The `germinationmetrics` Package: A Brief Introduction

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Contents

Overview

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

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

Installation

The package can be installed using the following functions:

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

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

Then the package can be loaded using the function

```
library(germinationmetrics)
```

Version History

The current version of the package is 0.1.8. The previous versions are as follows.

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

Version	Date
0.1.0	2018-04-17
0.1.1	2018-07-26
0.1.1.1	2018-10-16
0.1.2	2018-10-31
0.1.3	2019-01-19
0.1.4	2020-06-16
0.1.5	2021-02-17
0.1.6	2022-06-15

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).

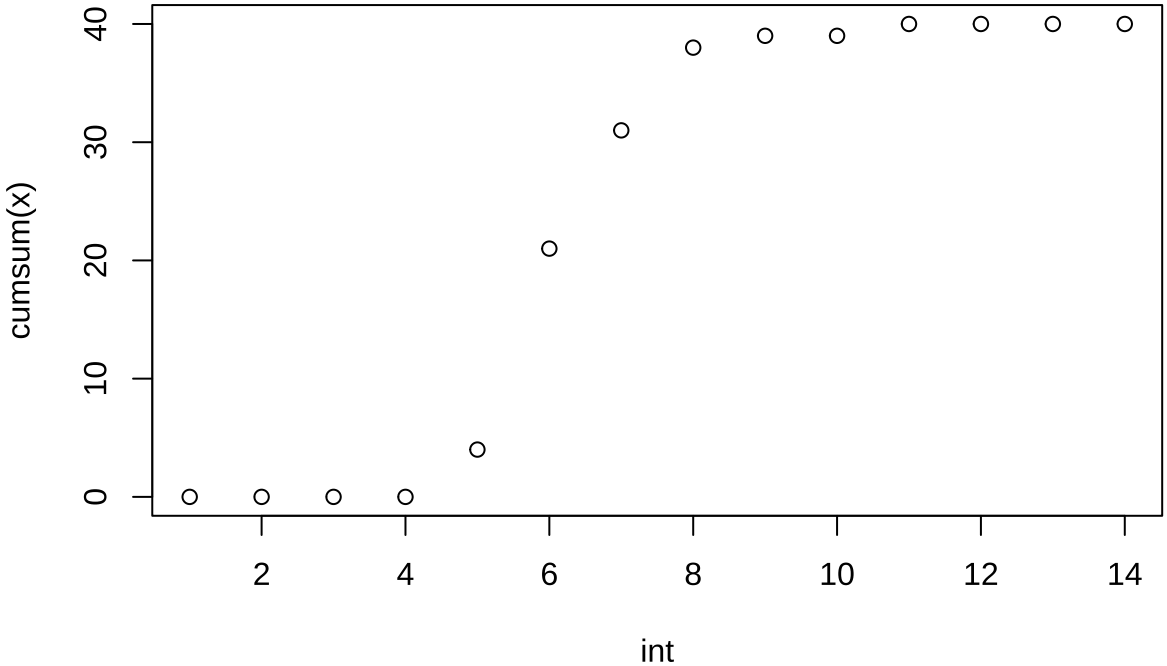
Table 2 : A typical germination count data.

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
```

```r
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 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	`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 germination rate index	`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.	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)
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)

Germination index	Function	Details	Unit	Measures	Reference
Timson's index [$\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$] or Germination energy index (GEI)	`TimsonsIndex`	It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time and is estimated in terms of cumulative germination percentage (G_i) as follows. $$\Sigma k = \sum_{i=1}^{k} G_i$$ Where, G_i is the cumulative germination percentage in time interval i, and k is the total number of time intervals. It also estimated in terms of partial germination percentage as follows. $$\Sigma k = \sum_{i=1}^{k} g_i(k-j)$$ Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to k), k is the total number of time intervals, and $j = i - 1$.	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)
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	Function	Details	Unit	Measures	Reference
Germination Index (GI) (Melville)	`GermIndex`	It is estimated as follows. $GI = \sum_{i=1}^{k} \frac{\lvert (T_k - T_i)\, N_i \rvert}{N_t}$ Where, T_i is the time from the start of the experiment to the ith interval (day for the example), N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), N_t is the total number of seeds used in the test, and k is the total number of time intervals.	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)
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)

Germination index	Function	Details	Unit	Measures	Reference
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 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 index	Function	Details	Unit	Measures	Reference
Germination value (GV) (Diavanshir and Pourbiek)	`GermValue`	It is computed as follows. $GV = \frac{\sum DGS}{N} \times GP \times c$ 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)
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)

Germination index	Function	Details	Unit	Measures	Reference
Synchrony of germination (Z index)	`GermSynchrony`	It is computed as follows. $$Z = \frac{\sum_{i=1}^{k} C_{N_i,2}}{C_{\Sigma N_i,2}}$$ Where, $C_{N_i,2}$ is the partial combination of the two germinated seeds from among N_i, the number of seeds germinated on the ith time 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 germinati
```

```
[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 g
```

```
[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)

# From partial germination counts
```

```r
#----------------------------------------------------------------------------
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 germi
```

```
[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)
```

```r
# 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
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.1534731
```

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

```
[1] 0.8653917
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

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

WeightGermPercent()

```
[1] 47.42857
```

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

```
[1] 47.42857
```

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

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

MeanGermPercent(), MeanGermNumber()

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```r
# 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)
```

```r
# 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)
```

EmergenceRateIndex()

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

```r
EmergenceRateIndex(germ.counts = x, intervals = int,
                   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, partial = FALSE)
```

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

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

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

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

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

$testend
[1] 16
```

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

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

[[2]]
```

```
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
1            0         1                      0                     0.0 0.000000
2            0         2                      0                     0.0 0.000000
3           34         3                     34                    17.0 5.666667
4           40         4                     74                    37.0 9.250000
5           21         5                     95                    47.5 9.500000
6           10         6                    105                    52.5 8.750000
7            4         7                    109                    54.5 7.785714
8            5         8                    114                    57.0 7.125000
9            3         9                    117                    58.5 6.500000
10           5        10                    122                    61.0 6.100000
11           8        11                    130                    65.0 5.909091
12           7        12                    137                    68.5 5.708333
13           7        13                    144                    72.0 5.538462
14           6        14                    150                    75.0 5.357143
15           6        15                    156                    78.0 5.200000
16           4        16                    160                    80.0 5.000000
17           0        17                    160                    80.0 4.705882
18           2        18                    162                    81.0 4.500000
19           0        19                    162                    81.0 4.263158
20           2        20                    164                    82.0 4.100000
```

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

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

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

$testend
[1] 16
```

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

```
[1] 9.5
```

```r
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
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS SumDGSbyN        GV
3           34         3                     34                    17.0 5.666667  5.666667  9.633333
4           40         4                     74                    37.0 9.250000  7.458333 27.595833
5           21         5                     95                    47.5 9.500000  8.138889 38.659722
6           10         6                    105                    52.5 8.750000  8.291667 43.531250
7            4         7                    109                    54.5 7.785714  8.190476 44.638095
8            5         8                    114                    57.0 7.125000  8.012897 45.673512
9            3         9                    117                    58.5 6.500000  7.796769 45.611097
10           5        10                    122                    61.0 6.100000  7.584673 46.266503
11           8        11                    130                    65.0 5.909091  7.398497 48.090230
12           7        12                    137                    68.5 5.708333  7.229481 49.521942
13           7        13                    144                    72.0 5.538462  7.075752 50.945411
14           6        14                    150                    75.0 5.357143  6.932534 51.994006
15           6        15                    156                    78.0 5.200000  6.799262 53.034246
```

```
16            4        16                     160                      80.0 5.000000  6.670744 53.365948
17            0        17                     160                      80.0 4.705882  6.539753 52.318022
18            2        18                     162                      81.0 4.500000  6.412268 51.939373
19            0        19                     162                      81.0 4.263158  6.285850 50.915385
20            2        20                     164                      82.0 4.100000  6.164414 50.548194

$testend
[1] 16
```

```r
GermValue(germ.counts = 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
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS SumDGSbyN        GV
1            0         1                      0                     0.0 0.000000  0.000000  0.000000
2            0         2                      0                     0.0 0.000000  0.000000  0.000000
3           34         3                     34                    17.0 5.666667  1.888889  3.211111
4           40         4                     74                    37.0 9.250000  3.729167 13.797917
5           21         5                     95                    47.5 9.500000  4.883333 23.195833
6           10         6                    105                    52.5 8.750000  5.527778 29.020833
7            4         7                    109                    54.5 7.785714  5.850340 31.884354
8            5         8                    114                    57.0 7.125000  6.009673 34.255134
9            3         9                    117                    58.5 6.500000  6.064153 35.475298
```

```
10          5        10                    122                     61.0 6.100000  6.067738 37.013202
11          8        11                    130                     65.0 5.909091  6.053316 39.346552
12          7        12                    137                     68.5 5.708333  6.024567 41.268285
13          7        13                    144                     72.0 5.538462  5.987174 43.107655
14          6        14                    150                     75.0 5.357143  5.942172 44.566291
15          6        15                    156                     78.0 5.200000  5.892694 45.963013
16          4        16                    160                     80.0 5.000000  5.836901 46.695205
17          0        17                    160                     80.0 4.705882  5.770370 46.162961
18          2        18                    162                     81.0 4.500000  5.699794 46.168331
19          0        19                    162                     81.0 4.263158  5.624182 45.555871
20          2        20                    164                     82.0 4.100000  5.547972 45.493374

$testend
[1] 16
```

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

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

CUGerm()

```
[1] 0.7092199
```

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

```
[1] 0.7092199
```

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

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

GermSynchrony(), GermUncertainty()

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

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

```
[1] 0.2666667
```

```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

Germination parameters	Details	Unit	Measures
D_{lag-50}	The duration between the time at germination onset (lag) and that at 50% germination (c).	time	Germination time
$t_{50_{total}}$	Time required for 50% of total seeds to germinate.	time	Germination time
$t_{50_{germinated}}$	Time required for 50% of viable/germinated seeds to germinate	time	Germination time
$t_{x_{total}}$	Time required for x% of total seeds to germinate.	time	Germination time
$t_{x_{germinated}}$	Time required for x% of viable/germinated seeds to germinate	time	Germination time
Uniformity ($U_{t_{max}-t_{min}}$)	It is the time interval between the percentages of viable seeds specified in the arguments `umin` and `umin` to germinate.	time	Germination time
Time at maximum germination rate ($TMGR$)	The partial derivative of the four-parameter hill function gives the instantaneous rate of germination (s) as follows. $$s = \frac{\partial y}{\partial x} = \frac{abc^b x^{b-1}}{(c^b + x^b)^2}$$ From this function for instantaneous rate of germination, $TMGR$ can be estimated as follows. $$TMGR = b\sqrt{\frac{c^b(b-1)}{b+1}}$$ It represents the point in time when the instantaneous rate of germination starts to decline.	time	Germination time
Area under the curve (AUC)	It is obtained by integration of the fitted curve between time 0 and time specified in the argument `tmax`.		Mixed
MGT	Calculated by integration of the fitted curve and proper normalisation.	time	Germination time
$Skewness$	It is computed as follows. $$\frac{MGT}{t_{50_{germinated}}}$$		

Examples

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

# From partial germination counts
#----------------------------------------------------------------------------
```

```
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 3.270090e-21

$Fit
    sigma isConv       finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.61522   TRUE 2.884804e-12 -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: df
  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: 8
Achieved convergence tolerance: 2.885e-12

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

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

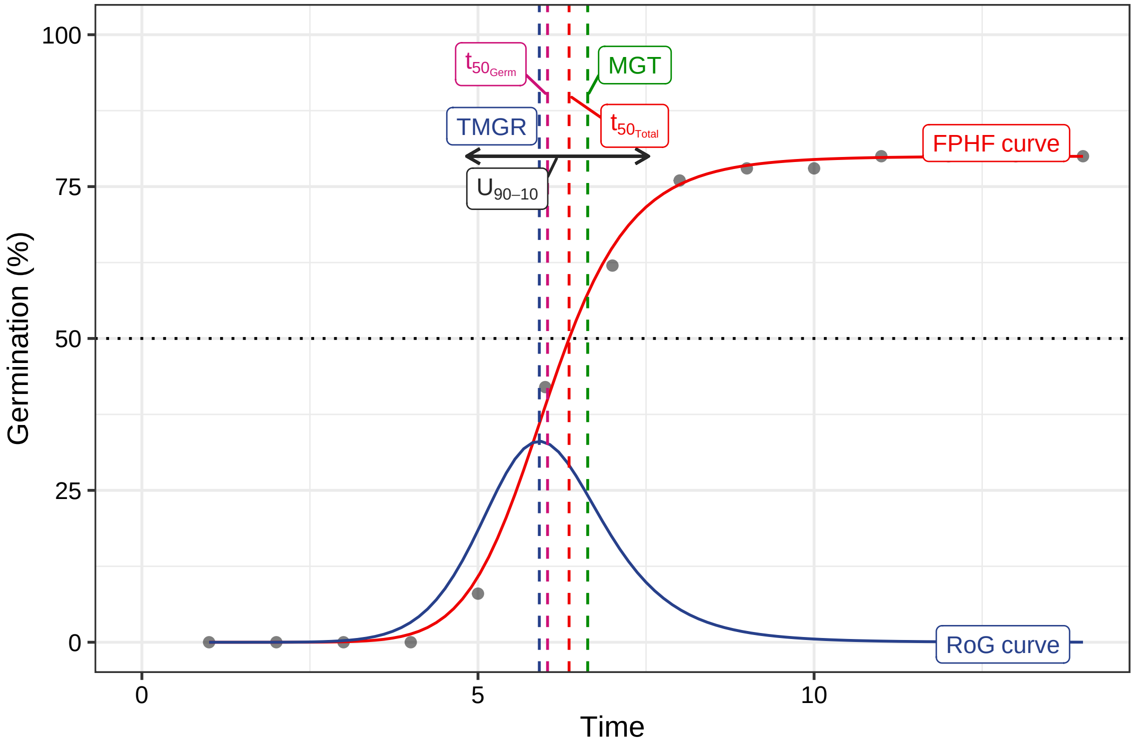
```
$data
   gp csgp intervals
1   0    0         1
2   0    0         2
```

```
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 3.270090e-21

$Fit
    sigma isConv       finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.61522   TRUE 2.884804e-12 -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
```

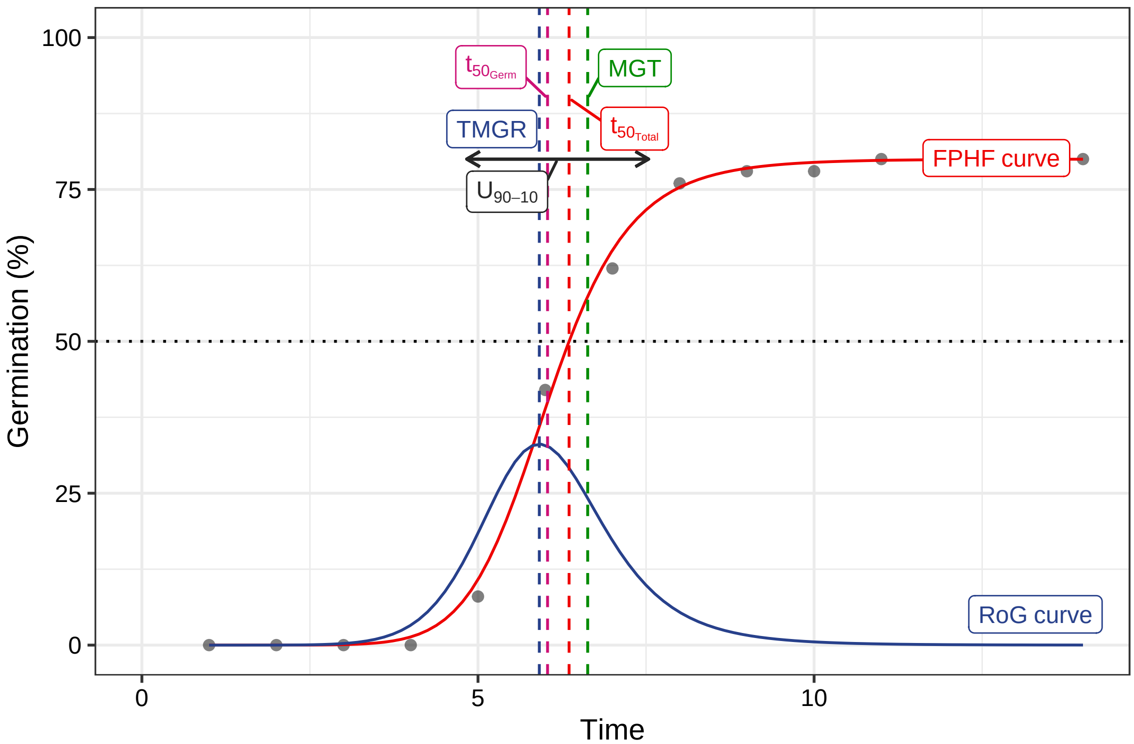
```
$Uniformity
       90        10 uniformity
  7.537690   4.831807   2.705882

$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: df
  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: 8
Achieved convergence tolerance: 2.885e-12

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

```
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
```

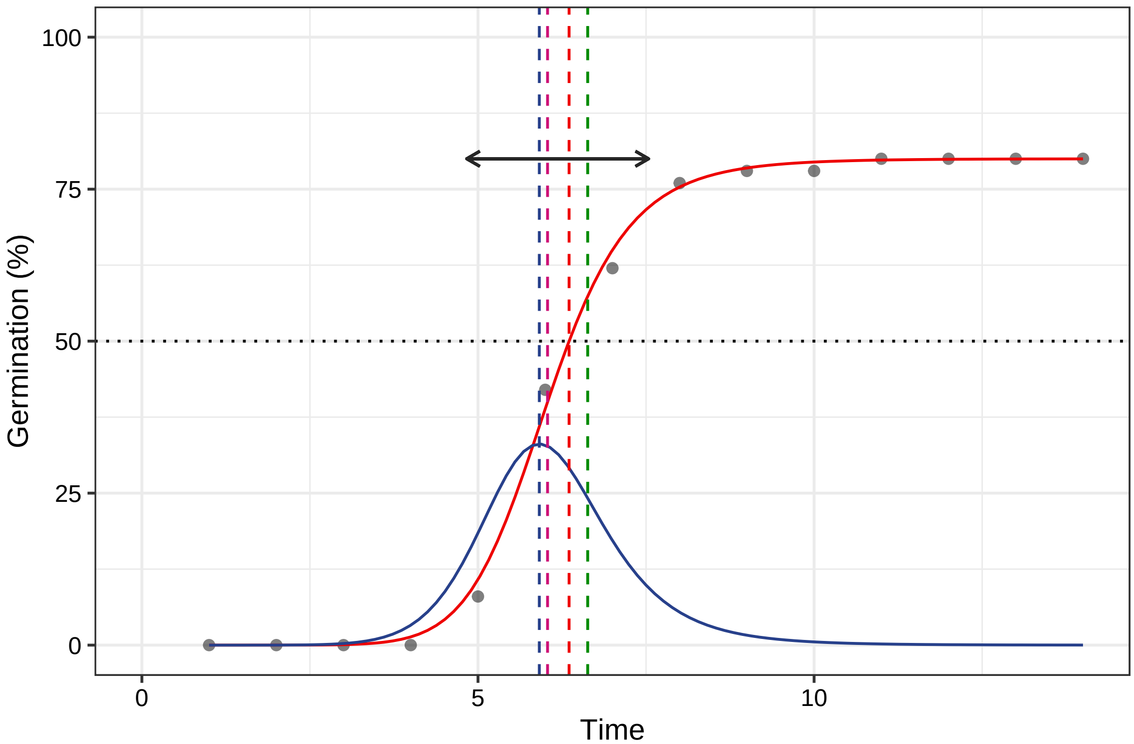
```r
plot(fit1)
```



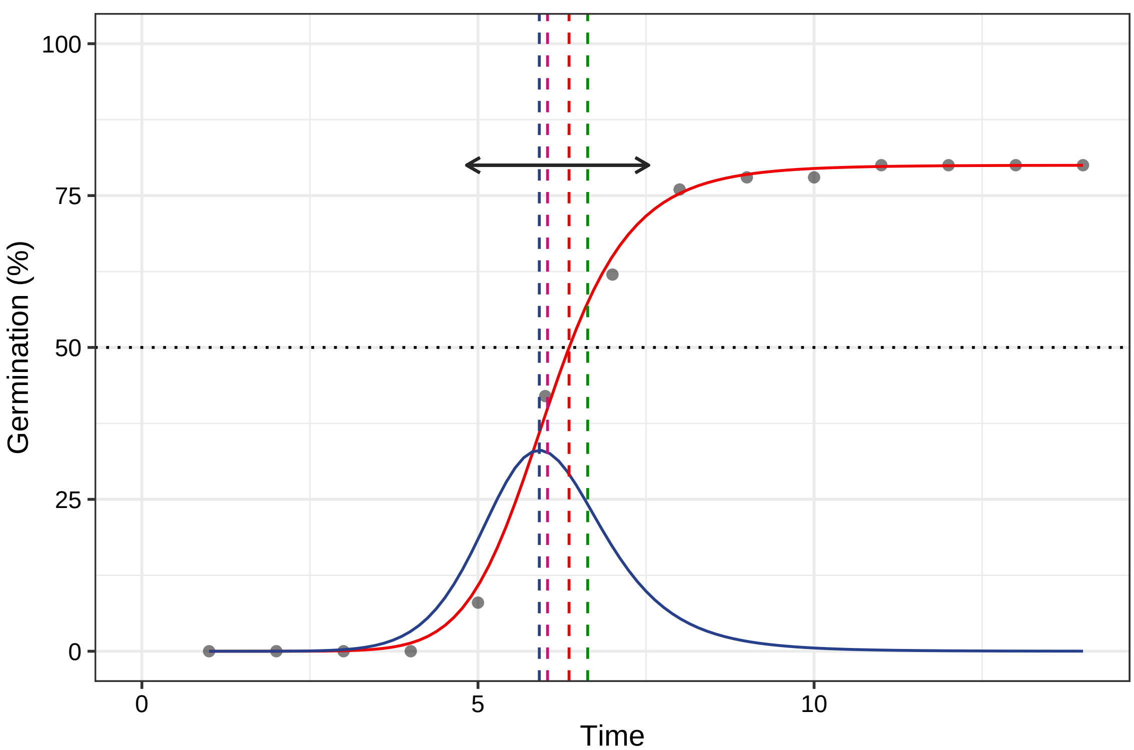

```r
plot(fit2)
```



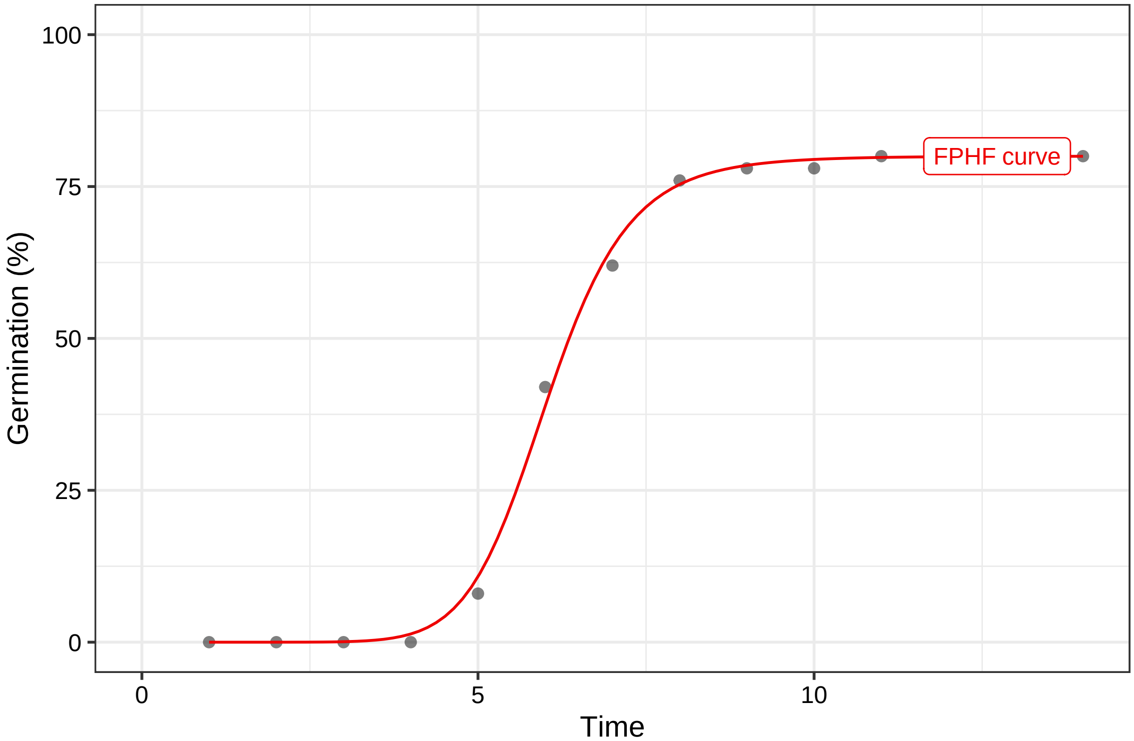

```r
# No labels
plot(fit1, plotlabels = FALSE)
```



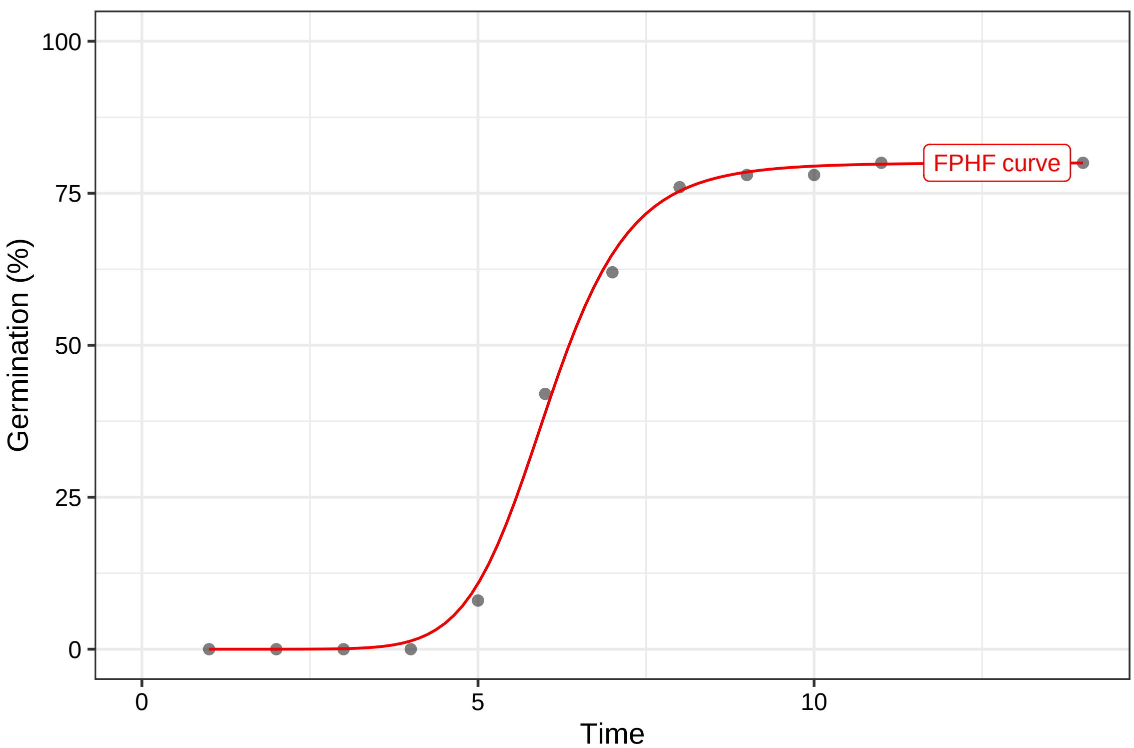

```r
plot(fit2, plotlabels = FALSE)
```



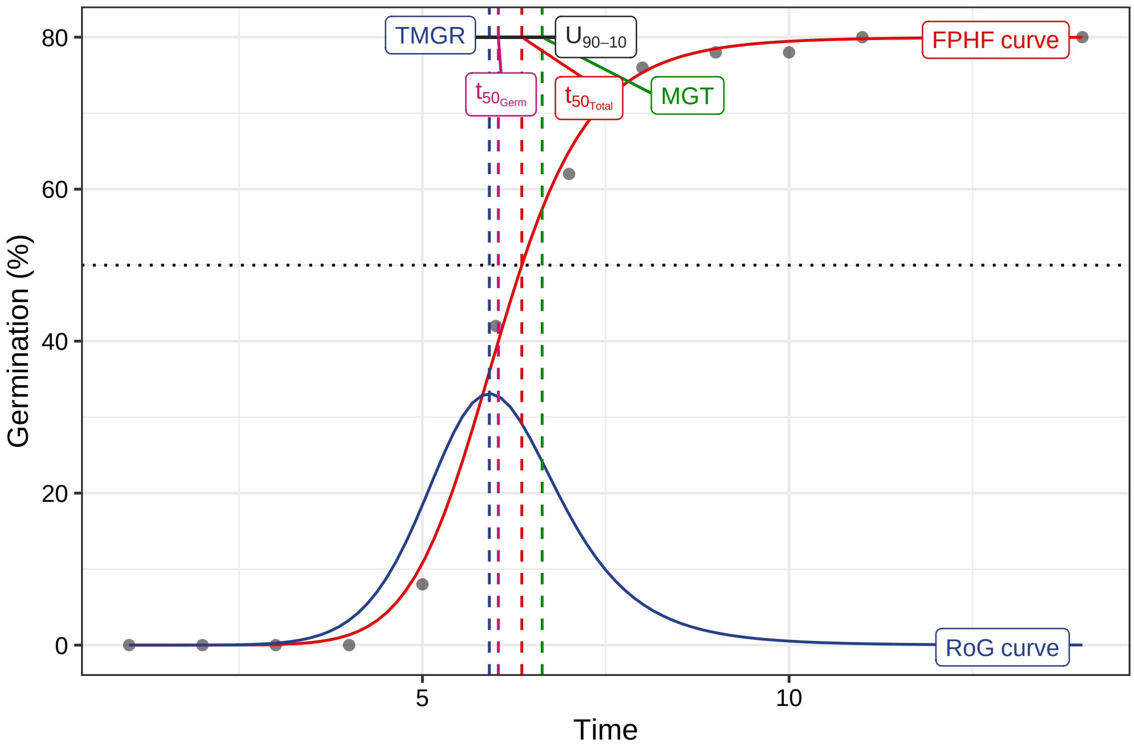

```r
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



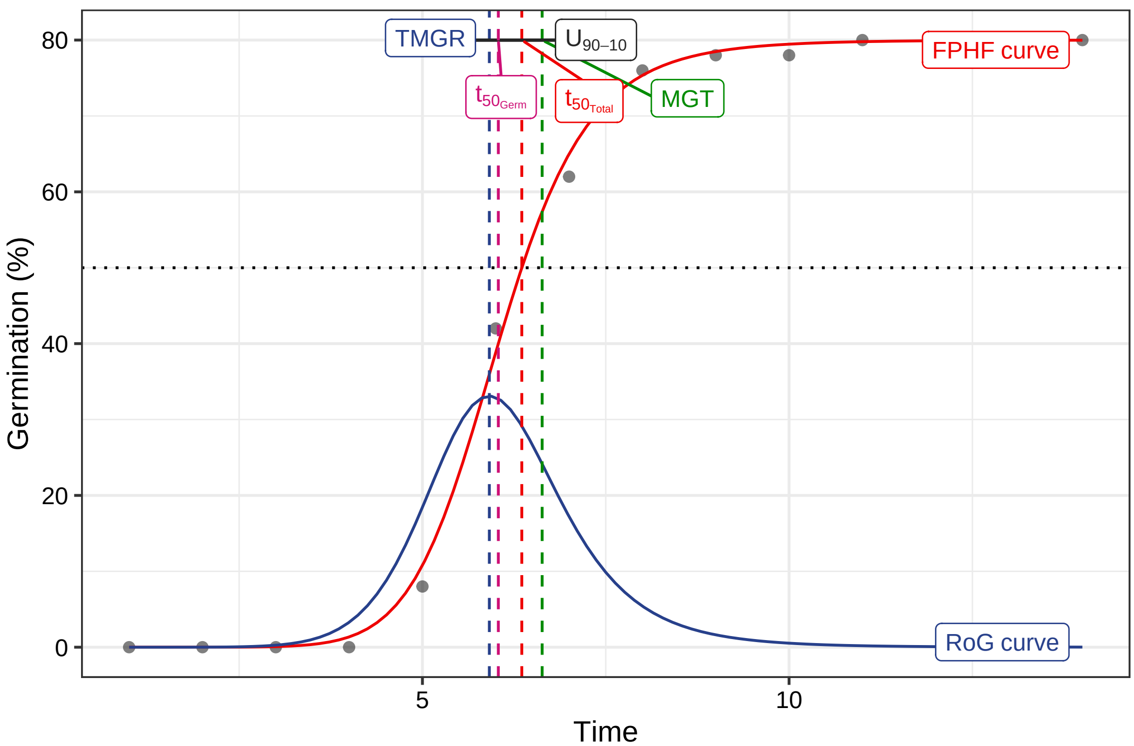

```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```




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




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



Wrapper functions

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

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

```r
data(gcdata)

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

```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14 Tota
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2        G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4        G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
5        G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1     0
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1     0
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0     0
   LastGermTime PeakGermTime TimeSpreadGerm t50_Coolbear t50_Farooq MeanGermTime VarGermTime SEGermTime
1            11            6              6     5.970588   5.941176     6.700000    1.446154  0.1901416
2            12            6              8     6.192308   6.153846     6.857143    2.027875  0.2197333
3            12            6              8     6.000000   5.972222     6.866667    2.572727  0.2391061
4            12            6              7     6.041667   6.000000     6.891304    2.187923  0.2180907
5            13            6              8     5.975000   5.950000     6.812500    2.368351  0.2221275
6            12            6              7     5.976190   5.952381     6.869565    2.071498  0.2122088
7            11            6              6     5.972222   5.944444     6.690476    1.389663  0.1818989
8            12            6              8     6.208333   6.166667     6.875000    2.112179  0.2297923
9            12            6              8     6.000000   5.973684     6.866667    2.300000  0.2260777
10           12            6              7     6.076923   6.038462     6.822222    1.831313  0.2017321
11           13            6              8     5.928571   5.904762     6.791667    2.381206  0.2227295
12           12            6              7     5.975000   5.950000     6.886364    2.149577  0.2210295
13           13            6              8     6.083333   6.041667     6.936170    2.539315  0.2324392
14           12            6              7     5.928571   5.904762     6.772727    1.900634  0.2078370
15           11            6              6     6.050000   6.000000     6.809524    1.670151  0.1994129
        CVG GermRateRecip_Coolbear GermRateRecip_Farooq GermSpeed_Count GermSpeed_Percent GermSpeedAccu
1  14.92537              0.1674877            0.1683168        6.138925          12.27785
2  14.58333              0.1614907            0.1625000        6.362698          12.47588
3  14.56311              0.1666667            0.1674419        6.882179          14.33787
4  14.51104              0.1655172            0.1666667        6.927417          13.58317
5  14.67890              0.1673640            0.1680672        7.318987          14.63797
6  14.55696              0.1673307            0.1680000        6.931782          14.14649
7  14.94662              0.1674419            0.1682243        6.448449          13.43427
8  14.54545              0.1610738            0.1621622        6.053175          12.87909
```

```
9  14.56311               0.1666667           0.1674009       6.830592          13.13575
10 14.65798               0.1645570           0.1656051       6.812698          13.62540
11 14.72393               0.1686747           0.1693548       7.342796          14.39764
12 14.52145               0.1673640           0.1680672       6.622258          12.98482
13 14.41718               0.1643836           0.1655172       7.052320          14.39249
14 14.76510               0.1686747           0.1693548       6.706782          13.97246
15 14.68531               0.1652893           0.1666667       6.363925          13.25818
   GermSpeedCorrected_Normal GermSpeedCorrected_Accumulated WeightGermPercent MeanGermPercent MeanGermNu
1                  0.1534731                      0.8653917          47.42857        5.714286        2.85
2                  0.1514928                      0.8462043          47.89916        5.882353        3.00
3                  0.1529373                      0.8510501          54.46429        6.696429        3.2
4                  0.1505960                      0.8409680          52.24090        6.442577        3.28
5                  0.1524789                      0.8543303          56.14286        6.857143        3.42
6                  0.1506909                      0.8429608          54.51895        6.705539        3.28
7                  0.1535345                      0.8663205          51.93452        6.250000        3.00
8                  0.1513294                      0.8442698          49.39210        6.079027        2.85
9                  0.1517909                      0.8470024          50.27473        6.181319        3.2
10                 0.1513933                      0.8487837          52.57143        6.428571        3.2
11                 0.1529749                      0.8578026          55.18207        6.722689        3.42
12                 0.1505059                      0.8410547          50.00000        6.162465        3.14
13                 0.1500494                      0.8360424          55.24781        6.851312        3.35
14                 0.1524269                      0.8567022          53.86905        6.547619        3.14
15                 0.1515220                      0.8499278          51.19048        6.250000        3.00
   TimsonsIndex_KhanUngar GermRateGeorge GermIndex GermIndex_mod EmergenceRateIndex_SG EmergenceRateInde
1               0.5714286              4  5.840000      7.300000                   292
2               0.7002801              5  5.882353      7.142857                   300
3               1.0416667              7  6.687500      7.133333                   321
4               0.5602241              4  6.411765      7.108696                   327
5               0.7142857              5  6.900000      7.187500                   345
6               0.4373178              3  6.693878      7.130435                   328
7               0.5952381              4  6.395833      7.309524                   307
8               0.7598784              5  6.063830      7.125000                   285
9               0.6868132              5  6.173077      7.133333                   321
10              0.5714286              4  6.460000      7.177778                   323
11              0.7002801              5  6.784314      7.208333                   346
12              0.4201681              3  6.137255      7.113636                   313
13              0.5830904              4  6.775510      7.063830                   332
14              0.4464286              3  6.625000      7.227273                   318
15              0.5952381              4  6.291667      7.190476                   302
   EmergenceRateIndex_Fakorede PeakValue GermValue_Czabator GermValue_DP GermValue_Czabator_mod GermValu
1                     8.375000  9.500000           54.28571     57.93890               54.28571
2                     8.326531  9.313725           54.78662     52.58713               54.78662
3                     7.324444 10.416667           69.75446     68.62289               69.75446
4                     7.640359 10.049020           64.74158     70.43331               64.74158
5                     7.096354 11.250000           77.14286     80.16914               77.14286
6                     7.317580 10.714286           71.84506     76.51983               71.84506
7                     7.646259 10.416667           65.10417     69.41325               65.10417
8                     8.078125  9.574468           58.20345     56.00669               58.20345
9                     7.934815  9.855769           60.92165     58.13477               60.92165
10                    7.580247 10.250000           65.89286     70.91875               65.89286
11                    7.216146 11.029412           74.14731     77.39782               74.14731
12                    7.981921  9.803922           60.41632     64.44988               60.41632
13                    7.231326 10.969388           75.15470     78.16335               75.15470
14                    7.388430 10.677083           69.90947     74.40140               69.90947
```

```
15                    7.782313 10.156250          63.47656     67.62031                63.47656
```

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

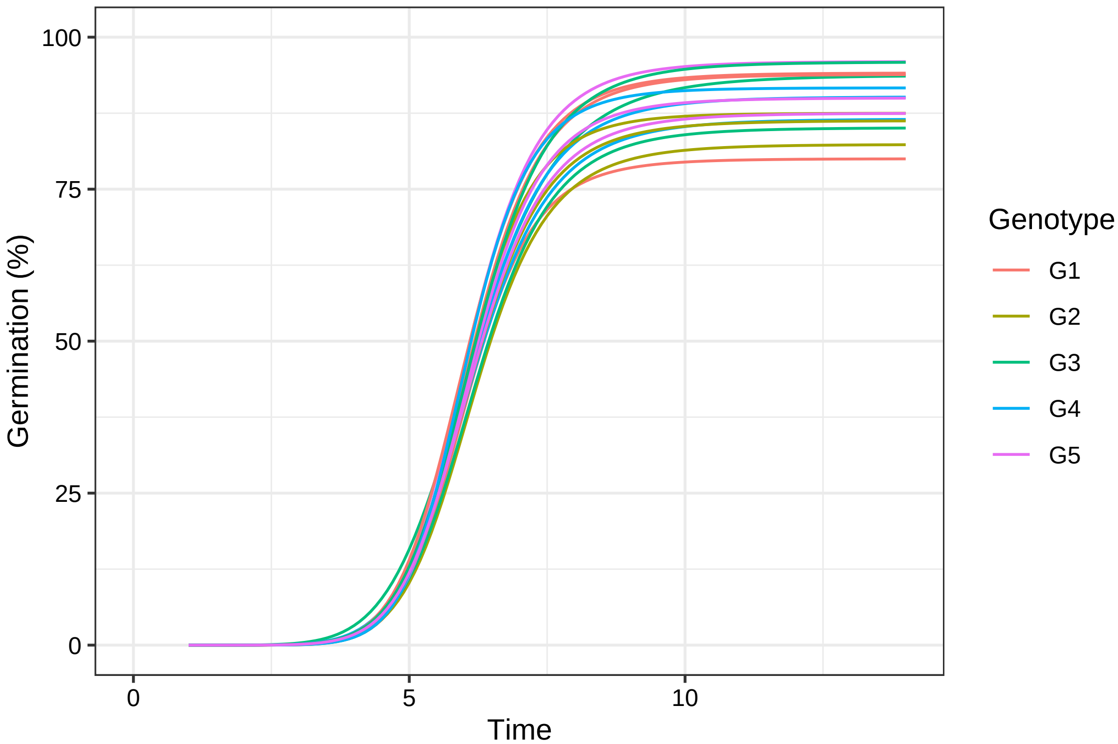
```r
data(gcdata)

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

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

```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14 Tota
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2        G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4        G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
5        G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1     0
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1     0
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0     0
                  c y0 lag           Dlag50        t50.total     txp.total_10     txp.total_60   t50.Ge
1  6.03495355423453  0   0 6.03495355423453  6.3551214973865 4.95626430994715  6.7445983463311 6.034953
2  6.17519294911323  0   0 6.17519294911323 6.47349044022769 4.98323617967833  6.8726033802361 6.175192
3  6.13811027378334  0   0 6.13811027378334 6.24419103019226 4.67302155573313 6.60843809234118 6.138110
4  6.12517308176588  0   0 6.12517308176588 6.27679437746254 4.85087548237175 6.61496814302537 6.125173
5  6.04964210720327  0   0 6.04964210720327 6.10343321091848 4.81412549010201 6.38678874941426 6.049642
6   6.0974148527557  0   0  6.0974148527557 6.18227860798315 4.86863251633358   6.477598609442  6.09741
7  6.02985089631599  0   0 6.02985089631599 6.20281219696422 4.93042184740182    6.51049505523 6.029850
8  6.18977354961439  0   0 6.18977354961439 6.43951015764455 4.94005695310539 6.82329908278267 6.189773
9  6.12512151399929  0   0 6.12512151399929 6.35217197764166 4.83665841861718 6.73327569782723 6.125121
10 6.10950363596761  0   0 6.10950363596761  6.2530432080492 4.92062915320932 6.56650619550494 6.109503
11 6.01875974061195  0   0 6.01875974061195 6.09943499335382 4.79862683383817  6.3912906236839 6.018759
12  6.1084516820797  0   0  6.1084516820797 6.32618435705024 4.89359557090626 6.68452626570581  6.10845
13 6.14901168717124  0   0 6.14901168717124 6.20750091190278 4.84130798420802 6.50995386860368 6.149011
14 6.01591019490093  0   0 6.01591019490093 6.12238872875573 4.91514013437311 6.39749098023249 6.015910
15 6.12157936163499  0   0 6.12157936163499 6.31739163301497 4.89250226946576 6.66724718740801 6.121579
      Uniformity_90    Uniformity_10       Uniformity             TMGR              AUC              MG
1  7.53768963497883 4.83180737938015 2.70588225559868 5.91219440464896 1108.97550938733 6.6322519662728
2  7.83540706385743 4.86675518553144 2.96865187832599 6.03128155445793 1128.55880085138 6.7844073567977
3  8.13734180246507 4.63006208264611 3.50727971981896 5.93817948943725 1283.69307344081 6.7727423283087
4  7.83480960415051 4.78859693817119 3.04621266597932 5.97268622562109 1239.88674124826 6.7396659272138
5  7.63902819750811 4.79094574322756 2.84808245428055 5.91428884333636 1328.32820017628 6.6549807574810
```

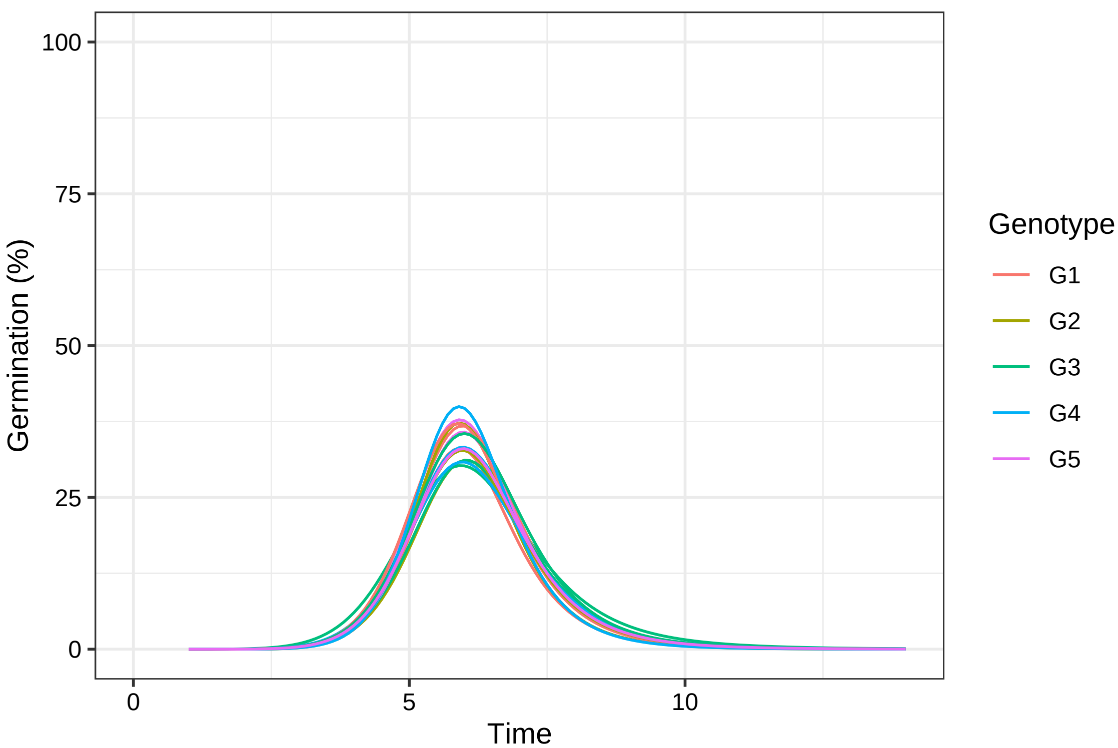
```
6  7.69346877523834 4.83247140825032 2.86099736698802 5.96187868660636 1294.46271441017 6.70247312632460
7  7.48364280989593 4.85847638047658 2.62516642941935 5.91405695229978 1213.90764565674 6.62241708548249
8  7.91416293168472 4.84110536088622 3.07305757079851 6.03619216805867 1164.34586106316 6.80400021213917
9  7.90404141879274 4.74657350251934  3.1574679162734  5.9616310497804 1188.79304149759  6.7452410863068
10 7.67917745255724  4.8606813566304 2.81849609592684 5.97811533043387 1240.22733172402 6.71189998824877
11 7.60361082322955 4.76424552194859 2.83936530128096 5.88355748786772 1305.20007906005 6.62424817630914
12 7.76385405638773 4.80601279742022 2.95784125896751  5.9640804983933  1188.0211599463 6.71863893649018
13 7.85034473566269 4.81639291039067 3.03395182527202 5.99827012362062 1316.40687308654 6.76227360530894
14  7.4323719910534 4.86939775305615 2.56297423799725  5.9051804897395 1273.38526597411  6.6049667882059
15 7.78580612916975 4.81308335438754 2.97272277478221 5.97608676470078 1203.66421628837 6.73226579042194
   Fit_isConv           Fit_finTol         Fit_logLik          Fit_AIC           Fit_BIC     Fit_deviance
1        TRUE 2.88480350718601e-12  -25.498681342686 56.9973626853719 58.9145346742177 31.3072289092405
2        TRUE 5.15498754793953e-12 -20.3147146781893 46.6294293563786 48.5466013452244 14.9286526064903
3        TRUE 8.43840552988695e-11 -31.2321314996742 68.4642629993484 70.3814349881942 71.0165774207971
4        TRUE 3.38218342221808e-12 -31.0226924019787 68.0453848039574 69.9625567928032  68.923242888336
5        TRUE 6.74447164783487e-11 -31.0406736477542 68.0813472955084 69.9985192843541 69.1005170158358
6        TRUE 3.97619714931352e-11  -34.328870450832 74.6577409016639 76.5749128905097 110.531949324479
7        TRUE 3.90798504668055e-12 -25.9069727183683 57.8139454367367 59.7311174255824 33.1876017805038
8        TRUE 4.32720526077901e-12 -20.3814877326307 46.7629754652615 48.6801474541073 15.0717385035725
9        TRUE 1.77209358298569e-11 -31.2163324798379 68.4326649596759 70.3498369485217 70.8564735497253
10       TRUE 8.14281975181075e-12 -26.1045565628368 58.2091131256735 60.1262851145193 34.1377096911127
11       TRUE 1.32729383039987e-11 -32.3138085946749 70.6276171893498 72.5447891781956 82.8837176958294
12       TRUE 3.51434437106946e-11 -33.5861335093548 73.1722670187096 75.0894390075554 99.4046940082808
13       TRUE 1.10560449684272e-11 -32.1879276469568 70.3758552939135 72.2930272827593  81.406542245287
14       TRUE 9.80548975348938e-13  -33.023419198233  72.046838396466 73.9640103853118  91.726523289527
15       TRUE 8.73967564984923e-13 -28.1644422917083 62.3288845834165 64.2460565722623 45.8177705510444
```

Multiple fitted curves generated in batch can also be plotted.

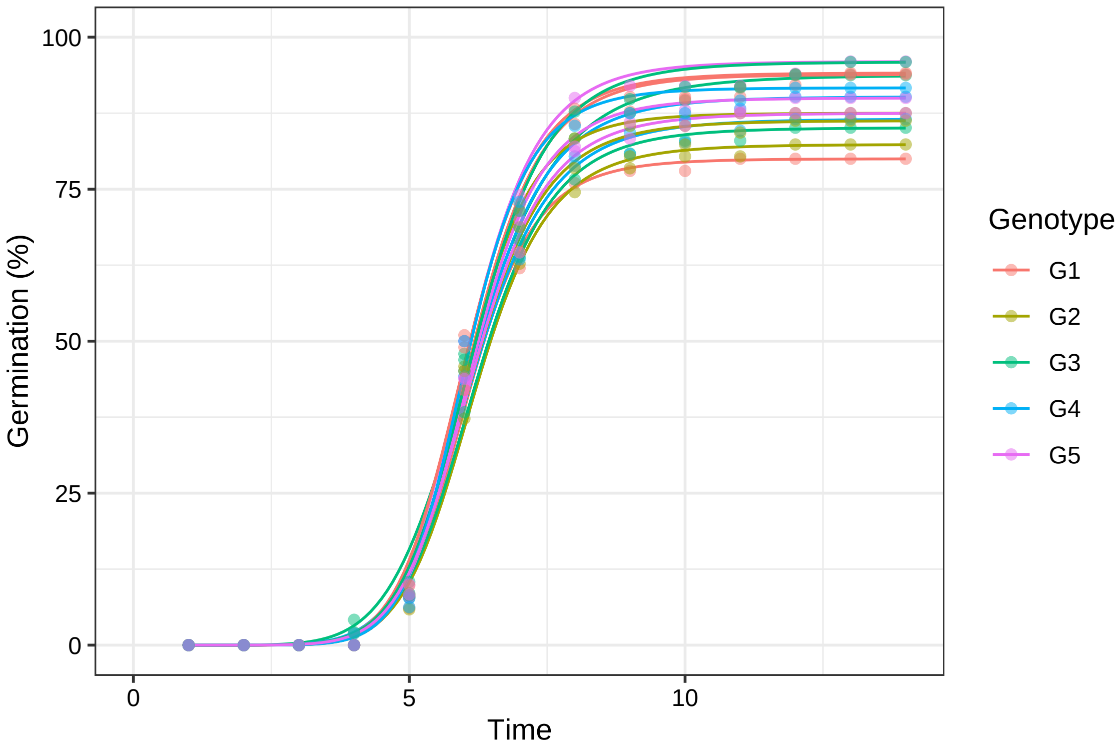
```r
data(gcdata)

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")
```



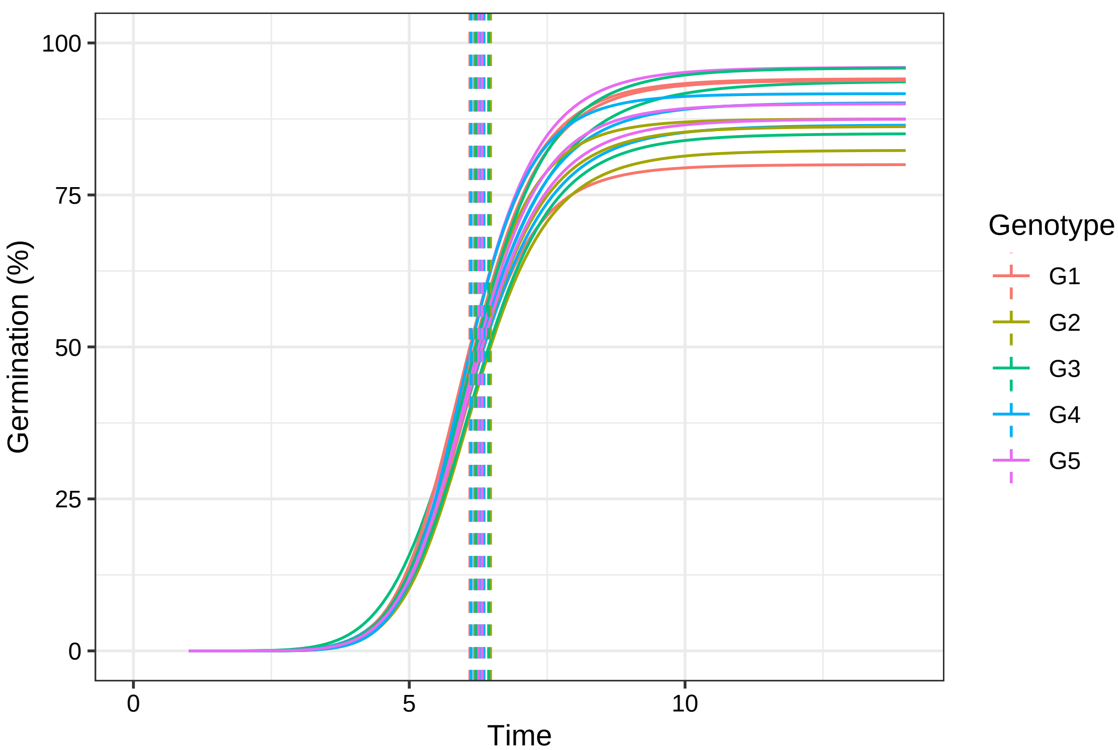

```r
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```



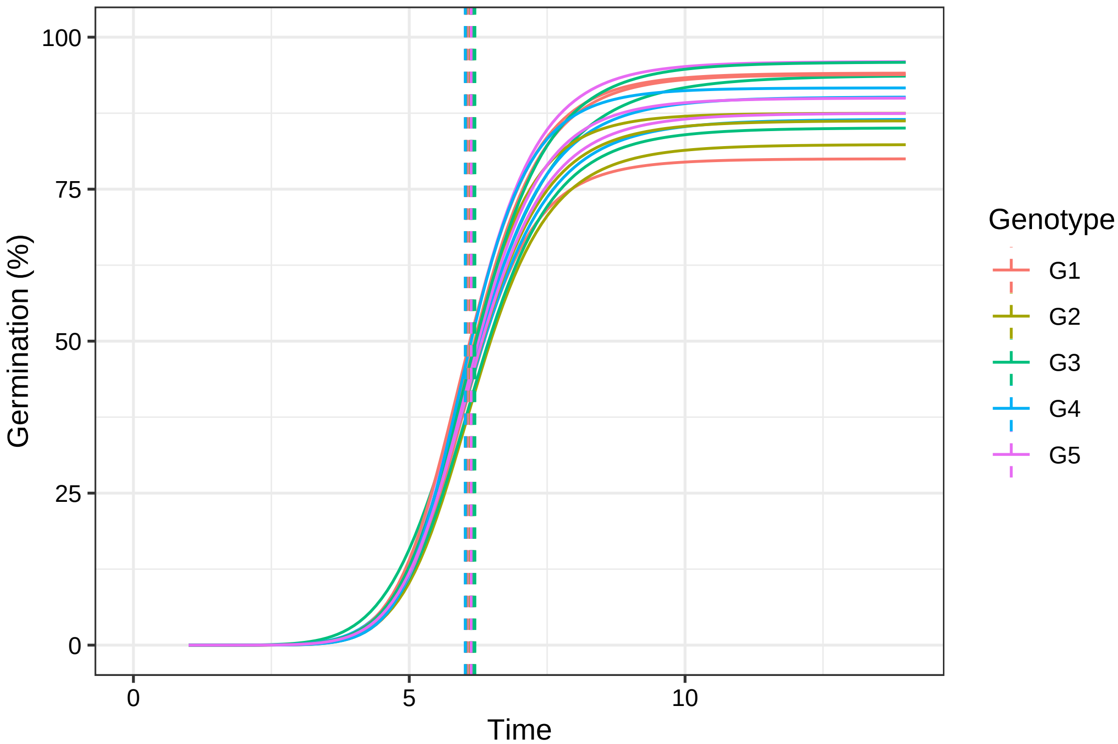

```r
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



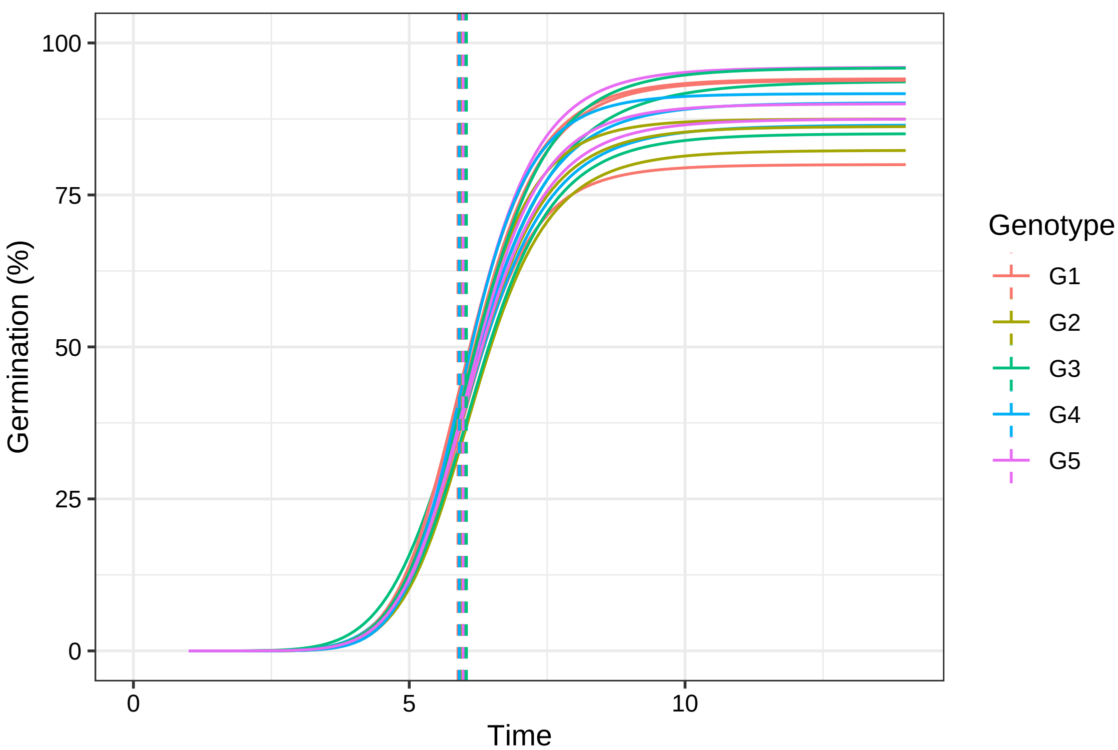

```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



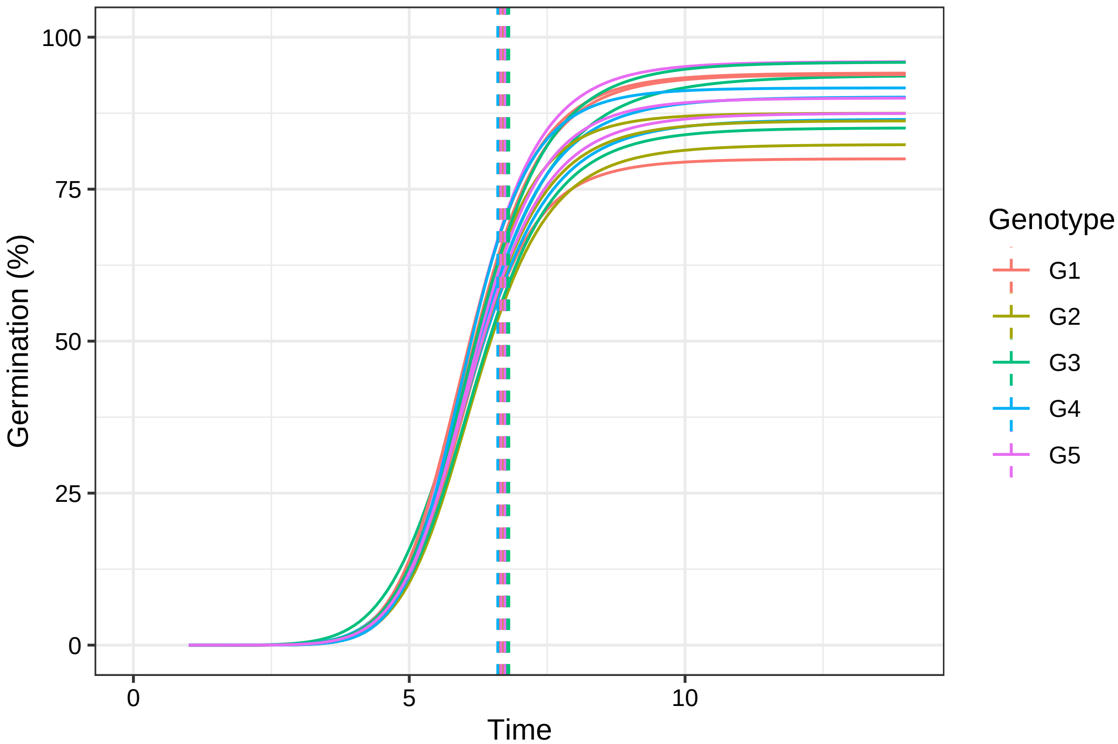

```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```




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

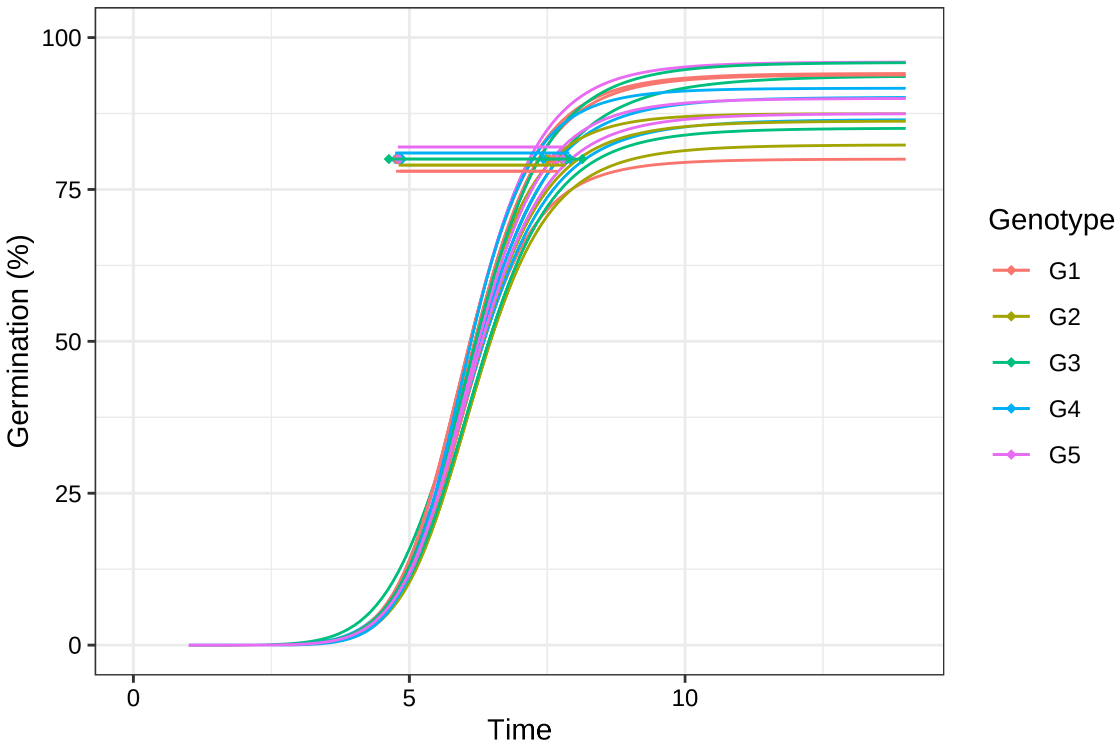



```r
plot(fits, group.col = "Genotype", annotate = "mgt")
```

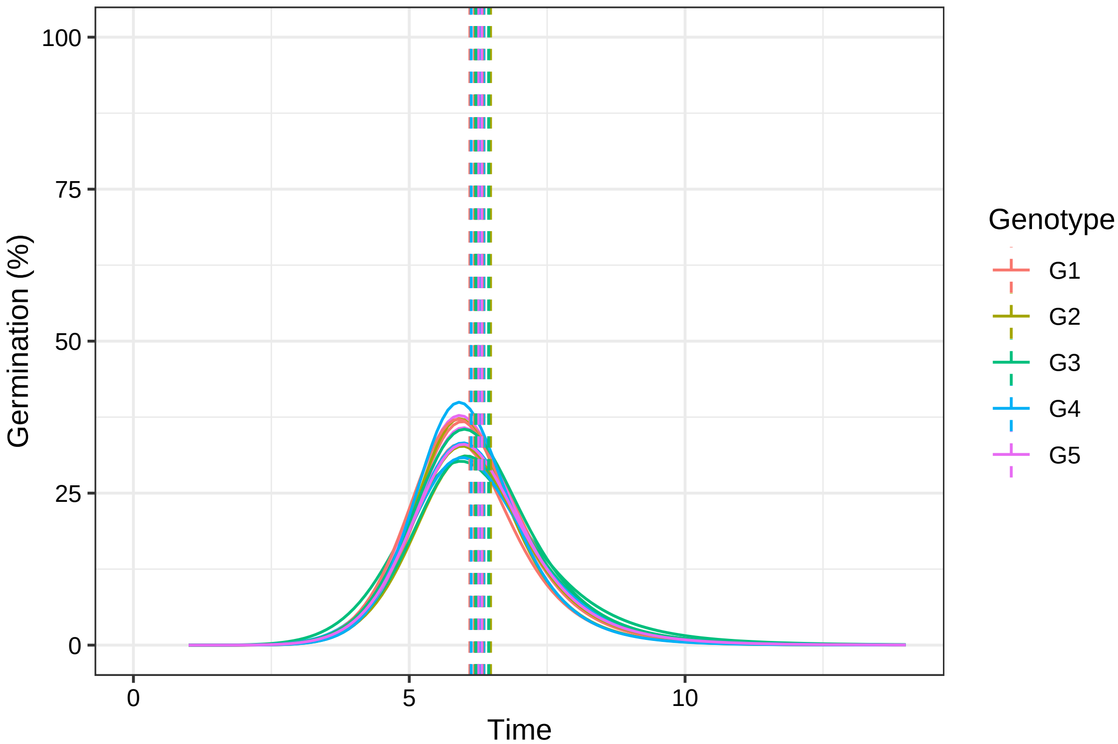



```r
plot(fits, group.col = "Genotype", annotate = "uniformity")
```

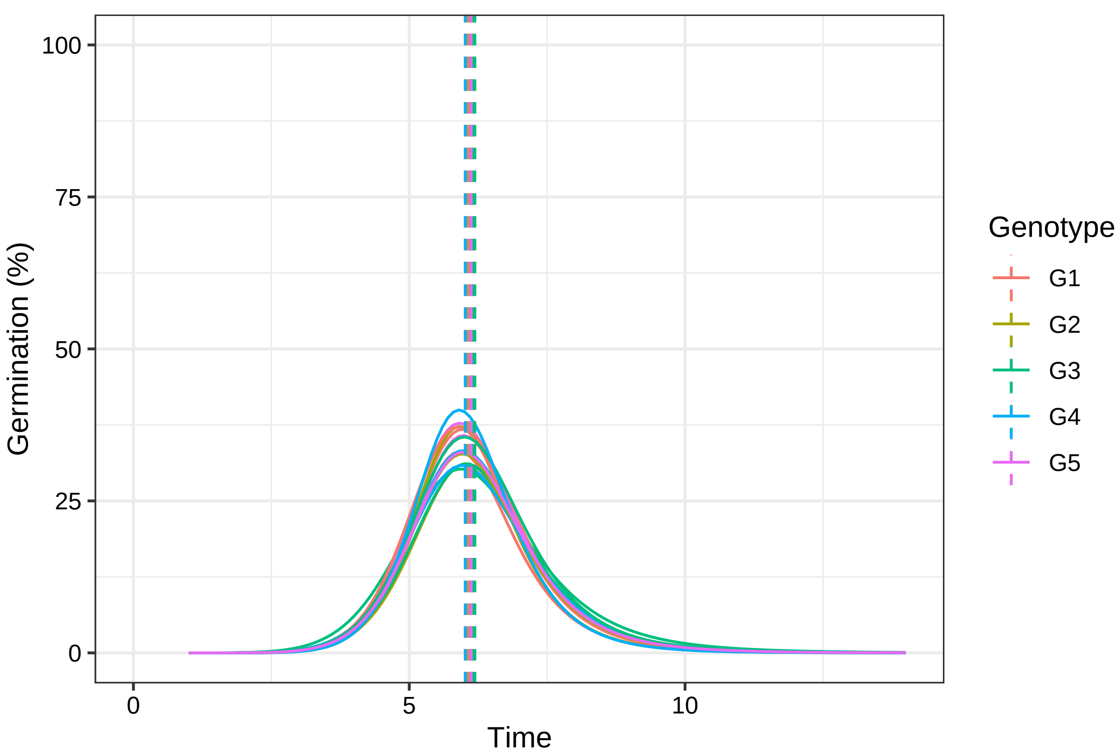
```
Warning: `position_dodge()` requires non-overlapping x intervals
`position_dodge()` requires non-overlapping x intervals
```



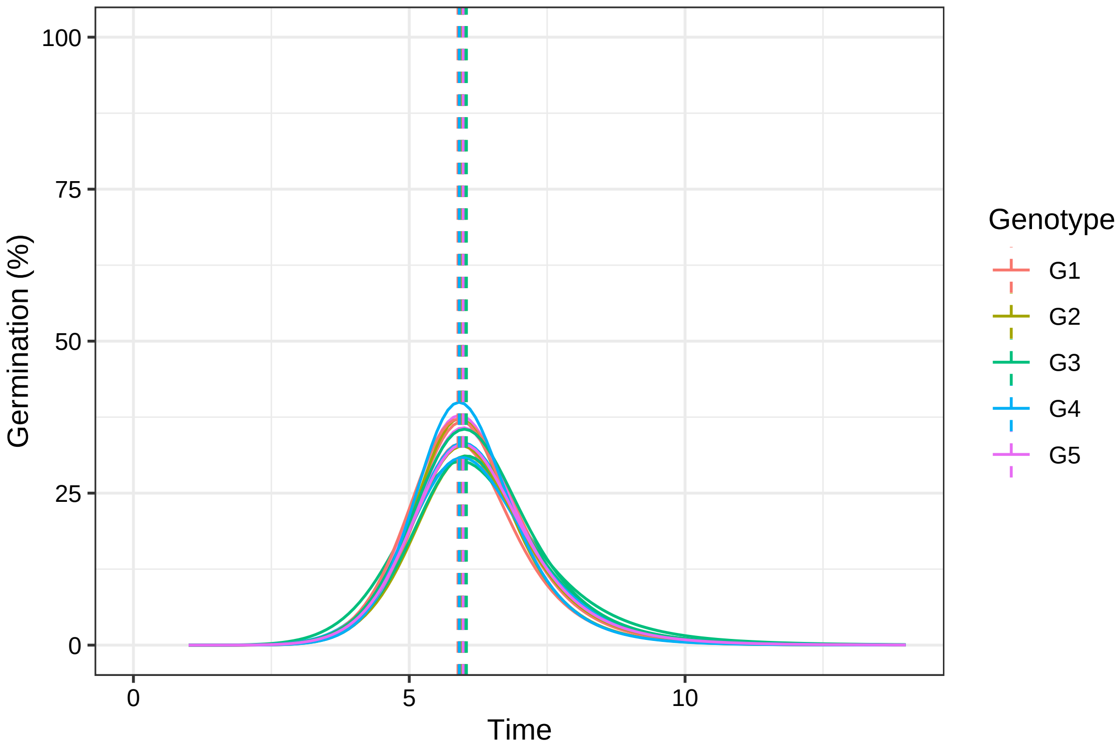

```r
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



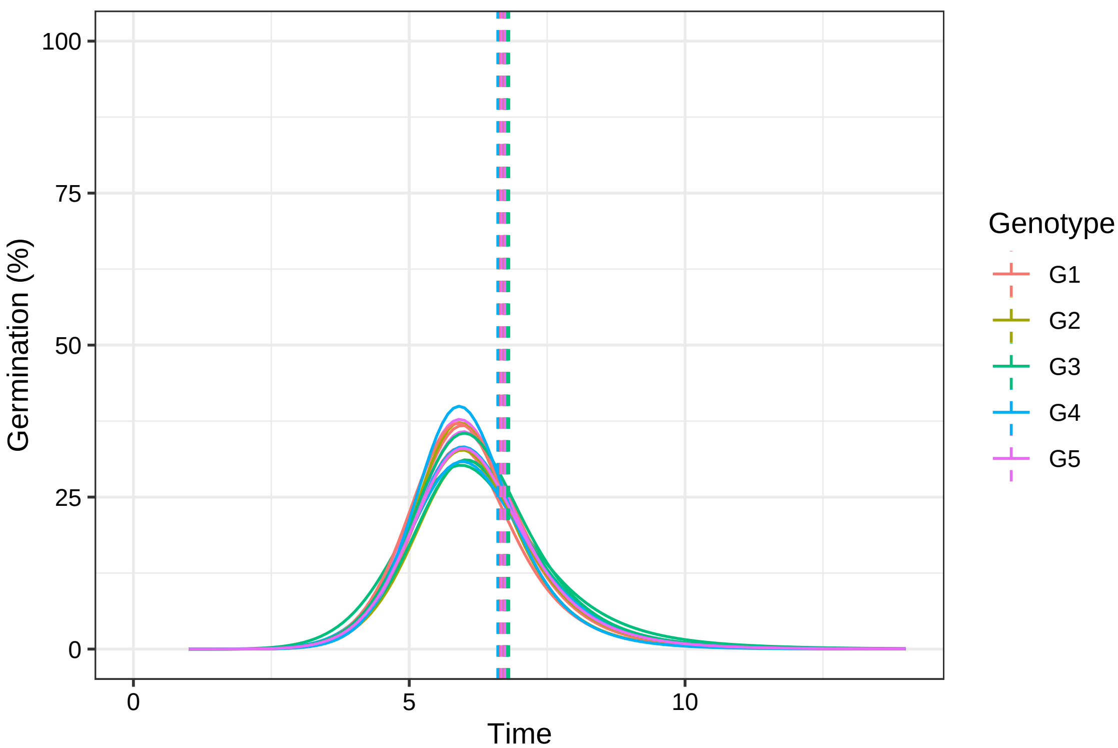

```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```




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

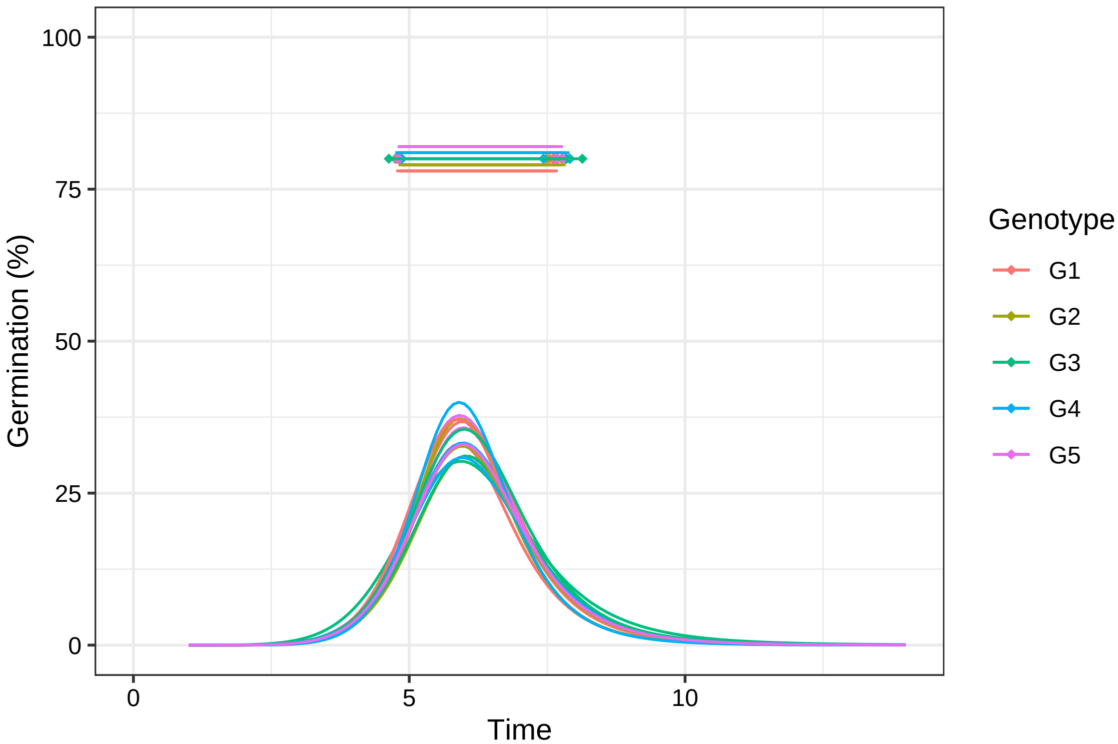



```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```

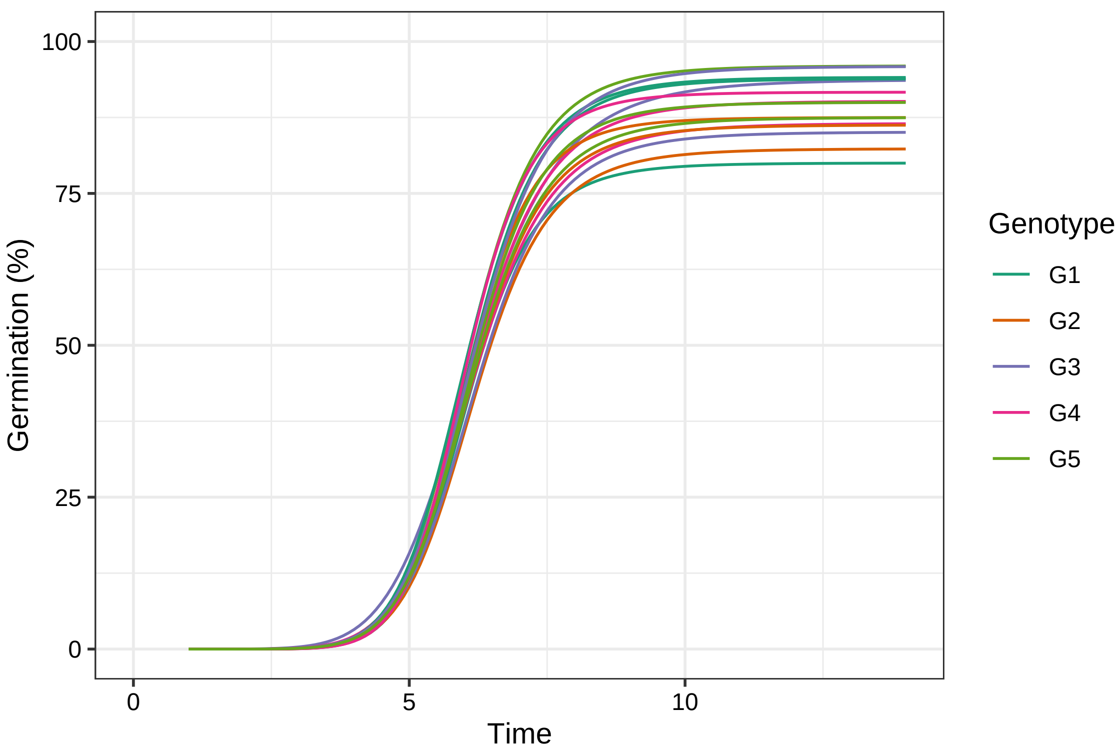



```r
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```

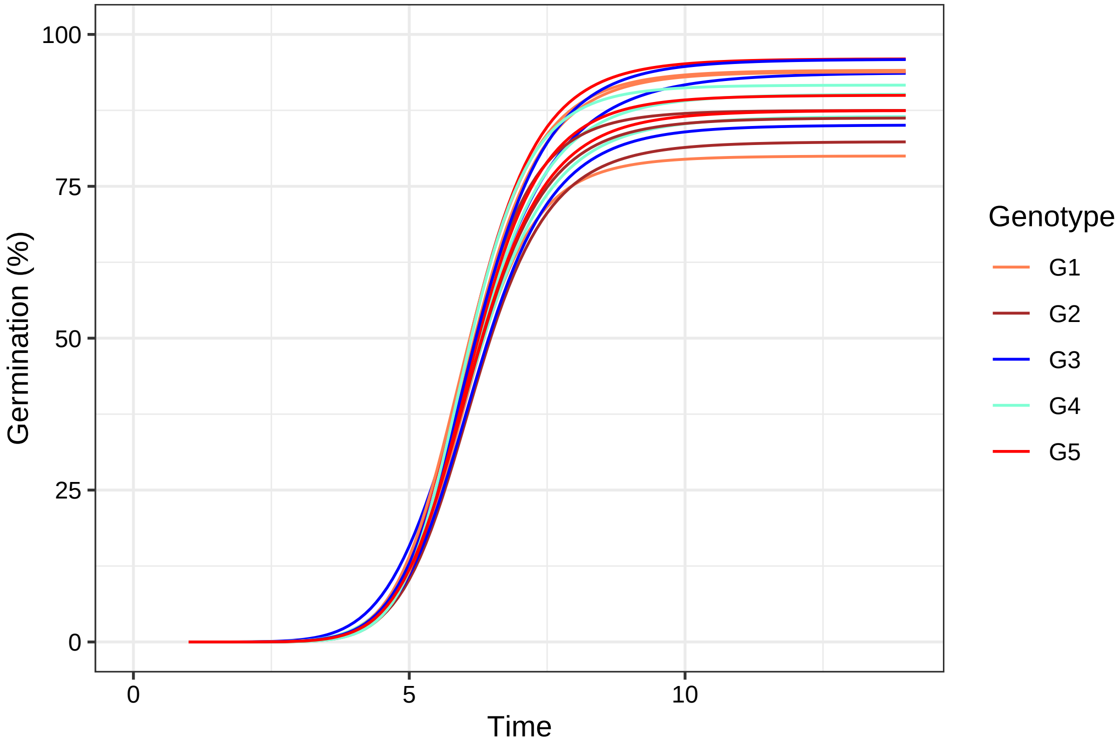
```
Warning: `position_dodge()` requires non-overlapping x intervals
`position_dodge()` requires non-overlapping x intervals
```




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

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



```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 ().  germinationmet
  Curve Fitting. R package version 0.1.8,
  https://github.com/aravind-j/germinationmetricshttps://cran.r-project.org/package=germinationmetrics.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
    author = {J. Aravind and S. {Vimala Devi} and J. Radhamani and Sherry Rachel Jacob and {Kalyani Sri
    note = {R package version 0.1.8 https://aravind-j.github.io/germinationmetrics/ https://CRAN.R-proj
  }

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

Session Info

```r
sessionInfo()
```

```
R Under development (unstable) (2023-08-09 r84924 ucrt)
Platform: x86_64-w64-mingw32/x64
```

```
Running under: Windows 11 x64 (build 22621)

Matrix products: default


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

time zone: Asia/Calcutta
tzcode source: internal

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

other attached packages:
[1] germinationmetrics_0.1.8 ggplot2_3.4.2            RCurl_1.98-1.12          testthat_3.1.10

loaded via a namespace (and not attached):
  [1] bitops_1.0-7       Rdpack_2.4         remotes_2.4.2.1    rlang_1.1.1        magrittr_2.0.3     hu
  [8] roxygen2_7.2.3     reshape2_1.4.4     callr_3.7.3        vctrs_0.6.3        stringr_1.5.0      pr
 [15] crayon_1.5.2       fastmap_1.1.1      backports_1.4.1    ellipsis_0.3.2     labeling_0.4.2     pa
 [22] promises_1.2.0.1   rmarkdown_2.23     sessioninfo_1.2.2  ps_1.7.5           tinytex_0.46       pu
 [29] gslnls_1.1.2       cachem_1.0.8       covr_3.6.2         jsonlite_1.8.7     highr_0.10         la
 [36] parallel_4.4.0     prettyunits_1.1.1  R6_2.5.1           RColorBrewer_1.1-3 stringi_1.7.12     pk
 [43] Rcpp_1.0.11        knitr_1.43         usethis_2.2.2      clisymbols_1.2.0   httpuv_1.6.11      Ma
 [50] rstudioapi_0.15.0  yaml_2.3.7         miniUI_0.1.1.1     curl_5.0.1         processx_3.8.2     pk
 [57] tibble_3.2.1       plyr_1.8.8         shiny_1.7.4.1      withr_2.5.0        evaluate_0.21      de
 [64] urlchecker_1.0.1   whoami_1.3.0       xml2_1.3.5         pillar_1.9.0       rex_1.2.1          pi
 [71] rprojroot_2.0.3    mathjaxr_1.6-0     xopen_1.0.0        munsell_0.5.0      codemetar_0.3.5    sc
 [78] glue_1.6.2         lazyeval_0.2.2     tools_4.4.0        data.table_1.14.8  goodpractice_1.0.4 XM
 [85] grid_4.4.0         tidyr_1.3.0        cyclocomp_1.1.0    rbibutils_2.2.14   lintr_3.1.0        de
 [92] cli_3.6.1          rcmdcheck_1.4.0    fansi_1.0.4        dplyr_1.1.2        praise_1.0.0       gt
 [99] ggrepel_0.9.3      farver_2.1.1       xmlparsedata_1.0.5 htmlwidgets_1.6.2  memoise_2.0.1      ht
[106] lifecycle_1.0.3    httr_1.4.6         mime_0.12
```

References

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