The `germinationmetrics` Package: A Brief Introduction

Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan

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ICAR-National Bureau of Plant Genetic Resources, New Delhi.

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 0.1.5.9000. 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

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

Germination count data

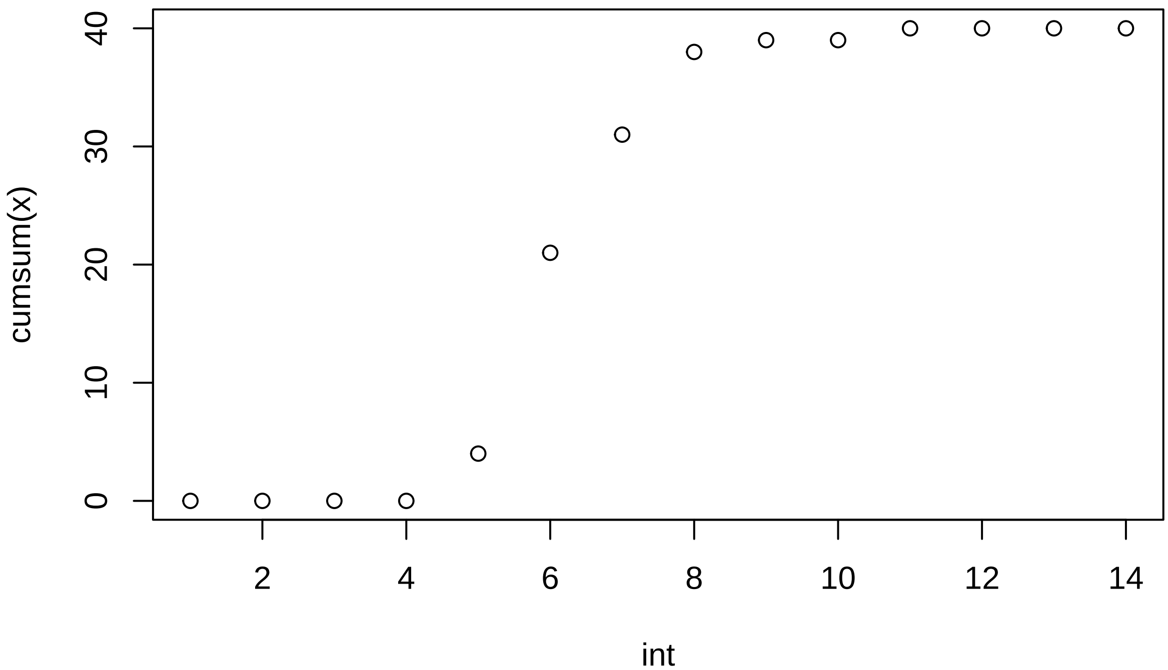
Typically in a germination test, the germination count data of a fixed number of seeds is recorded at regular intervals for a definite period of time or until all the seeds have germinated. These germination count data can be either partial or cumulative (Table 2).

Table 2 : A typical germination count data.

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

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

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

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

plot(int, cumsum(x))
```



Single-value germination indices

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

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	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.	% day $^{-1}$	Germination rate	Kotowski (1926), Nichols and Heydecker (1968); Bewley and Black (1994); Labouriau (1983b); Scott et al. (1984)
Variance of germination rate (s_{V}^{2})	`VarGermRate`	It is calculated according to the following formula. $$s_{V}^{2} = \overline{V}^{4} \times s_{T}^{2}$$ Where, s_{T}^{2} is the variance of germination time.	time^{-2}	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
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}	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}	Mixed	Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004)
Corrected germination rate index	`GermSpeedCorrected`	It is computed as follows. $$S_{corrected} = \frac{S}{FGP}$$ Where, FGP is the final germination percentage or germinability.	time^{-1}	Mixed	Evetts and Burnside (1972)
Weighted germination percentage (WGP)	`WeightGermPercent`	It is estimated as follows. $$WGP = \frac{\sum_{i=1}^{k} (k - i + 1) N_i}{k \times N} \times 100$$ Where, N_i is the number of seeds that germinated in the time interval i (not cumulative, but partial count), N is the total number of seeds tested, and k is the total number of time intervals.		Mixed	Reddy et al. (1985); Reddy (1978)
Mean germination percentage per unit time ($\overline{GP}$)	`MeanGermPercent`	It is estimated as follows. $$\overline{GP} = \frac{GP}{T_k}$$ Where, GP is the final germination percentage, T_k is the time at the kth time interval, and k is the total number of time intervals required for final germination.		Mixed	Czabator (1962)
Number of seeds germinated per unit time $\overline{N}$	`MeanGermNumber`	It is estimated as follows. $$\overline{N} = \frac{N_g}{T_k}$$ Where, N_g is the number of germinated seeds at the end of the germination test, T_k is the time at the kth time interval, and k is the total number of time intervals required for final germination.		Mixed	Khamassi et al. (2013)

Germination index	Function	Details	Unit	Measures	Reference
Timson's index [$\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$] or Germination energy index (GEI)	`TimsonsIndex`	It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time and is estimated in terms of cumulative germination percentage (G_i) as follows. $\Sigma k = \sum_{i=1}^{k} G_i$ Where, G_i is the cumulative germination percentage in time interval i, and k is the total number of time intervals. It also estimated in terms of partial germination percentage as follows. $\Sigma k = \sum_{i=1}^{k} g_i (k - j)$ Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to k), k is the total number of time intervals, and $j = i - 1$.		Mixed	Grose and Zimmer (1958); Timson (1965); Lyon and Coffelt (1966); Chaudhary and Ghildyal (1970); Negm and Smith (1978); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971)
Modified Timson's index (Σk_{mod}) (Labouriau)	`TimsonsIndex`	It is estimated as Timson's index Σk divided by the sum of partial germination percentages. $\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}$		Mixed	Ranal and Santana (2006)
Modified Timson's index (Σk_{mod}) (Khan and Unger)	`TimsonsIndex`	It is estimated as Timson's index (Σk) divided by the total time period of germination (T_k). $\Sigma k_{mod} = \frac{\Sigma k}{T_k}$		Mixed	Khan and Ungar (1984)
George's index (GR)	`GermRateGeorge`	It is estimated as follows. $GR = \sum_{i=1}^{k} N_i K_i$ Where N_i is the number of seeds germinated by ith interval and K_i is the number of intervals(eg. days) until the end of the test, and and k is the total number of time intervals.		Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968)

Germination index	Function	Details	Unit	Measures	Reference
Germination Index (GI) (Melville)	`GermIndex`	It is estimated as follows. $GI = \sum_{i=1}^{k} \frac{\lvert (T_{k} - T_{i})\, N_{i} \rvert}{N_{t}}$ Where, T_{i} is the time from the start of the experiment to the ith interval (day for the example), N_{i} is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), N_{t} is the total number of seeds used in the test, and k is the total number of time intervals.		Mixed	Melville et al. (1980)
Germination Index (GI_{mod}) (Melville; Santana and Ranal)	`GermIndex`	It is estimated as follows. $GI_{mod} = \sum_{i=1}^{k} \frac{\lvert (T_{k} - T_{i})\, N_{i} \rvert}{N_{g}}$ Where, T_{i} is the time from the start of the experiment to the ith interval (day for the example), N_{i} is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), N_{g} is the total number of germinated seeds at the end of the test, and k is the total number of time intervals.		Mixed	Melville et al. (1980); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (ERI) or Germination Rate Index (Shmueli and Goldberg)	`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.		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.		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.		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.		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.		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.		Mixed	Djavanshir and Pourbeik (1976); Brown and Mayer (1988)
Coefficient of uniformity of germination (CUG)	`CUGerm`	It is computed as follows. $$CUG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k}(\overline{T} - T_i)^2 N_i}$$ Where, $\overline{T}$ is the the mean germination time, T_i is the time from the start of the experiment to the ith interval (day for the example), N_i is the number of seeds germinated in the ith time interval (not the accumulated number, but the number corresponding to the ith interval), and k is the total number of time intervals.		Germination unifromity	Heydecker (1972); Bewley and Black (1994)
Coefficient of variation of the germination time (CV_T)	`CVGermTime`	It is estimated as follows. $$CV_T = \sqrt{\frac{s_T^2}{\overline{T}}}$$ Where, s_T^2 is the variance of germination time and $\overline{T}$ is the mean germination time.		Germination unifromity	Gomes (1960); Ranal and Santana (2006)
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.		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 = z, intervals = int, total.seeds = 50,
                partial = FALSE)
```

```
[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
#----------------------------------------------------------------------------
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
```

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

```
[1] 5.970588
```

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

```
[1] 5.941176
```

```

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

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

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

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

```
[1] 6.7
```

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

```
[1] 19.04012
```

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

```
[1] 0.2394781
```

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

```
[1] 0.6512685
```

```

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

# From partial germination counts
```

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

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.0007176543
```

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

```
[1] 0.004235724
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

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

```
[1] 0.1492537
```

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

```
[1] 14.92537
```

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

```
[1] 0.009448666
```

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

```
[1] 0.005334776
```

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

```
[1] 0.1674877
```

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

```
[1] 0.1683168
```

```

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

# From partial germination counts
```

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

```
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] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

```
[1] 6.138925
```

```
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] 0.07673656
```

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

```
[1] 0.4326958
```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

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

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

WeightGermPercent()

```
[1] 47.42857
```

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

```
[1] 47.42857
```

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

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

MeanGermPercent(), MeanGermNumber()

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

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

```
[1] 2.857143
```

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

```
[1] 5.714286
```

```r

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

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

TimsonsIndex(), GermRateGeorge()

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

```
[1] 172
```

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

```
[1] 332
```

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

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

GermIndex()

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

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

EmergenceRateIndex()

```
[1] 292
```

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

```
[1] 292
```

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

```
[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 = "melville")
```

```
[1] 292
```

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

```
[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
```

```
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
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS SumDGSbyN        GV
1            0         1                      0                     0.0 0.000000  0.000000  0.000000
2            0         2                      0                     0.0 0.000000  0.000000  0.000000
3           34         3                     34                    17.0 5.666667  1.888889  3.211111
4           40         4                     74                    37.0 9.250000  3.729167 13.797917
5           21         5                     95                    47.5 9.500000  4.883333 23.195833
6           10         6                    105                    52.5 8.750000  5.527778 29.020833
7            4         7                    109                    54.5 7.785714  5.850340 31.884354
8            5         8                    114                    57.0 7.125000  6.009673 34.255134
9            3         9                    117                    58.5 6.500000  6.064153 35.475298
10           5        10                    122                    61.0 6.100000  6.067738 37.013202
11           8        11                    130                    65.0 5.909091  6.053316 39.346552
12           7        12                    137                    68.5 5.708333  6.024567 41.268285
13           7        13                    144                    72.0 5.538462  5.987174 43.107655
14           6        14                    150                    75.0 5.357143  5.942172 44.566291
15           6        15                    156                    78.0 5.200000  5.892694 45.963013
```

```
16          4        16                    160                     80.0 5.000000  5.836901 46.695205
17          0        17                    160                     80.0 4.705882  5.770370 46.162961
18          2        18                    162                     81.0 4.500000  5.699794 46.168331
19          0        19                    162                     81.0 4.263158  5.624182 45.555871
20          2        20                    164                     82.0 4.100000  5.547972 45.493374

$testend
[1] 16
```

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

```
[1] 9.5
```

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

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

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

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS SumDGSbyN        GV
3           34         3                     34                    17.0 5.666667  5.666667  9.633333
4           40         4                     74                    37.0 9.250000  7.458333 27.595833
5           21         5                     95                    47.5 9.500000  8.138889 38.659722
6           10         6                    105                    52.5 8.750000  8.291667 43.531250
7            4         7                    109                    54.5 7.785714  8.190476 44.638095
```

```
8             5          8                     114                    57.0 7.125000  8.012897 45.673512
9             3          9                     117                    58.5 6.500000  7.796769 45.611097
10            5         10                     122                    61.0 6.100000  7.584673 46.266503
11            8         11                     130                    65.0 5.909091  7.398497 48.090230
12            7         12                     137                    68.5 5.708333  7.229481 49.521942
13            7         13                     144                    72.0 5.538462  7.075752 50.945411
14            6         14                     150                    75.0 5.357143  6.932534 51.994006
15            6         15                     156                    78.0 5.200000  6.799262 53.034246
16            4         16                     160                    80.0 5.000000  6.670744 53.365948
17            0         17                     160                    80.0 4.705882  6.539753 52.318022
18            2         18                     162                    81.0 4.500000  6.412268 51.939373
19            0         19                     162                    81.0 4.263158  6.285850 50.915385
20            2         20                     164                    82.0 4.100000  6.164414 50.548194

$testend
[1] 16
```

```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] 0.05267935
```

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

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

GermSynchrony(), GermUncertainty()

```
[1] 0.2666667
```

```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".

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

Germination parameters	Details	Unit	Measures
lag	It is the time at germination onset and is computed by solving four-parameter hill function after setting y to 0 as follows. $$lag = b\sqrt{\frac{-y_0 c^b}{a + y_0}}$$	time	Germination time
D_{lag-50}	The duration between the time at germination onset (lag) and that at 50% germination (c).	time	Germination time
$t_{50_{total}}$	Time required for 50% of total seeds to germinate.	time	Germination time
$t_{50_{germinated}}$	Time required for 50% of viable/germinated seeds to germinate	time	Germination time
$t_{x_{total}}$	Time required for x% of total seeds to germinate.	time	Germination time
$t_{x_{germinated}}$	Time required for x% of viable/germinated seeds to germinate	time	Germination time
Uniformity ($U_{t_{max}-t_{min}}$)	It is the time interval between the percentages of viable seeds specified in the arguments `umin` and `umin` to germinate.	time	Germination time
Time at maximum germination rate ($TMGR$)	The partial derivative of the four-parameter hill function gives the instantaneous rate of germination (s) as follows. $$s = \frac{\partial y}{\partial x} = \frac{abc^b x^{b-1}}{(c^b + x^b)^2}$$ From this function for instantaneous rate of germination, $TMGR$ can be estimated as follows. $$TMGR = b\sqrt{\frac{c^b(b-1)}{b+1}}$$ It represents the point in time when the instantaneous rate of germination starts to decline.	time	Germination time
Area under the curve (AUC)	It is obtained by integration of the fitted curve between time 0 and time specified in the argument `tmax`.		Mixed
MGT	Calculated by integration of the fitted curve and proper normalisation.	time	Germination time
$Skewness$	It is computed as follows. $$\frac{MGT}{t_{50_{germinated}}}$$		

Examples

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

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

FourPHFfit()

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

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

$Fit
     sigma isConv       finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723          10   14

$a
[1] 80

$b
[1] 9.881947

$c
[1] 6.034954

$y0
[1] 0

$lag
[1] 0
```

```
$Dlag50
[1] 6.034954

$t50.total
[1] 6.355122

$txp.total
      10       60
4.956266 6.744598

$t50.Germinated
[1] 6.034954

$txp.Germinated
      10       60
4.831809 6.287724

$Uniformity
        90         10 uniformity
  7.537688   4.831809   2.705880

$TMGR
[1] 5.912195

$AUC
[1] 1108.975

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

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

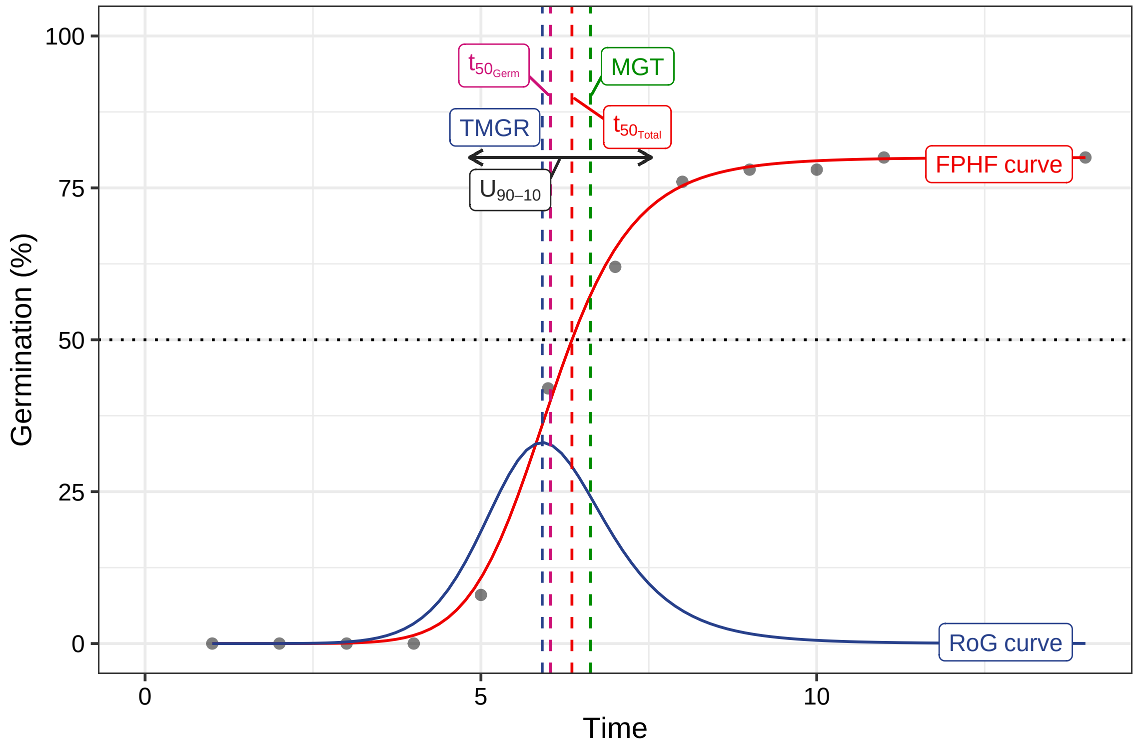
```
# From cumulative germination counts
#----------------------------------------------------------------------------
FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, tmax = 20,
partial = FALSE)
```

```
$data
   gp csgp intervals
1   0    0         1
2   0    0         2
3   0    0         3
4   0    0         4
5   8    8         5
```

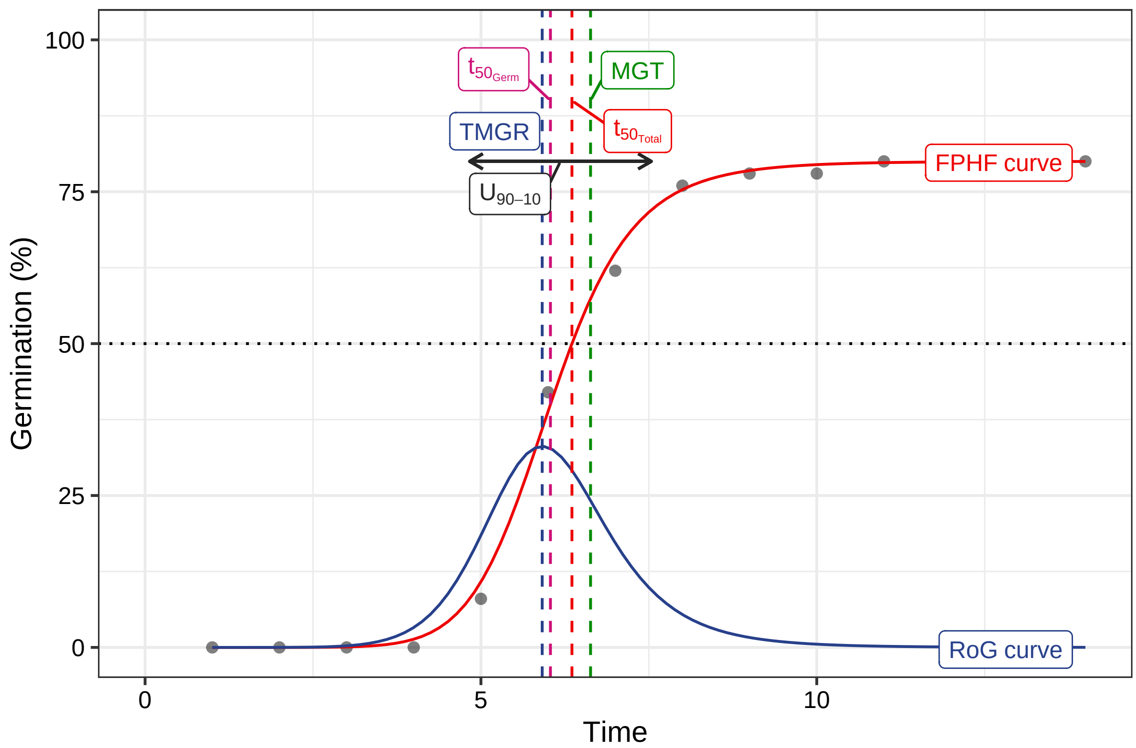
```
6  34   42         6
7  20   62         7
8  14   76         8
9   2   78         9
10  0   78        10
11  2   80        11
12  0   80        12
13  0   80        13
14  0   80        14

$Parameters
  term  estimate std.error statistic      p.value
1    a 80.000000 1.2415867  64.43368 1.973252e-14
2    b  9.881927 0.7077918  13.96163 6.952270e-08
3    c  6.034953 0.0495266 121.85275 3.399437e-17
4   y0  0.000000 0.9160705   0.00000 1.000000e+00

$Fit
     sigma isConv       finTol    logLik      AIC      BIC deviance df.residual nobs
1 1.769385   TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723          10   14

$a
[1] 80

$b
[1] 9.881927

$c
[1] 6.034953

$y0
[1] 0

$lag
[1] 0

$Dlag50
[1] 6.034953

$t50.total
[1] 6.355121

$txp.total
      10       60
4.956263 6.744599

$t50.Germinated
[1] 6.034953

$txp.Germinated
      10       60
4.831806 6.287723

$Uniformity
```

```
       90        10 uniformity
  7.537691   4.831806   2.705885

$TMGR
[1] 5.912194

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

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

$isConv
[1] TRUE

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

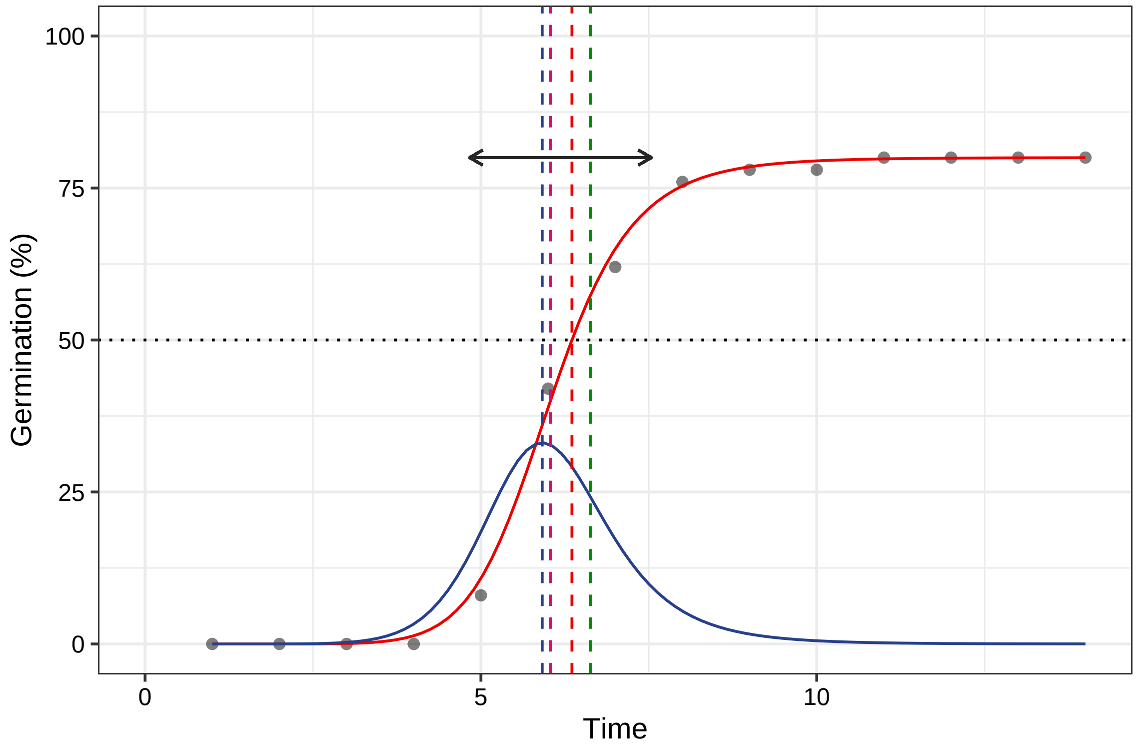
```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

# 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
plot(fit1)
```



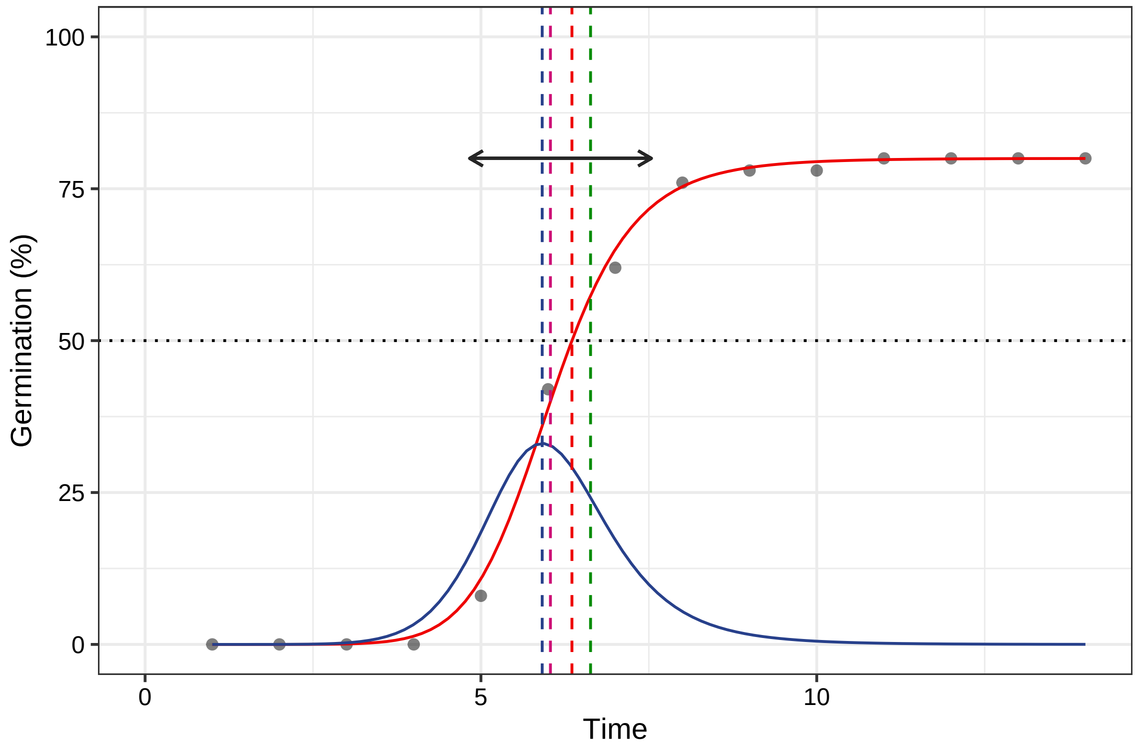

```
plot(fit2)
```



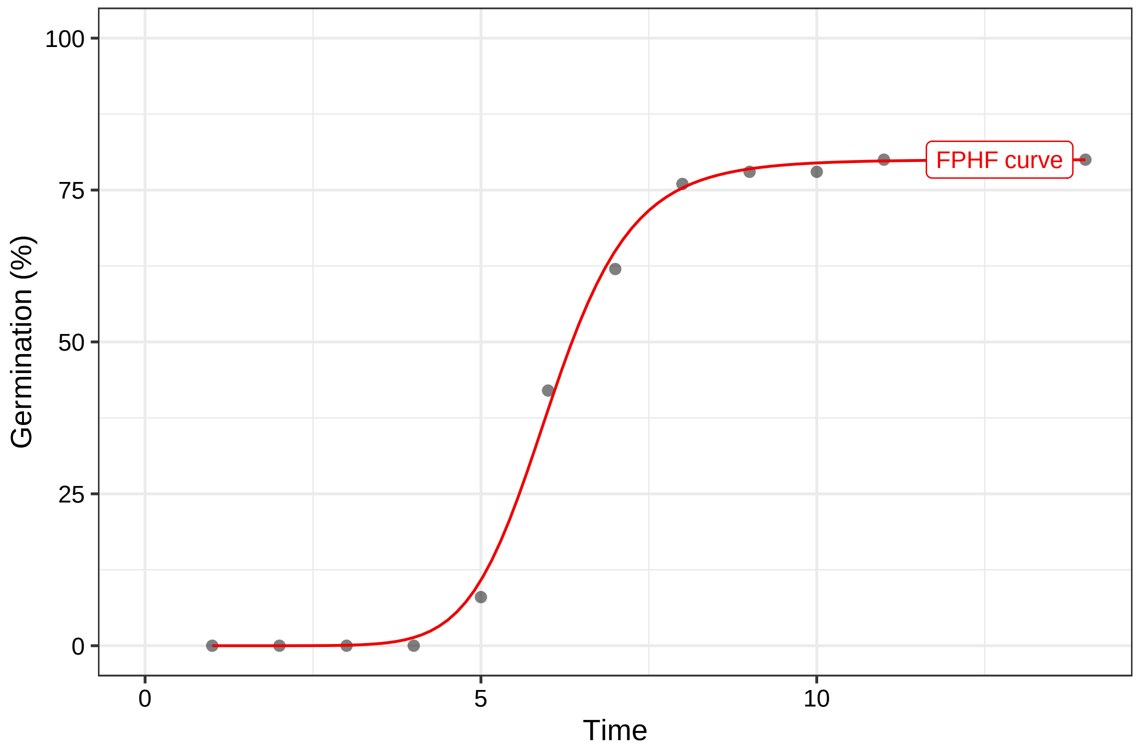

```
# No labels
plot(fit1, plotlabels = FALSE)
```



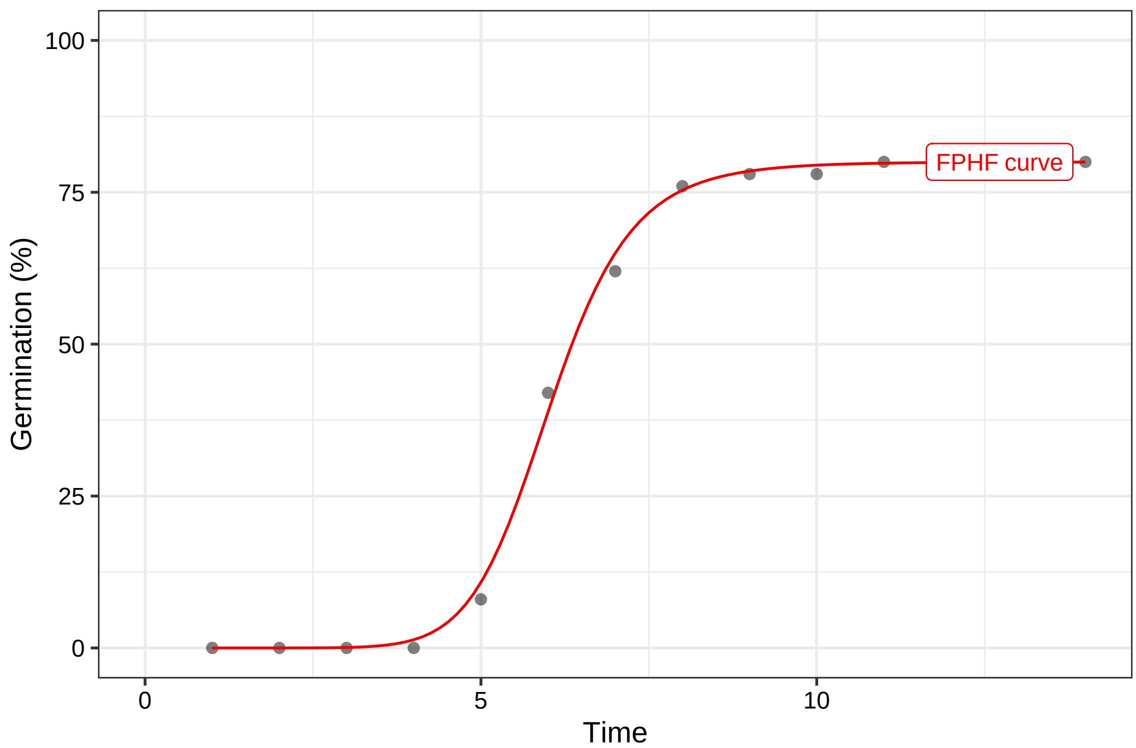

```
plot(fit2, plotlabels = FALSE)
```



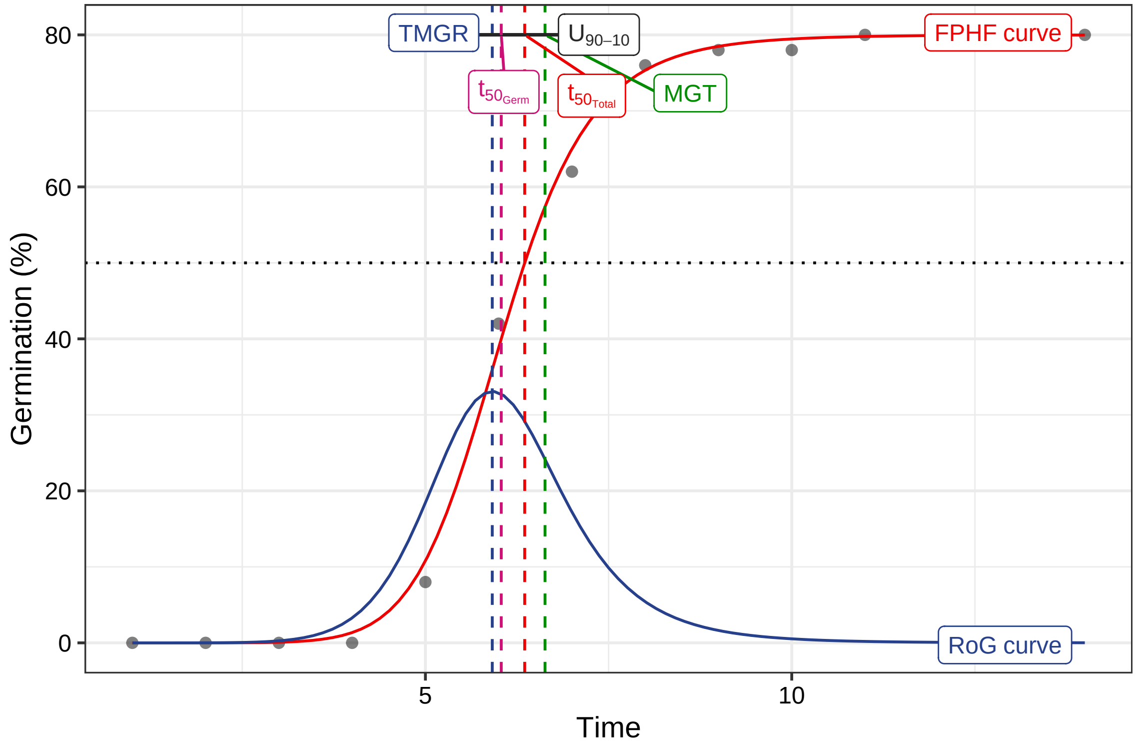

```
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



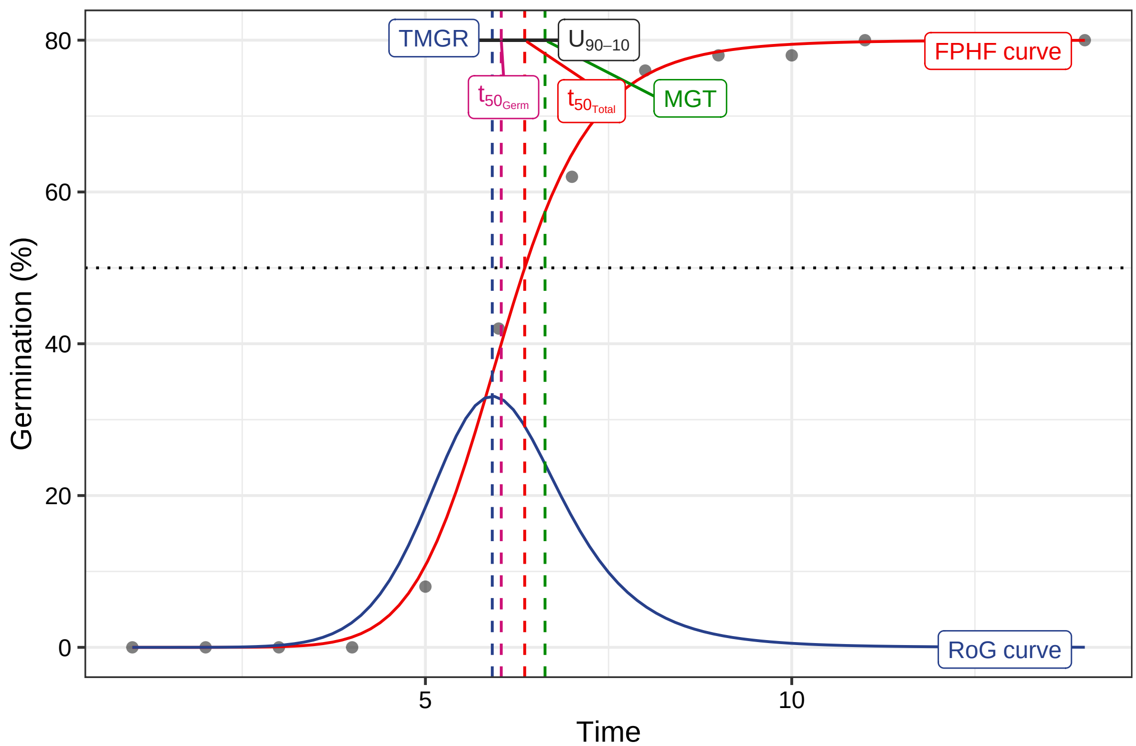

```r
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



```
# 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
   PeakGermPercent FirstGermTime LastGermTime PeakGermTime TimeSpreadGerm t50_Coolbear t50_Farooq MeanGe
1         34.00000             5           11            6              6     5.970588   5.941176      6
2         29.41176             4           12            6              8     6.192308   6.153846      6
3         37.50000             4           12            6              8     6.000000   5.972222      6
4         37.25490             5           12            6              7     6.041667   6.000000      6
5         40.00000             5           13            6              8     5.975000   5.950000      6
6         42.85714             5           12            6              7     5.976190   5.952381      6
7         37.50000             5           11            6              6     5.972222   5.944444      6
8         29.78723             4           12            6              8     6.208333   6.166667      6
9         36.53846             4           12            6              8     6.000000   5.973684      6
10        36.00000             5           12            6              7     6.076923   6.038462      6
11        41.17647             5           13            6              8     5.928571   5.904762      6
12        39.21569             5           12            6              7     5.975000   5.950000      6
13        38.77551             5           13            6              8     6.083333   6.041667      6
14        43.75000             5           12            6              7     5.928571   5.904762      6
15        35.41667             5           11            6              6     6.050000   6.000000      6
   SEGermTime CVGermTime MeanGermRate  VarGermRate   SEGermRate      CVG GermRateRecip_Coolbear GermRateR
1   0.1901416  0.1794868    0.1492537 0.0007176543 0.004235724 14.92537             0.1674877
2   0.2197333  0.2076717    0.1458333 0.0009172090 0.004673148 14.58333             0.1614907
3   0.2391061  0.2335882    0.1456311 0.0011572039 0.005071059 14.56311             0.1666667
4   0.2180907  0.2146419    0.1451104 0.0009701218 0.004592342 14.51104             0.1655172
```

```
5   0.2221275  0.2259002    0.1467890 0.0010995627 0.004786184 14.67890           0.1673640
6   0.2122088  0.2095140    0.1455696 0.0009301809 0.004496813 14.55696           0.1673307
7   0.1818989  0.1761967    0.1494662 0.0006935558 0.004063648 14.94662           0.1674419
8   0.2297923  0.2113940    0.1454545 0.0009454531 0.004861721 14.54545           0.1610738
9   0.2260777  0.2208604    0.1456311 0.0010345321 0.004794747 14.56311           0.1666667
10  0.2017321  0.1983606    0.1465798 0.0008453940 0.004334343 14.65798           0.1645570
11  0.2227295  0.2272072    0.1472393 0.0011191581 0.004828643 14.72393           0.1686747
12  0.2210295  0.2129053    0.1452145 0.0009558577 0.004660905 14.52145           0.1673640
13  0.2324392  0.2297410    0.1441718 0.0010970785 0.004831366 14.41718           0.1643836
14  0.2078370  0.2035568    0.1476510 0.0009033254 0.004531018 14.76510           0.1686747
15  0.1994129  0.1897847    0.1468531 0.0007767634 0.004300508 14.68531           0.1652893
   GermSpeed_Percent GermSpeedAccumulated_Count GermSpeedAccumulated_Percent GermSpeedCorrected_Normal
1           12.27785                   34.61567                     69.23134                0.07673656
2           12.47588                   35.54058                     69.68741                0.07726134
3           14.33787                   38.29725                     79.78594                0.07340991
4           13.58317                   38.68453                     75.85202                0.07680397
5           14.63797                   41.00786                     82.01571                0.07623944
6           14.14649                   38.77620                     79.13509                0.07383855
7           13.43427                   36.38546                     75.80304                0.07369656
8           12.87909                   33.77079                     71.85275                0.07112480
9           13.13575                   38.11511                     73.29829                0.07893128
10          13.62540                   38.19527                     76.39054                0.07569665
11          14.39764                   41.17452                     80.73436                0.07801721
12          12.98482                   37.00640                     72.56158                0.07675799
13          14.39249                   39.29399                     80.19182                0.07352419
14          13.97246                   37.69490                     78.53103                0.07316490
15          13.25818                   35.69697                     74.36868                0.07273057
   GermSpeedCorrected_Accumulated WeightGermPercent MeanGermPercent MeanGermNumber TimsonsIndex TimsonsI
1                       0.4326958          47.42857        5.714286       2.857143     8.000000
2                       0.4315642          47.89916        5.882353       3.000000     9.803922
3                       0.4085040          54.46429        6.696429       3.214286    14.583333
4                       0.4288937          52.24090        6.442577       3.285714     7.843137
5                       0.4271652          56.14286        6.857143       3.428571    10.000000
6                       0.4130508          54.51895        6.705539       3.285714     6.122449
7                       0.4158338          51.93452        6.250000       3.000000     8.333333
8                       0.3968068          49.39210        6.079027       2.857143    10.638298
9                       0.4404413          50.27473        6.181319       3.214286     9.615385
10                      0.4243919          52.57143        6.428571       3.214286     8.000000
11                      0.4374793          55.18207        6.722689       3.428571     9.803922
12                      0.4289379          50.00000        6.162465       3.142857     5.882353
13                      0.4096608          55.24781        6.851312       3.357143     8.163265
14                      0.4112171          53.86905        6.547619       3.142857     6.250000
15                      0.4079653          51.19048        6.250000       3.000000     8.333333
   TimsonsIndex_KhanUngar GermRateGeorge GermIndex GermIndex_mod EmergenceRateIndex_Melville EmergenceRa
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_BilbroWanjura EmergenceRateIndex_Fakorede PeakValue GermValue_Czabator GermValue_I
1                          5.970149                    8.375000  9.500000           54.28571     57.9389
2                          6.125000                    8.326531  9.313725           54.78662     52.5871
3                          6.553398                    7.324444 10.416667           69.75446     68.6228
4                          6.675079                    7.640359 10.049020           64.74158     70.4333
5                          7.045872                    7.096354 11.250000           77.14286     80.1691
6                          6.696203                    7.317580 10.714286           71.84506     76.5198
7                          6.277580                    7.646259 10.416667           65.10417     69.4132
8                          5.818182                    8.078125  9.574468           58.20345     56.0060
9                          6.553398                    7.934815  9.855769           60.92165     58.1347
10                         6.596091                    7.580247 10.250000           65.89286     70.9187
11                         7.067485                    7.216146 11.029412           74.14731     77.3978
12                         6.389439                    7.981921  9.803922           60.41632     64.4498
13                         6.776074                    7.231326 10.969388           75.15470     78.1633
14                         6.496644                    7.388430 10.677083           69.90947     74.4014
15                         6.167832                    7.782313 10.156250           63.47656     67.6203
   GermValue_DP_mod    CUGerm GermSynchrony GermUncertainty
1          39.56076 0.7092199     0.2666667        2.062987
2          40.99260 0.5051546     0.2346109        2.321514
3          53.42809 0.3975265     0.2242424        2.462012
4          48.86825 0.4672113     0.2502415        2.279215
5          56.23935 0.4312184     0.2606383        2.146051
6          53.06435 0.4934701     0.2792271        2.160545
7          47.37690 0.7371500     0.2729384        2.040796
8          43.67948 0.4855842     0.2256410        2.357249
9          45.30801 0.4446640     0.2494949        2.321080
10         49.10820 0.5584666     0.2555556        2.187983
11         54.27520 0.4288905     0.2686170        2.128670
12         44.71582 0.4760266     0.2737844        2.185245
13         54.94192 0.4023679     0.2506938        2.241181
14         51.41913 0.5383760     0.2991543        2.037680
15         46.48043 0.6133519     0.2497096        2.185028
```

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

```r
data(gcdata)

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

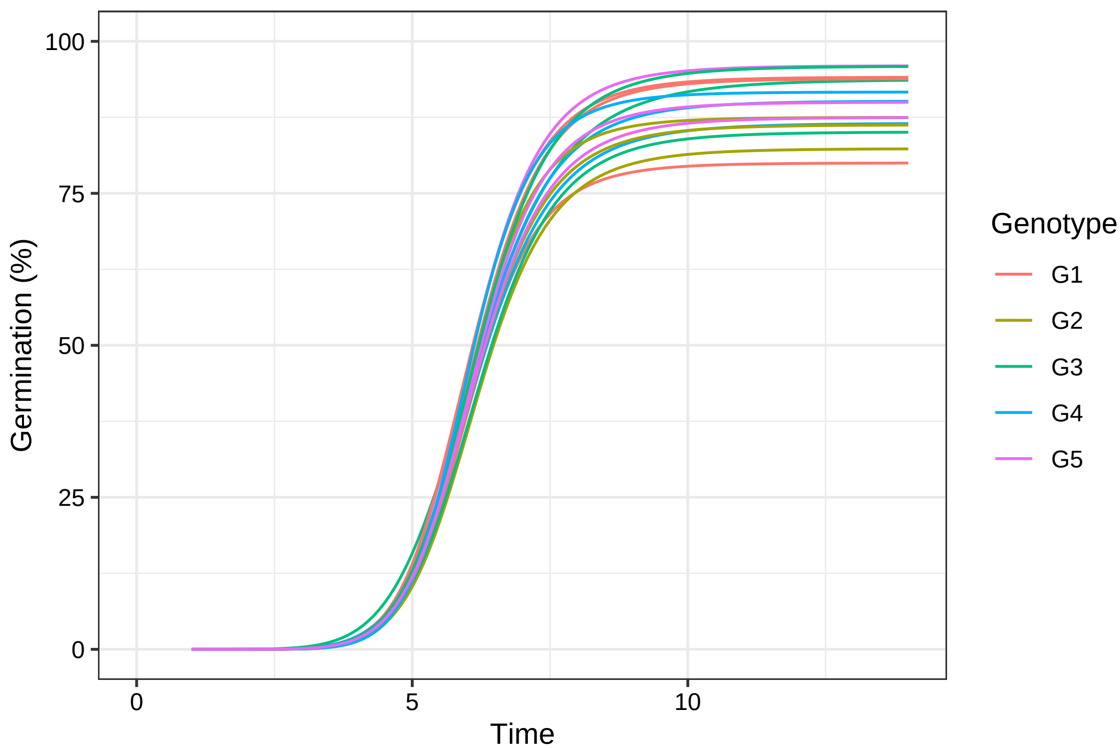
```
   Genotype Rep Day01 Day02 Day03 Day04 Day05 Day06 Day07 Day08 Day09 Day10 Day11 Day12 Day13 Day14 Tota
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
```

```
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 t50.Germinated     TMGR      AUC      MGT Skewness
1  6.034954  0   0 6.034954  6.355122       6.034954 5.912195 1108.975 6.632252 1.098973
2  6.175193  0   0 6.175193  6.473490       6.175193 6.031282 1128.559 6.784407 1.098655
3  6.138110  0   0 6.138110  6.244190       6.138110 5.938179 1283.693 6.772742 1.103392
4  6.125172  0   0 6.125172  6.276793       6.125172 5.972686 1239.887 6.739665 1.100323
5  6.049641  0   0 6.049641  6.103433       6.049641 5.914289 1328.328 6.654980 1.100062
6  6.097412  0   0 6.097412  6.182276       6.097412 5.961877 1294.463 6.702470 1.099232
7  6.029851  0   0 6.029851  6.202812       6.029851 5.914057 1213.908 6.622417 1.098272
8  6.189774  0   0 6.189774  6.439510       6.189774 6.036193 1164.346 6.804000 1.099232
9  6.125121  0   0 6.125121  6.352172       6.125121 5.961631 1188.793 6.745241 1.101242
10 6.109503  0   0 6.109503  6.253042       6.109503 5.978115 1240.227 6.711899 1.098600
11 6.018759  0   0 6.018759  6.099434       6.018759 5.883558 1305.200 6.624247 1.100600
12 6.108449  0   0 6.108449  6.326181       6.108449 5.964079 1188.021 6.718636 1.099892
13 6.149011  0   0 6.149011  6.207500       6.149011 5.998270 1316.407 6.762272 1.099733
14 6.015907  0   0 6.015907  6.122385       6.015907 5.905179 1273.386 6.604963 1.097916
15 6.121580  0   0 6.121580  6.317392       6.121580 5.976088 1203.664 6.732267 1.099760
                                                       msg isConv txp.total_10 txp.total_60 Uniforn
1  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.956266     6.744598       7
2  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.983236     6.872603       7
3  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.673022     6.608437       8
4  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.850876     6.614967       7
5  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.814126     6.386788       7
6  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.868635     6.477594       7
7  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.930423     6.510495       7
8  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.940058     6.823299       7
9  #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.836659     6.733275       7
10 #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.920629     6.566505       7
11 #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.798630     6.391288       7
12 #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.893597     6.684521       7
13 #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.841310     6.509952       7
14 #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.915143     6.397486       7
15 #1. Relative error in the sum of squares is at most `ftol'.   TRUE     4.892505     6.667247       7
   Uniformity
1    2.705880
2    2.968652
3    3.507277
4    3.046208
5    2.848078
6    2.860984
7    2.625165
```

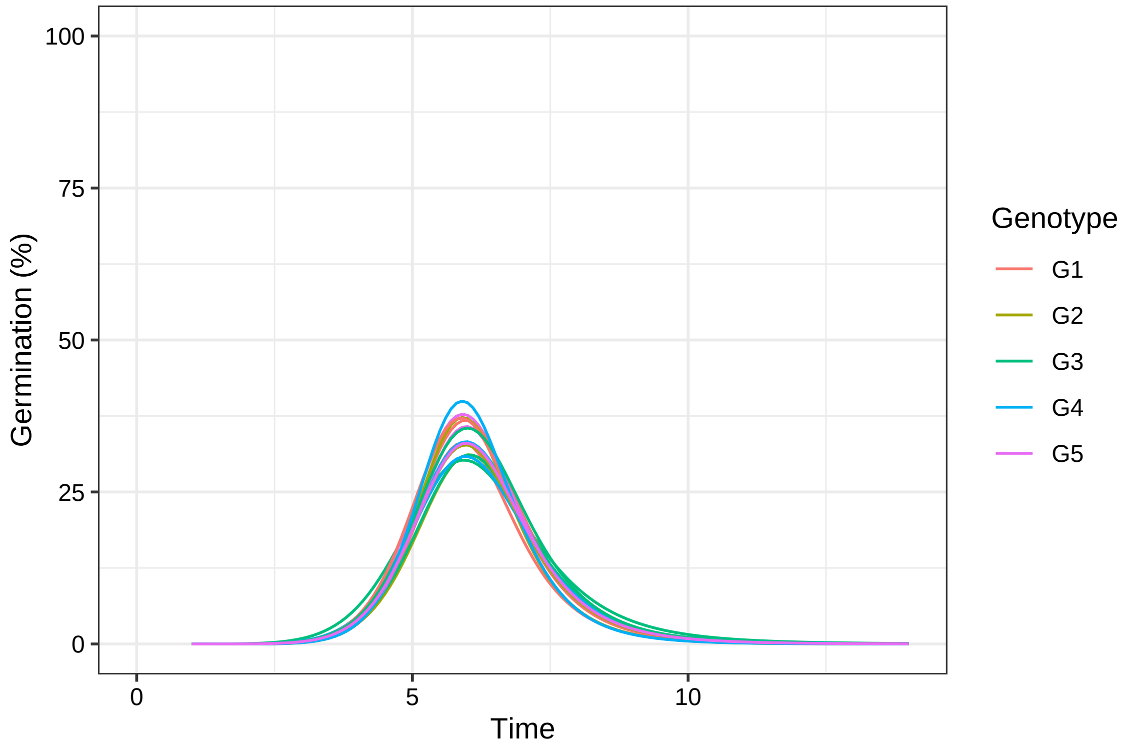
```
8     3.073056
9     3.157466
10    2.818494
11    2.839354
12    2.957830
13    3.033943
14    2.562960
15    2.972718
```

Multiple fitted curves generated in batch can also be plotted.

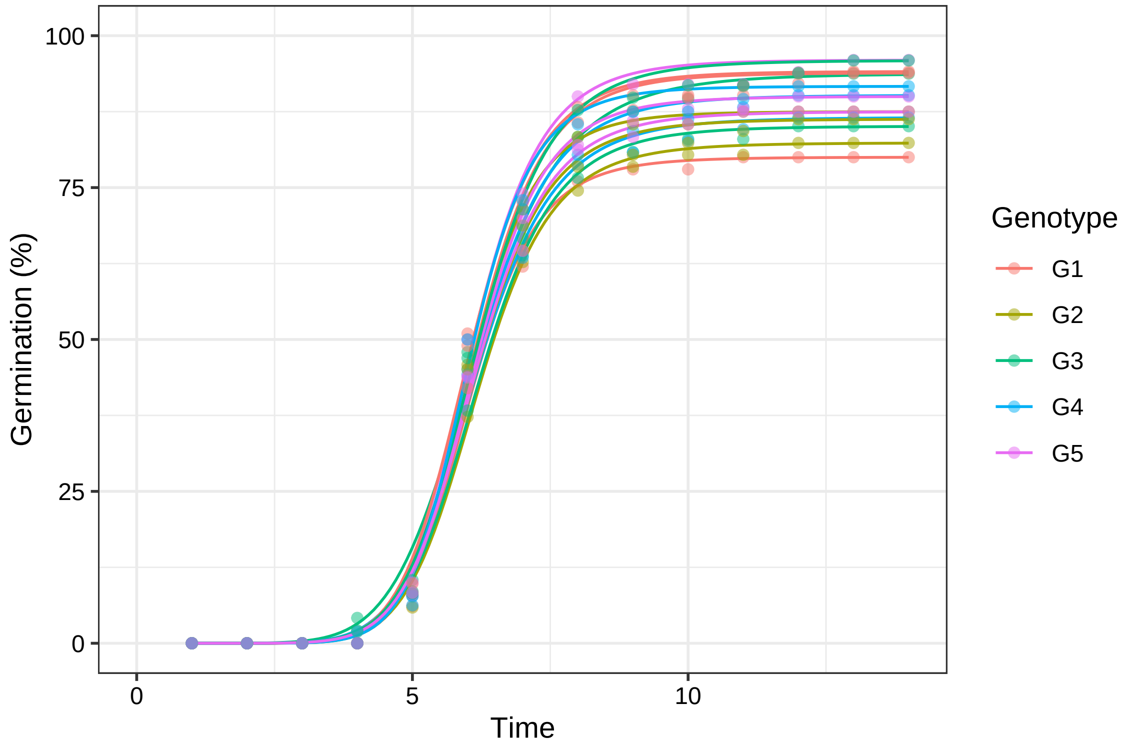
```r
data(gcdata)

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

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

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



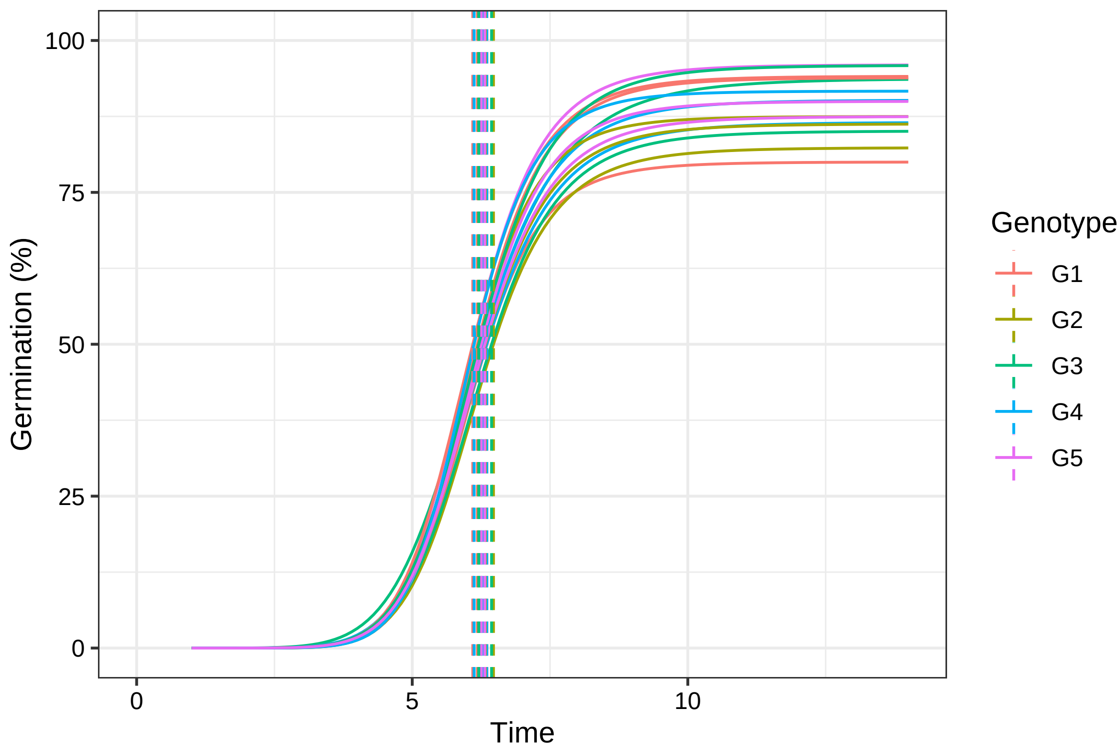

```r
# Plot ROG curves
plot(fits, rog = TRUE, group.col = "Genotype")
```



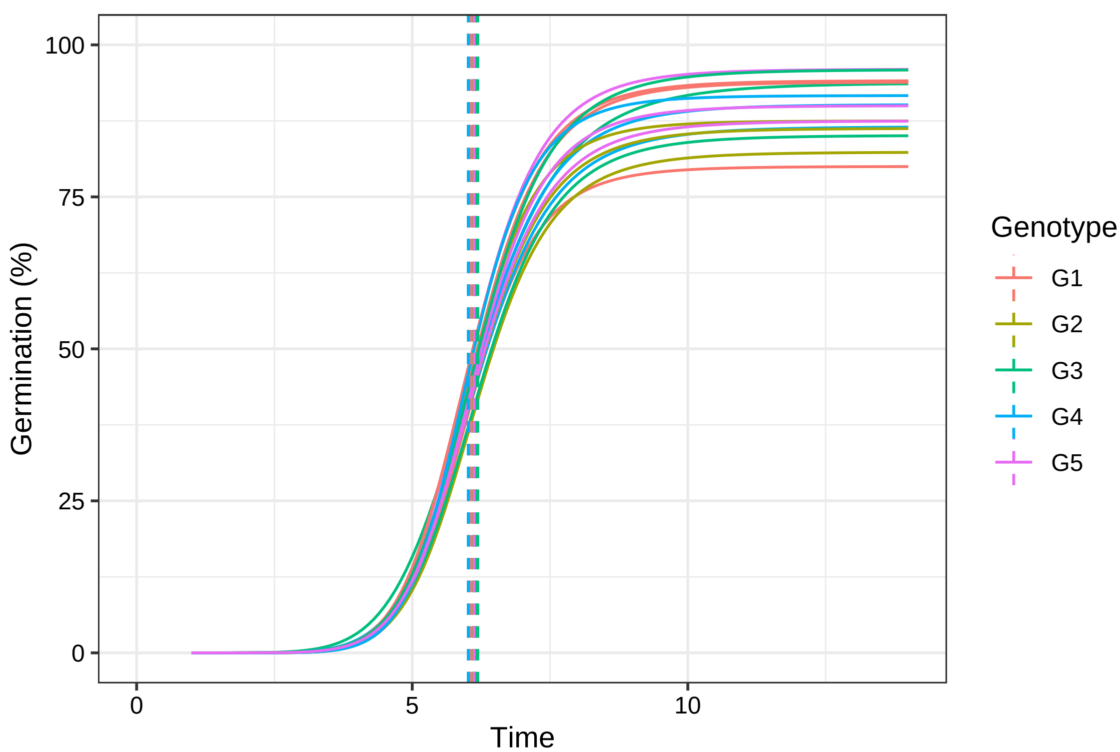

```r
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



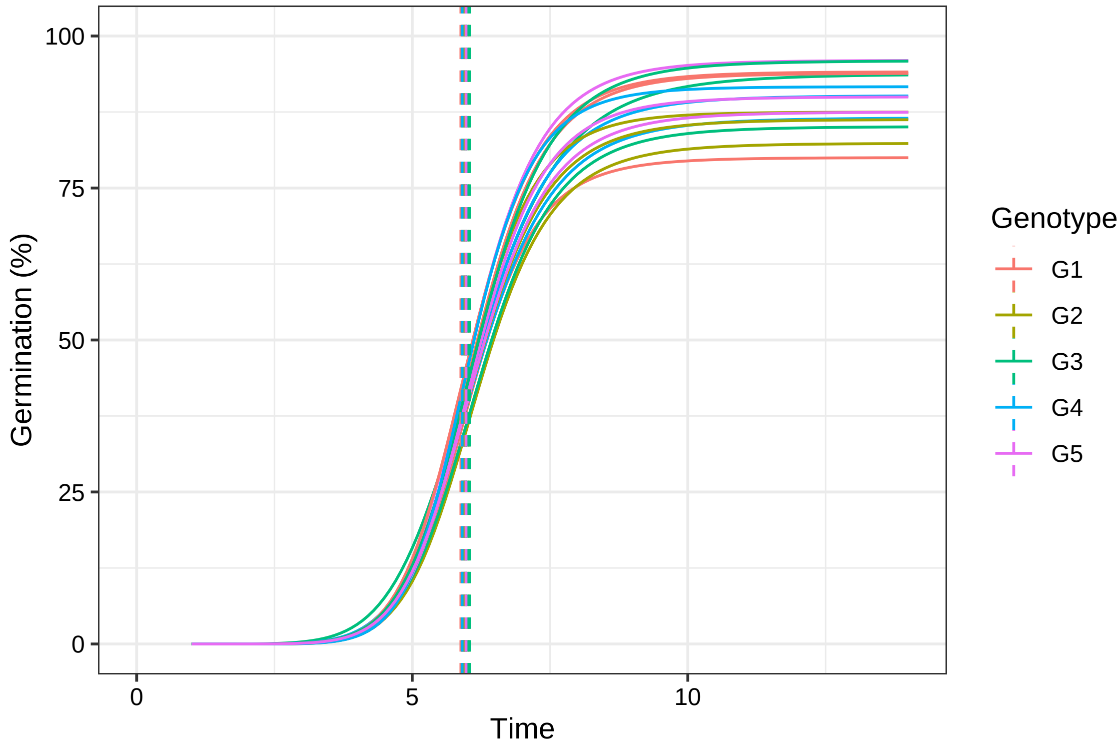

```r
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



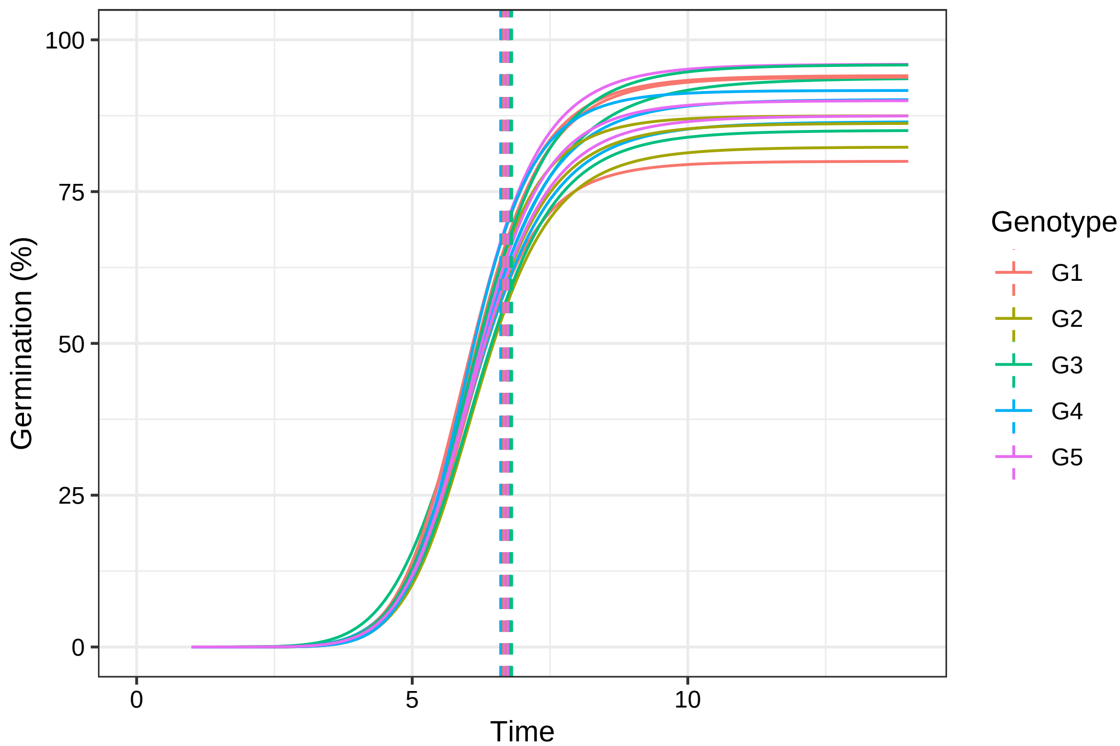

```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```




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

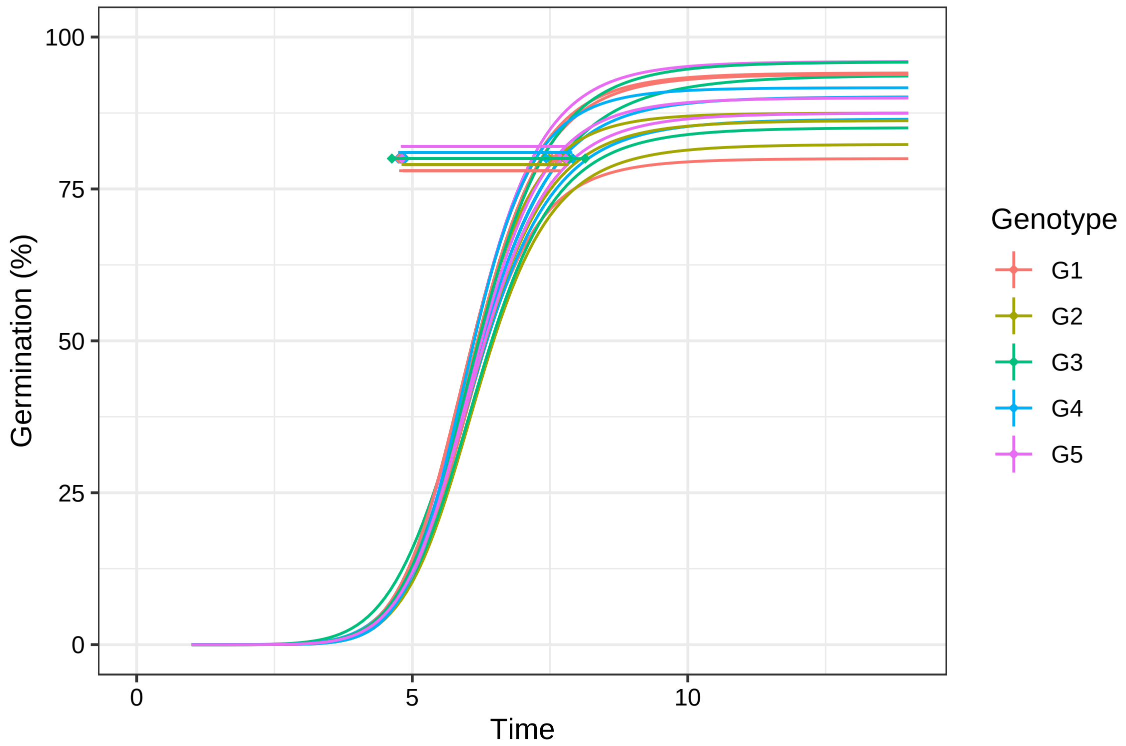



```
plot(fits, group.col = "Genotype", annotate = "mgt")
```

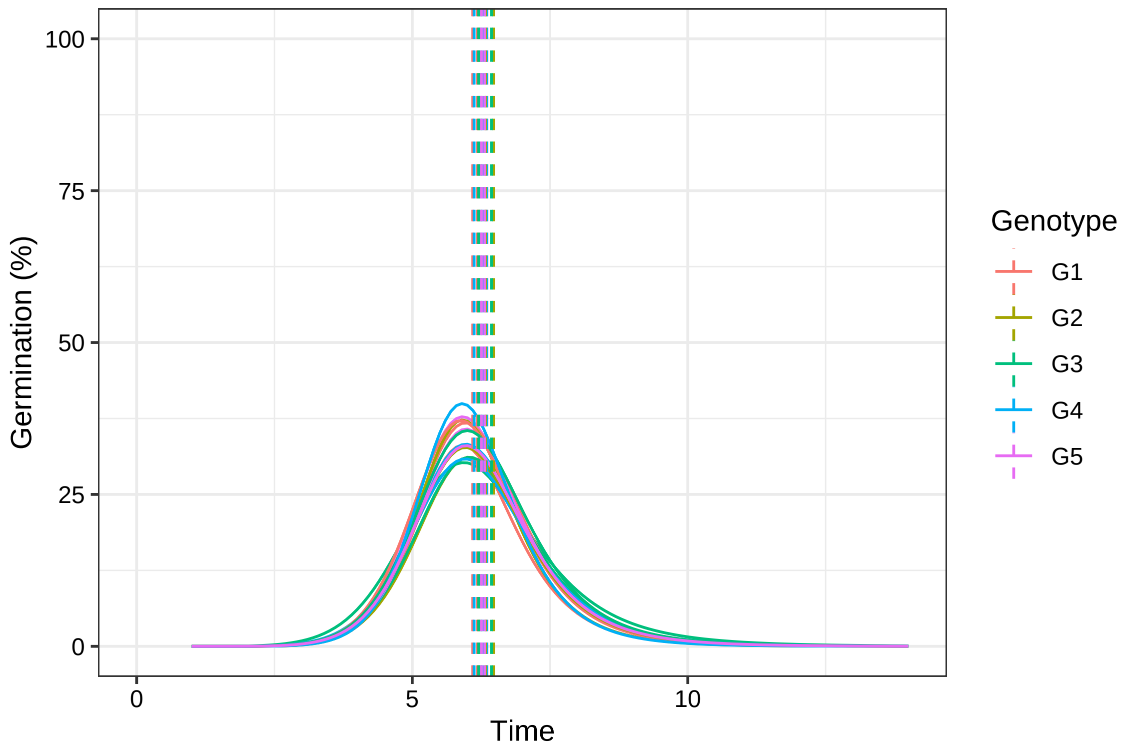



```
plot(fits, group.col = "Genotype", annotate = "uniformity")

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

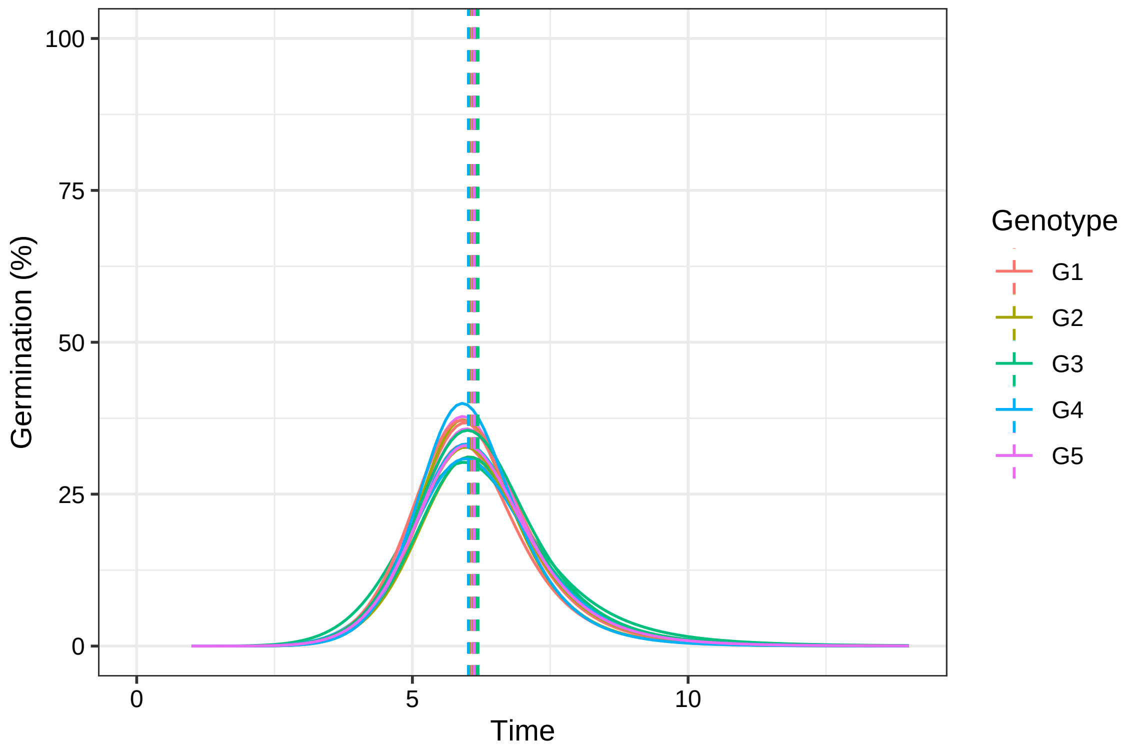
```
position_dodge requires non-overlapping x intervals
```



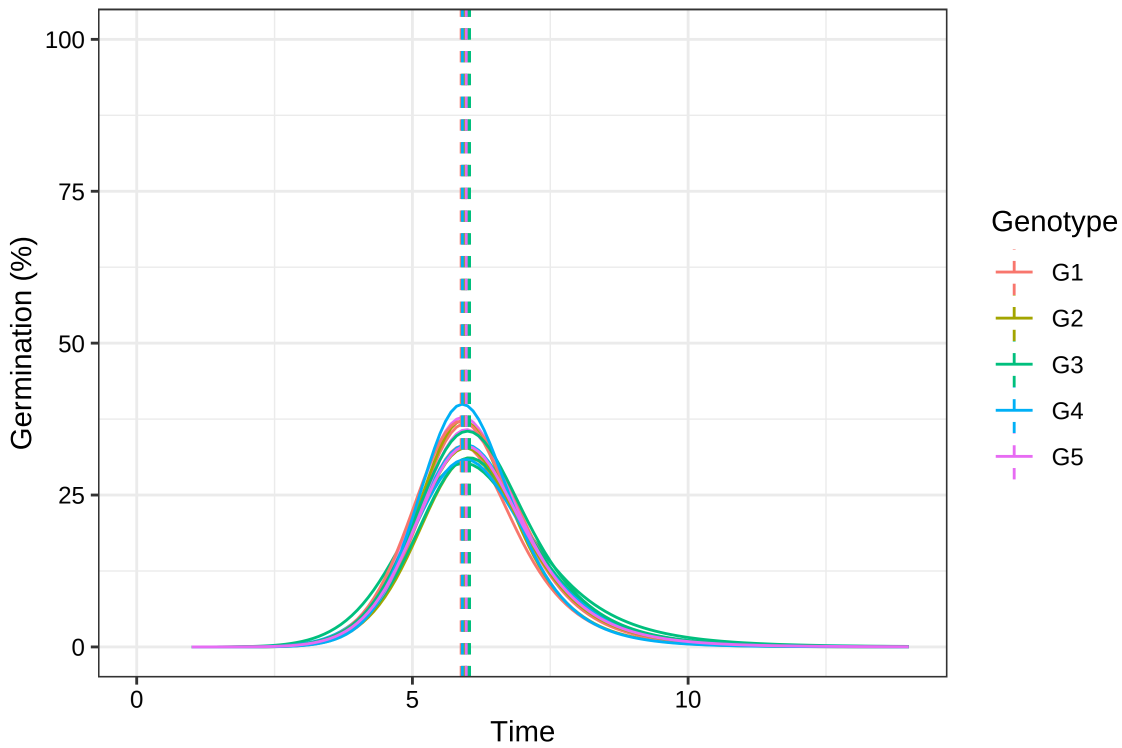

```r
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



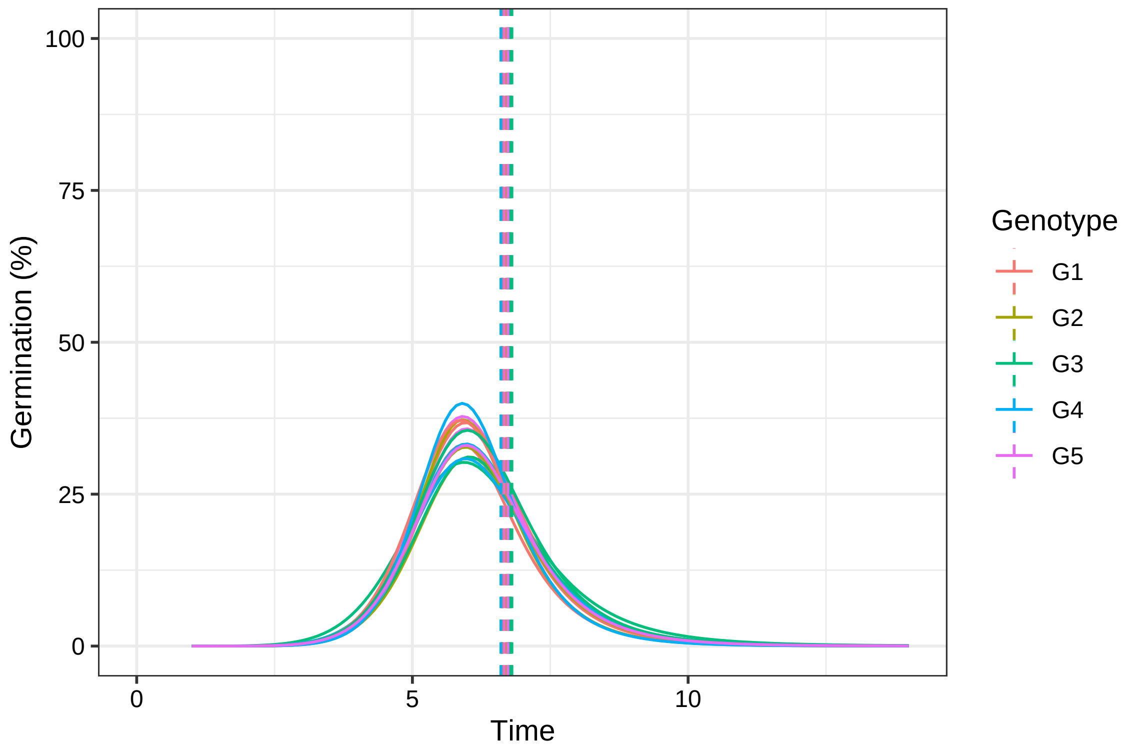
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```




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

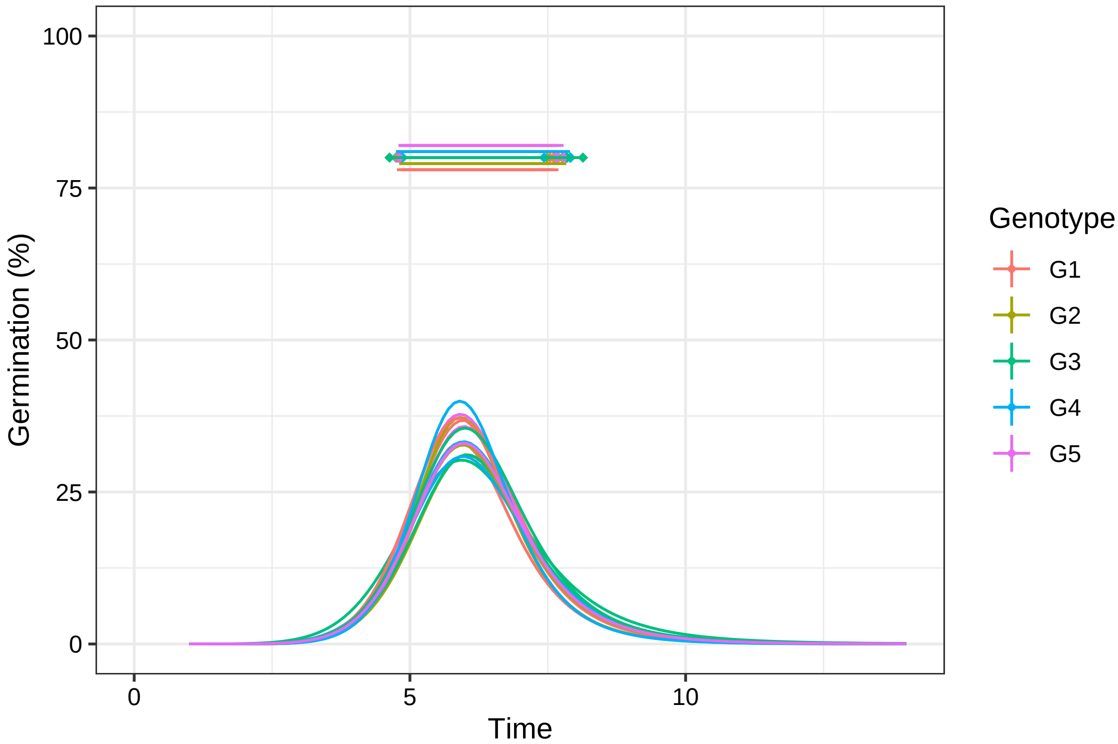


```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```




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

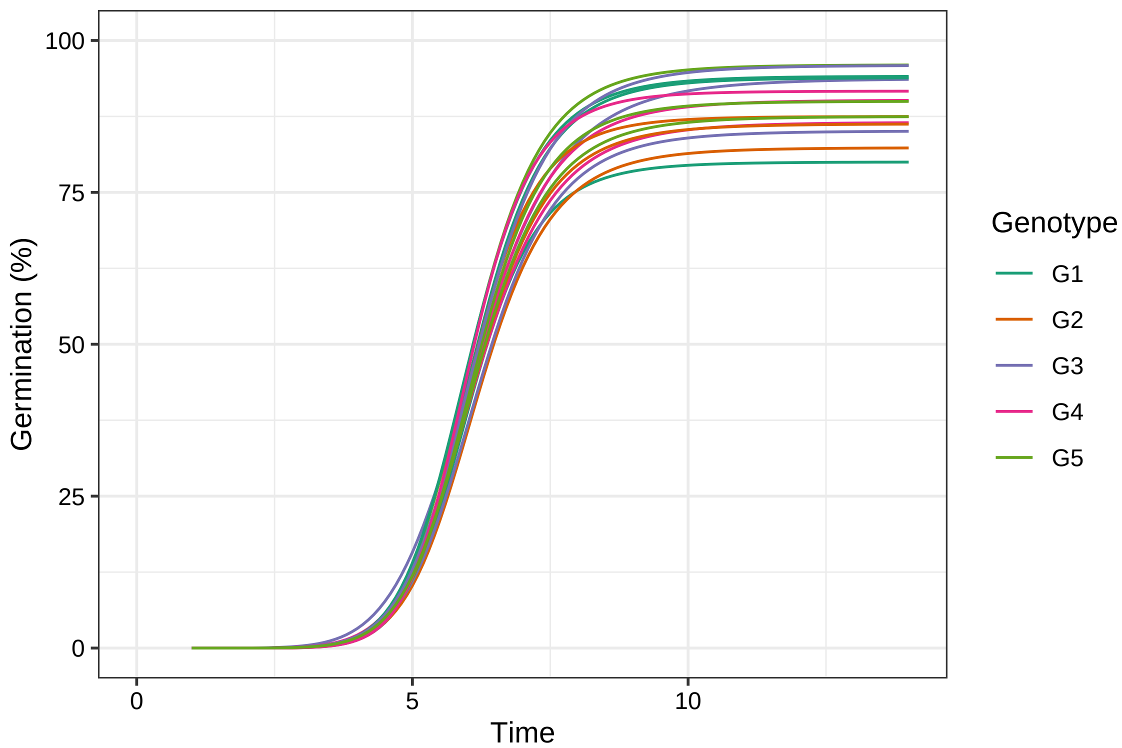
```
Warning: position_dodge requires non-overlapping x intervals
position_dodge requires non-overlapping x intervals
```



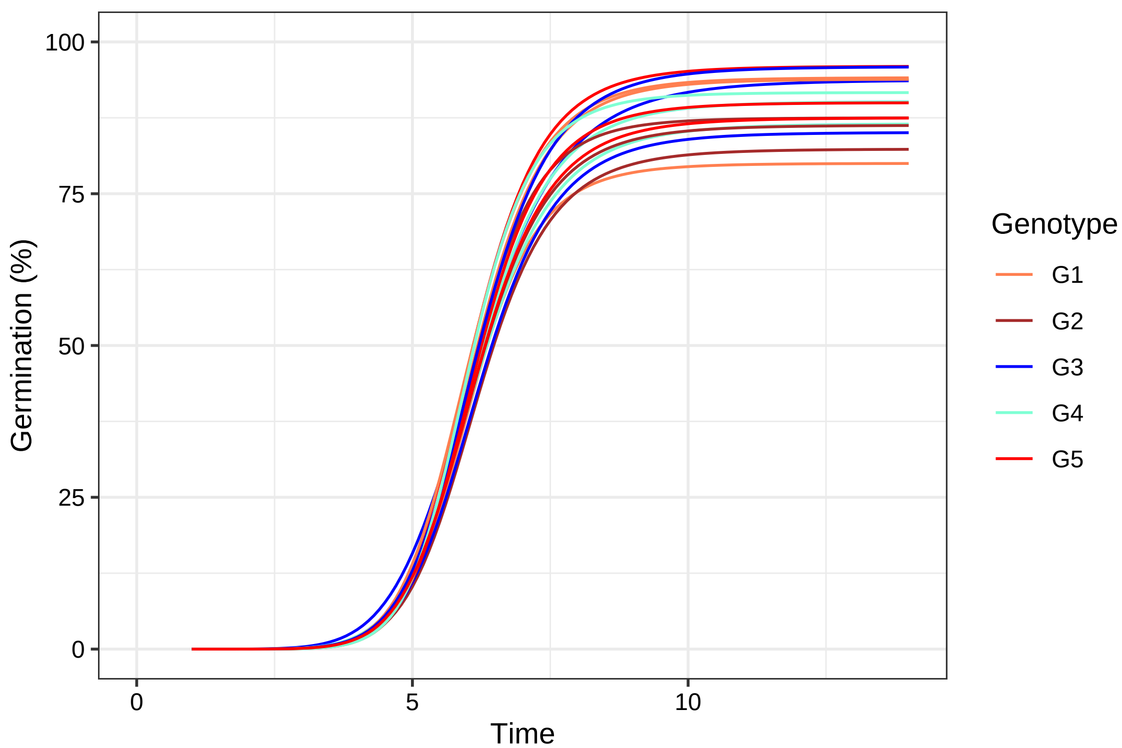

```
# Change colour of curves using ggplot2 options
library(ggplot2)
```

```
Need help getting started? Try the R Graphics Cookbook: https://r-graphics.org
```

```
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 (2022).  germinatio
  Germination Indices and Curve Fitting. R package version 0.1.5.9000,
  https://github.com/aravind-j/germinationmetricshttps://cran.r-project.org/package=germinationmetrics.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
    author = {J. Aravind and S. {Vimala Devi} and J. Radhamani and Sherry Rachel Jacob and {Kalyani Sri
    year = {2022},
    note = {R package version 0.1.5.9000},
    note = {https://github.com/aravind-j/germinationmetrics},
    note = {https://cran.r-project.org/package=germinationmetrics},
  }

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

Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2022-06-05 r82452 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 19044)

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

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

other attached packages:
[1] germinationmetrics_0.1.5.9000 ggplot2_3.3.6                 readxl_1.4.0

loaded via a namespace (and not attached):
 [1] tidyselect_1.1.2   farver_2.1.0       dplyr_1.0.9        bitops_1.0-7       RCurl_1.98-1.6     fas
 [7] lazyeval_0.2.2     xopen_1.0.0        mathjaxr_1.6-0     XML_3.99-0.9       rex_1.2.1          dig
[13] lifecycle_1.0.1    ellipsis_0.3.2     processx_3.5.3     magrittr_2.0.3     compiler_4.3.0     rla
[19] tools_4.3.0        utf8_1.2.2         yaml_2.3.5         data.table_1.14.2  knitr_1.39         lab
[25] prettyunits_1.1.1  pkgbuild_1.3.1     curl_4.3.2         xmlparsedata_1.0.5 RColorBrewer_1.1-3 ply
[31] xml2_1.3.3         pkgload_1.2.4      covr_3.5.1         withr_2.5.0        purrr_0.3.4        des
[37] hunspell_3.0.1     grid_4.3.0         goodpractice_1.0.2 fansi_1.0.3        colorspace_2.0-3   who
[43] scales_1.2.0       cli_3.3.0          rmarkdown_2.14     crayon_1.5.1       generics_0.1.2     rem
[49] rstudioapi_0.13    reshape2_1.4.4     httr_1.4.3         sessioninfo_1.2.2  DBI_1.1.2          cac
[55] pander_0.6.5       stringr_1.4.0      assertthat_0.2.1   cellranger_1.1.0   vctrs_0.4.1        dev
[61] jsonlite_1.8.0     minpack.lm_1.2-2   callr_3.7.0        rcmdcheck_1.4.0    ggrepel_0.9.1      tes
```

```
[67] cyclocomp_1.1.0    tidyr_1.2.0        glue_1.6.2         pkgdown_2.0.3      ps_1.7.0           stri
[73] gtable_0.3.0       munsell_0.5.0      tibble_3.1.7       pillar_1.7.0       clisymbols_1.2.0   html
[79] brio_1.1.3         praise_1.0.0       R6_2.5.1           lintr_2.0.1        Rdpack_2.3         rpro
[85] evaluate_0.15      highr_0.9          rbibutils_2.2.8    backports_1.4.1    memoise_2.0.1      broo
[91] Rcpp_1.0.8.3       xfun_0.31          fs_1.5.2           usethis_2.1.6      pkgconfig_2.0.3
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