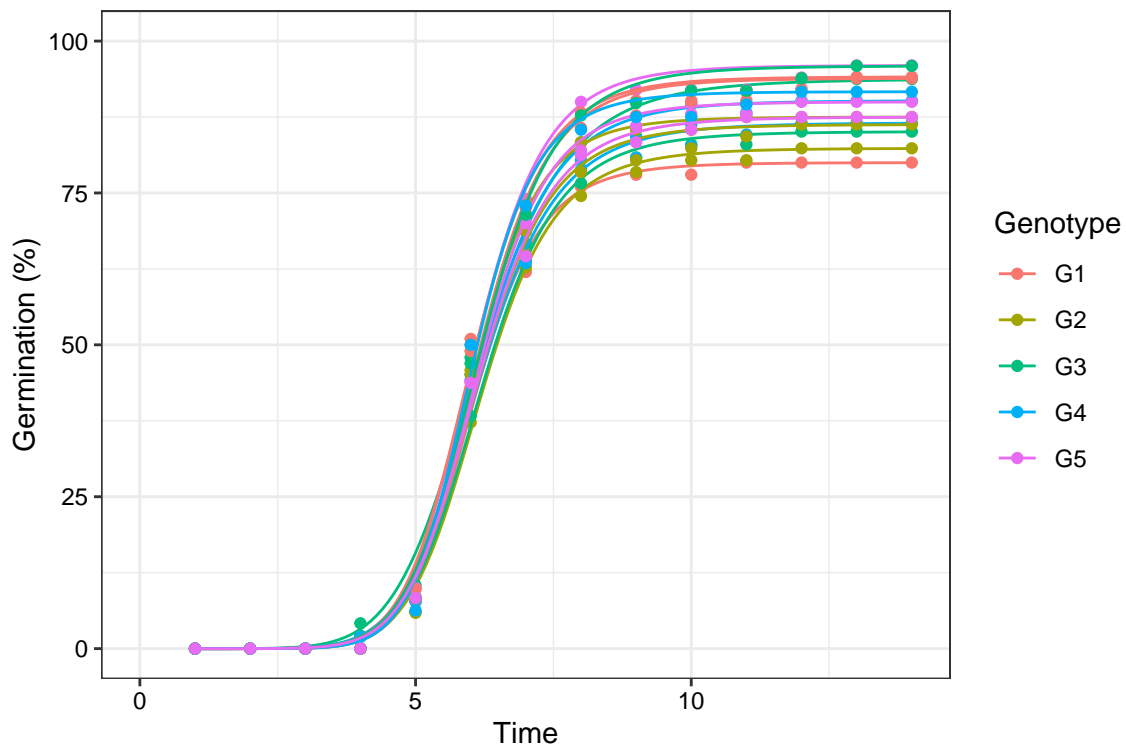


```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```
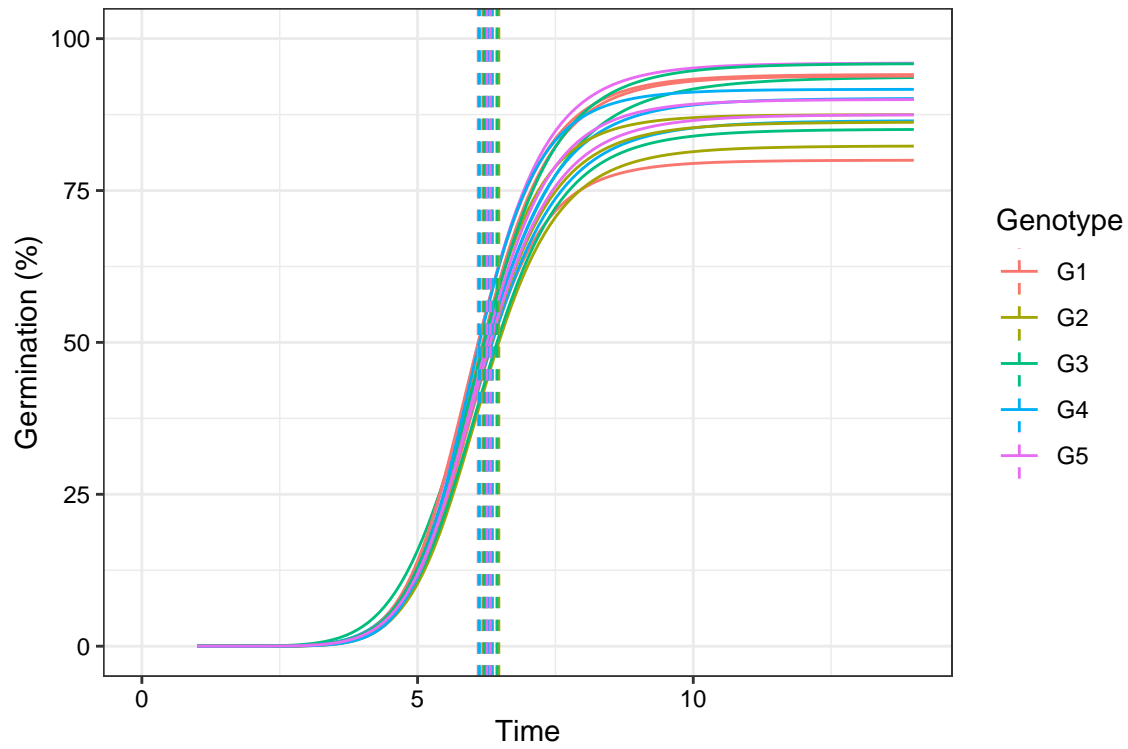
```r
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```



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

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



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

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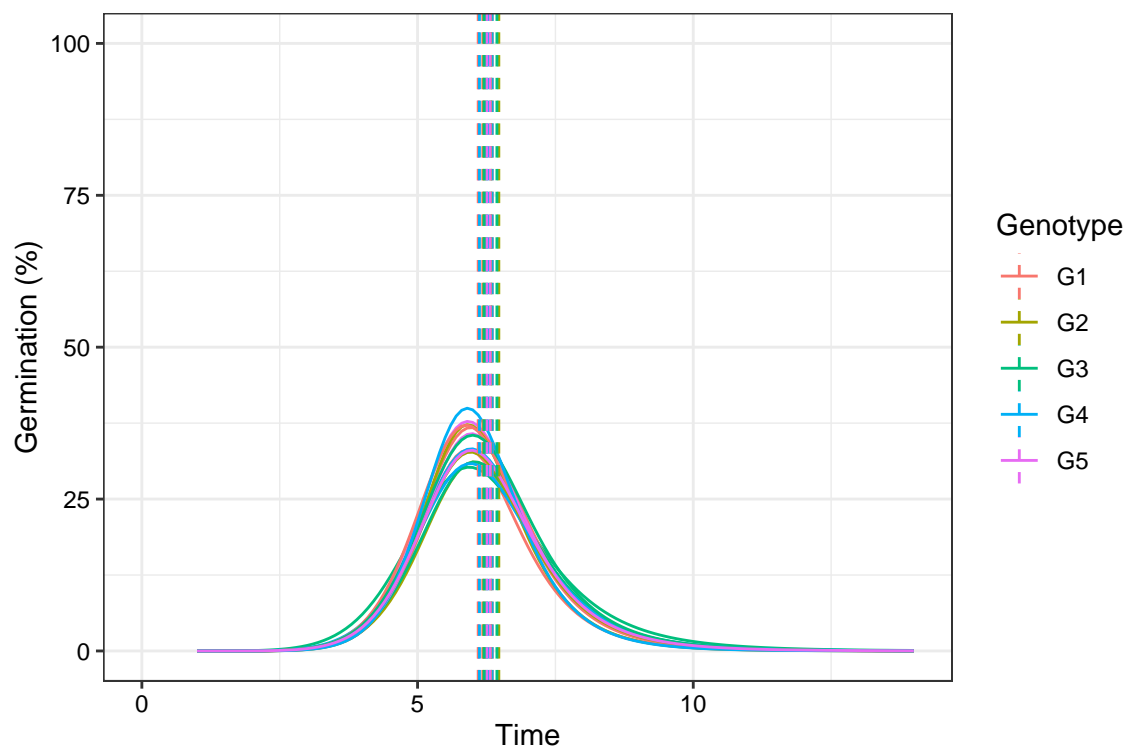


```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```
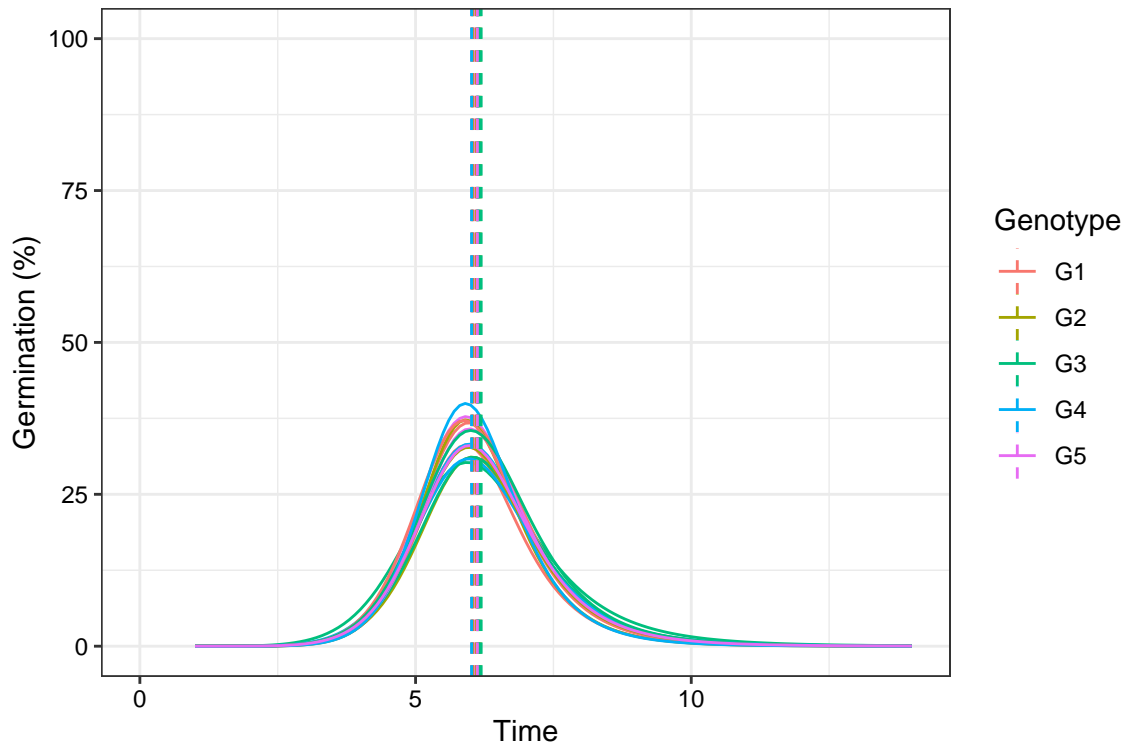
```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "tmgr")
```



```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```

```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```
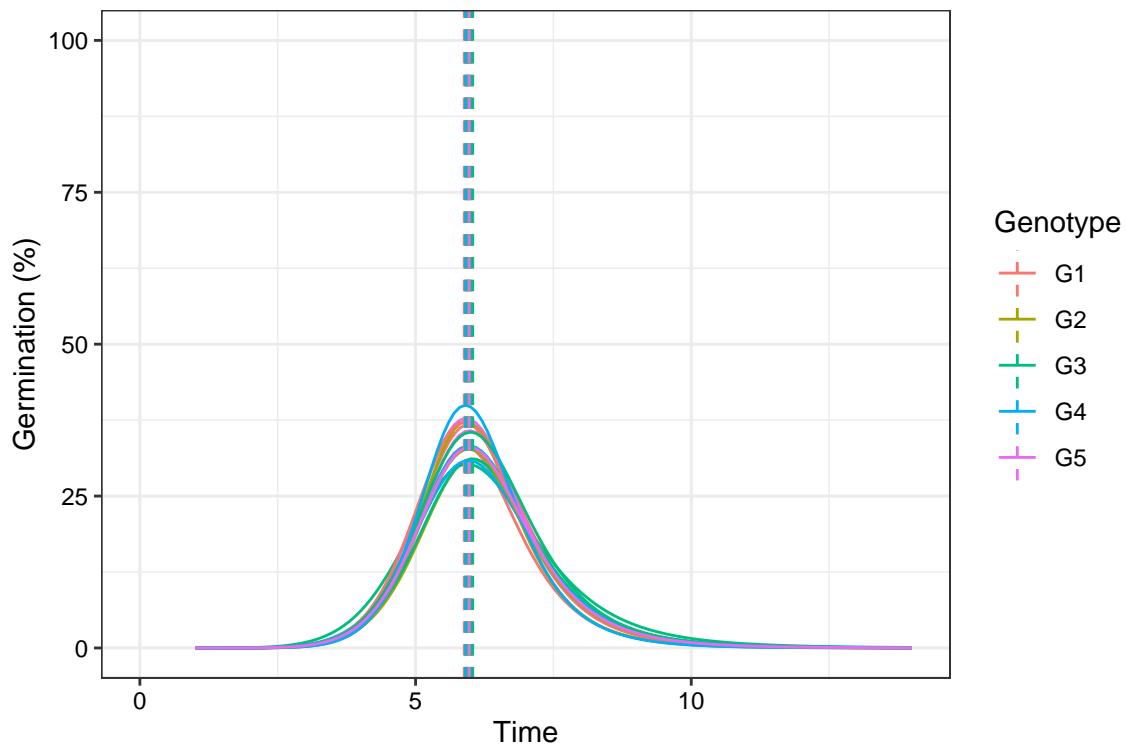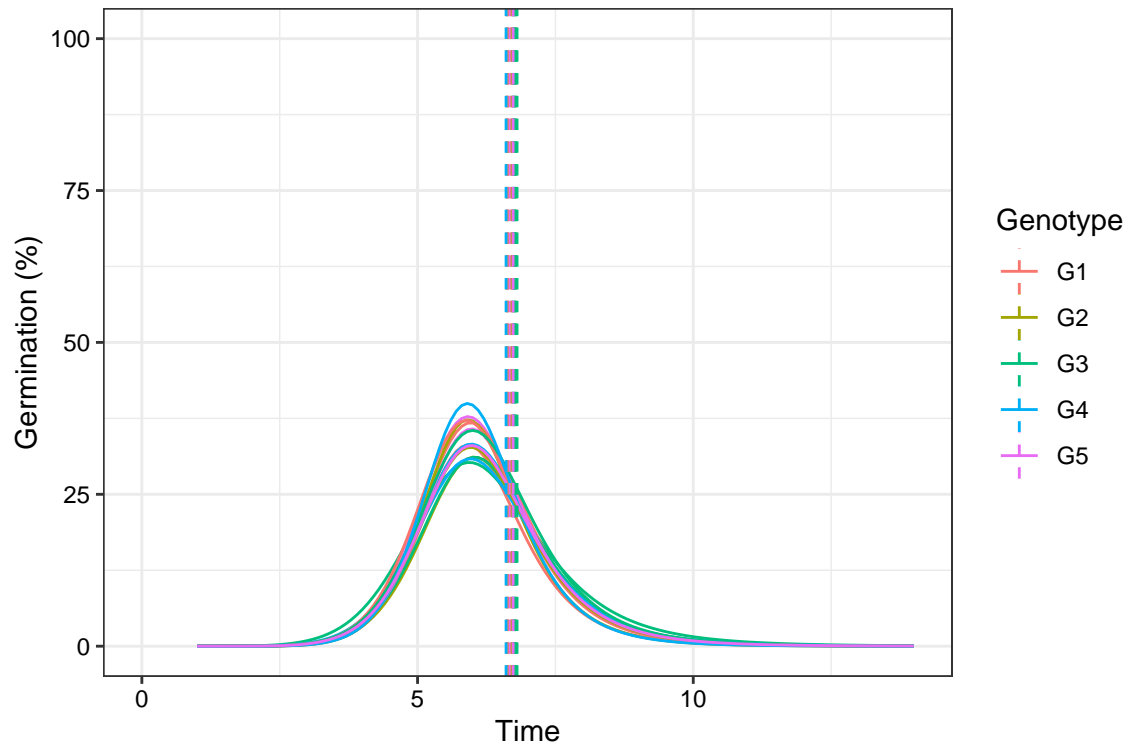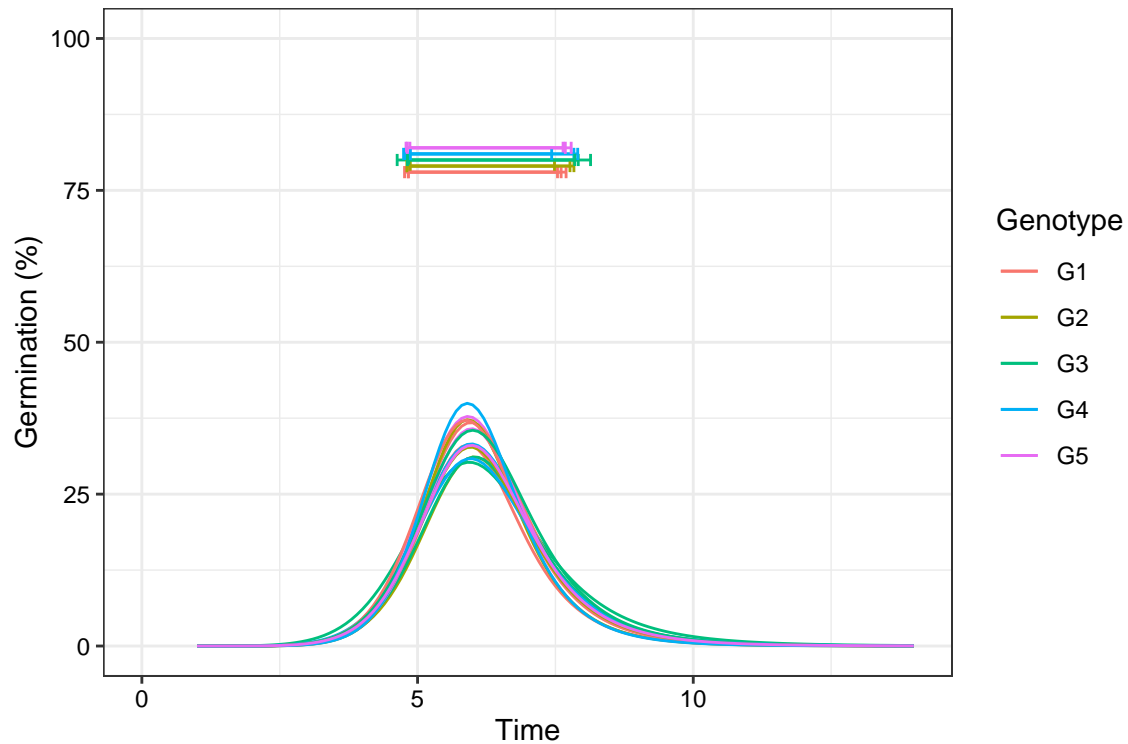


```r
# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

# 'Dark2' palette from RColorBrewer
```

```
curvesplot + scale_colour_brewer(palette = "Dark2")
```
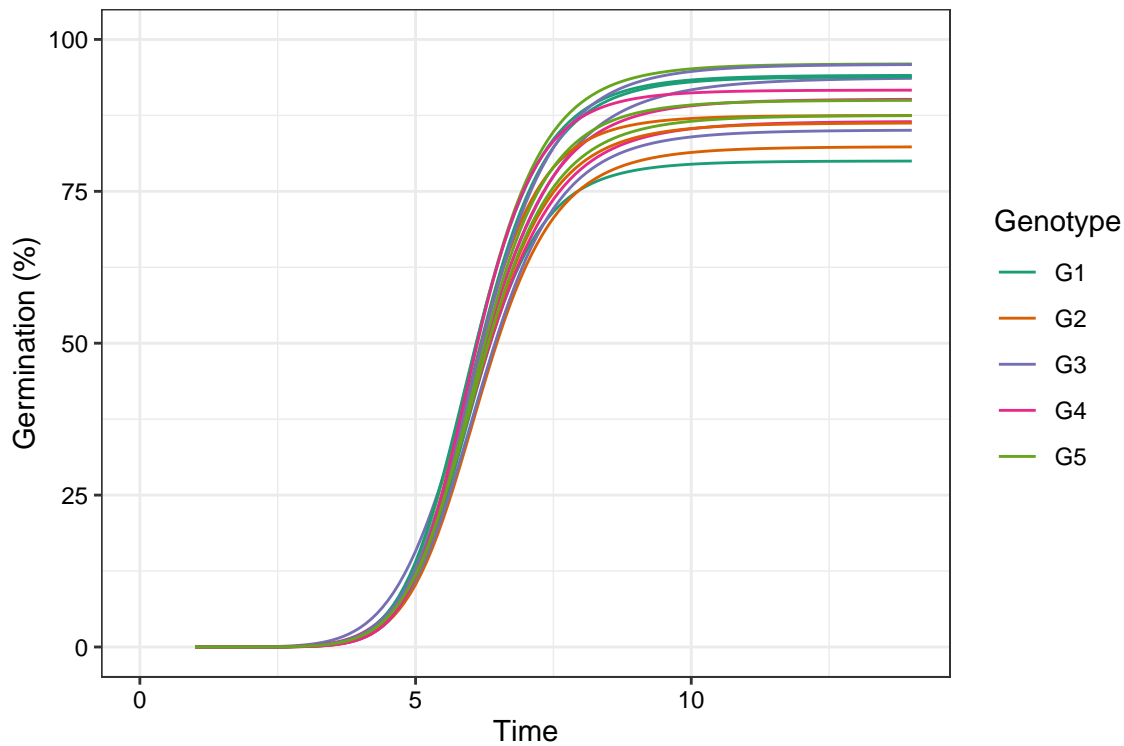


```
# Manual colours
curvesplot +
  scale_colour_manual(values = c("Coral", "Brown", "Blue",
                                 "Aquamarine", "Red"))
```
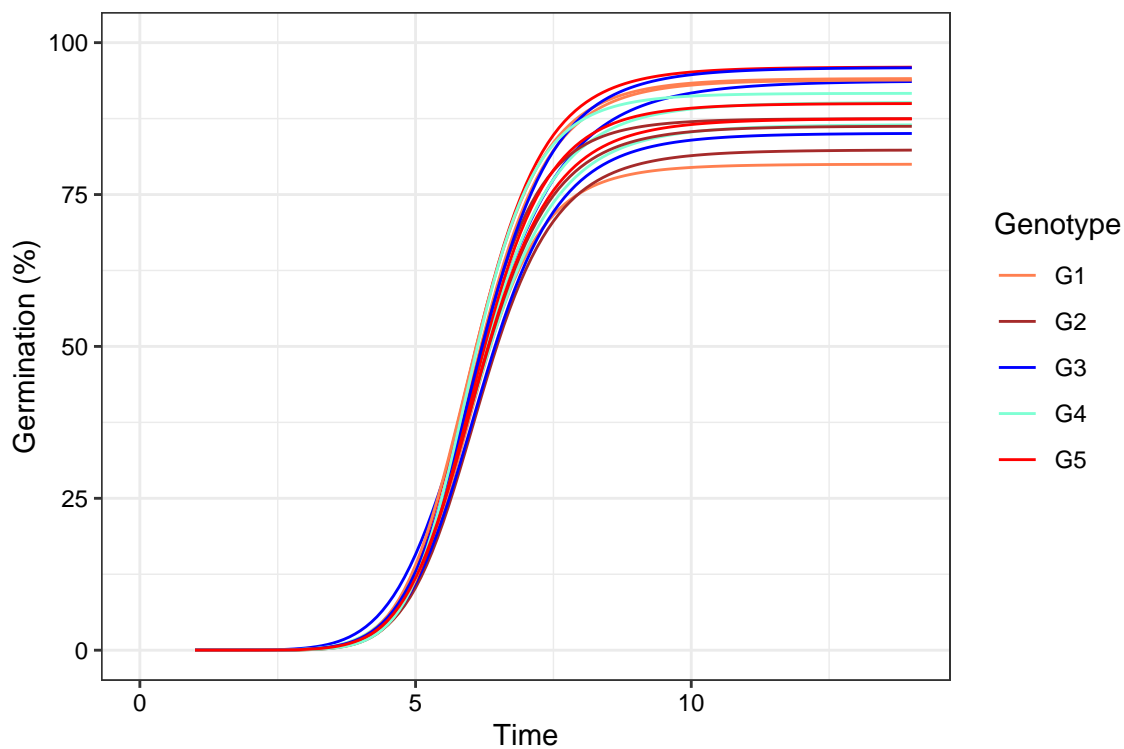
Citing `germinationmetrics`

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

  Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan (). germinationmet
  Indices and Curve Fitting. R package version 0.1.8.9000,
  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
    note = {R package version 0.1.8.9000 https://aravind-j.github.io/germinationmetrics/ https://CRAN.R-
  }

This free and open-source software implements academic research by the authors and co-workers. If you u
project by citing the package.

Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2025-07-21 r88439 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 26100)

Matrix products: default
  LAPACK version 3.12.1

locale:
[1] LC_COLLATE=English_India.utf8  LC_CTYPE=English_India.utf8    LC_MONETARY=English_India.utf8 LC_NUM
[5] LC_TIME=English_India.utf8

time zone: Asia/Calcutta
tzcode source: internal

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

other attached packages:
[1] germinationmetrics_0.1.8.9000 ggplot2_3.5.2.9002            readxl_1.4.5                  testthat_3

loaded via a namespace (and not attached):
 [1] Rdpack_2.6.4      bitops_1.0-9      remotes_2.5.0.9000 rlang_1.1.6       magrittr_2.0.3    comp
 [8] callr_3.7.6       vctrs_0.6.5       reshape2_1.4.4    stringr_1.5.1     profvis_0.4.0     pkg
[15] backports_1.5.0   ellipsis_0.3.2    labeling_0.4.3    pander_0.6.6      promises_1.3.3    rma
[22] ps_1.9.1          tinytex_0.57      purrr_1.1.0       xfun_0.52         gslnls_1.4.1      cac
[29] broom_1.0.9       parallel_4.6.0    R6_2.6.1          stringi_1.8.7     RColorBrewer_1.1-3 pkg
[36] cellranger_1.1.0  Rcpp_1.1.0        knitr_1.50        usethis_3.1.0     httpuv_1.6.16     Mat
[43] rstudioapi_0.17.1 dichromat_2.0-0.1 yaml_2.3.10       miniUI_0.1.2      curl_6.4.0        pro
[50] lattice_0.22-7    tibble_3.3.0      plyr_1.8.9        shiny_1.11.1      withr_3.0.2       S7_
[57] desc_1.4.3        rJava_1.0-11      urlchecker_1.0.1  xml2_1.3.8        pillar_1.11.0     rsc
[64] rprojroot_2.1.0   mathjaxr_1.8-0    RCurl_1.98-1.17   scales_1.4.0      xtable_1.8-4      glu
```

```
[71] data.table_1.17.8  fs_1.6.6           XML_3.99-0.18     grid_4.6.0       tidyr_1.3.1      rbi
[78] cli_3.6.5          dplyr_1.1.4        gtable_0.3.6      digest_0.6.37    ggrepel_0.9.6    htm
[85] memoise_2.0.1      htmltools_0.5.8.1  pkgdown_2.1.3.9000 lifecycle_1.0.4  httr_1.4.7       mim
```

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