

The `germinationmetrics` Package: A Brief Introduction

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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 0.1.10. The previous versions are as follows.

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

Version	Date
0.1.0	2018-04-17
0.1.1	2018-07-26
0.1.1.1	2018-10-16
0.1.2	2018-10-31
0.1.3	2019-01-19
0.1.4	2020-06-16
0.1.5	2021-02-17
0.1.6	2022-06-15
0.1.7	2022-08-28
0.1.8	2023-08-18
0.1.9	2025-12-14

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

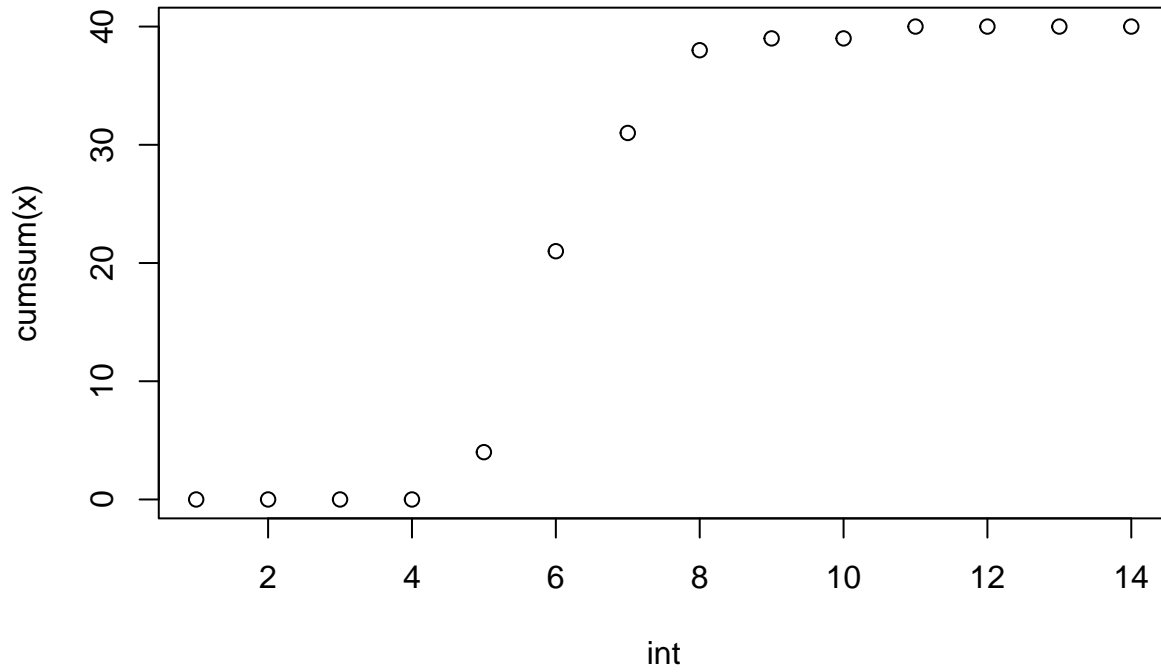
The time-course of germination can be plotted as follows.

```
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 i th interval and N_i is the number of seeds germinated in the i th time interval (not the accumulated number, but the number corresponding to the i th 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 i th interval and N_i is the number of seeds germinated in the i th time interval (not the accumulated number, but the number corresponding to the i th 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). $\text{Time spread of germination} = t_g - t_0$	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 i th interval, N_i is the number of seeds germinated in the i th time interval (not the accumulated number, but the number corresponding to the i th 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	<p>It is the time to reach 50% of final/maximum germination. With argument <code>method</code> specified as "coolbear", it is computed as follows.</p> $t_{50} = T_i + \frac{(\frac{N+1}{2} - N_i)(T_j - T_i)}{N_j - N_i}$ <p>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 $N_i < \frac{N+1}{2} < N_j$.</p>	time	Germination time	Coolbear et al. (1984)
Median germination time (t_{50}) (Farooq)	t50	<p>With argument <code>method</code> specified as "farooq", it is computed as follows.</p> $t_{50} = T_i + \frac{(\frac{N}{2} - N_i)(T_j - T_i)}{N_j - N_i}$ <p>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 $N_i < \frac{N}{2} < N_j$.</p>	time	Germination time	Farooq et al. (2005)
Mean germination time or Mean length of incubation time (\bar{T}) or Germination resistance (GR) or Sprouting index (SI) or Emergence index (EI)	MeanGermTime	<p>It is the average length of time required for maximum germination of a seed lot and is estimated according to the following formula.</p> $\bar{T} = \frac{\sum_{i=1}^k N_i T_i}{\sum_{i=1}^k N_i}$ <p>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.</p> <p>It is the inverse of mean germination rate (\bar{V}).</p> $\bar{T} = \frac{1}{\bar{V}}$	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	<p>It is computed according to the following formula.</p> $s_T^2 = \frac{\sum_{i=1}^k N_i (T_i - \bar{T})^2}{\sum_{i=1}^k N_i - 1}$ <p>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.</p>	time ⁻¹	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Standard error of germination time ($s_{\bar{T}}$)	SEGermTime	<p>It signifies the accuracy of the calculation of the mean germination time. It is estimated according to the following formula:</p> $s_{\bar{T}} = \sqrt{\frac{s_T^2}{\sum_{i=1}^k N_i}}$ <p>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.</p>	time	Germination time	Labouriau (1983a); Ranal and Santana (2006)
Mean germination rate (\bar{V})	MeanGermRate	<p>It is computed according to the following formula:</p> $\bar{V} = \frac{\sum_{i=1}^k N_i}{\sum_{i=1}^k N_i T_i}$ <p>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 (\bar{T}).</p> $\bar{V} = \frac{1}{\bar{T}}$	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 (<i>CVG</i>) or Coefficient of rate of germination (<i>CRG</i>) or Kotowski's coefficient of velocity	CVG	<p>It is estimated according to the following formula.</p> $CVG = \frac{\sum_{i=1}^k N_i}{\sum_{i=1}^k N_i T_i} \times 100$ $CVG = \bar{V} \times 100$ <p>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.</p>	% time ⁻¹	Germination rate	Kotowski (1926), Nichols and Heydecker (1968); Bewley and Black (1994); Labouriau (1983b); Scott et al. (1984)
Variance of germination rate (s_V^2)	VarGermRate	<p>It is calculated according to the following formula.</p> $s_V^2 = \bar{V}^4 \times s_T^2$ <p>Where, s_T^2 is the variance of germination time.</p>	time ⁻²	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Standard error of germination rate ($s_{\bar{V}}$)	SEGermRate	<p>It is estimated according to the following formula.</p> $s_{\bar{V}} = \sqrt{\frac{s_V^2}{\sum_{i=1}^k N_i}}$ <p>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.</p>	time ⁻¹	Germination rate	Labouriau (1983b); Ranal and Santana (2006)
Germination rate as the reciprocal of the median time (v_{50})	GermRateRecip	<p>It is the reciprocal of the median germination time (t_{50}).</p> $v_{50} = \frac{1}{t_{50}}$	time ⁻¹	Germination rate	Went (1957); Labouriau (1983b); Ranal and Santana (2006)
Speed of germination (S) or Germination rate Index or index of velocity of germination or Emergence rate index (Allan, Vogel and Peterson; Erbach; Hsu and Nelson) or Germination index (AOSA)	GermSpeed	<p>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.</p> $S = \sum_{i=1}^k \frac{N_i}{T_i}$ <p>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.</p>	% time ⁻¹ or count time ⁻¹	Mixed	Throneberry and Smith (1955); Maguire (1962); Allan et al. (1962); Kendrick and Frankland (1969); Bouton et al. (1976); Erbach (1982); AOSA (1983); Khandakar and Bradbeer (1983); Hsu and Nelson (1986); Bradbeer (1988); Wardle et al. (1991)

Germination index	Function	Details	Unit	Measures	Reference
Speed of accumulated germination ($S_{accumulated}$)	GermSpeedAccumulate	<p>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.</p> $S_{accumulated} = \sum_{i=1}^k \frac{\sum_{j=1}^i N_j}{T_i}$ <p>Where, T_i is the time from the start of the experiment to the ith interval, $\sum_{j=1}^i N_j$ is the cumulative/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.</p>	% time ⁻¹ or count time ⁻¹	Mixed	Bradbeer (1988); Wardle et al. (1991); Haugland and Brandsaeter (1996); Santana and Ranal (2004)
Corrected speed of germination or Corrected germination rate index (\hat{S})	GermSpeedCorrected	<p>It is computed as follows.</p> $S_{corrected} = \frac{S}{FGP}$ <p>Where, S is the germination speed computed with germination percentage instead of counts and FGP is the final germination percentage or germinability. It can also be computed from speed of accumulated germination (computed with germination percentage).</p> $\hat{S}_{accumulated} = \frac{S_{accumulated}}{FGP}$ <p>Where, $S_{accumulated}$ is the speed of accumulated germination computed with germination percentage instead of counts and FGP is the final germination percentage or germinability.</p>	time ⁻¹	Mixed	Evetts and Burnside (1972)
Weighted germination percentage (WGP)	WeightGermPercent	<p>It is estimated as follows.</p> $WGP = \frac{\sum_{i=1}^k (k-i+1)N_i}{k \times N} \times 100$ <p>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.</p>	Percentage (%)	Mixed	Reddy et al. (1985); Reddy (1978)
Mean germination percentage per unit time (\overline{GP})	MeanGermPercent	<p>It is estimated as follows.</p> $\overline{GP} = \frac{GP}{T_k}$ <p>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.</p>	% time ⁻¹	Mixed	Czabator (1962)

Germination index	Function	Details	Unit	Measures	Reference
Number of seeds germinated per unit time \bar{N}	MeanGermNumber	It is estimated as follows. $\bar{N} = \frac{N_g}{T_k}$ Where, N_g is the number of germinated seeds at the end of the germination test, T_k is the time at the k th time interval, and k is the total number of time intervals required for final germination.	count time ⁻¹	Mixed	Khamassi et al. (2013)
Timson's index [$\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$] or Germination energy index (GEI)	TimsonsIndex	It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time and is estimated in terms of cumulative germination percentage (G_i) as follows. $\Sigma k = \sum_{i=1}^k G_i$ Where, G_i is the cumulative germination percentage in time interval i , and k is the total number of time intervals. It also estimated in terms of partial germination percentage as follows. $\Sigma k = \sum_{i=1}^k g_i(k-j)$ Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to k), k is the total number of time intervals, and $j = i - 1$.	Percentage (%)	Mixed	Grose and Zimmer (1958); Timson (1965); Lyon and Coffelt (1966); Chaudhary and Ghildyal (1970); Negm and Smith (1978); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971)
Modified Timson's index (Σk_{mod}) (Labouriau)	TimsonsIndex	It is estimated as Timson's index Σk divided by the sum of partial germination percentages. $\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^k g_i}$	no unit	Mixed	Ranal and Santana (2006)
Modified Timson's index (Σk_{mod}) (Khan and Unger)	TimsonsIndex	It is estimated as Timson's index (Σk) divided by the total time period of germination (T_k). $\Sigma k_{mod} = \frac{\Sigma k}{T_k}$	% time ⁻¹	Mixed	Khan and Ungar (1984)

Germination index	Function	Details	Unit	Measures	Reference
George's index (<i>GR</i>)	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 i th interval and K_i is the number of intervals(eg. days) until the end of the test, and k is the total number of time intervals.	count time	Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968); Chopra and Chaudhary (1980)
Germination Index (<i>GI</i>) (Melville)	GermIndex	It is estimated as follows. $GI = \sum_{i=1}^k \frac{ (T_k - T_i) N_i }{N_t}$ Where, T_i is the time from the start of the experiment to the i th interval (day for the example), N_i is the number of seeds germinated in the i th time interval (not the accumulated number, but the number corresponding to the i th interval), N_t is the total number of seeds used in the test, and k is the total number of time intervals.	time	Mixed	Melville et al. (1980)
Germination Index (<i>GI_{mod}</i>) (Melville; Santana and Ranal)	GermIndex	It is estimated as follows. $GI_{mod} = \sum_{i=1}^k \frac{ (T_k - T_i) N_i }{N_g}$ Where, T_i is the time from the start of the experiment to the i th interval (day for the example), N_i is the number of seeds germinated in the i th time interval (not the accumulated number, but the number corresponding to the i th interval), N_g is the total number of germinated seeds at the end of the test, and k is the total number of time intervals.	time	Mixed	Melville et al. (1980); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (<i>ERI</i>) 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 i th time interval (not the accumulated number, but the number corresponding to the i th interval), i_0 is the time interval when emergence/germination started, and k is the total number of time intervals.	count	Mixed	Shmueli and Goldberg (1971)

Germination index	Function	Details	Unit	Measures	Reference
Modified Emergence Rate Index (ERI_{mod}) or Modified Germination Rate Index (Shmueli and Goldberg; Santana and Ranal)	EmergenceRateIndex	<p>It is estimated by dividing Emergence rate index (ERI) by total number of emerged seedlings (or germinated seeds).</p> $ERI_{mod} = \frac{\sum_{i=i_0}^{k-1} N_i(k-i)}{N_g} = \frac{ERI}{N_g}$ <p>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.</p>	no unit	Mixed	Shmueli and Goldberg (1971); Santana and Ranal (2004); Ranal and Santana (2006)
Emergence Rate Index (ERI) or Germination Rate Index (Bilbro & Wanjura)	EmergenceRateIndex	<p>It is the estimated as follows.</p> $ERI = \frac{\sum_{i=1}^k N_i}{\bar{T}} = \frac{N_g}{\bar{T}}$ <p>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 \bar{T} is the mean germination time or mean emergence time.</p>	count time ⁻¹	Mixed	Bilbro and Wanjura (1982)
Emergence Rate Index (ERI) or Germination Rate Index (Fakorede)	EmergenceRateIndex	<p>It is estimated as follows.</p> $ERI = \frac{\bar{T}}{FGP/100}$ <p>Where, \bar{T} is the Mean germination time and FGP is the final germination time.</p>	time count ⁻¹	Mixed	Fakorede and Ayoola (1980); Fakorede and Ojo (1981); Fakorede and Agbana (1983)
Peak value(PV) (Czabator) or Emergence Energy (EE)	PeakValue	<p>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.</p> $PV = \max\left(\frac{G_1}{T_1}, \frac{G_2}{T_2}, \dots, \frac{G_k}{T_k}\right)$ <p>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.</p>	% time ⁻¹	Mixed	Czabator (1962); Bonner (1967)

Germination index	Function	Details	Unit	Measures	Reference
Germination value (<i>GV</i>) (Czabator)	GermValue	<p>It is computed as follows.</p> $GV = PV \times MDG$ <p>Where, <i>PV</i> is the peak value and <i>MDG</i> 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 <i>MDG</i> with the mean germination percentage per unit time (\overline{GP}). <i>GV</i> value can be modified (<i>GV_{mod}</i>), to consider the entire duration from the beginning of the test instead of just from the onset of germination.</p>	% ² time ⁻²	Mixed	Czabator (1962); Brown and Mayer (1988)
Germination value (<i>GV</i>) (Diavanshir and Pourbiek)	GermValue	<p>It is computed as follows.</p> $GV = \frac{\sum DGS}{N} \times GP \times c$ <p>Where, <i>DGS</i> is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the onset of germination, <i>N</i> is the frequency or number of DGS calculated during the test, <i>GP</i> is the germination percentage expressed over 100, and <i>c</i> is a constant. The value of <i>c</i> is decided on the basis of average daily speed of germination ($\frac{\sum DGS}{N}$). If it is less than 10, then <i>c</i> value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for <i>c</i>. <i>GV</i> value can be modified (<i>GV_{mod}</i>), to consider the entire duration from the beginning of the test instead of just from the onset of germination.</p>	% ² time ⁻¹	Mixed	Djavanshir and Pourbeik (1976); Brown and Mayer (1988)
Coefficient of uniformity of germination (<i>CUG</i>)	CUGerm	<p>It is computed as follows.</p> $CUG = \frac{\sum_{i=1}^k N_i}{\sum_{i=1}^k (\overline{T} - T_i)^2 N_i}$ <p>Where, \overline{T} is the mean germination time, <i>T_i</i> is the time from the start of the experiment to the <i>i</i>th interval (day for the example), <i>N_i</i> is the number of seeds germinated in the <i>i</i>th time interval (not the accumulated number, but the number corresponding to the <i>i</i>th interval), and <i>k</i> is the total number of time intervals.</p>	time ⁻²	Germination uniformity	Heydecker (1972); Bewley and Black (1994)
Coefficient of variation of the germination time (<i>CV_T</i>)	CVGermTime	<p>It is estimated as follows.</p> $CV_T = \sqrt{\frac{s_T^2}{\overline{T}}}$ <p>Where, s_T^2 is the variance of germination time and \overline{T} is the mean germination time.</p>	no unit	Germination uniformity	Gomes (1960); Ranal and Santana (2006)

Germination index	Function	Details	Unit	Measures	Reference
Synchronization index (\bar{E}) or Uncertainty of the germination process (U) or informational entropy (H)	GermUncertainty	<p>It is estimated as follows.</p> $\bar{E} = - \sum_{i=1}^k f_i \log_2 f_i$ <p>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.</p>	bit	Germination synchrony	Shannon (1948); Labouriau and Valadares (1976); Labouriau (1983b)
Synchrony of germination (Z index)	GermSynchrony	<p>It is computed as follows.</p> $Z = \frac{\sum_{i=1}^k C_{N_i,2}}{C_{\sum N_i,2}}$ <p>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 $C_{\sum N_i,2}$ 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.</p>	no unit	Germination synchrony	Primack (1985); Ranal and Santana (2006)

Examples

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
z <- c(0, 0, 0, 0, 11, 11, 9, 7, 1, 0, 1, 0, 0, 0)
int <- 1:length(x)
```

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

```
GermPercent()
```

```
[1] 80
```

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

```
[1] 34
```

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

Warning in PeakGermPercent(germ.counts = z, intervals = int, total.seeds = 50): Multiple peak germination times exist.

```
[1] 22
```

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

```
[1] 80
```

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

```
[1] 34
```

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

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

```
[1] 22
```

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

```
[1] 80
```

```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
z <- c(0, 0, 0, 0, 11, 11, 9, 7, 1, 0, 1, 0, 0, 0)
int <- 1:length(x)
```

```

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

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

[1] 5
LastGermTime(germ.counts = x, intervals = int)

[1] 11
TimeSpreadGerm(germ.counts = x, intervals = int)

[1] 6
PeakGermTime(germ.counts = x, intervals = int)

[1] 6
# For multiple peak germination times
PeakGermTime(germ.counts = z, intervals = int)

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

[1] 5 6
# From cumulative germination counts
#-----
FirstGermTime(germ.counts = y, intervals = int, partial = FALSE)

[1] 5
LastGermTime(germ.counts = y, intervals = int, partial = FALSE)

[1] 11
TimeSpreadGerm(germ.counts = y, intervals = int, partial = FALSE)

[1] 6
PeakGermTime(germ.counts = y, intervals = int, partial = FALSE)

[1] 6
# For multiple peak germination time
PeakGermTime(germ.counts = cumsum(z), intervals = int, partial = FALSE)

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

[1] 5 6

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

# From partial germination counts
#-----
t50(germ.counts = x, intervals = int, method = "coolbear")

```

```
t50()
```

```
[1] 5.970588
```

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

```
[1] 5.941176
```

```
# From cumulative germination counts
```

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

```
[1] 5.970588
```

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

```
[1] 5.941176
```

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

```
# From partial germination counts
```

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

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

```
# From cumulative germination counts
```

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

```
[1] 6.7
```

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

```
[1] 1.446154
```

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

```
[1] 0.1901416
```

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

```
[1] 0.1794868
```

```

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

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

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

[1] 0.1492537
CVG(germ.counts = x, intervals = int)

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

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

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

[1] 0.1674877
GermRateRecip(germ.counts = x, intervals = int, method = "farooq")

[1] 0.1683168

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

[1] 0.1492537
CVG(germ.counts = y, intervals = int, partial = FALSE)

[1] 14.92537
VarGermRate(germ.counts = y, intervals = int, partial = FALSE)

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

[1] 0.004235724
GermRateRecip(germ.counts = y, intervals = int,
               method = "coolbear", partial = FALSE)

[1] 0.1674877
GermRateRecip(germ.counts = y, intervals = int,
               method = "farooq", partial = FALSE)

[1] 0.1683168

```

```

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

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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()

[1] 6.138925

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

[1] 34.61567

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

[1] 0.1534731

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

[1] 0.8653917

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

[1] 12.27785

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

[1] 69.23134

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

[1] 6.138925

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

[1] 34.61567

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

[1] 0.1534731

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

[1] 0.8653917

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

```

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

```
[1] 12.27785
```

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

```
[1] 69.23134
```

```
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
```

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

```
[1] 5.714286
```

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

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

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

```
[1] 664
```

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

```
[1] 664
```

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

```
[1] 8.3
```

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

```
[1] 47.42857
```

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

```
[1] 332
```

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

```
[1] 344
```

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

```
[1] 344
```

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

```
[1] 4.410256
```

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

```
[1] 24.57143
```

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

[1] 172

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

[1] 332

```
# From cumulative germination counts
```

```
#-----
```

```
# Without max specified
```

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

[1] 664

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

[1] 664

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

[1] 8.3

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

[1] 47.42857

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

[1] 332

```
# With max specified
```

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

[1] 344

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

[1] 344

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

[1] 4.410256

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

[1] 24.57143

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

```
[1] 172
```

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

```
[1] 332
```

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

```
# From partial germination counts
```

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

```
GermIndex()
```

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

```
# From cumulative germination counts
```

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

```
[1] 5.84
```

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

```
[1] 5.84
```

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

```
[1] 7.3
```

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

```
# From partial germination counts
```

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

```
EmergenceRateIndex()
```

[1] 292

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

[1] 292

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

[1] 7.3

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

[1] 5.970149

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

[1] 8.375

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

[1] 292

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

[1] 292

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

[1] 7.3

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

[1] 5.970149

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

[1] 8.375

```
x <- c(0, 0, 34, 40, 21, 10, 4, 5, 3, 5, 8, 7, 7, 6, 6, 4, 0, 2, 0, 2)
y <- c(0, 0, 34, 74, 95, 105, 109, 114, 117, 122, 130, 137, 144, 150,
      156, 160, 160, 162, 162, 164)
int <- 1:length(x)
total.seeds = 200

# From partial germination counts
```

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

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

```
[1] 9.5
```

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

```
$`Germination Value`
```

```
[1] 38.95
```

```
[[2]]
```

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

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

```
$`Germination Value`
```

```
[1] 53.36595
```

```
[[2]]
```

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

```

17      0      17      160      80.0 4.705882  6.539753
18      2      18      162      81.0 4.500000  6.412268
19      0      19      162      81.0 4.263158  6.285850
20      2      20      164      82.0 4.100000  6.164414

```

```

GV
3  9.633333
4 27.595833
5 38.659722
6 43.531250
7 44.638095
8 45.673512
9 45.611097
10 46.266503
11 48.090230
12 49.521942
13 50.945411
14 51.994006
15 53.034246
16 53.365948
17 52.318022
18 51.939373
19 50.915385
20 50.548194

```

```
$testend
```

```
[1] 16
```

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

```
GV
```

1	0.000000
2	0.000000
3	3.211111
4	13.797917
5	23.195833
6	29.020833
7	31.884354
8	34.255134
9	35.475298
10	37.013202
11	39.346552
12	41.268285
13	43.107655
14	44.566291
15	45.963013
16	46.695205
17	46.162961
18	46.168331
19	45.555871
20	45.493374

```
$testend
```

```
[1] 16
```

```
# From cumulative germination counts
```

```
#-----
```

```
PeakValue(germ.counts = y, interval = int, total.seeds = 200,
           partial = FALSE)
```

```
[1] 9.5
```

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

```
$`Germination Value`
```

```
[1] 38.95
```

```
[[2]]
```

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

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

```
$`Germination Value`
```

```
[1] 53.36595
```

```
[[2]]
```

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

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

GV

```

3  9.633333
4 27.595833
5 38.659722
6 43.531250
7 44.638095
8 45.673512
9 45.611097
10 46.266503
11 48.090230
12 49.521942
13 50.945411
14 51.994006
15 53.034246
16 53.365948
17 52.318022
18 51.939373
19 50.915385
20 50.548194

```

\$testend

[1] 16

```

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

```

\$`Germination Value`

[1] 38.95

[[2]]

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

```
20          2          20          164          82.0 4.100000
```

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

```
$`Germination Value`
```

```
[1] 46.6952
```

```
[[2]]
```

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

```
GV
```

```
1 0.000000
2 0.000000
3 3.211111
4 13.797917
5 23.195833
6 29.020833
7 31.884354
8 34.255134
9 35.475298
10 37.013202
11 39.346552
12 41.268285
13 43.107655
14 44.566291
15 45.963013
16 46.695205
17 46.162961
18 46.168331
19 45.555871
20 45.493374
```

```
$testend
```

```
[1] 16
```

```
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)
int <- 1:length(x)
```

```
# From partial germination counts
```

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

```
CUGerm()
```

```
[1] 0.7092199
```

```
# From cumulative germination counts
```

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

```
[1] 0.7092199
```

```
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)
int <- 1:length(x)
```

```
# From partial germination counts
```

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

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

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

```
# From cumulative germination counts
```

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

```
[1] 0.2666667
```

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

```
[1] 2.062987
```

Non-linear regression analysis

Several mathematical functions have been used to fit the cumulative germination count data and describe the germination process by non-linear regression analysis. They include functions such as Richard's, Weibull, logistic, log-logistic, gaussian, four-parameter hill function etc. Currently `germinationmetrics` implements the four-parameter hill function to fit the count data and computed various associated metrics.

Four-parameter hill function

The four-parameter hill function defined as follows (El-Kassaby et al., 2008).

$$f(x) = y = y_0 + \frac{ax^b}{x^b + c^b}$$

Where, y is the cumulative germination percentage at time x , y_0 is the intercept on the y axis, a is the asymptote, b is a mathematical parameter controlling the shape and steepness of the germination curve and c is the “half-maximal activation level”.

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

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

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

The details of various parameters that are computed from this function are given in Table 4.

Table 4 Germination parameters estimated from the four-parameter hill function.

Germination parameters	Details	Unit	Measures
y intercept (y_0)	The intercept on the y axis.		
Asymptote (a)	It is the maximum cumulative germination percentage, which is equivalent to germination capacity.	%	Germination capacity
Shape and steepness (b)	Mathematical parameter controlling the shape and steepness of the germination curve. The larger the b , the steeper the rise toward the asymptote a , and the shorter the time between germination onset and maximum germination.		Germination rate
Half-maximal activation level (c)	Time required for 50% of viable seeds to germinate.	time	Germination time
lag	It is the time at germination onset and is computed by solving four-parameter hill function after setting y to 0 as follows.	time	Germination time
	$lag = b\sqrt{\frac{-y_0c^b}{a + y_0}}$		
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 <code>umin</code> and <code>umin</code> to germinate.	time	Germination time

Germination parameters	Details	Unit	Measures
Time at maximum germination rate (<i>TMGR</i>)	<p>The partial derivative of the four-parameter hill function gives the instantaneous rate of germination (<i>s</i>) as follows.</p> $s = \frac{\partial y}{\partial x} = \frac{abc^b x^{b-1}}{(c^b + x^b)^2}$ <p>From this function for instantaneous rate of germination, <i>TMGR</i> can be estimated as follows.</p> $TMGR = b \sqrt{\frac{c^b(b-1)}{b+1}}$ <p>It represents the point in time when the instantaneous rate of germination starts to decline.</p>	time	Germination time
Area under the curve (<i>AUC</i>)	It is obtained by integration of the fitted curve between time 0 and time specified in the argument tmax .		Mixed
<i>MGT</i>	Calculated by integration of the fitted curve and proper normalisation.	time	Germination time
<i>Skewness</i>	It is computed as follows.		
	$\frac{MGT}{t_{50_{germinated}}}$		

Examples

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

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

FourPHFfit()

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

```

10 0 78      10
11 2 80      11
12 0 80      12
13 0 80      13
14 0 80      14

```

\$Parameters

```

      term estimate  std.error statistic      p.value
1  bta 2.290709 0.05602634  40.88628 2.965932e-14
2    c 6.034954 0.03872162 155.85488 3.270089e-21

```

\$Fit

```

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

```

\$a

```
[1] 80
```

\$b

```
[1] 9.881937
```

\$c

```
[1] 6.034954
```

\$y0

```
[1] 0
```

\$lag

```
[1] 0
```

\$Dlag50

```
[1] 6.034954
```

\$t50.total

```
[1] 6.355121
```

\$txp.total

```

      10      60
4.956264 6.744598

```

\$t50.Germinated

```
[1] 6.034954
```

\$txp.Germinated

```

      10      60
4.831807 6.287724

```

\$Uniformity

```

      90      10 uniformity
7.537690 4.831807 2.705882

```

\$TMGR

```
[1] 5.912194
```

```

$AUC
[1] 1108.976

$MGT
[1] 6.632252

$Skewness
[1] 1.098973

$msg
[1] "#1. success "

$isConv
[1] TRUE

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

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

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

attr(,"class")
[1] "FourPHFfit" "list"
# From cumulative germination counts
#-----
FourPHFfit(germ.counts = y, intervals = int, total.seeds = 50, tmax = 20,
           partial = FALSE)

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

$Parameters
  term estimate  std.error statistic      p.value

```

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

```
$Fit
```

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

```
$a
```

```
[1] 80
```

```
$b
```

```
[1] 9.881937
```

```
$c
```

```
[1] 6.034954
```

```
$y0
```

```
[1] 0
```

```
$lag
```

```
[1] 0
```

```
$Dlag50
```

```
[1] 6.034954
```

```
$t50.total
```

```
[1] 6.355121
```

```
$txp.total
```

```
      10      60
4.956264 6.744598
```

```
$t50.Germinated
```

```
[1] 6.034954
```

```
$txp.Germinated
```

```
      10      60
4.831807 6.287724
```

```
$Uniformity
```

```
      90      10 uniformity
7.537690 4.831807 2.705882
```

```
$TMGR
```

```
[1] 5.912194
```

```
$AUC
```

```
[1] 1108.976
```

```
$MGT
```

```
[1] 6.632252
```

```
$Skewness
```

```
[1] 1.098973
```

```

$msg
[1] "#1. success "

$isConv
[1] TRUE

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

```

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

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

```

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

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

# From partial germination counts
#-----
fit1 <- FourPHFfit(germ.counts = x, intervals = int,
                  total.seeds = 50, tmax = 20)

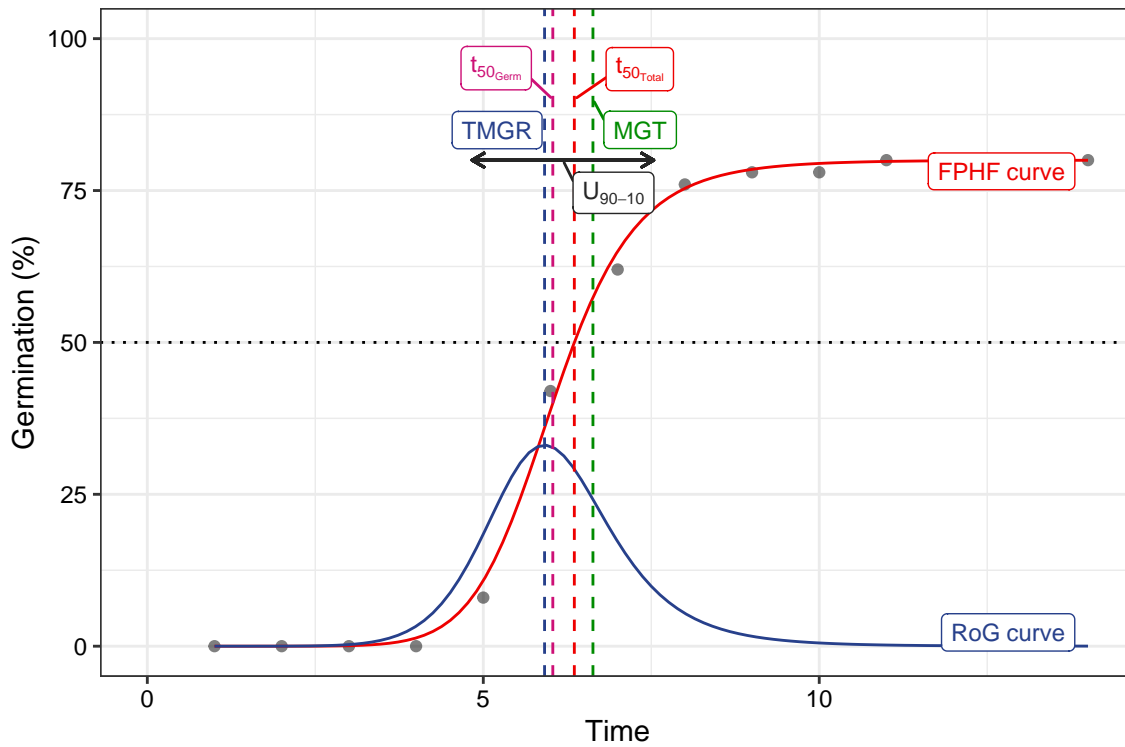
# From cumulative germination counts
#-----
fit2 <- FourPHFfit(germ.counts = y, intervals = int,
                  total.seeds = 50, tmax = 20, partial = FALSE)

# Default plots
plot(fit1)

```

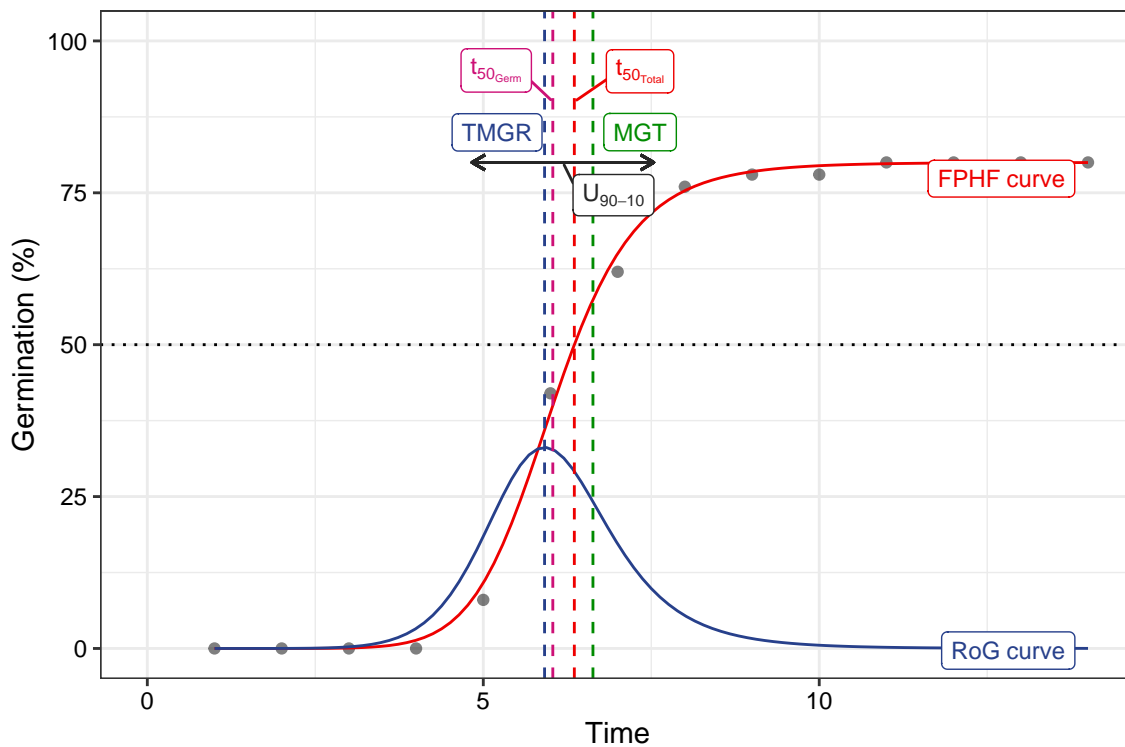
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have 1 value. Please consider using `annotate()` or provide this layer with data containing a single row.

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



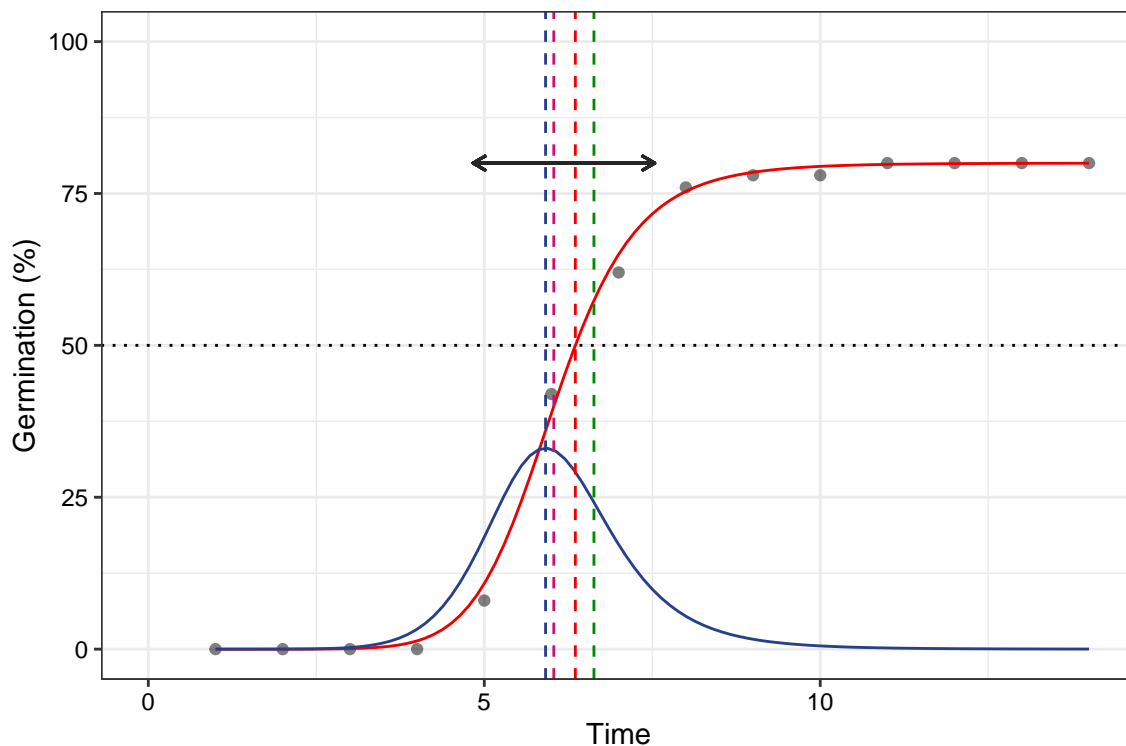
```
plot(fit2)
```

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



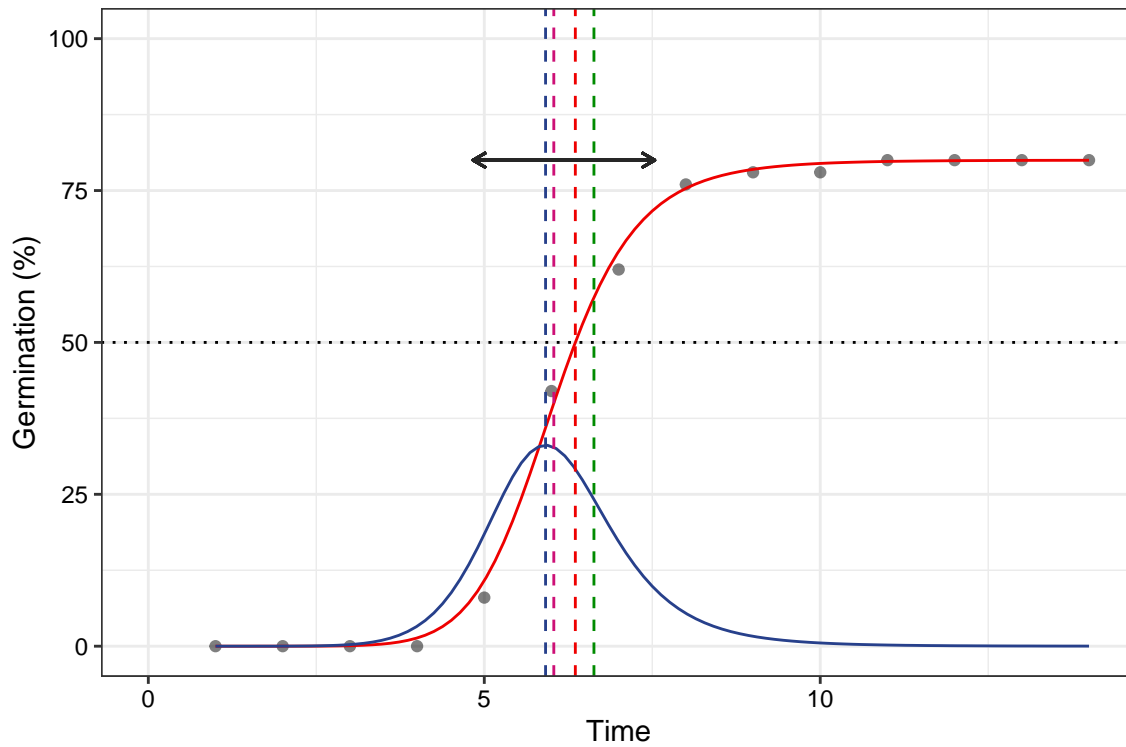
```
# No labels
plot(fit1, plotlabels = FALSE)
```

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

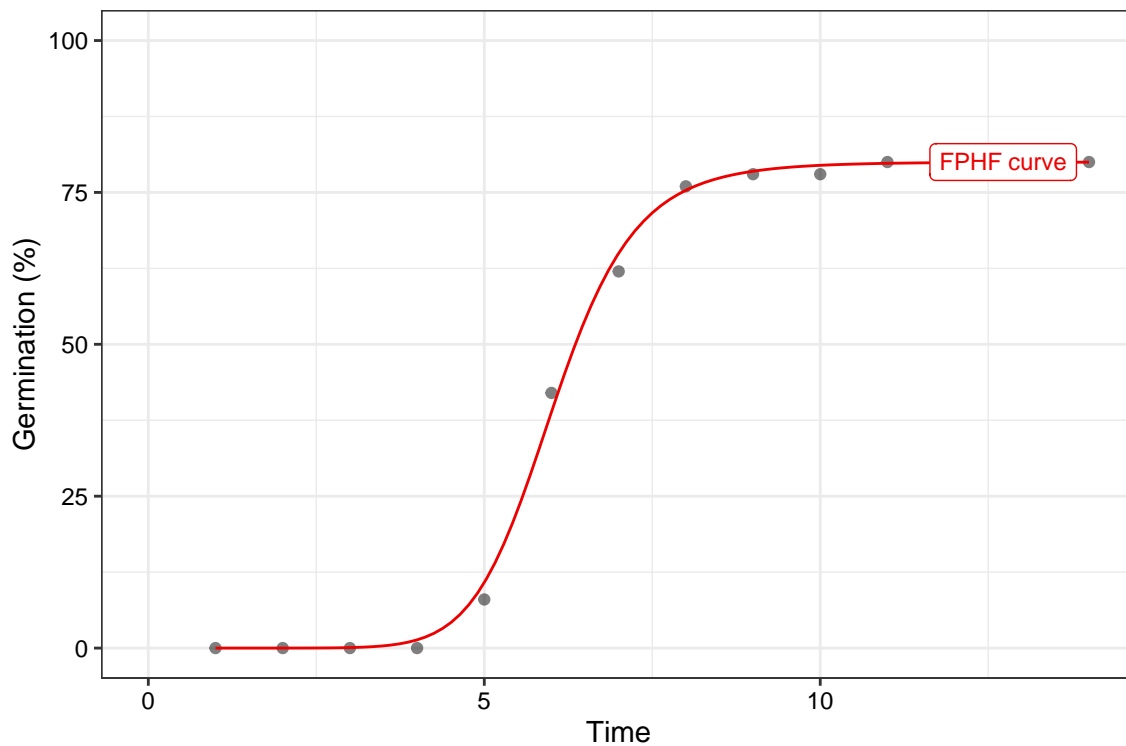


```
plot(fit2, plotlabels = FALSE)
```

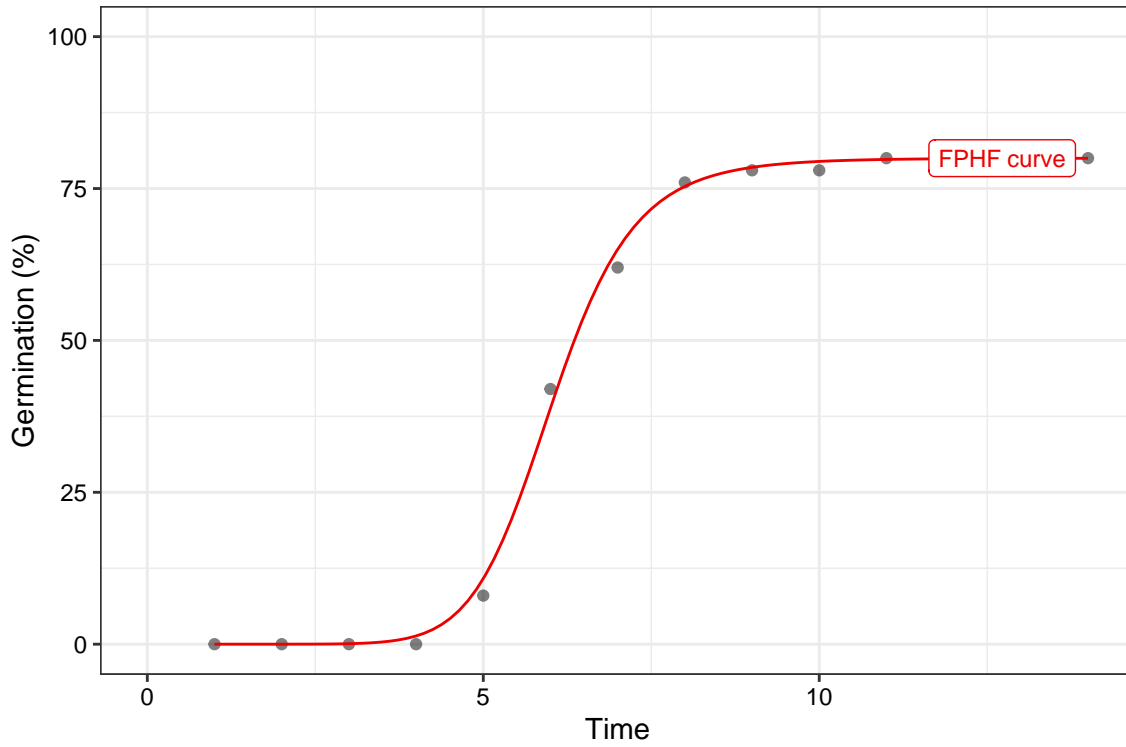
Warning in geom_segment(aes(x = UfmMin, xend = UfmMax, y = ypos2, yend = ypos2), : All aesthetics have length 1, but the data has 14 rows.
 i Please consider using `annotate()` or provide this layer with data containing a single row.
 All aesthetics have length 1, but the data has 14 rows.
 i Please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



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

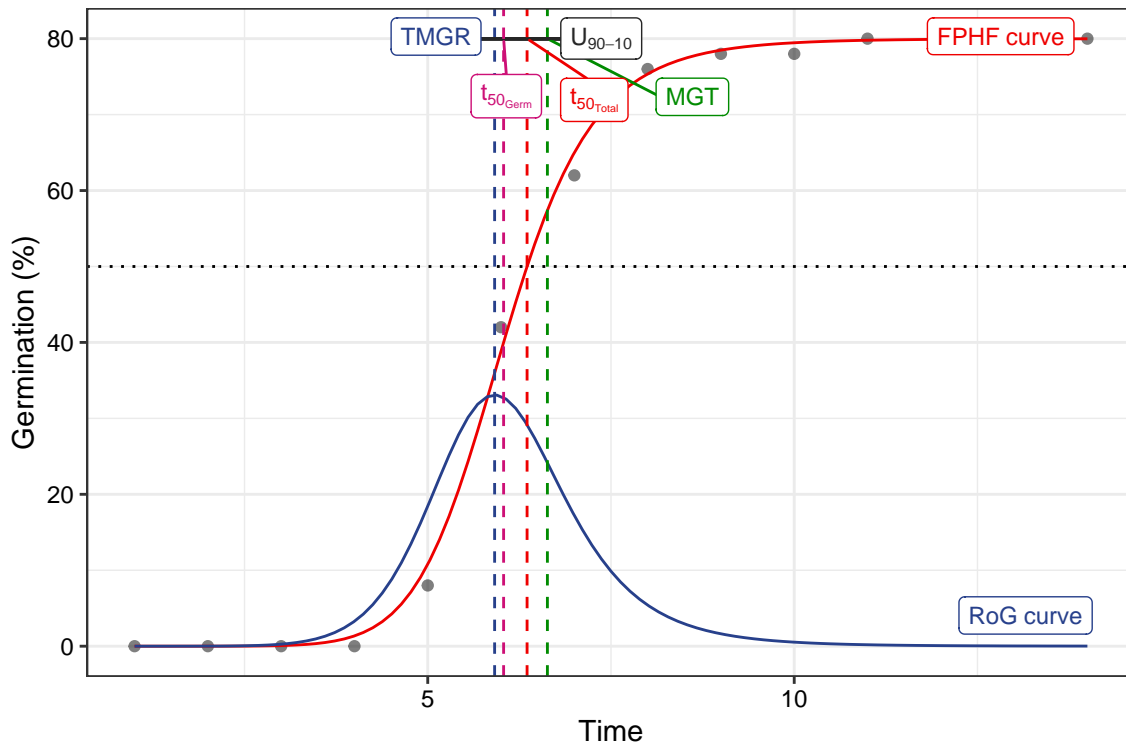


```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



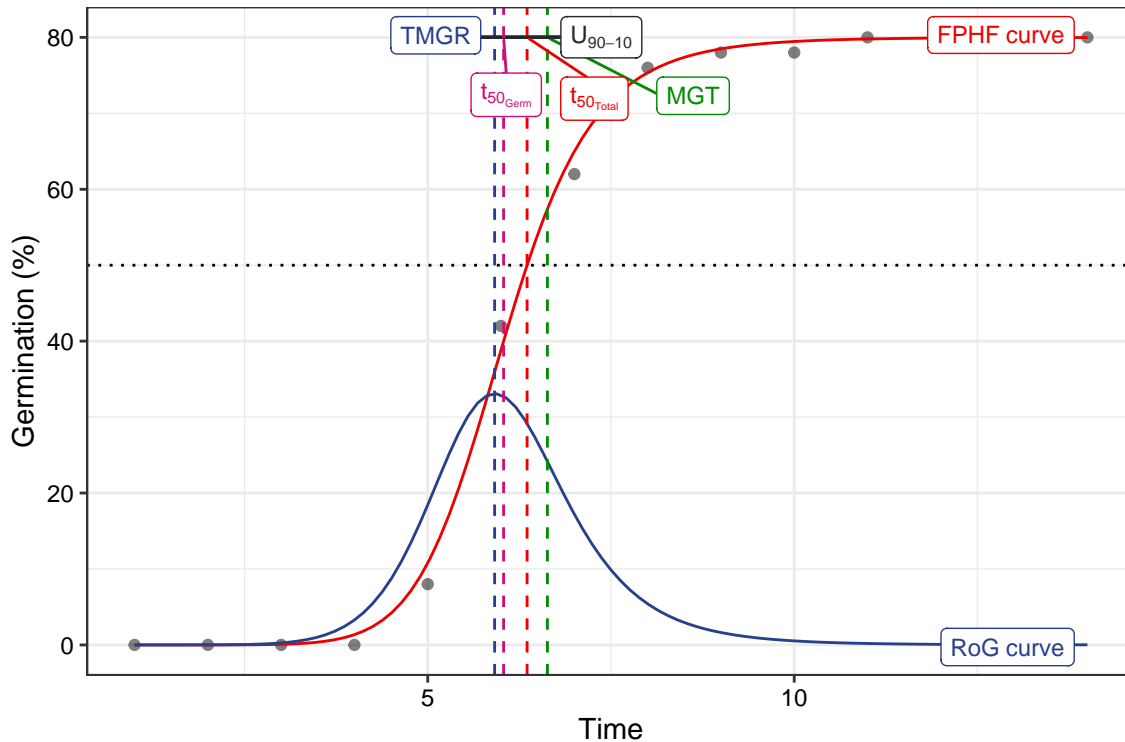
```
# Without y axis limits adjustment
plot(fit1, limits = FALSE)
```

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



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

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



Wrapper functions

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

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

```
data(gcdata)
```

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

```
germination.indices(gcdata, total.seeds.col = "Total Seeds",
                   counts.intervals.cols = counts.per.intervals,
                   intervals = 1:14, partial = TRUE, max.int = 5)
```

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

6	G1	2	0	0	0	0	3	21	11	7	1	1	1	1	0
7	G2	2	0	0	0	0	4	18	11	7	1	0	1	0	0
8	G3	2	0	0	0	1	3	14	12	6	2	1	0	1	0
9	G4	2	0	0	0	1	3	19	10	8	1	1	1	1	0
10	G5	2	0	0	0	0	4	18	13	6	2	1	0	1	0
11	G1	3	0	0	0	0	5	21	11	8	1	0	0	1	1
12	G2	3	0	0	0	0	3	20	10	7	1	1	1	1	0
13	G3	3	0	0	0	0	4	19	12	8	1	1	0	1	1
14	G4	3	0	0	0	0	3	21	11	6	1	0	1	1	0
15	G5	3	0	0	0	0	4	17	10	8	1	1	1	0	0

	Day14	Total	Seeds	GermPercent	PeakGermPercent	FirstGermTime	LastGermTime	PeakGermTime	
1	0		50	80.00000	34.00000		5	11	6
2	0		51	82.35294	29.41176		4	12	6
3	0		48	93.75000	37.50000		4	12	6
4	0		51	90.19608	37.25490		5	12	6
5	0		50	96.00000	40.00000		5	13	6
6	0		49	93.87755	42.85714		5	12	6
7	0		48	87.50000	37.50000		5	11	6
8	0		47	85.10638	29.78723		4	12	6
9	0		52	86.53846	36.53846		4	12	6
10	0		50	90.00000	36.00000		5	12	6
11	0		51	94.11765	41.17647		5	13	6
12	0		51	86.27451	39.21569		5	12	6
13	0		49	95.91837	38.77551		5	13	6
14	0		48	91.66667	43.75000		5	12	6
15	0		48	87.50000	35.41667		5	11	6

	TimeSpreadGerm	t50_Coolbear	t50_Farooq	MeanGermTime	VarGermTime	SEGermTime	CVGermTime
1	6	5.970588	5.941176	6.700000	1.446154	0.1901416	0.1794868
2	8	6.192308	6.153846	6.857143	2.027875	0.2197333	0.2076717
3	8	6.333333	5.972222	6.866667	2.572727	0.2391061	0.2335882
4	7	6.041667	6.225806	6.891304	2.187923	0.2180907	0.2146419
5	8	5.975000	5.950000	6.812500	2.368351	0.2221275	0.2259002
6	7	5.976190	5.952381	6.869565	2.071498	0.2122088	0.2095140
7	6	5.972222	5.944444	6.690476	1.389663	0.1818989	0.1761967
8	8	6.208333	6.166667	6.875000	2.112179	0.2297923	0.2113940
9	8	6.310345	5.973684	6.866667	2.300000	0.2260777	0.2208604
10	7	6.076923	6.038462	6.822222	1.831313	0.2017321	0.1983606
11	8	5.928571	5.904762	6.791667	2.381206	0.2227295	0.2272072
12	7	5.975000	5.950000	6.886364	2.149577	0.2210295	0.2129053
13	8	6.083333	6.041667	6.936170	2.539315	0.2324392	0.2297410
14	7	5.928571	5.904762	6.772727	1.900634	0.2078370	0.2035568
15	6	6.050000	6.259259	6.809524	1.670151	0.1994129	0.1897847

	MeanGermRate	VarGermRate	SEGermRate	CVGermRate	GermRateRecip_Coolbear	GermRateRecip_Farooq
1	0.1492537	0.0007176543	0.004235724	14.92537	0.1674877	0.1683168
2	0.1458333	0.0009172090	0.004673148	14.58333	0.1614907	0.1625000
3	0.1456311	0.0011572039	0.005071059	14.56311	0.1578947	0.1674419
4	0.1451104	0.0009701218	0.004592342	14.51104	0.1655172	0.1606218
5	0.1467890	0.0010995627	0.004786184	14.67890	0.1673640	0.1680672
6	0.1455696	0.0009301809	0.004496813	14.55696	0.1673307	0.1680000
7	0.1494662	0.0006935558	0.004063648	14.94662	0.1674419	0.1682243
8	0.1454545	0.0009454531	0.004861721	14.54545	0.1610738	0.1621622
9	0.1456311	0.0010345321	0.004794747	14.56311	0.1584699	0.1674009
10	0.1465798	0.0008453940	0.004334343	14.65798	0.1645570	0.1656051
11	0.1472393	0.0011191581	0.004828643	14.72393	0.1686747	0.1693548

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

2	5.882353	7.142857	300	7.142857
3	6.687500	7.133333	321	7.133333
4	6.411765	7.108696	327	7.108696
5	6.900000	7.187500	345	7.187500
6	6.693878	7.130435	328	7.130435
7	6.395833	7.309524	307	7.309524
8	6.063830	7.125000	285	7.125000
9	6.173077	7.133333	321	7.133333
10	6.460000	7.177778	323	7.177778
11	6.784314	7.208333	346	7.208333
12	6.137255	7.113636	313	7.113636
13	6.775510	7.063830	332	7.063830
14	6.625000	7.227273	318	7.227273
15	6.291667	7.190476	302	7.190476

	EmergenceRateIndex_BilbroWanjura	EmergenceRateIndex_Fakorede	PeakValue	GermValue_Czabator
1	5.970149	8.375000	9.500000	54.28571
2	6.125000	8.326531	9.313725	54.78662
3	6.553398	7.324444	10.416667	69.75446
4	6.675079	7.640359	10.049020	64.74158
5	7.045872	7.096354	11.250000	77.14286
6	6.696203	7.317580	10.714286	71.84506
7	6.277580	7.646259	10.416667	65.10417
8	5.818182	8.078125	9.574468	58.20345
9	6.553398	7.934815	9.855769	60.92165
10	6.596091	7.580247	10.250000	65.89286
11	7.067485	7.216146	11.029412	74.14731
12	6.389439	7.981921	9.803922	60.41632
13	6.776074	7.231326	10.969388	75.15470
14	6.496644	7.388430	10.677083	69.90947
15	6.167832	7.782313	10.156250	63.47656

	GermValue_DP	GermValue_Czabator_mod	GermValue_DP_mod	CUGerm	GermSynchrony
1	57.93890	54.28571	39.56076	0.7092199	0.2666667
2	52.58713	54.78662	40.99260	0.5051546	0.2346109
3	68.62289	69.75446	53.42809	0.3975265	0.2242424
4	70.43331	64.74158	48.86825	0.4672113	0.2502415
5	80.16914	77.14286	56.23935	0.4312184	0.2606383
6	76.51983	71.84506	53.06435	0.4934701	0.2792271
7	69.41325	65.10417	47.37690	0.7371500	0.2729384
8	56.00669	58.20345	43.67948	0.4855842	0.2256410
9	58.13477	60.92165	45.30801	0.4446640	0.2494949
10	70.91875	65.89286	49.10820	0.5584666	0.2555556
11	77.39782	74.14731	54.27520	0.4288905	0.2686170
12	64.44988	60.41632	44.71582	0.4760266	0.2737844
13	78.16335	75.15470	54.94192	0.4023679	0.2506938
14	74.40140	69.90947	51.41913	0.5383760	0.2991543
15	67.62031	63.47656	46.48043	0.6133519	0.2497096

	GermUncertainty
1	2.062987
2	2.321514
3	2.462012
4	2.279215
5	2.146051
6	2.160545
7	2.040796

```

8      2.357249
9      2.321080
10     2.187983
11     2.128670
12     2.185245
13     2.241181
14     2.037680
15     2.185028

```

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

```

data(gcdata)

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

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

```

	Genotype	Rep	Day01	Day02	Day03	Day04	Day05	Day06	Day07	Day08	Day09	Day10	Day11	Day12	Day13
1	G1	1	0	0	0	0	4	17	10	7	1	0	1	0	0
2	G2	1	0	0	0	1	3	15	13	6	2	1	0	1	0
3	G3	1	0	0	0	2	3	18	9	8	2	1	1	1	0
4	G4	1	0	0	0	0	4	19	12	6	2	1	1	1	0
5	G5	1	0	0	0	0	5	20	12	8	1	0	0	1	1
6	G1	2	0	0	0	0	3	21	11	7	1	1	1	1	0
7	G2	2	0	0	0	0	4	18	11	7	1	0	1	0	0
8	G3	2	0	0	0	1	3	14	12	6	2	1	0	1	0
9	G4	2	0	0	0	1	3	19	10	8	1	1	1	1	0
10	G5	2	0	0	0	0	4	18	13	6	2	1	0	1	0
11	G1	3	0	0	0	0	5	21	11	8	1	0	0	1	1
12	G2	3	0	0	0	0	3	20	10	7	1	1	1	1	0
13	G3	3	0	0	0	0	4	19	12	8	1	1	0	1	1
14	G4	3	0	0	0	0	3	21	11	6	1	0	1	1	0
15	G5	3	0	0	0	0	4	17	10	8	1	1	1	0	0
	Day14	Total	Seeds	a	b	c	y0	lag	Dlag50	t50.total	t10.total	t60.total			
1	0	50	80.00000	9.881937	6.034954	0	0	6.034954	6.355121	4.956264	6.744598				
2	0	51	82.35294	9.227666	6.175193	0	0	6.175193	6.473490	4.983236	6.872603				
3	0	48	93.75000	7.793051	6.138110	0	0	6.138110	6.244191	4.673022	6.608438				
4	0	51	90.19608	8.925655	6.125173	0	0	6.125173	6.276794	4.850875	6.614968				
5	0	50	96.00000	9.419181	6.049642	0	0	6.049642	6.103433	4.814125	6.386789				
6	0	49	93.87755	9.450149	6.097415	0	0	6.097415	6.182279	4.868632	6.477599				
7	0	48	87.50000	10.172459	6.029851	0	0	6.029851	6.202812	4.930422	6.510495				
8	0	47	85.10638	8.940696	6.189774	0	0	6.189774	6.439510	4.940057	6.823299				
9	0	52	86.53846	8.617391	6.125122	0	0	6.125122	6.352172	4.836658	6.733276				
10	0	50	90.00000	9.608844	6.109504	0	0	6.109504	6.253043	4.920629	6.566506				
11	0	51	94.11765	9.400212	6.018760	0	0	6.018760	6.099435	4.798627	6.391291				
12	0	51	86.27451	9.162526	6.108452	0	0	6.108452	6.326184	4.893596	6.684526				
13	0	49	95.91837	8.995210	6.149012	0	0	6.149012	6.207501	4.841308	6.509954				
14	0	48	91.66667	10.391845	6.015910	0	0	6.015910	6.122389	4.915140	6.397491				

```

15      0          48 87.50000  9.136744 6.121579  0   0 6.121579  6.317392  4.892502  6.667247
      t50.Germinated t10.Germinated t60.Germinated Uniformity_90 Uniformity_10 Uniformity
1         6.034954         4.831807         6.287724         7.537690         4.831807         2.705882
2         6.175193         4.866755         6.452582         7.835407         4.866755         2.968652
3         6.138110         4.630062         6.465924         8.137342         4.630062         3.507280
4         6.125173         4.788597         6.409838         7.834810         4.788597         3.046213
5         6.049642         4.790946         6.315746         7.639028         4.790946         2.848083
6         6.097415         4.832471         6.364722         7.693469         4.832471         2.860997
7         6.029851         4.858476         6.275050         7.483643         4.858476         2.625166
8         6.189774         4.841105         6.476945         7.914163         4.841105         3.073058
9         6.125122         4.746573         6.420208         7.904041         4.746573         3.157468
10        6.109504         4.860681         6.372823         7.679177         4.860681         2.818496
11        6.018760         4.764246         6.284051         7.603611         4.764246         2.839365
12        6.108452         4.806013         6.384836         7.763854         4.806013         2.957841
13        6.149012         4.816393         6.432524         7.850345         4.816393         3.033952
14        6.015910         4.869398         6.255276         7.432372         4.869398         2.562974
15        6.121579         4.813083         6.399357         7.785806         4.813083         2.972723
      TMGR      AUC      MGT Skewness      msg      sigma      finTol      logLik      AIC
1  5.912194 1108.976 6.632252 1.098973 #1. success 1.615220 7.105427e-14 -25.49868 56.99736
2  6.031282 1128.559 6.784407 1.098655 #1. success 1.115372 2.309264e-14 -20.31471 46.62943
3  5.938180 1283.693 6.772742 1.103392 #1. success 2.432704 9.947598e-14 -31.23213 68.46426
4  5.972686 1239.887 6.739666 1.100323 #1. success 2.396582 5.684342e-14 -31.02269 68.04538
5  5.914289 1328.328 6.654981 1.100062 #1. success 2.399662 1.094236e-12 -31.04067 68.08135
6  5.961879 1294.463 6.702473 1.099232 #1. success 3.034962 1.563194e-13 -34.32887 74.65774
7  5.914057 1213.908 6.622417 1.098272 #1. success 1.663019 1.421085e-13 -25.90697 57.81395
8  6.036192 1164.346 6.804000 1.099232 #1. success 1.120704 4.327205e-12 -20.38149 46.76298
9  5.961631 1188.793 6.745241 1.101242 #1. success 2.429960 7.958079e-13 -31.21633 68.43266
10 5.978115 1240.227 6.711900 1.098600 #1. success 1.686656 8.142820e-12 -26.10456 58.20911
11 5.883557 1305.200 6.624248 1.100600 #1. success 2.628113 1.989520e-13 -32.31381 70.62762
12 5.964080 1188.021 6.718639 1.099892 #1. success 2.878146 1.151079e-12 -33.58613 73.17227
13 5.998270 1316.407 6.762274 1.099733 #1. success 2.604588 2.984279e-13 -32.18793 70.37586
14 5.905180 1273.385 6.604967 1.097916 #1. success 2.764756 9.805490e-13 -33.02342 72.04684
15 5.976087 1203.664 6.732266 1.099760 #1. success 1.954008 8.739676e-13 -28.16444 62.32888
      BIC deviance df.residual nobs
1  58.91453 31.30723      12  14
2  48.54660 14.92865      12  14
3  70.38143 71.01658      12  14
4  69.96256 68.92324      12  14
5  69.99852 69.10052      12  14
6  76.57491 110.53195      12  14
7  59.73112 33.18760      12  14
8  48.68015 15.07174      12  14
9  70.34984 70.85647      12  14
10 60.12629 34.13771      12  14
11 72.54479 82.88372      12  14
12 75.08944 99.40469      12  14
13 72.29303 81.40654      12  14
14 73.96401 91.72652      12  14
15 64.24606 45.81777      12  14

```

Multiple fitted curves generated in batch can also be plotted.

```
data(gcdata)
```

```
counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",
```

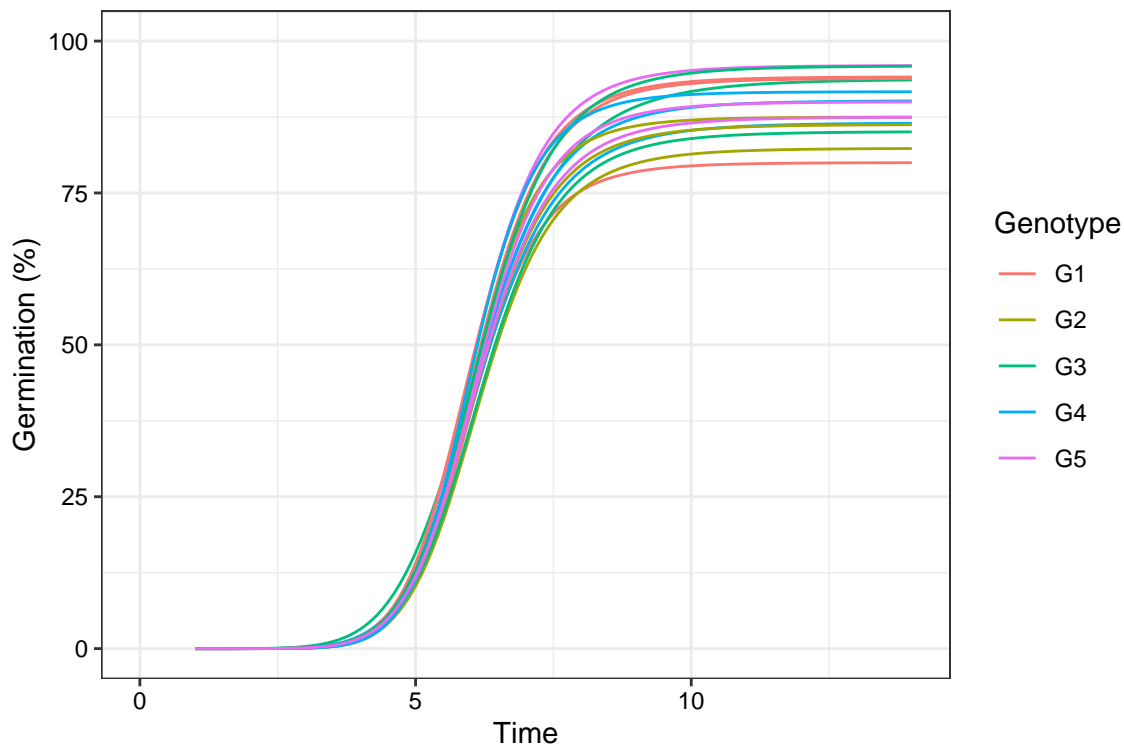
```

      "Day06", "Day07", "Day08", "Day09", "Day10",
      "Day11", "Day12", "Day13", "Day14")

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

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

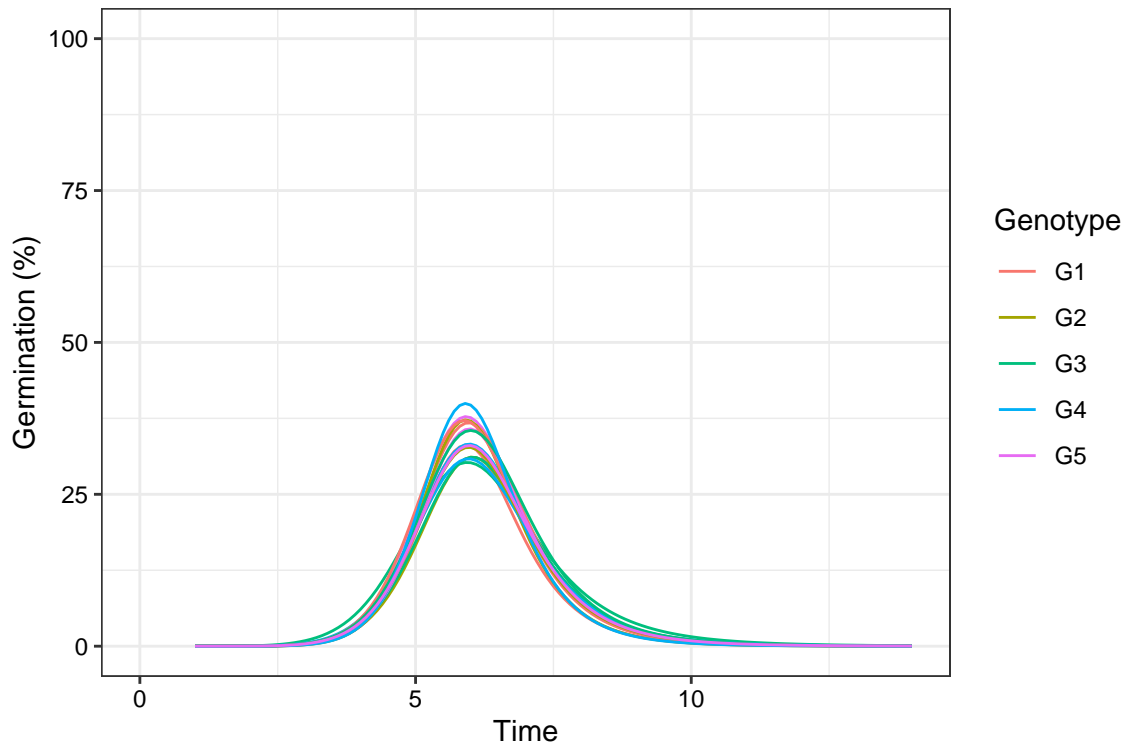
```



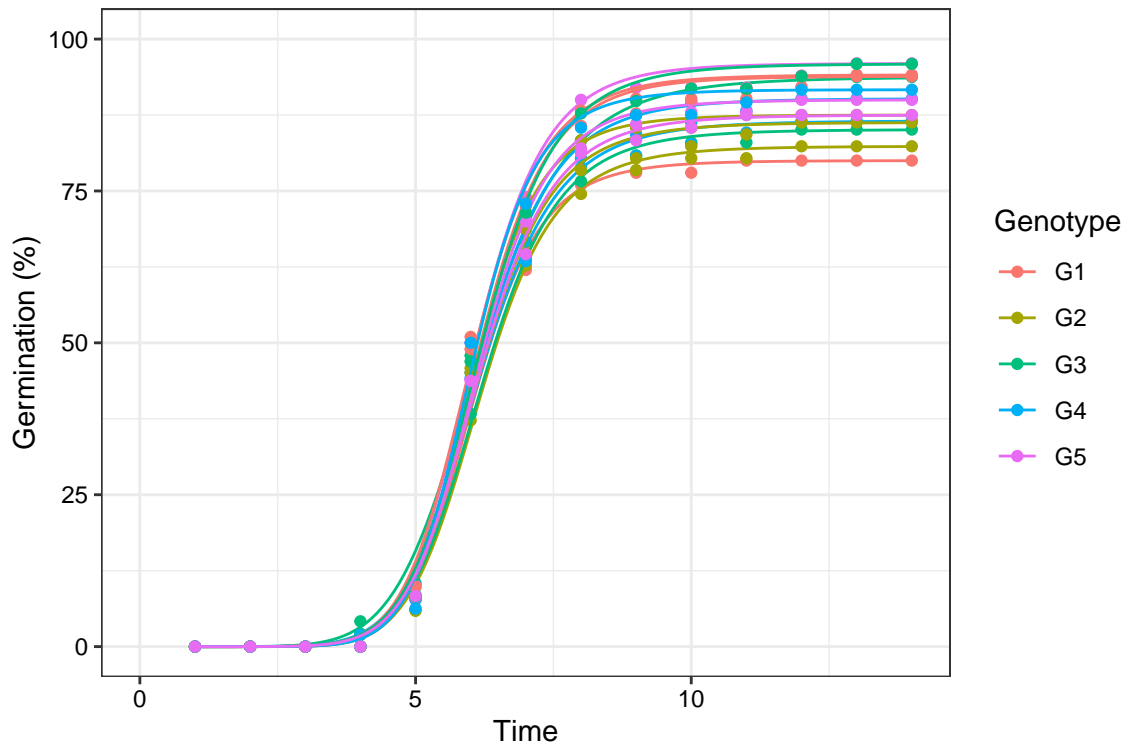
```

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

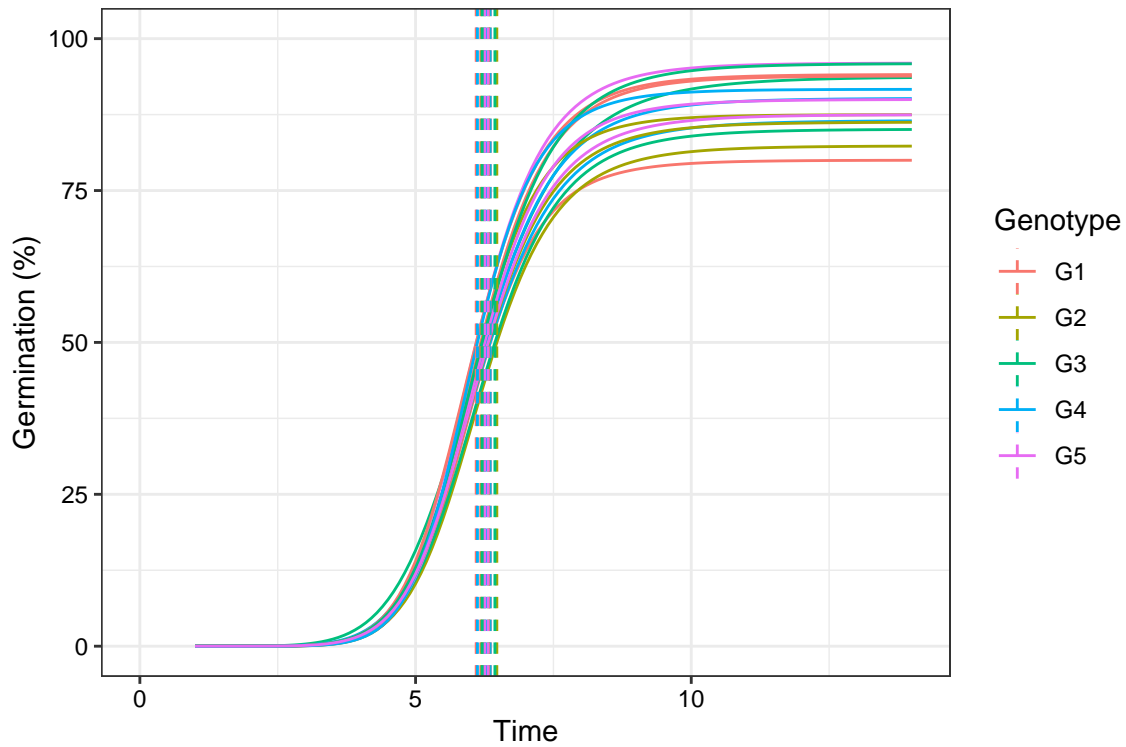
```



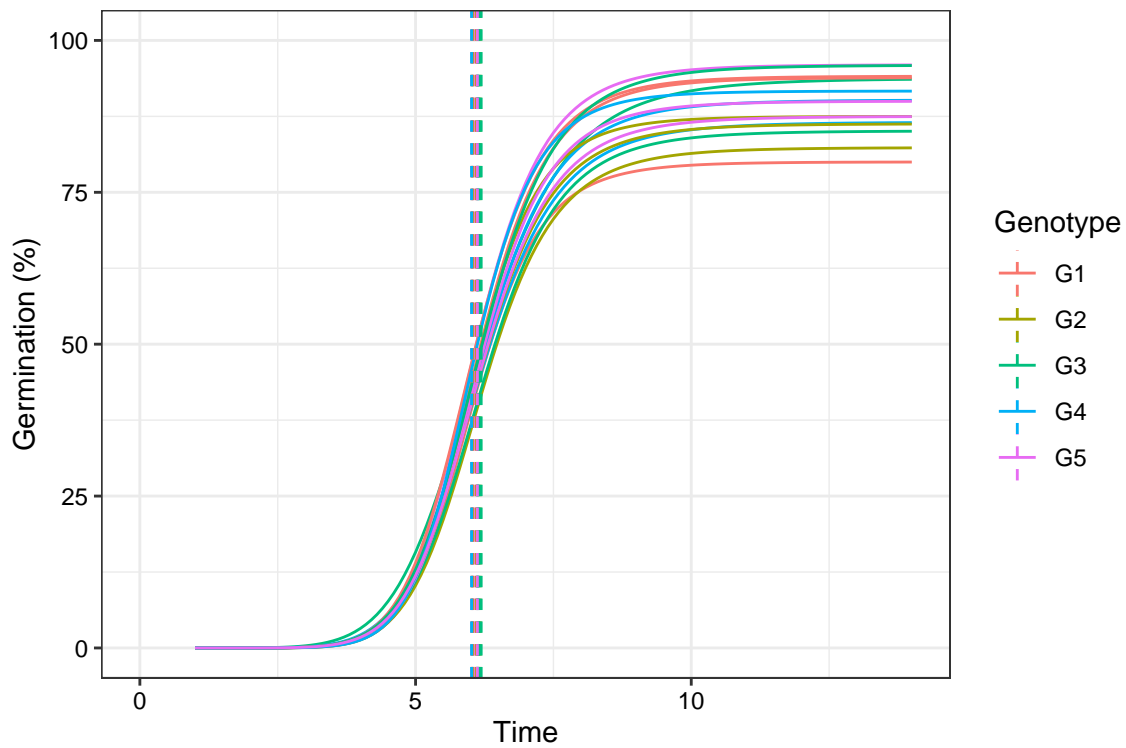
```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



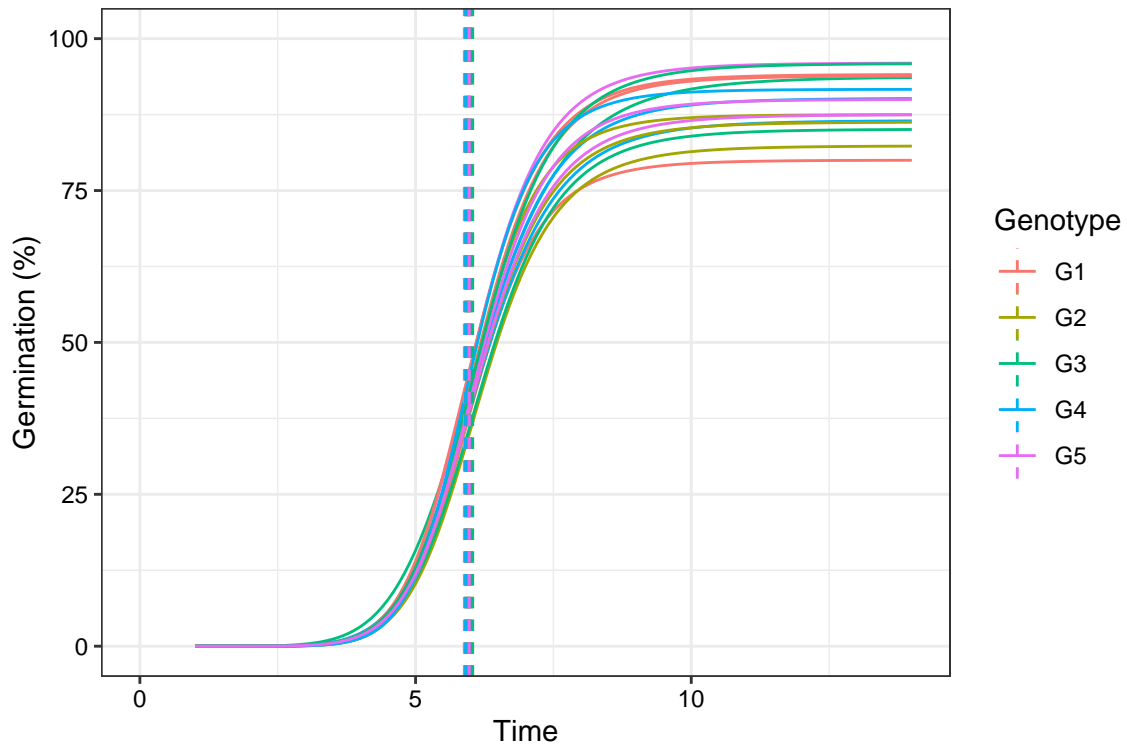
```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



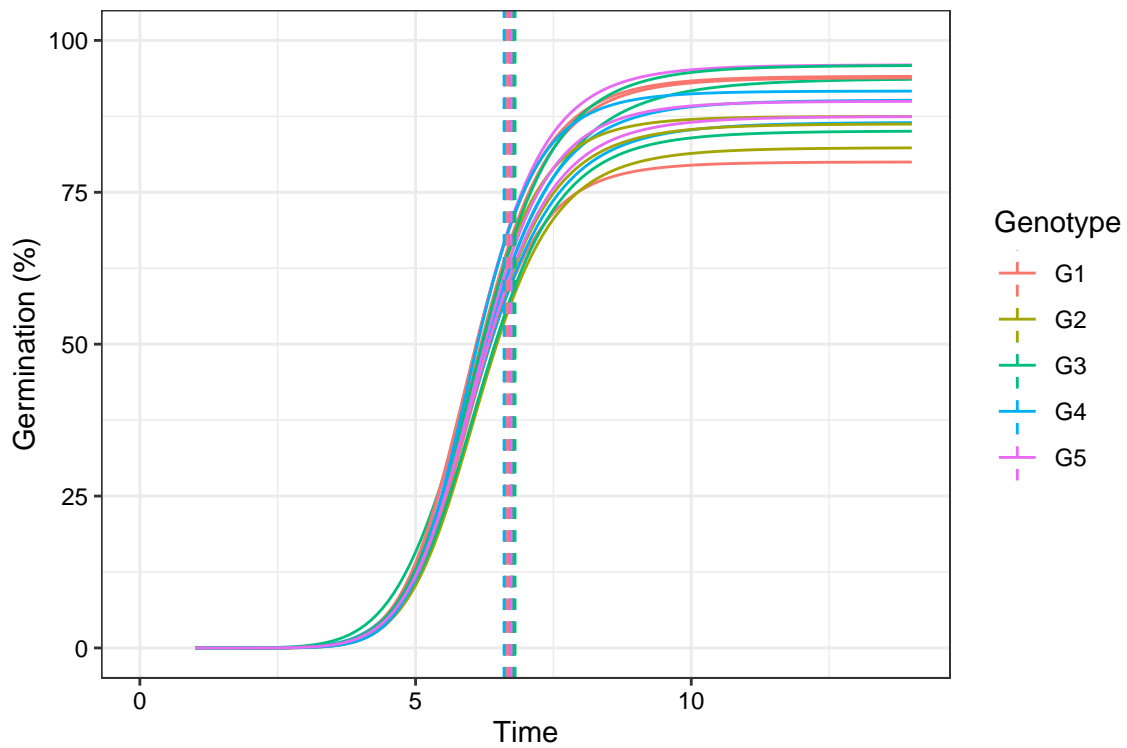
```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```



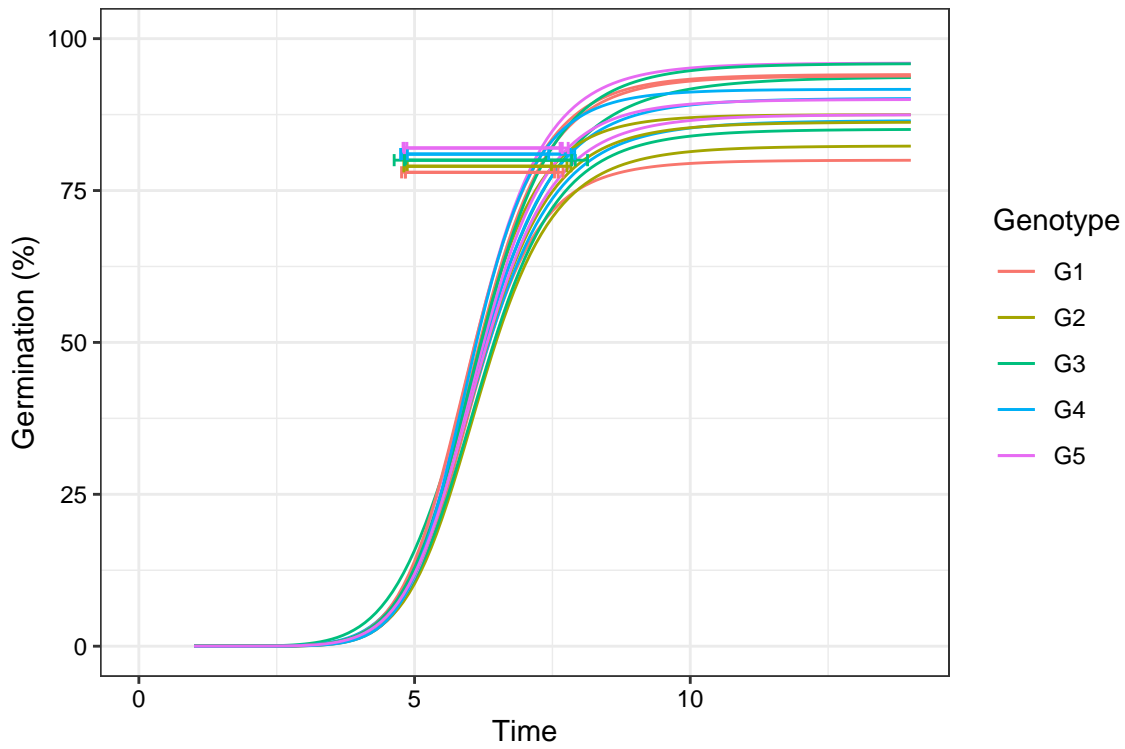
```
plot(fits, group.col = "Genotype", annotate = "tmgr")
```



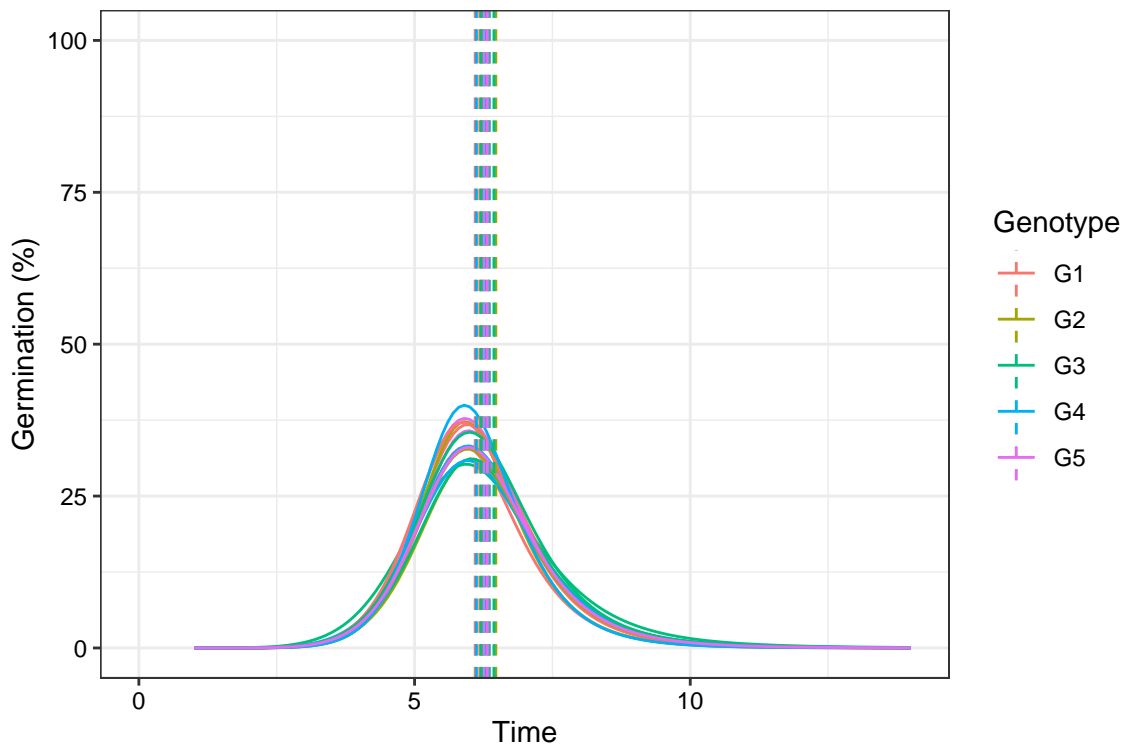
```
plot(fits, group.col = "Genotype", annotate = "mgt")
```



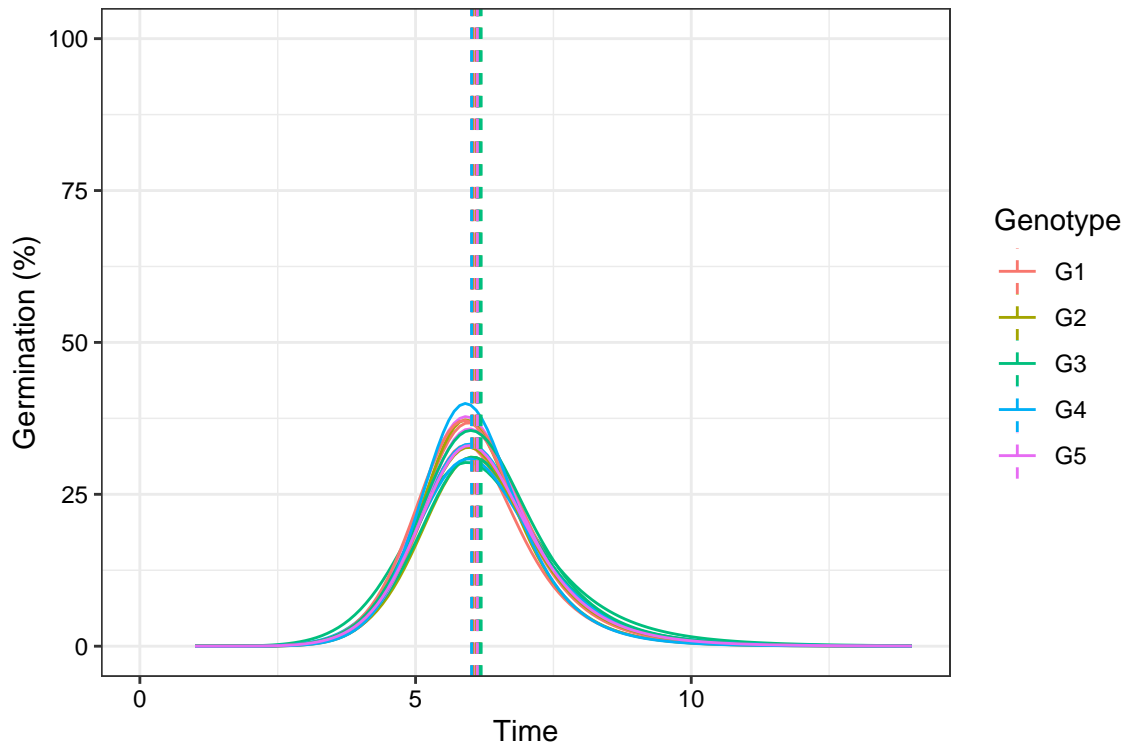
```
plot(fits, group.col = "Genotype", annotate = "uniformity")
```



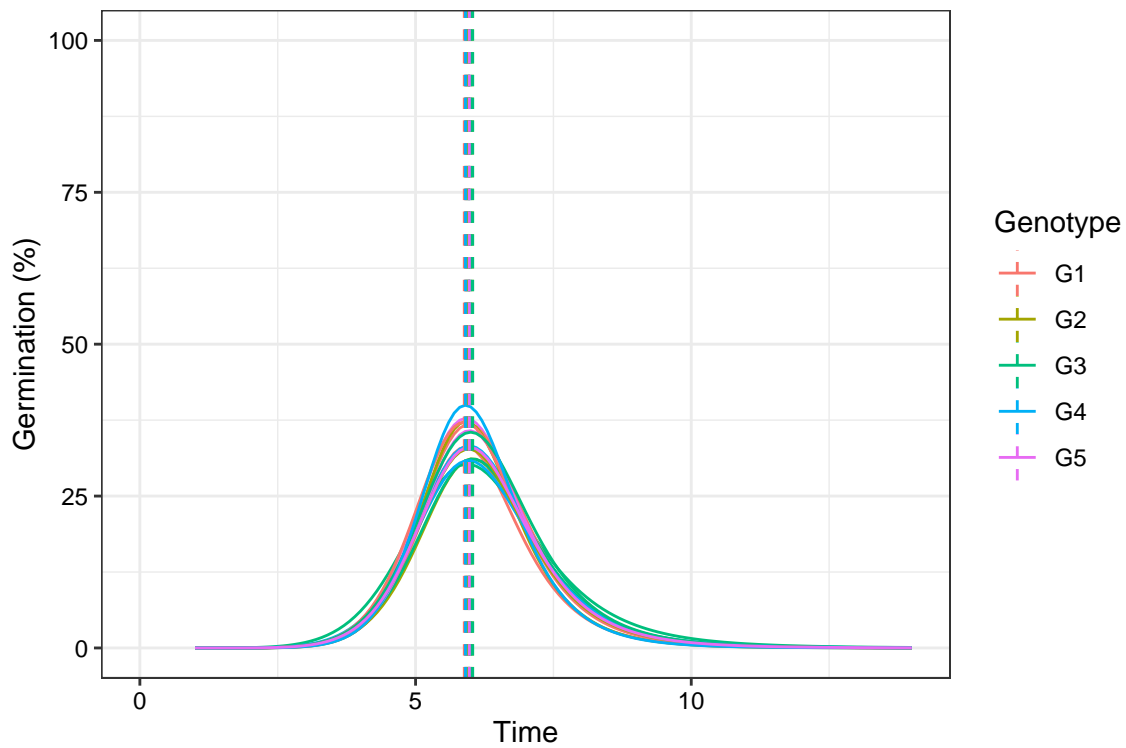
```
# Plot ROG curves with annotations
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



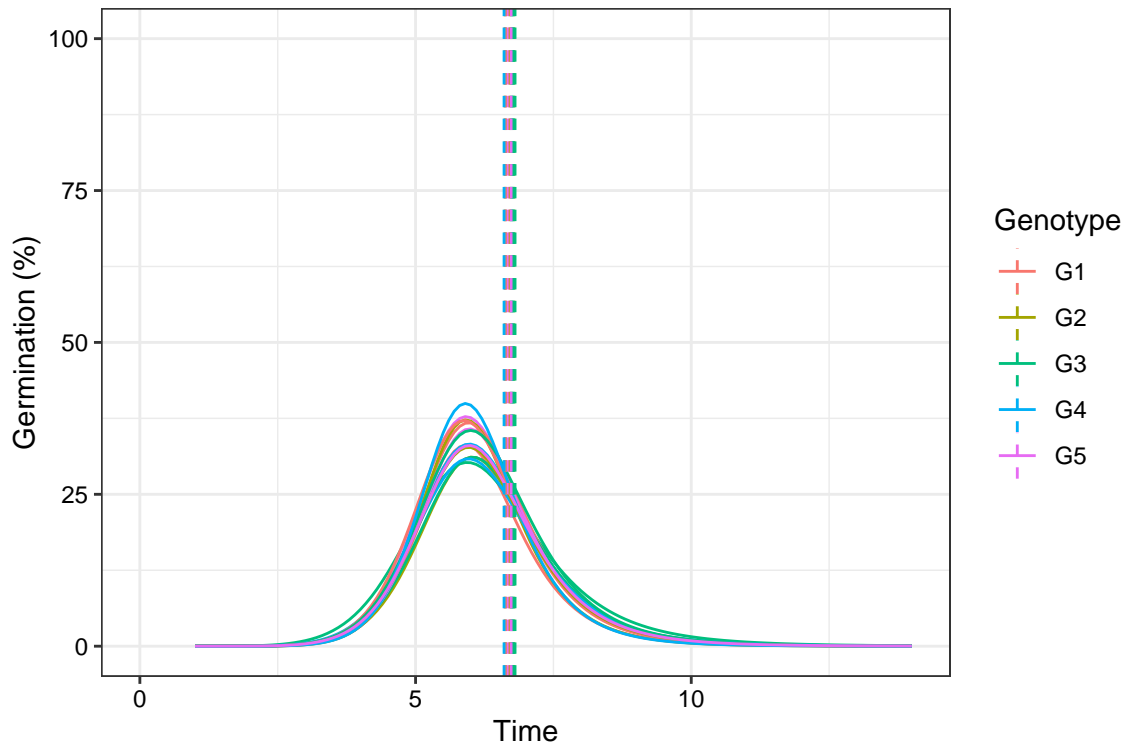
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```



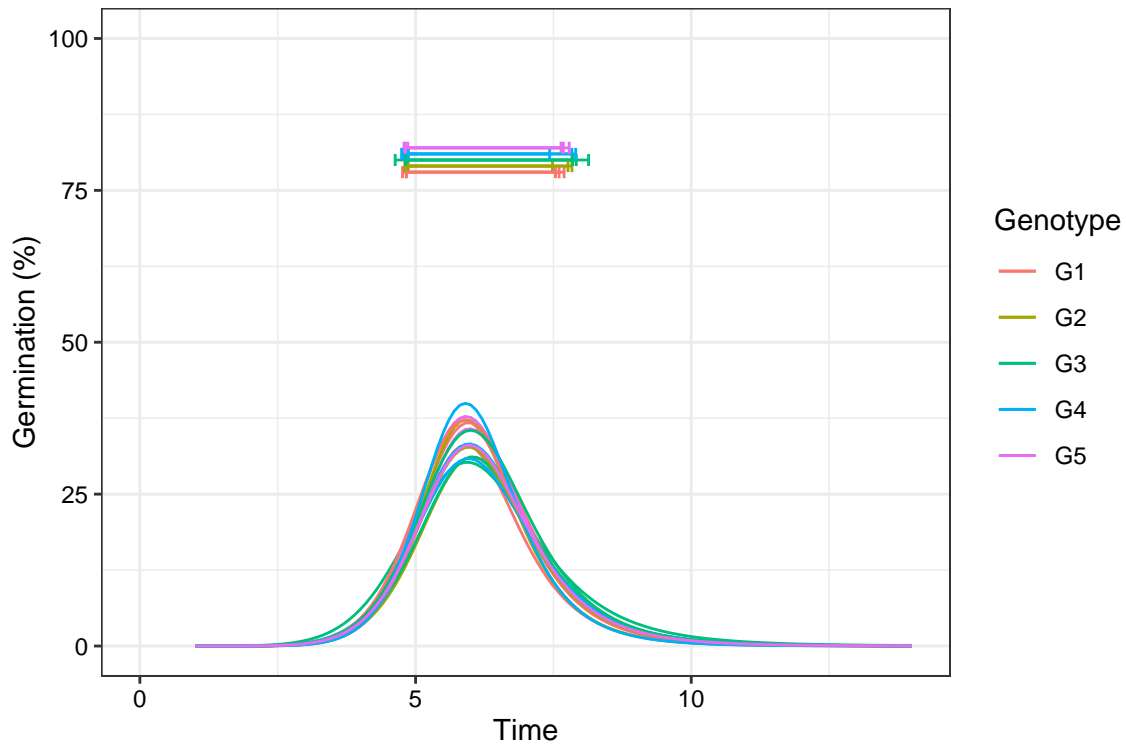
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "tmgr")
```



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



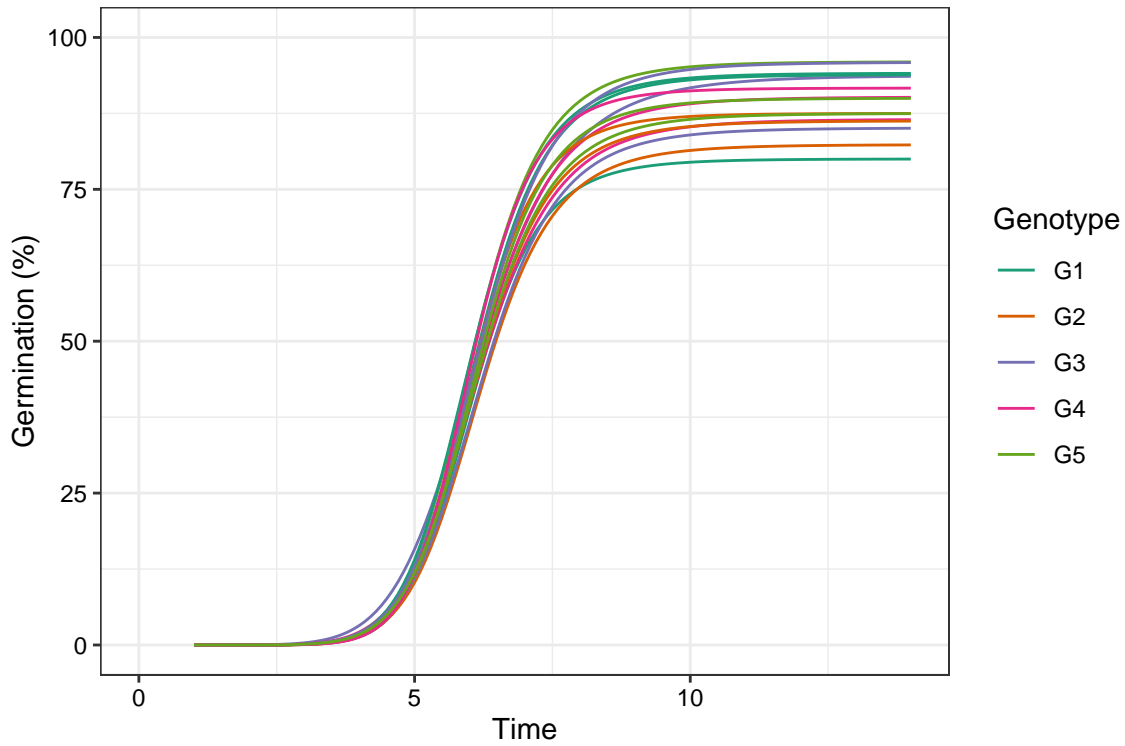
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "uniformity")
```



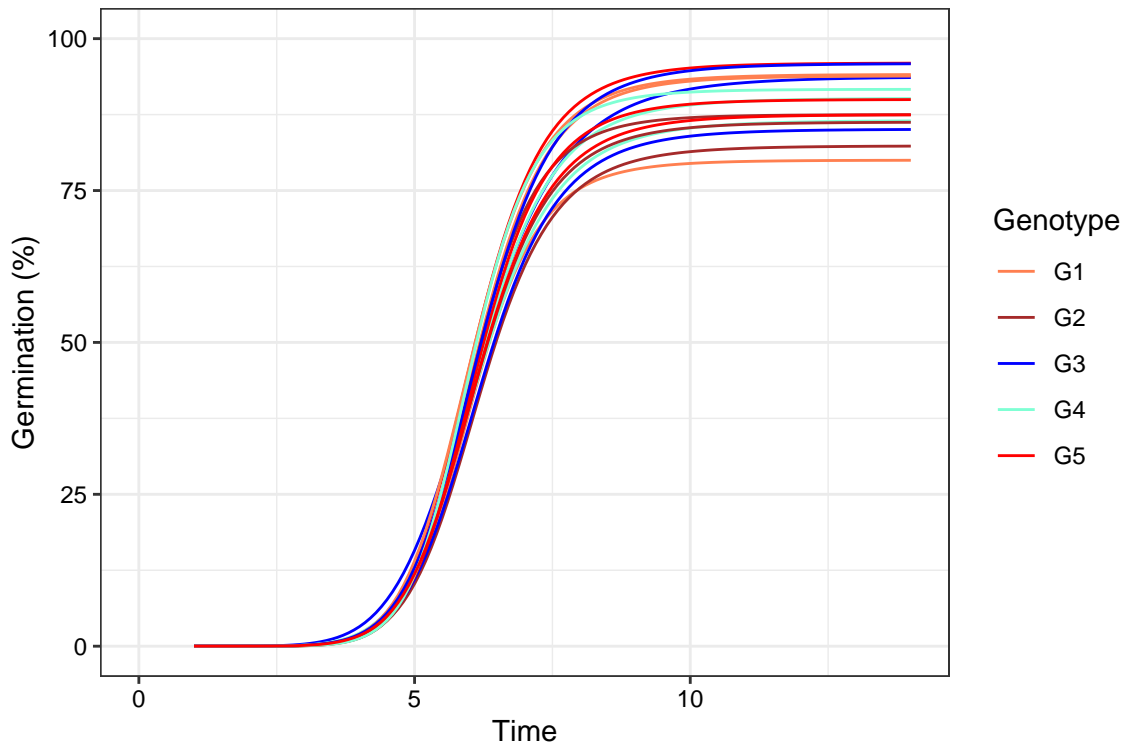
```
# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

# 'Dark2' palette from RColorBrewer
```

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



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



Citing germinationmetrics

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

Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan (2026). germinationmetrics: Seed Germination Indices and Curve Fitting. R package version 0.1.10.9000, <https://github.com/aravind-j/germinationmetrics> <https://cran.r-project.org/package=germinationmetrics>.

A BibTeX entry for LaTeX users is

```
@Manual{,
  title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
  author = {J. Aravind and S. {Vimala Devi} and J. Radhamani and Sherry Rachel Jacob and {Kalyani Sri},
  note = {R package version 0.1.10.9000 https://aravind-j.github.io/germinationmetrics/ https://CRAN.r-project.org/package=germinationmetrics},
  year = {2026},
}
```

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

Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2026-04-17 r89908 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 26200)
```

```
Matrix products: default
LAPACK version 3.12.1
```

```
locale:
[1] LC_COLLATE=English_India.utf8 LC_CTYPE=English_India.utf8
[3] LC_MONETARY=English_India.utf8 LC_NUMERIC=C
[5] LC_TIME=English_India.utf8
```

```
time zone: Asia/Calcutta
tzcode source: internal
```

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

```
other attached packages:
[1] germinationmetrics_0.1.10.9000 ggplot2_4.0.2
[3] readxl_1.4.5                  curl_7.0.0
[5] testthat_3.3.2
```

```
loaded via a namespace (and not attached):
[1] gtable_0.3.6      xfun_0.56          devtools_2.5.1.9000 processx_3.8.6
[5] ggrepel_0.9.7    rJava_1.0-14      lattice_0.22-9    callr_3.7.6
[9] mathjaxr_2.0-0   vctrs_0.7.3       tools_4.7.0      pak_0.9.4
[13] Rdpack_2.6.6     ps_1.9.1          generics_0.1.4   stats4_4.7.0
[17] parallel_4.7.0  tibble_3.3.1      pkgconfig_2.0.3  gslnls_1.4.2
```

[21] Matrix_1.7-5	data.table_1.18.2.1	RColorBrewer_1.1-3	S7_0.2.1-1
[25] desc_1.4.3	lifecycle_1.0.5	compiler_4.7.0	farver_2.1.2
[29] stringr_1.6.0	brio_1.1.5	tinytex_0.58	htmltools_0.5.9
[33] usethis_3.2.1	yaml_2.3.12	pillar_1.11.1	tidyr_1.3.2
[37] ellipsis_0.3.3	rsconnect_1.7.0	cachem_1.1.0	sessioninfo_1.2.3
[41] tidyselect_1.2.1	digest_0.6.39	stringi_1.8.7	reshape2_1.4.5
[45] pander_0.6.6	dplyr_1.2.0	purrr_1.2.1	labeling_0.4.3
[49] rprojroot_2.1.1	fastmap_1.2.0	grid_4.7.0	cli_3.6.6
[53] magrittr_2.0.5	XML_3.99-0.22	dichromat_2.0-0.1	pkgbuild_1.4.8
[57] broom_1.0.12	withr_3.0.2	scales_1.4.0	backports_1.5.0
[61] httr_1.4.8	roxygen2_7.3.3	rmarkdown_2.30	otel_0.2.0
[65] cellranger_1.1.0	memoise_2.0.1	evaluate_1.0.5	knitr_1.51
[69] rbibutils_2.4.1	rlang_1.2.0	Rcpp_1.1.1	glue_1.8.1
[73] xml2_1.5.2	pkgload_1.5.1	rstudioapi_0.18.0	R6_2.6.1
[77] plyr_1.8.9	fs_2.1.0		

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