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 0.1.9. 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
0.1.8	2023-08-18

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).

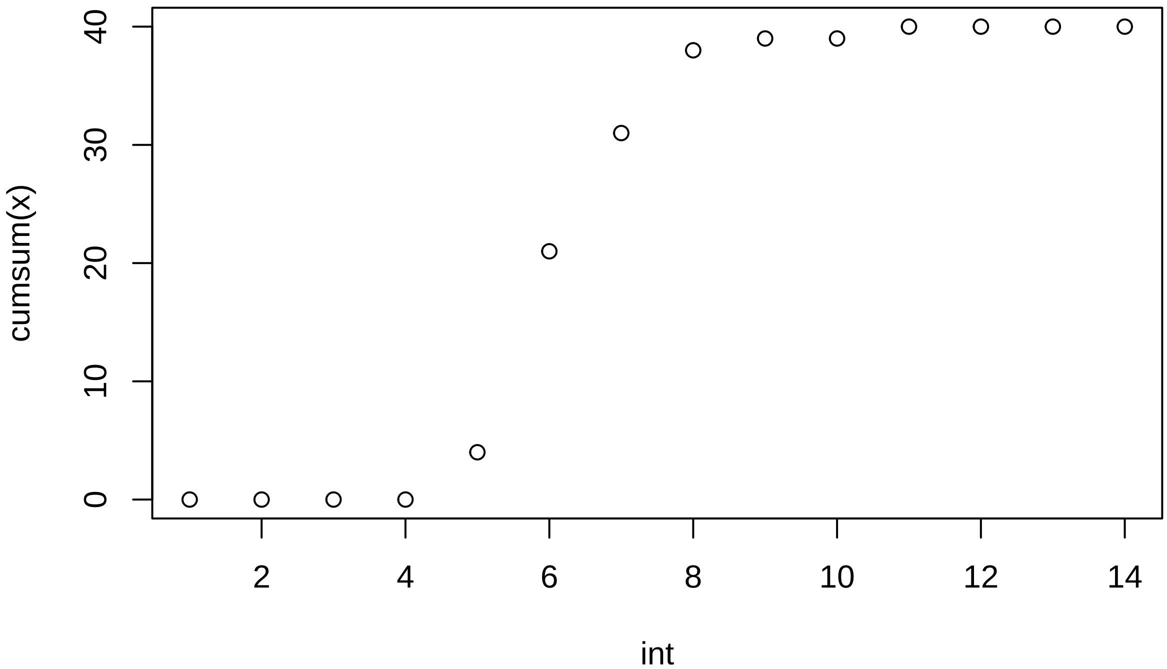
Table 2 : A typical germination count data.

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 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} 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. $GI = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i) N_i \rvert}{N_t}$ 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.	time	Mixed	Melville et al. (1980)
Germination Index (GI_{mod}) (Melville; Santana and Ranal)	`GermIndex`	It is estimated as follows. $GI_{mod} = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i) N_i \rvert}{N_g}$ 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.	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

```
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)
```

GermPercent()

```
[1] 80
```

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

```
[1] 34
```

```
# 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
germination times exist.
```

```
[1] 22
```

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

```
[1] 80
```

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

```
[1] 34
```

```
# 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 germination times exist.
```

```
[1] 22
```

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

```
[1] 80
```

```
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)
```

```r
# 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
```

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

```
[1] 6
```

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

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

```
[1] 5 6
```

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

```
[1] 5
```

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

```
[1] 11
```

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

```
[1] 6
```

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

```
[1] 6
```

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

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

```
[1] 5 6
```

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

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
```

```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
```

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.0007176543
```

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

```
[1] 0.004235724
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

```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] 0.1534731
```

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

```
[1] 0.8653917
```

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

```r
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
```

```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
```

```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
```

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

```r
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)
```

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)
```

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
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

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

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

```
[1] 8.375
```

```r

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
```

```r
#----------------------------------------------------------------------------
PeakValue(germ.counts = x, intervals = int, total.seeds = 200)
```

PeakValue(), GermValue()

```
[1] 9.5
```

```r
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
3           34         3                     34                    17.0 5.666667  5.666667
4           40         4                     74                    37.0 9.250000  7.458333
5           21         5                     95                    47.5 9.500000  8.138889
6           10         6                    105                    52.5 8.750000  8.291667
7            4         7                    109                    54.5 7.785714  8.190476
8            5         8                    114                    57.0 7.125000  8.012897
9            3         9                    117                    58.5 6.500000  7.796769
10           5        10                    122                    61.0 6.100000  7.584673
11           8        11                    130                    65.0 5.909091  7.398497
12           7        12                    137                    68.5 5.708333  7.229481
13           7        13                    144                    72.0 5.538462  7.075752
14           6        14                    150                    75.0 5.357143  6.932534
15           6        15                    156                    78.0 5.200000  6.799262
16           4        16                    160                    80.0 5.000000  6.670744
```

```
17            0        17                      160                      80.0 4.705882  6.539753
18            2        18                      162                      81.0 4.500000  6.412268
19            0        19                      162                      81.0 4.263158  6.285850
20            2        20                      164                      82.0 4.100000  6.164414
          GV
3   9.633333
4  27.595833
5  38.659722
6  43.531250
7  44.638095
8  45.673512
9  45.611097
10 46.266503
11 48.090230
12 49.521942
13 50.945411
14 51.994006
15 53.034246
16 53.365948
17 52.318022
18 51.939373
19 50.915385
20 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
1            0         1                      0                     0.0 0.000000  0.000000
2            0         2                      0                     0.0 0.000000  0.000000
3           34         3                     34                    17.0 5.666667  1.888889
4           40         4                     74                    37.0 9.250000  3.729167
5           21         5                     95                    47.5 9.500000  4.883333
6           10         6                    105                    52.5 8.750000  5.527778
7            4         7                    109                    54.5 7.785714  5.850340
8            5         8                    114                    57.0 7.125000  6.009673
9            3         9                    117                    58.5 6.500000  6.064153
10           5        10                    122                    61.0 6.100000  6.067738
11           8        11                    130                    65.0 5.909091  6.053316
12           7        12                    137                    68.5 5.708333  6.024567
13           7        13                    144                    72.0 5.538462  5.987174
14           6        14                    150                    75.0 5.357143  5.942172
15           6        15                    156                    78.0 5.200000  5.892694
16           4        16                    160                    80.0 5.000000  5.836901
17           0        17                    160                    80.0 4.705882  5.770370
18           2        18                    162                    81.0 4.500000  5.699794
19           0        19                    162                    81.0 4.263158  5.624182
20           2        20                    164                    82.0 4.100000  5.547972
          GV
1   0.000000
2   0.000000
3   3.211111
4  13.797917
5  23.195833
6  29.020833
7  31.884354
8  34.255134
9  35.475298
10 37.013202
11 39.346552
12 41.268285
13 43.107655
14 44.566291
15 45.963013
16 46.695205
17 46.162961
18 46.168331
19 45.555871
20 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
3           34         3                     34                    17.0 5.666667  5.666667
4           40         4                     74                    37.0 9.250000  7.458333
5           21         5                     95                    47.5 9.500000  8.138889
6           10         6                    105                    52.5 8.750000  8.291667
7            4         7                    109                    54.5 7.785714  8.190476
8            5         8                    114                    57.0 7.125000  8.012897
9            3         9                    117                    58.5 6.500000  7.796769
10           5        10                    122                    61.0 6.100000  7.584673
11           8        11                    130                    65.0 5.909091  7.398497
12           7        12                    137                    68.5 5.708333  7.229481
13           7        13                    144                    72.0 5.538462  7.075752
14           6        14                    150                    75.0 5.357143  6.932534
15           6        15                    156                    78.0 5.200000  6.799262
```

```
16          4         16                     160                    80.0 5.000000  6.670744
17          0         17                     160                    80.0 4.705882  6.539753
18          2         18                     162                    81.0 4.500000  6.412268
19          0         19                     162                    81.0 4.263158  6.285850
20          2         20                     164                    82.0 4.100000  6.164414
          GV
3   9.633333
4  27.595833
5  38.659722
6  43.531250
7  44.638095
8  45.673512
9  45.611097
10 46.266503
11 48.090230
12 49.521942
13 50.945411
14 51.994006
15 53.034246
16 53.365948
17 52.318022
18 51.939373
19 50.915385
20 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
1            0         1                      0                     0.0 0.000000  0.000000
2            0         2                      0                     0.0 0.000000  0.000000
3           34         3                     34                    17.0 5.666667  1.888889
4           40         4                     74                    37.0 9.250000  3.729167
5           21         5                     95                    47.5 9.500000  4.883333
6           10         6                    105                    52.5 8.750000  5.527778
7            4         7                    109                    54.5 7.785714  5.850340
8            5         8                    114                    57.0 7.125000  6.009673
9            3         9                    117                    58.5 6.500000  6.064153
10           5        10                    122                    61.0 6.100000  6.067738
11           8        11                    130                    65.0 5.909091  6.053316
12           7        12                    137                    68.5 5.708333  6.024567
13           7        13                    144                    72.0 5.538462  5.987174
14           6        14                    150                    75.0 5.357143  5.942172
15           6        15                    156                    78.0 5.200000  5.892694
16           4        16                    160                    80.0 5.000000  5.836901
17           0        17                    160                    80.0 4.705882  5.770370
18           2        18                    162                    81.0 4.500000  5.699794
19           0        19                    162                    81.0 4.263158  5.624182
20           2        20                    164                    82.0 4.100000  5.547972
          GV
1   0.000000
2   0.000000
3   3.211111
4  13.797917
5  23.195833
6  29.020833
7  31.884354
8  34.255134
9  35.475298
10 37.013202
11 39.346552
12 41.268285
13 43.107655
14 44.566291
15 45.963013
16 46.695205
17 46.162961
18 46.168331
19 45.555871
20 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
```

```r
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. $$lag = b\sqrt{\frac{-y_0c^b}{a+y_0}}$$	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

Germination parameters	Details	Unit	Measures
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  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"
```

```
# 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
```

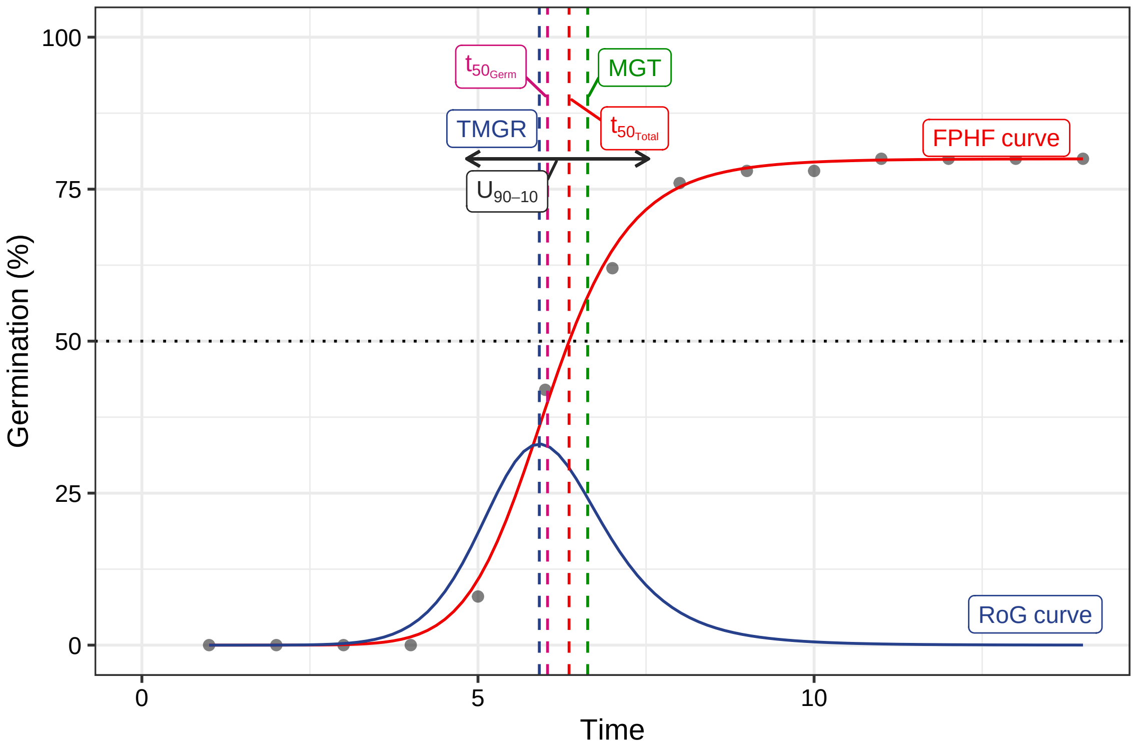
```
1  bta 2.290709 0.05602634  40.88628 2.965932e-14
2    c 6.034954 0.03872162 155.85488 3.270089e-21

$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)
```

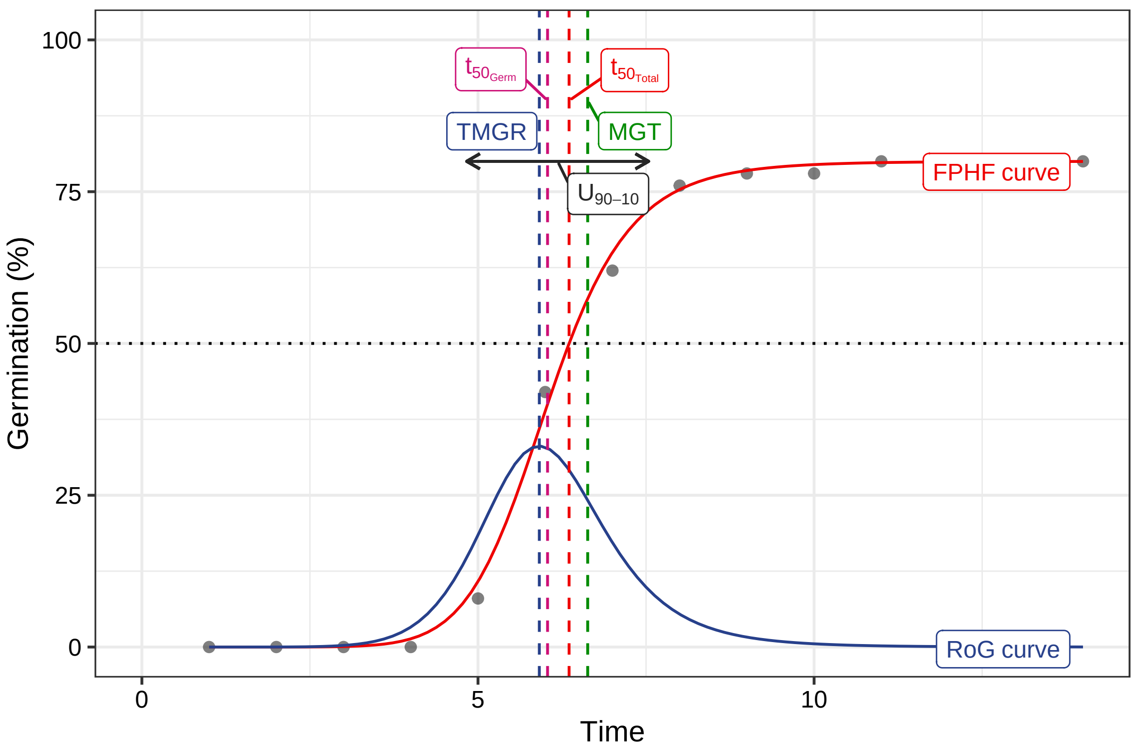
```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have
i Please consider using `annotate()` or provide this layer with data containing a single row.
```

```
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.
```



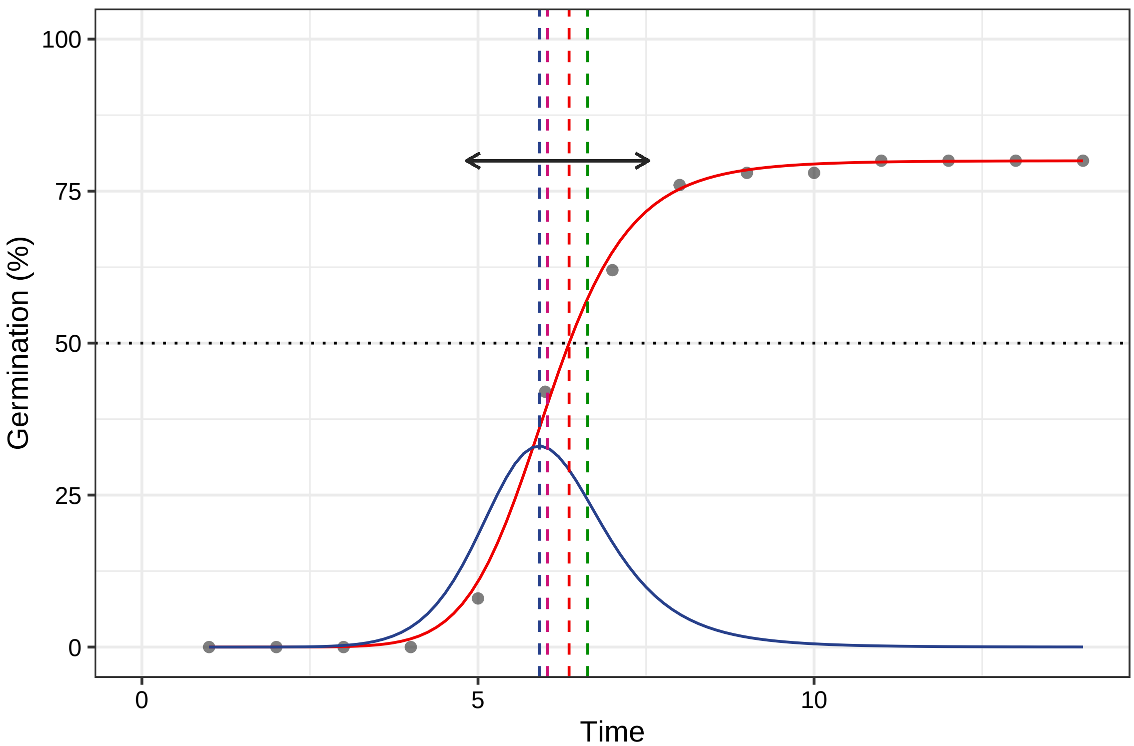

```
plot(fit2)
```

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



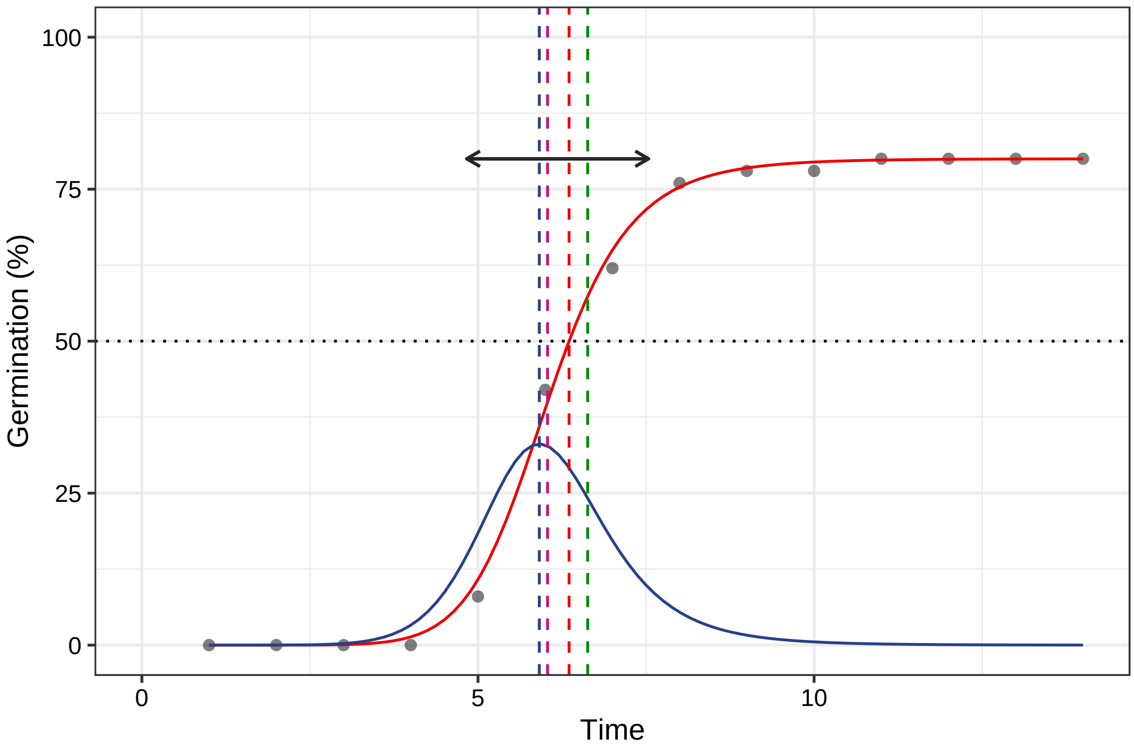
```r
# No labels
plot(fit1, plotlabels = FALSE)
```

```
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.
```

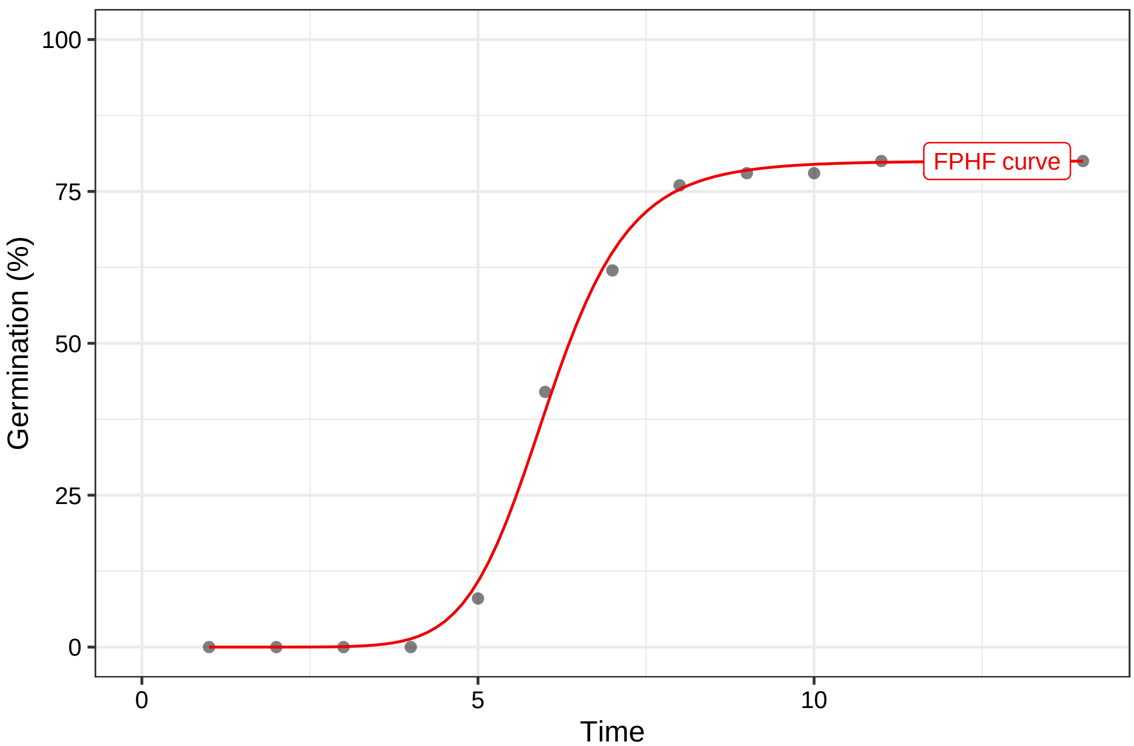



```r
plot(fit2, plotlabels = FALSE)
```

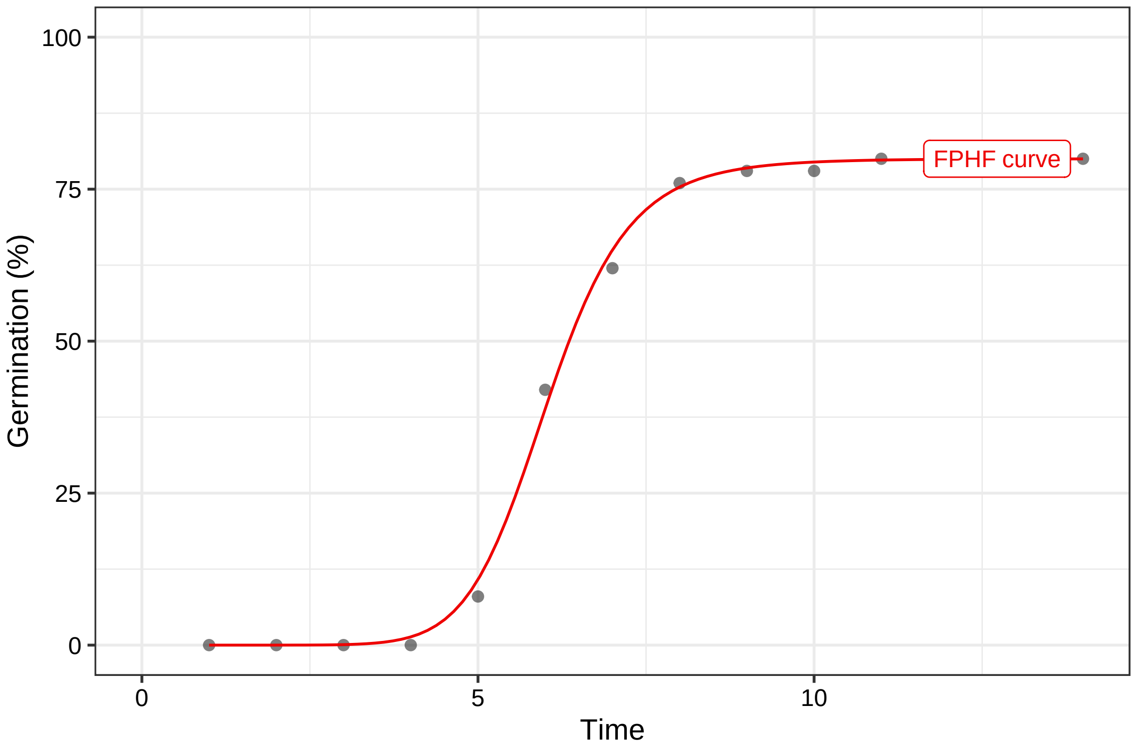
```
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have l
i Please consider using `annotate()` or provide this layer with data containing a single row.
All aesthetics have length 1, but the data has 14 rows.
i Please consider using `annotate()` or provide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




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

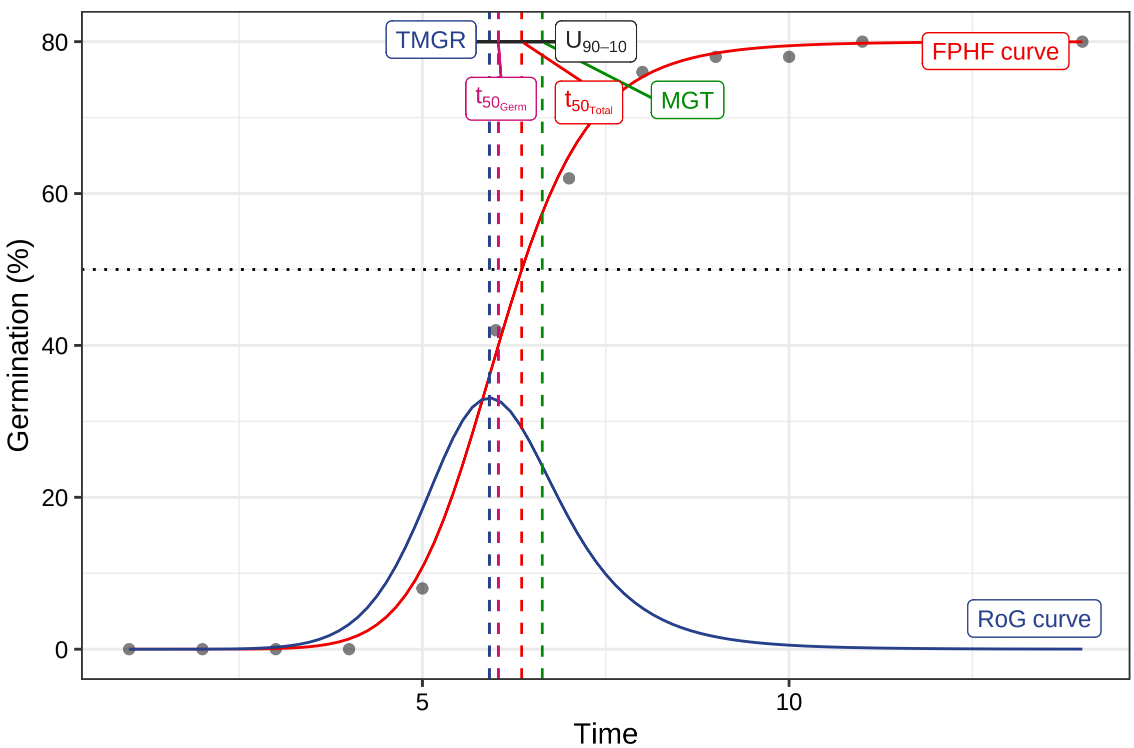



```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



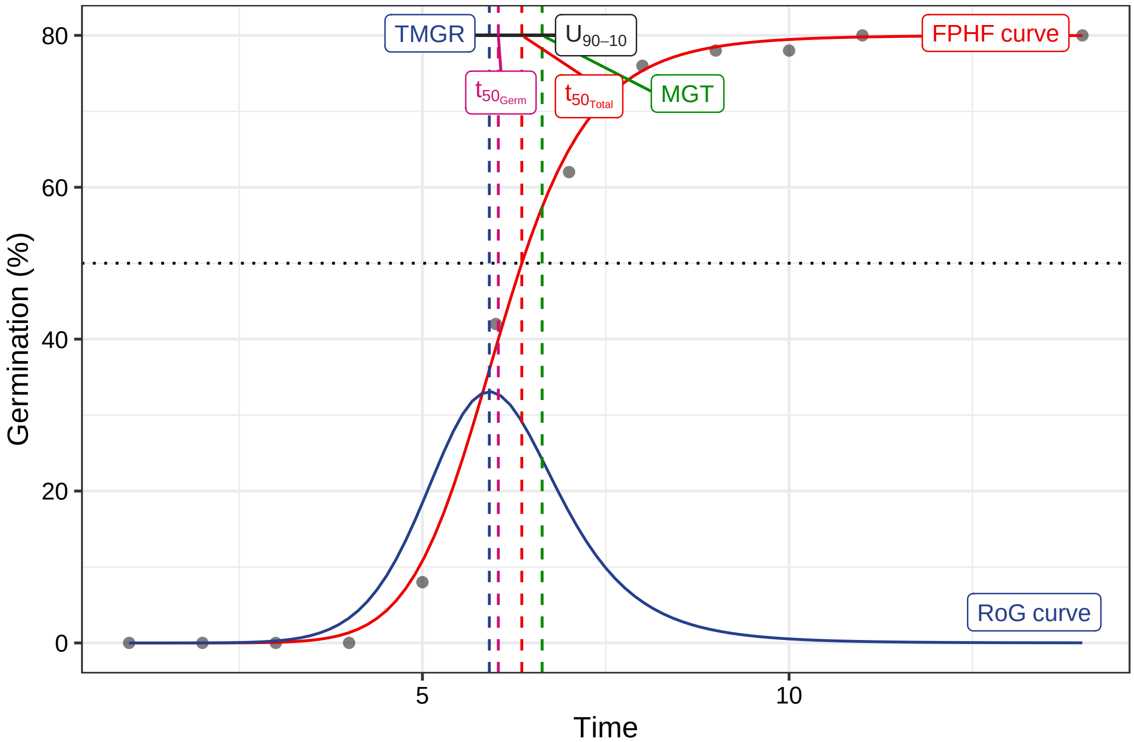

```r
# Without y axis limits adjustment
plot(fit1, limits = FALSE)
```

```
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.
```



```r
plot(fit2, limits = 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.
```



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
1       G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0
2       G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0
3       G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0
4       G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0
5       G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1
```

```
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0
   Day14 Total Seeds GermPercent PeakGermPercent FirstGermTime LastGermTime PeakGermTime
1      0          50    80.00000        34.00000             5           11            6
2      0          51    82.35294        29.41176             4           12            6
3      0          48    93.75000        37.50000             4           12            6
4      0          51    90.19608        37.25490             5           12            6
5      0          50    96.00000        40.00000             5           13            6
6      0          49    93.87755        42.85714             5           12            6
7      0          48    87.50000        37.50000             5           11            6
8      0          47    85.10638        29.78723             4           12            6
9      0          52    86.53846        36.53846             4           12            6
10     0          50    90.00000        36.00000             5           12            6
11     0          51    94.11765        41.17647             5           13            6
12     0          51    86.27451        39.21569             5           12            6
13     0          49    95.91837        38.77551             5           13            6
14     0          48    91.66667        43.75000             5           12            6
15     0          48    87.50000        35.41667             5           11            6
   TimeSpreadGerm t50_Coolbear t50_Farooq MeanGermTime VarGermTime SEGermTime CVGermTime
1               6     5.970588   5.941176     6.700000    1.446154  0.1901416  0.1794868
2               8     6.192308   6.153846     6.857143    2.027875  0.2197333  0.2076717
3               8     6.333333   5.972222     6.866667    2.572727  0.2391061  0.2335882
4               7     6.041667   6.225806     6.891304    2.187923  0.2180907  0.2146419
5               8     5.975000   5.950000     6.812500    2.368351  0.2221275  0.2259002
6               7     5.976190   5.952381     6.869565    2.071498  0.2122088  0.2095140
7               6     5.972222   5.944444     6.690476    1.389663  0.1818989  0.1761967
8               8     6.208333   6.166667     6.875000    2.112179  0.2297923  0.2113940
9               8     6.310345   5.973684     6.866667    2.300000  0.2260777  0.2208604
10              7     6.076923   6.038462     6.822222    1.831313  0.2017321  0.1983606
11              8     5.928571   5.904762     6.791667    2.381206  0.2227295  0.2272072
12              7     5.975000   5.950000     6.886364    2.149577  0.2210295  0.2129053
13              8     6.083333   6.041667     6.936170    2.539315  0.2324392  0.2297410
14              7     5.928571   5.904762     6.772727    1.900634  0.2078370  0.2035568
15              6     6.050000   6.259259     6.809524    1.670151  0.1994129  0.1897847
   MeanGermRate  VarGermRate  SEGermRate      CVG GermRateRecip_Coolbear GermRateRecip_Farooq
1     0.1492537 0.0007176543 0.004235724 14.92537              0.1674877            0.1683168
2     0.1458333 0.0009172090 0.004673148 14.58333              0.1614907            0.1625000
3     0.1456311 0.0011572039 0.005071059 14.56311              0.1578947            0.1674419
4     0.1451104 0.0009701218 0.004592342 14.51104              0.1655172            0.1606218
5     0.1467890 0.0010995627 0.004786184 14.67890              0.1673640            0.1680672
6     0.1455696 0.0009301809 0.004496813 14.55696              0.1673307            0.1680000
7     0.1494662 0.0006935558 0.004063648 14.94662              0.1674419            0.1682243
8     0.1454545 0.0009454531 0.004861721 14.54545              0.1610738            0.1621622
9     0.1456311 0.0010345321 0.004794747 14.56311              0.1584699            0.1674009
10    0.1465798 0.0008453940 0.004334343 14.65798              0.1645570            0.1656051
11    0.1472393 0.0011191581 0.004828643 14.72393              0.1686747            0.1693548
```

```
12    0.1452145 0.0009558577 0.004660905 14.52145            0.1673640            0.1680672
13    0.1441718 0.0010970785 0.004831366 14.41718            0.1643836            0.1655172
14    0.1476510 0.0009033254 0.004531018 14.76510            0.1686747            0.1693548
15    0.1468531 0.0007767634 0.004300508 14.68531            0.1652893            0.1597633
   GermSpeed_Count GermSpeed_Percent GermSpeedAccumulated_Count GermSpeedAccumulated_Percent
1         6.138925          12.27785                   34.61567                     69.23134
2         6.362698          12.47588                   35.54058                     69.68741
3         6.882179          14.33787                   38.29725                     79.78594
4         6.927417          13.58317                   38.68453                     75.85202
5         7.318987          14.63797                   41.00786                     82.01571
6         6.931782          14.14649                   38.77620                     79.13509
7         6.448449          13.43427                   36.38546                     75.80304
8         6.053175          12.87909                   33.77079                     71.85275
9         6.830592          13.13575                   38.11511                     73.29829
10        6.812698          13.62540                   38.19527                     76.39054
11        7.342796          14.39764                   41.17452                     80.73436
12        6.622258          12.98482                   37.00640                     72.56158
13        7.052320          14.39249                   39.29399                     80.19182
14        6.706782          13.97246                   37.69490                     78.53103
15        6.363925          13.25818                   35.69697                     74.36868
   GermSpeedCorrected_Normal GermSpeedCorrected_Accumulated WeightGermPercent MeanGermPercent
1                  0.1534731                      0.8653917          47.42857        5.714286
2                  0.1514928                      0.8462043          47.89916        5.882353
3                  0.1529373                      0.8510501          54.46429        6.696429
4                  0.1505960                      0.8409680          52.24090        6.442577
5                  0.1524789                      0.8543303          56.14286        6.857143
6                  0.1506909                      0.8429608          54.51895        6.705539
7                  0.1535345                      0.8663205          51.93452        6.250000
8                  0.1513294                      0.8442698          49.39210        6.079027
9                  0.1517909                      0.8470024          50.27473        6.181319
10                 0.1513933                      0.8487837          52.57143        6.428571
11                 0.1529749                      0.8578026          55.18207        6.722689
12                 0.1505059                      0.8410547          50.00000        6.162465
13                 0.1500494                      0.8360424          55.24781        6.851312
14                 0.1524269                      0.8567022          53.86905        6.547619
15                 0.1515220                      0.8499278          51.19048        6.250000
   MeanGermNumber TimsonsIndex TimsonsIndex_Labouriau TimsonsIndex_KhanUngar GermRateGeorge
1        2.857143     8.000000                   1.00              0.5714286              4
2        3.000000     9.803922                   1.25              0.7002801              5
3        3.214286    14.583333                   1.40              1.0416667              7
4        3.285714     7.843137                   1.00              0.5602241              4
5        3.428571    10.000000                   1.00              0.7142857              5
6        3.285714     6.122449                   1.00              0.4373178              3
7        3.000000     8.333333                   1.00              0.5952381              4
8        2.857143    10.638298                   1.25              0.7598784              5
9        3.214286     9.615385                   1.25              0.6868132              5
10       3.214286     8.000000                   1.00              0.5714286              4
11       3.428571     9.803922                   1.00              0.7002801              5
12       3.142857     5.882353                   1.00              0.4201681              3
13       3.357143     8.163265                   1.00              0.5830904              4
14       3.142857     6.250000                   1.00              0.4464286              3
15       3.000000     8.333333                   1.00              0.5952381              4
   GermIndex GermIndex_mod EmergenceRateIndex_SG EmergenceRateIndex_SG_mod
1   5.840000      7.300000                   292                  7.300000
```

```
2   5.882353      7.142857                     300                  7.142857
3   6.687500      7.133333                     321                  7.133333
4   6.411765      7.108696                     327                  7.108696
5   6.900000      7.187500                     345                  7.187500
6   6.693878      7.130435                     328                  7.130435
7   6.395833      7.309524                     307                  7.309524
8   6.063830      7.125000                     285                  7.125000
9   6.173077      7.133333                     321                  7.133333
10  6.460000      7.177778                     323                  7.177778
11  6.784314      7.208333                     346                  7.208333
12  6.137255      7.113636                     313                  7.113636
13  6.775510      7.063830                     332                  7.063830
14  6.625000      7.227273                     318                  7.227273
15  6.291667      7.190476                     302                  7.190476
   EmergenceRateIndex_BilbroWanjura EmergenceRateIndex_Fakorede PeakValue GermValue_Czabator
1                          5.970149                    8.375000  9.500000          54.28571
2                          6.125000                    8.326531  9.313725          54.78662
3                          6.553398                    7.324444 10.416667          69.75446
4                          6.675079                    7.640359 10.049020          64.74158
5                          7.045872                    7.096354 11.250000          77.14286
6                          6.696203                    7.317580 10.714286          71.84506
7                          6.277580                    7.646259 10.416667          65.10417
8                          5.818182                    8.078125  9.574468          58.20345
9                          6.553398                    7.934815  9.855769          60.92165
10                         6.596091                    7.580247 10.250000          65.89286
11                         7.067485                    7.216146 11.029412          74.14731
12                         6.389439                    7.981921  9.803922          60.41632
13                         6.776074                    7.231326 10.969388          75.15470
14                         6.496644                    7.388430 10.677083          69.90947
15                         6.167832                    7.782313 10.156250          63.47656
   GermValue_DP GermValue_Czabator_mod GermValue_DP_mod    CUGerm GermSynchrony GermUncertainty
1      57.93890               54.28571         39.56076 0.7092199     0.2666667        2.062987
2      52.58713               54.78662         40.99260 0.5051546     0.2346109        2.321514
3      68.62289               69.75446         53.42809 0.3975265     0.2242424        2.462012
4      70.43331               64.74158         48.86825 0.4672113     0.2502415        2.279215
5      80.16914               77.14286         56.23935 0.4312184     0.2606383        2.146051
6      76.51983               71.84506         53.06435 0.4934701     0.2792271        2.160545
7      69.41325               65.10417         47.37690 0.7371500     0.2729384        2.040796
8      56.00669               58.20345         43.67948 0.4855842     0.2256410        2.357249
9      58.13477               60.92165         45.30801 0.4446640     0.2494949        2.321080
10     70.91875               65.89286         49.10820 0.5584666     0.2555556        2.187983
11     77.39782               74.14731         54.27520 0.4288905     0.2686170        2.128670
12     64.44988               60.41632         44.71582 0.4760266     0.2737844        2.185245
13     78.16335               75.15470         54.94192 0.4023679     0.2506938        2.241181
14     74.40140               69.90947         51.41913 0.5383760     0.2991543        2.037680
15     67.62031               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.

```r
data(gcdata)

counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
                          "Day06", "Day07", "Day08", "Day09", "Day10",
```

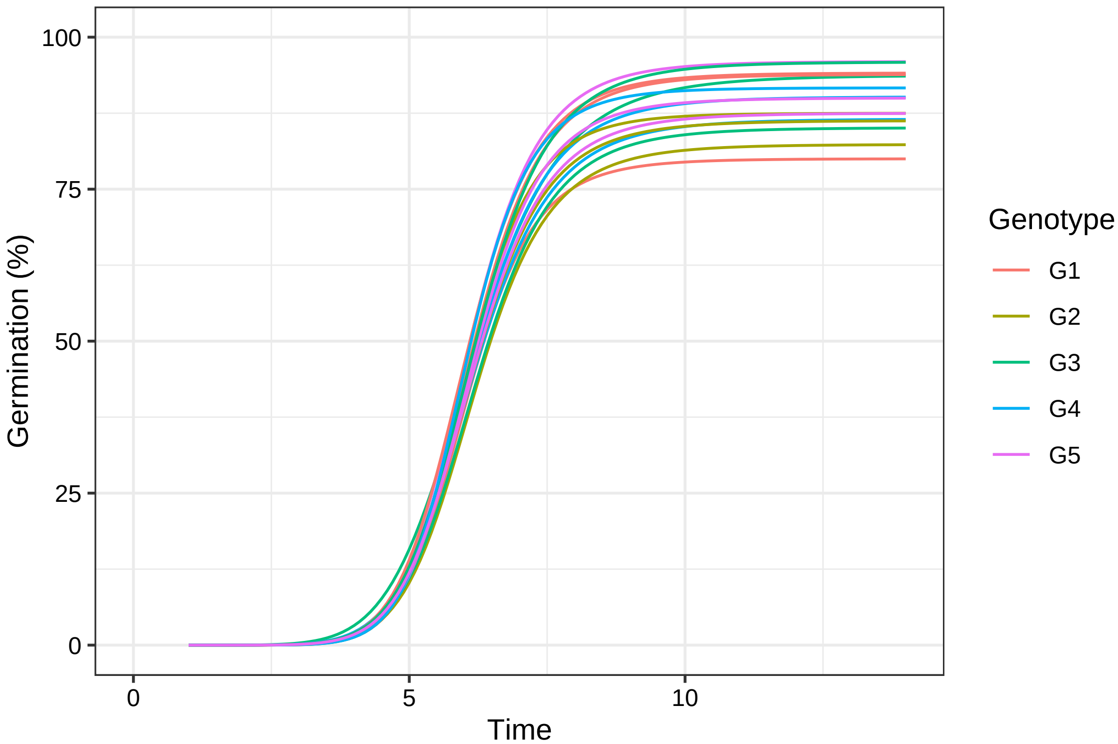
```r
                          "Day11", "Day12", "Day13", "Day14")

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
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0
2        G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0
4        G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0
5        G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0
   Day14 Total Seeds        a         b        c y0 lag   Dlag50 t50.total t10.total t60.total
1      0          50 80.00000  9.881937 6.034954  0   0 6.034954  6.355121  4.956264  6.744598
2      0          51 82.35294  9.227666 6.175193  0   0 6.175193  6.473490  4.983236  6.872603
3      0          48 93.75000  7.793051 6.138110  0   0 6.138110  6.244191  4.673022  6.608438
4      0          51 90.19608  8.925655 6.125173  0   0 6.125173  6.276794  4.850875  6.614968
5      0          50 96.00000  9.419181 6.049642  0   0 6.049642  6.103433  4.814125  6.386789
6      0          49 93.87755  9.450149 6.097415  0   0 6.097415  6.182279  4.868632  6.477599
7      0          48 87.50000 10.172459 6.029851  0   0 6.029851  6.202812  4.930422  6.510495
8      0          47 85.10638  8.940696 6.189774  0   0 6.189774  6.439510  4.940057  6.823299
9      0          52 86.53846  8.617391 6.125122  0   0 6.125122  6.352172  4.836658  6.733276
10     0          50 90.00000  9.608844 6.109504  0   0 6.109504  6.253043  4.920629  6.566506
11     0          51 94.11765  9.400212 6.018760  0   0 6.018760  6.099435  4.798627  6.391291
12     0          51 86.27451  9.162526 6.108452  0   0 6.108452  6.326184  4.893596  6.684526
13     0          49 95.91837  8.995210 6.149012  0   0 6.149012  6.207501  4.841308  6.509954
14     0          48 91.66667 10.391845 6.015910  0   0 6.015910  6.122389  4.915140  6.397491
15     0          48 87.50000  9.136744 6.121579  0   0 6.121579  6.317392  4.892502  6.667247
   t50.Germinated t10.Germinated t60.Germinated Uniformity_90 Uniformity_10 Uniformity     TMGR
1        6.034954       4.831807       6.287724      7.537690      4.831807   2.705882 5.912194
2        6.175193       4.866755       6.452582      7.835407      4.866755   2.968652 6.031282
3        6.138110       4.630062       6.465924      8.137342      4.630062   3.507280 5.938180
4        6.125173       4.788597       6.409838      7.834810      4.788597   3.046213 5.972686
5        6.049642       4.790946       6.315746      7.639028      4.790946   2.848083 5.914289
6        6.097415       4.832471       6.364722      7.693469      4.832471   2.860997 5.961879
7        6.029851       4.858476       6.275050      7.483643      4.858476   2.625166 5.914057
8        6.189774       4.841105       6.476945      7.914163      4.841105   3.073058 6.036192
9        6.125122       4.746573       6.420208      7.904041      4.746573   3.157468 5.961631
10       6.109504       4.860681       6.372823      7.679177      4.860681   2.818496 5.978115
11       6.018760       4.764246       6.284051      7.603611      4.764246   2.839365 5.883557
12       6.108452       4.806013       6.384836      7.763854      4.806013   2.957841 5.964080
13       6.149012       4.816393       6.432524      7.850345      4.816393   3.033952 5.998270
```

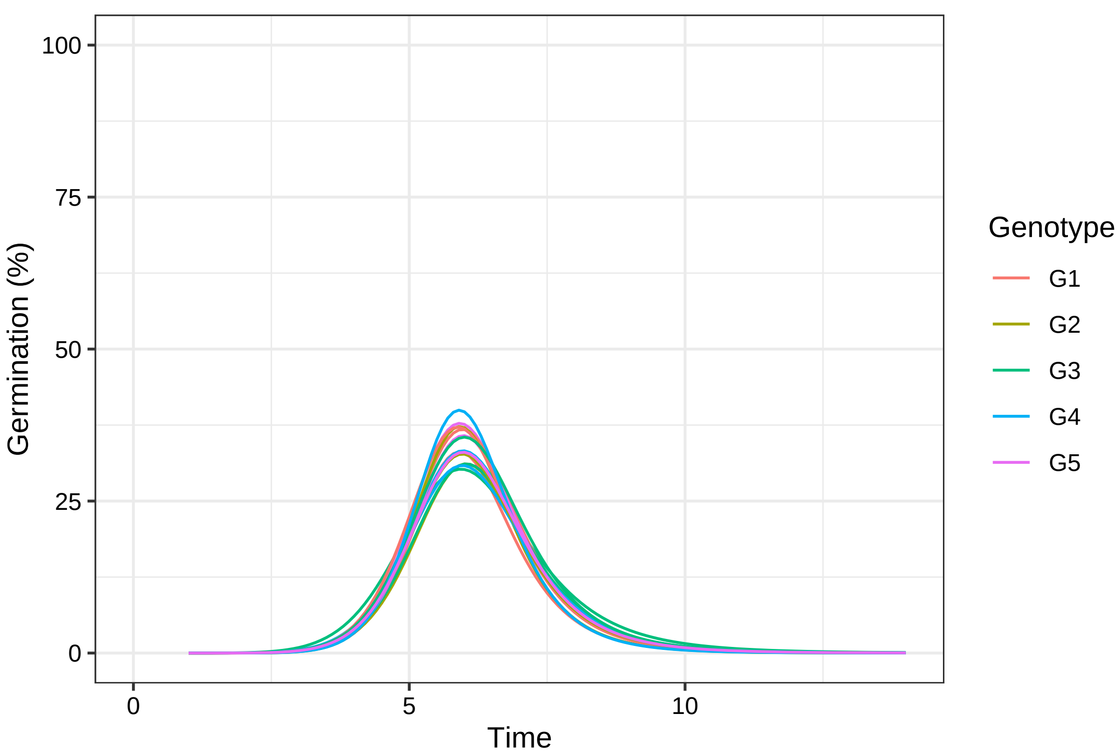
```
14       6.015910       4.869398       6.255276       7.432372       4.869398   2.562974 5.905180
15       6.121579       4.813083       6.399357       7.785806       4.813083   2.972723 5.976087
        AUC      MGT Skewness          msg    sigma       finTol    logLik      AIC      BIC
1  1108.976 6.632252 1.098973 #1. success  1.615220 7.105427e-14 -25.49868 56.99736 58.91453
2  1128.559 6.784407 1.098655 #1. success  1.115372 2.309264e-14 -20.31471 46.62943 48.54660
3  1283.693 6.772742 1.103392 #1. success  2.432704 9.947598e-14 -31.23213 68.46426 70.38143
4  1239.887 6.739666 1.100323 #1. success  2.396582 5.684342e-14 -31.02269 68.04538 69.96256
5  1328.328 6.654981 1.100062 #1. success  2.399662 1.094236e-12 -31.04067 68.08135 69.99852
6  1294.463 6.702473 1.099232 #1. success  3.034962 1.563194e-13 -34.32887 74.65774 76.57491
7  1213.908 6.622417 1.098272 #1. success  1.663019 1.421085e-13 -25.90697 57.81395 59.73112
8  1164.346 6.804000 1.099232 #1. success  1.120704 4.327205e-12 -20.38149 46.76298 48.68015
9  1188.793 6.745241 1.101242 #1. success  2.429960 7.958079e-13 -31.21633 68.43266 70.34984
10 1240.227 6.711900 1.098600 #1. success  1.686656 8.142820e-12 -26.10456 58.20911 60.12629
11 1305.200 6.624248 1.100600 #1. success  2.628113 1.989520e-13 -32.31381 70.62762 72.54479
12 1188.021 6.718639 1.099892 #1. success  2.878146 1.151079e-12 -33.58613 73.17227 75.08944
13 1316.407 6.762274 1.099733 #1. success  2.604588 2.984279e-13 -32.18793 70.37586 72.29303
14 1273.385 6.604967 1.097916 #1. success  2.764756 9.805490e-13 -33.02342 72.04684 73.96401
15 1203.664 6.732266 1.099760 #1. success  1.954008 8.739676e-13 -28.16444 62.32888 64.24606
    deviance df.residual nobs
1   31.30723          12   14
2   14.92865          12   14
3   71.01658          12   14
4   68.92324          12   14
5   69.10052          12   14
6  110.53195          12   14
7   33.18760          12   14
8   15.07174          12   14
9   70.85647          12   14
10  34.13771          12   14
11  82.88372          12   14
12  99.40469          12   14
13  81.40654          12   14
14  91.72652          12   14
15  45.81777          12   14
```

Multiple fitted curves generated in batch can also be plotted.

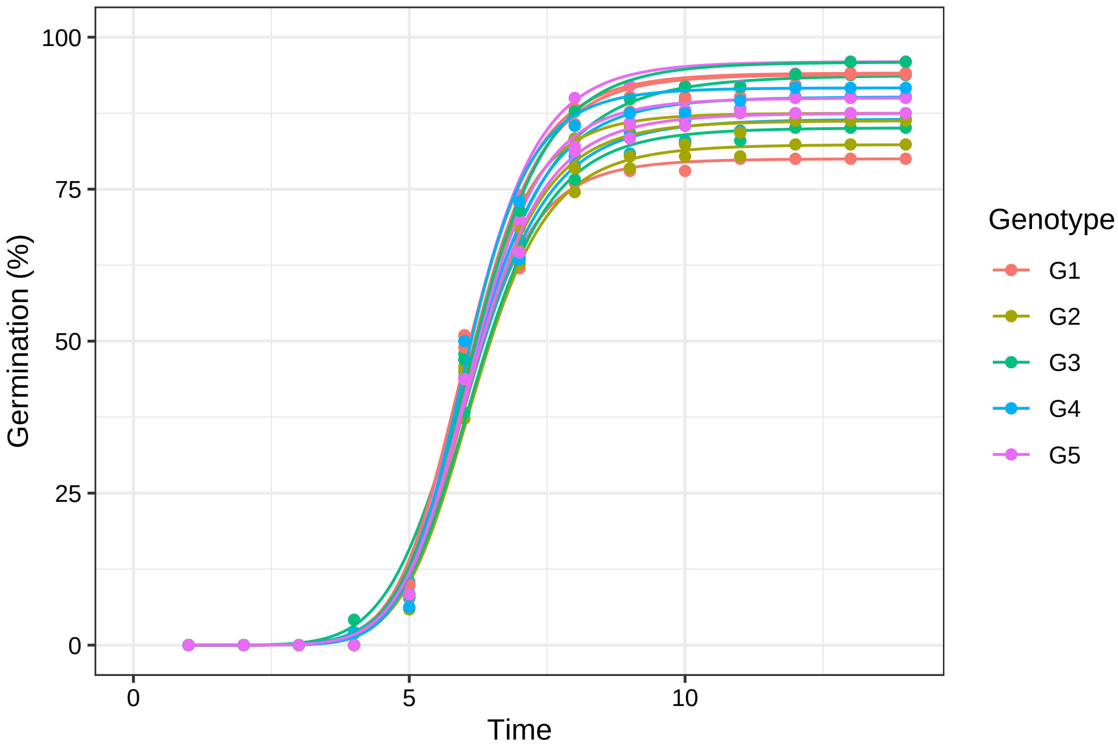
```r
data(gcdata)

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")
```



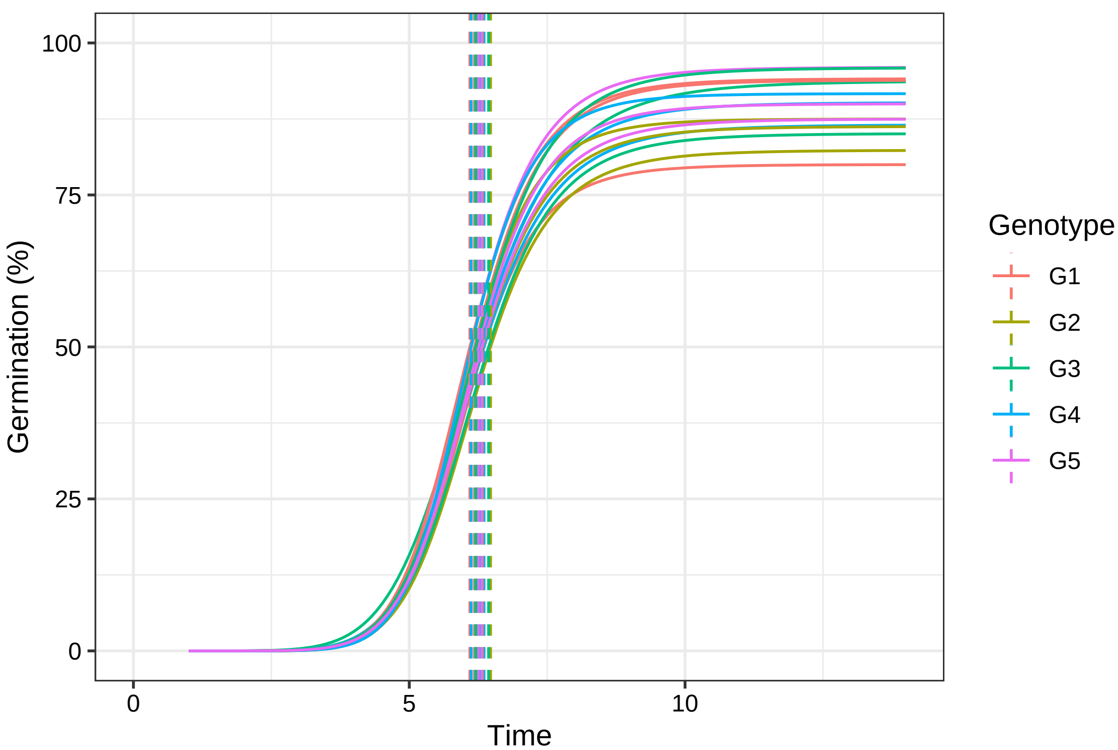

```r
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```



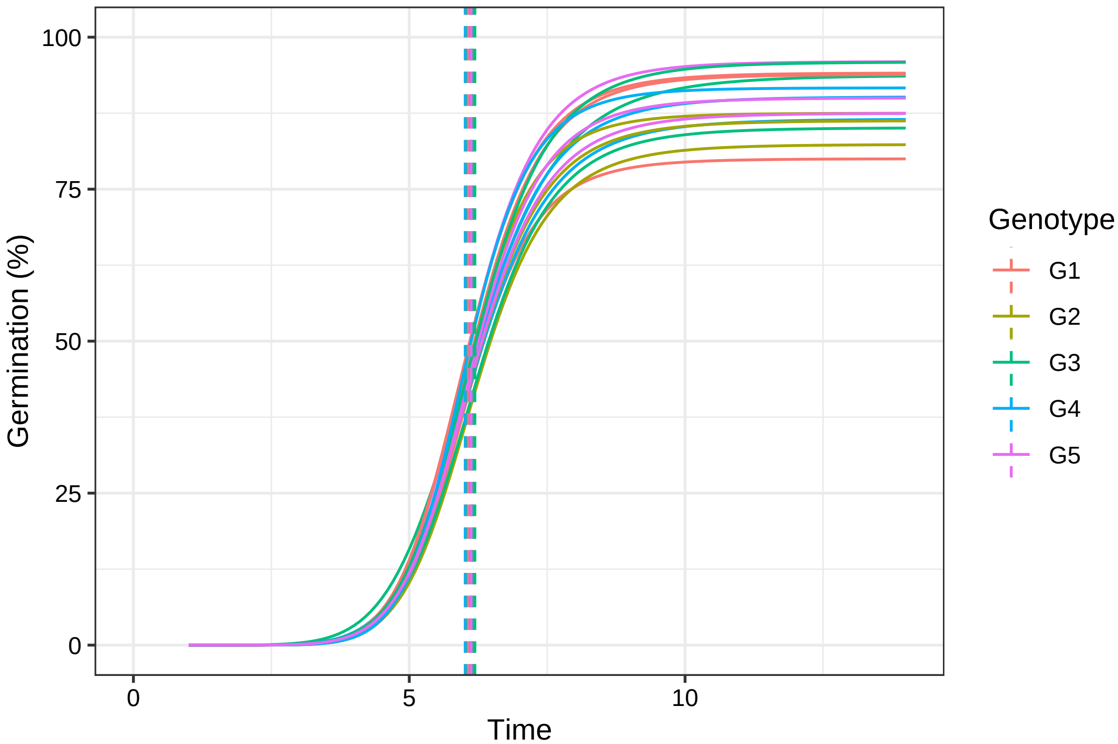

```r
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



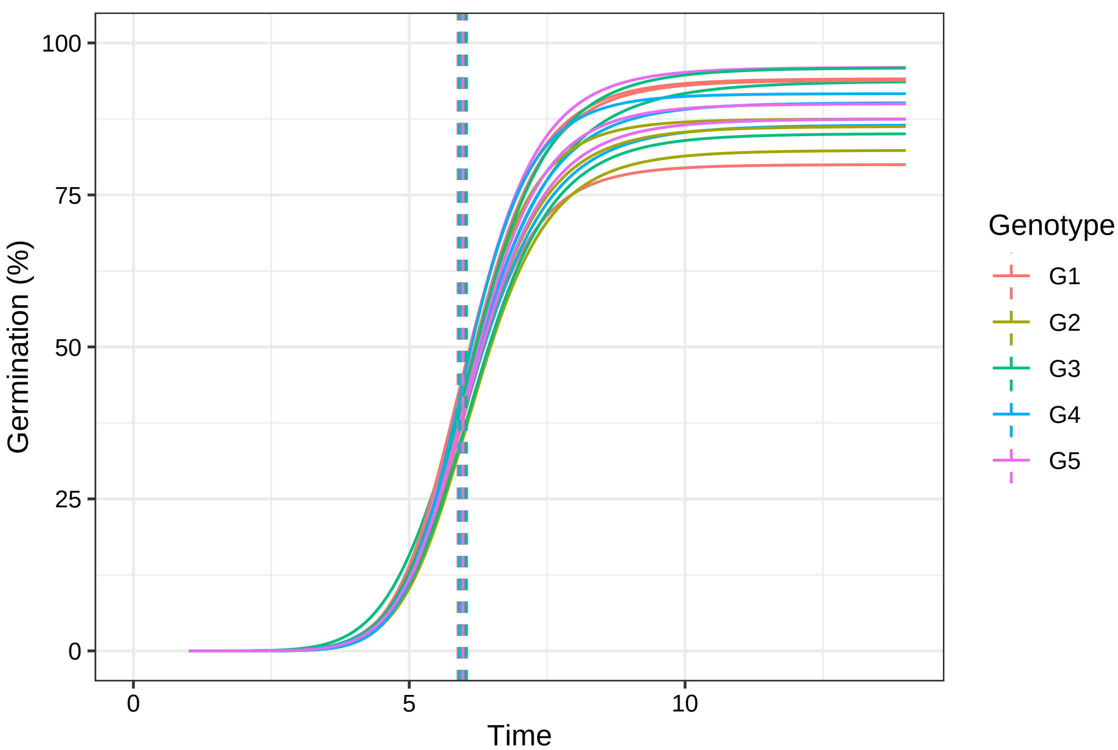

```r
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



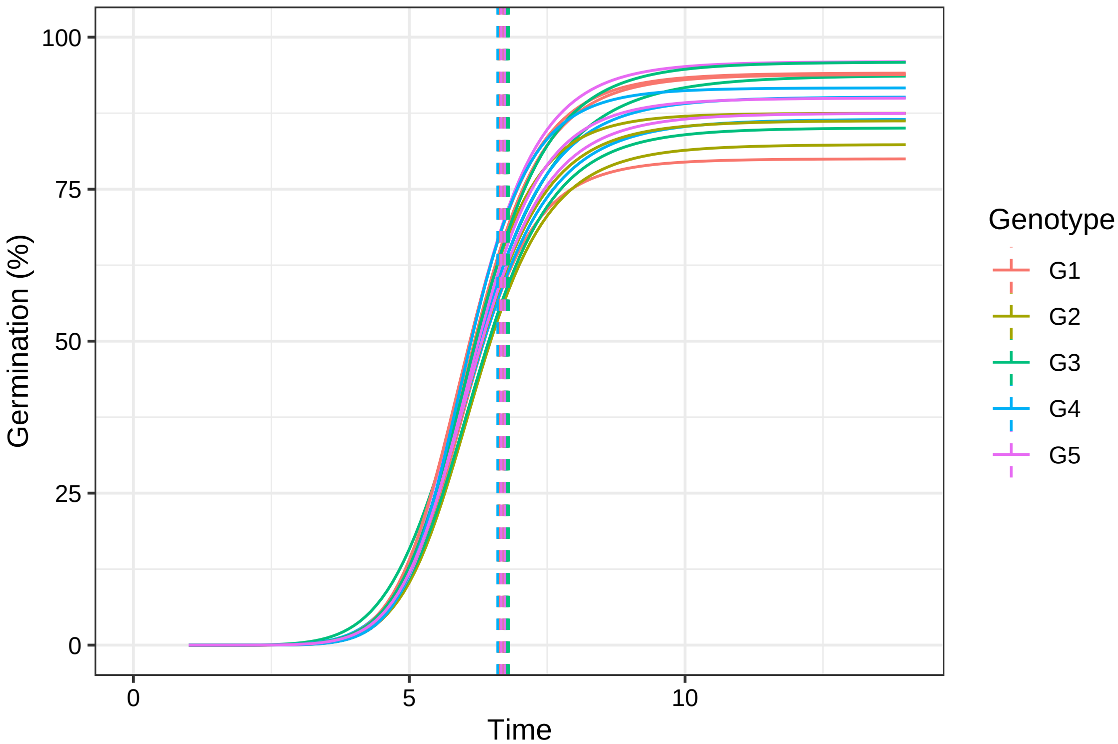

```r
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```



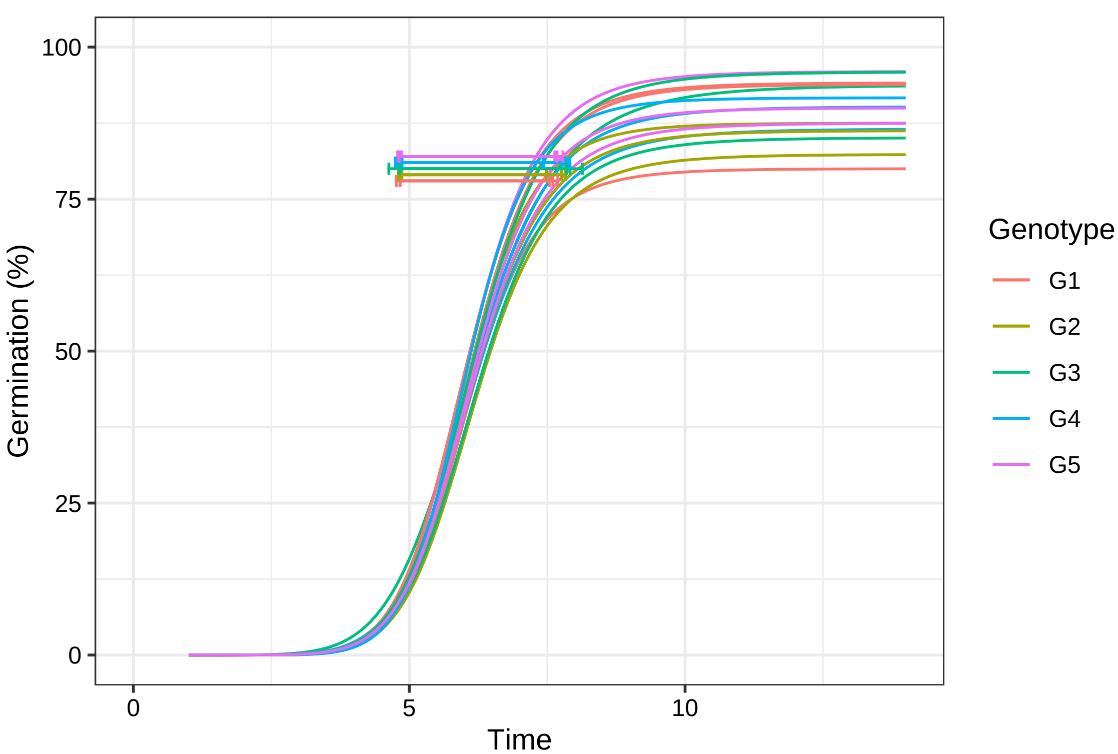

```r
plot(fits, group.col = "Genotype", annotate = "tmgr")
```



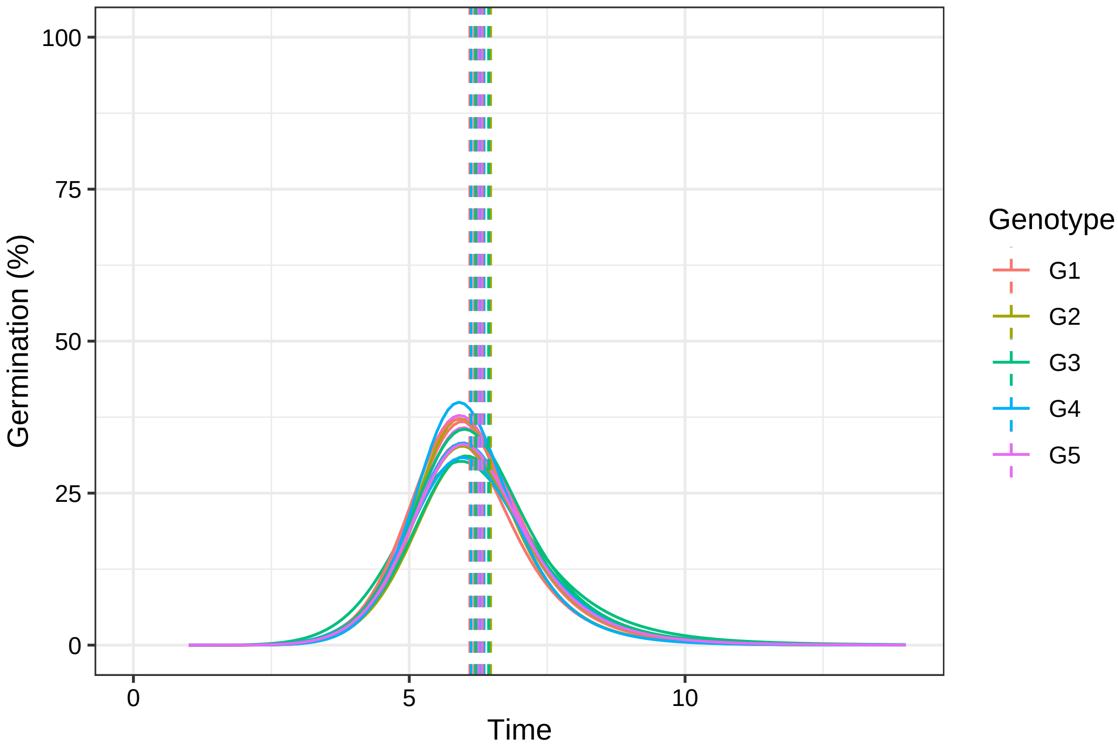

```r
plot(fits, group.col = "Genotype", annotate = "mgt")
```



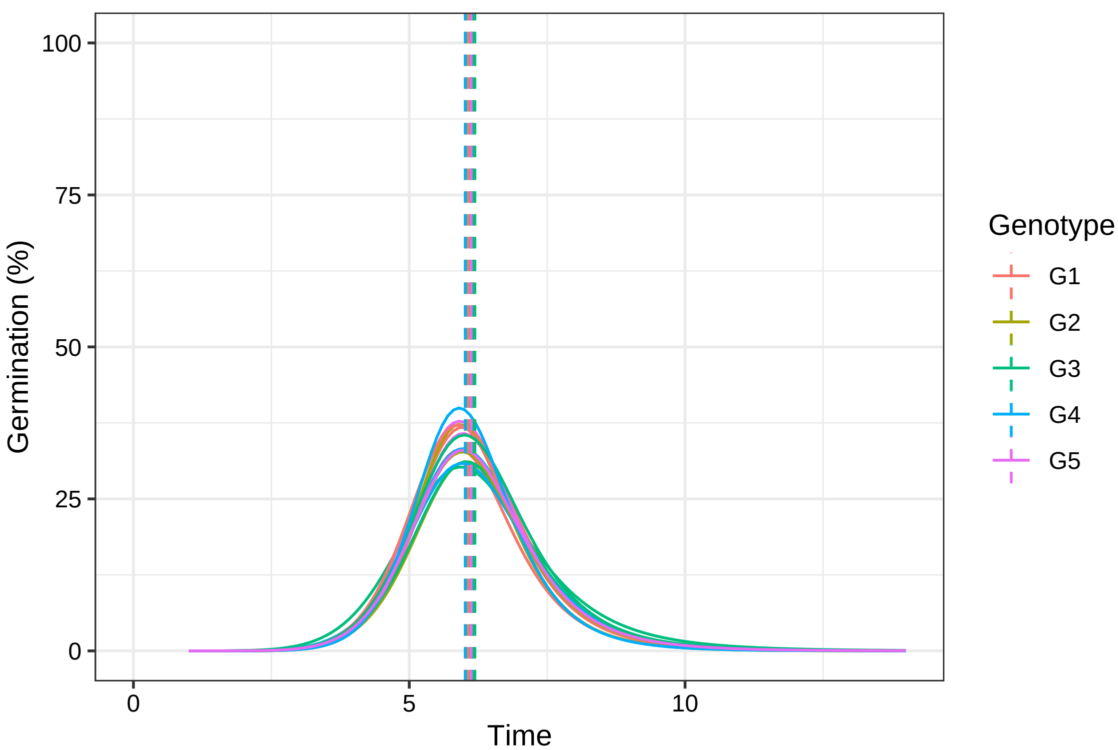

```r
plot(fits, group.col = "Genotype", annotate = "uniformity")
```



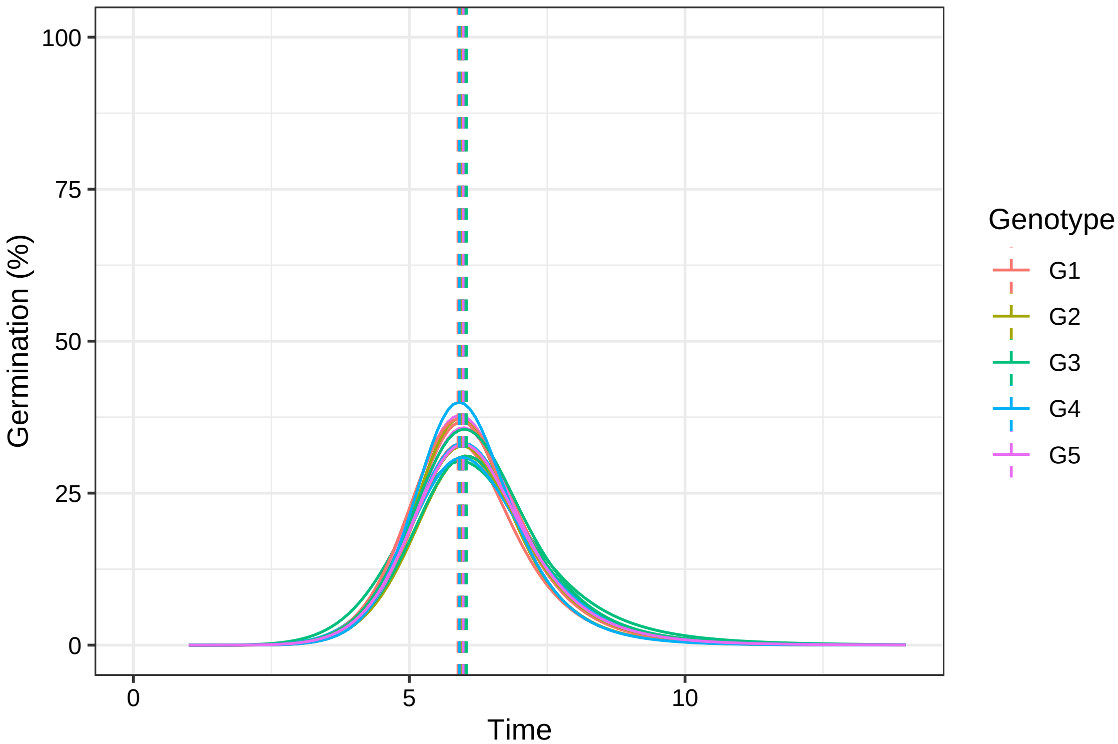

```r
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



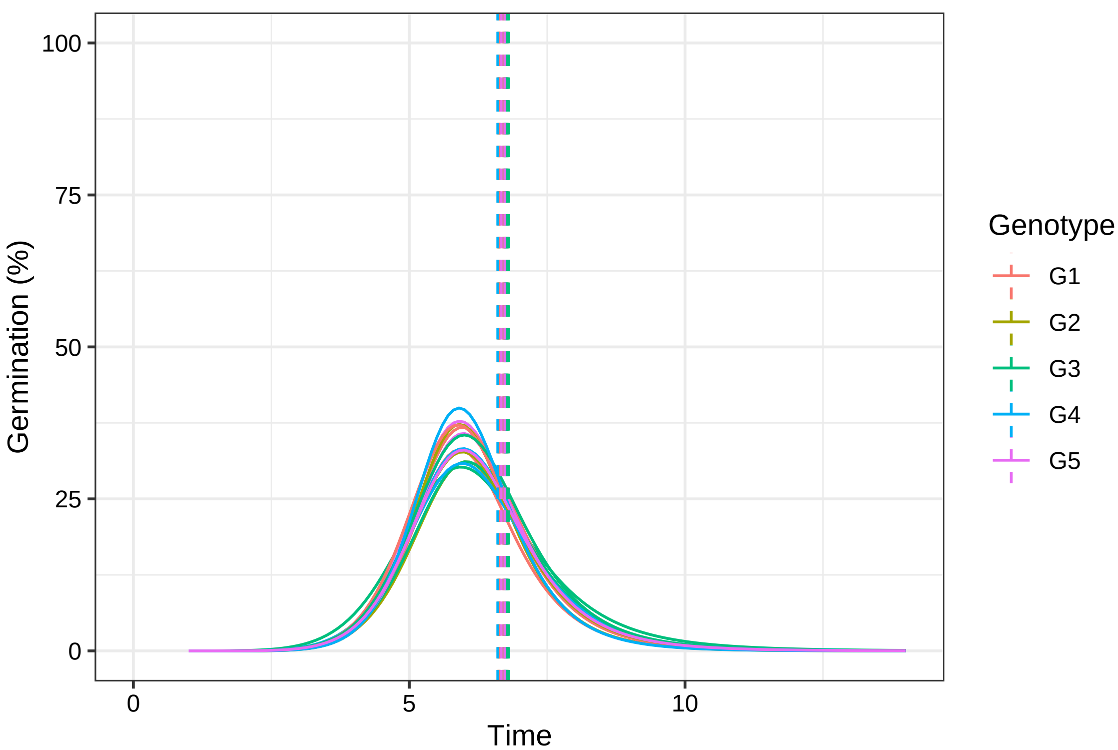

```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```



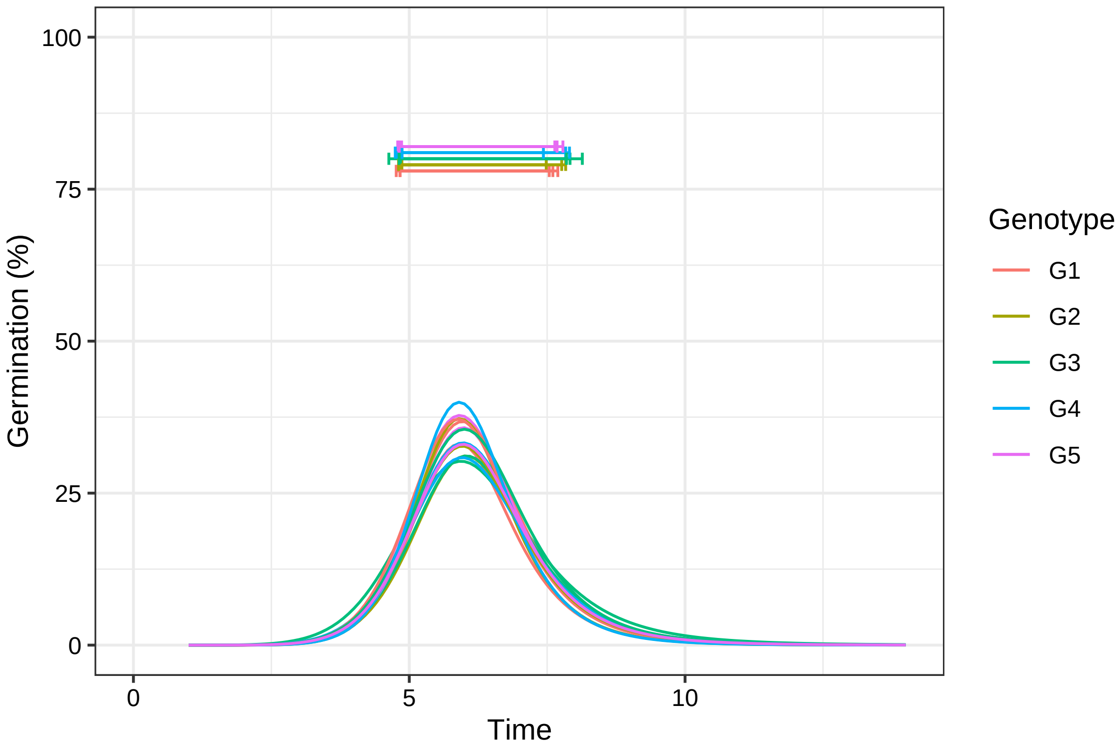

```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "tmgr")
```



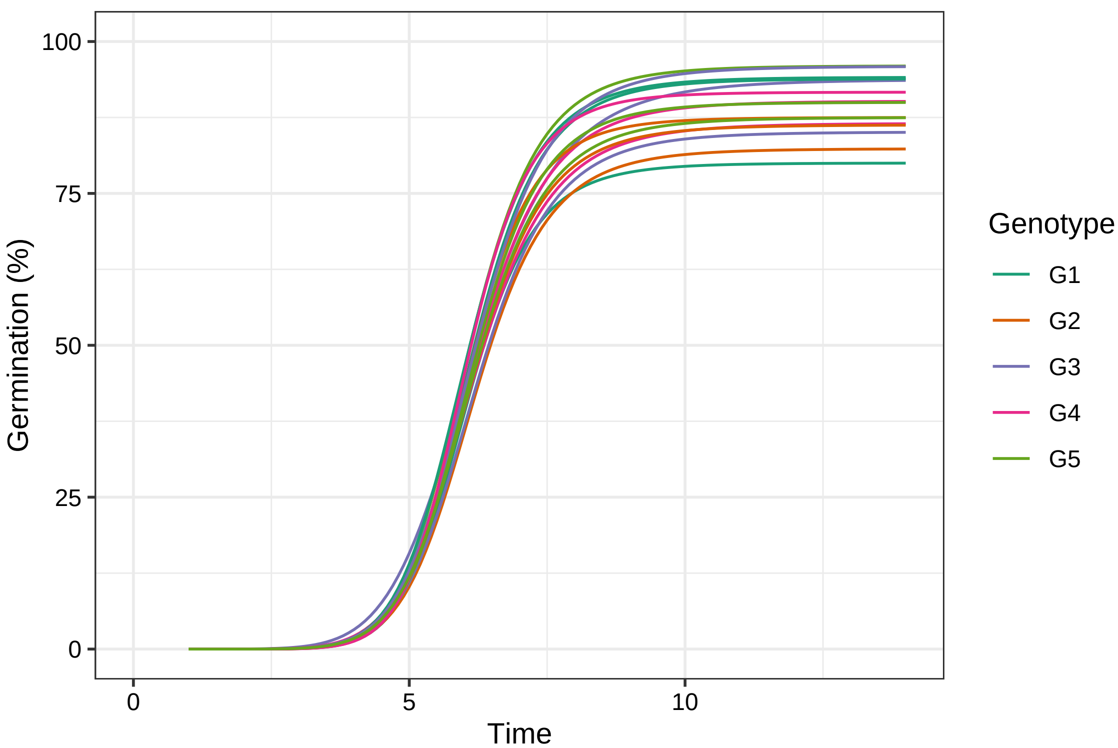

```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```



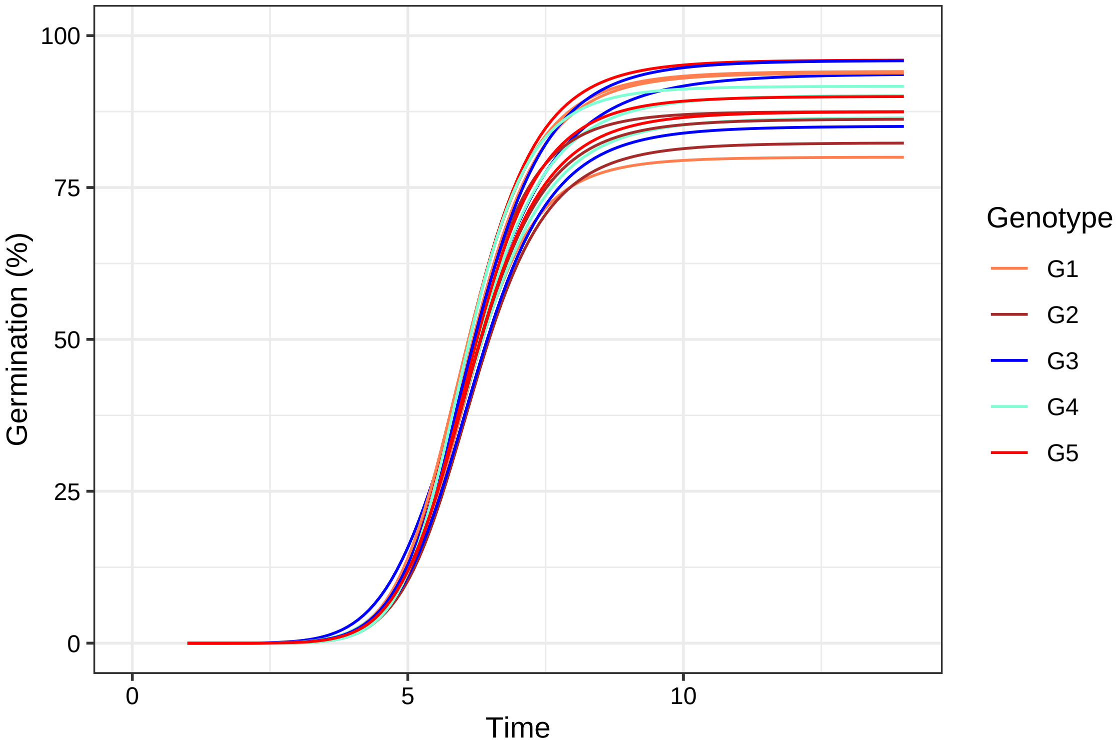

```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```




```
# 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")
```



```r
# 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
  (2025).  germinationmetrics: Seed Germination Indices and Curve Fitting. R package
  version 0.1.9.9000, https://github.com/aravind-j/germinationmetrics
  https://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 Srin
    note = {R package version 0.1.9.9000 https://aravind-j.github.io/germinationmetrics/ https://CRAN.R-
    year = {2025},
  }

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

Session Info

```r
sessionInfo()
```

```
R Under development (unstable) (2025-12-09 r89129 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 26200)

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
[4] LC_NUMERIC=C                   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_0.1.9.9000 ggplot2_4.0.1                 readxl_1.4.5
[4] RCurl_1.98-1.17               testthat_3.3.1

loaded via a namespace (and not attached):
 [1] gtable_0.3.6       xfun_0.55          devtools_2.4.6     remotes_2.5.0.9000
 [5] processx_3.8.6     ggrepel_0.9.6      rJava_1.0-11       lattice_0.22-7
 [9] callr_3.7.6        mathjaxr_2.0-0     bitops_1.0-9       vctrs_0.6.5
[13] tools_4.6.0        Rdpack_2.6.4       ps_1.9.1           generics_0.1.4
[17] stats4_4.6.0       curl_7.0.0         parallel_4.6.0     tibble_3.3.0
[21] pkgconfig_2.0.3    gslnls_1.4.2       Matrix_1.7-4       data.table_1.17.8
[25] RColorBrewer_1.1-3 S7_0.2.1           desc_1.4.3         lifecycle_1.0.4
[29] compiler_4.6.0     farver_2.1.2       stringr_1.6.0      brio_1.1.5
[33] tinytex_0.58       htmltools_0.5.9    usethis_3.2.1      yaml_2.3.12
[37] pillar_1.11.1      tidyr_1.3.2        ellipsis_0.3.2     rsconnect_1.7.0
[41] cachem_1.1.0       sessioninfo_1.2.3  tidyselect_1.2.1   digest_0.6.39
[45] stringi_1.8.7      reshape2_1.4.5     pander_0.6.6       dplyr_1.1.4
[49] purrr_1.2.0        labeling_0.4.3     rprojroot_2.1.1    fastmap_1.2.0
[53] grid_4.6.0         cli_3.6.5          magrittr_2.0.4     XML_3.99-0.20
[57] dichromat_2.0-0.1  pkgbuild_1.4.8     broom_1.0.11       withr_3.0.2
[61] scales_1.4.0       backports_1.5.0    httr_1.4.7         roxygen2_7.3.3
[65] rmarkdown_2.30     cellranger_1.1.0   memoise_2.0.1      evaluate_1.0.5
[69] knitr_1.50         rbibutils_2.4      rlang_1.1.6        Rcpp_1.1.0.8.1
[73] glue_1.8.0         xml2_1.5.1         pkgload_1.4.1      rstudioapi_0.17.1
[77] R6_2.6.1           plyr_1.8.9         fs_1.6.6
```

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