

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.

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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)
```

Welcome to `germinationmetrics` version 0.1.5

```
# To know how to use this package type:
  browseVignettes(package = 'germinationmetrics')
  for the package vignette.

# To know whats new in this version type:
  news(package='germinationmetrics')
  for the NEWS file.

# To cite the methods in the package type:
  citation(package='germinationmetrics')

# To suppress this message use:
  suppressPackageStartupMessages(library(germinationmetrics))
```

Version History

The current version of the package is 0.1.5. 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

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.

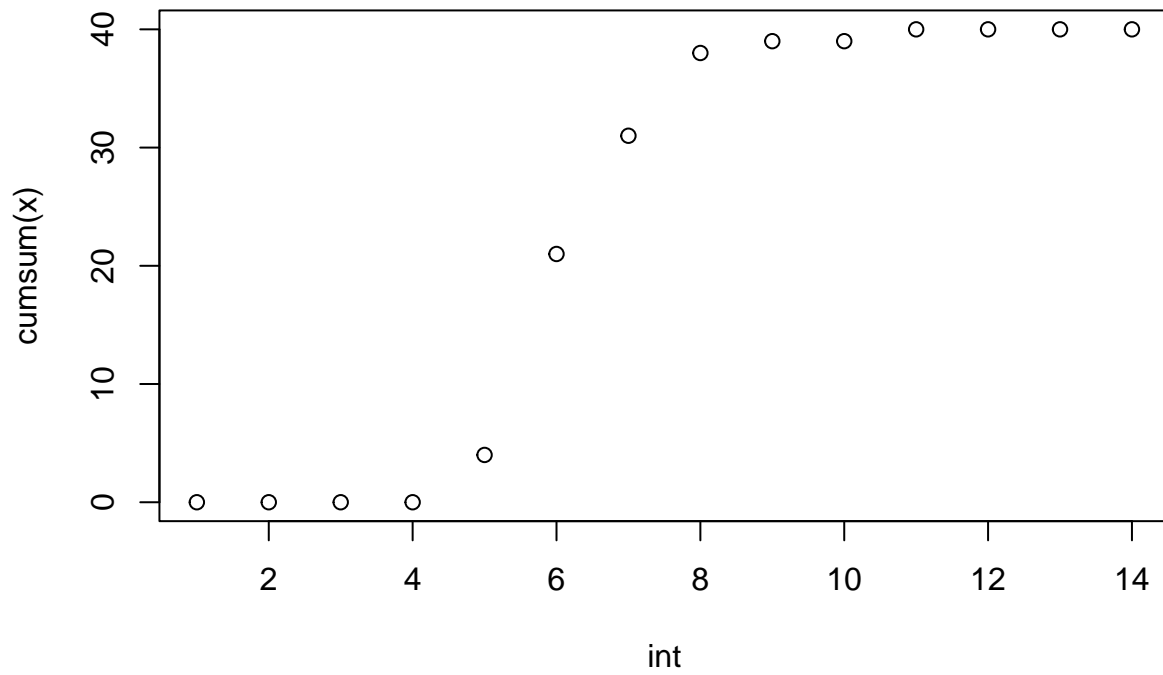
intervals	counts	cumulative.counts
1	0	0
2	0	0
3	0	0
4	0	0
5	4	4
6	17	21
7	10	31
8	7	38
9	1	39
10	0	39
11	1	40
12	0	40
13	0	40
14	0	40

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)
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)	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)	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	PeakGermTime	It is the time in which highest frequency of germinated seeds are observed and need not be unique.	time	Germination time	Ranal and Santana (2006)
Median germination time (t_{50}) (Coolbear)	t50	It is the time to reach 50% of final/maximum germination. With argument <code>method</code> 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 <code>method</code> 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)

Germination index	Function	Details	Unit	Measures	Reference
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)
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	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.</p> <p>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)

Germination index	Function	Details	Unit	Measures	Reference
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.</p> <p>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)
Coefficient of velocity of germination (CVG) or Coefficient of rate of germination (CRG) 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>	% 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	<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)

Germination index	Function	Details	Unit	Measures	Reference
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	<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.</p> <p>Instead of germination counts, germination percentages may also be used for computation of speed of germination.</p>	% 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)
Speed of accumulated germination	GermSpeedAccumulated	<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.</p> <p>Instead of germination counts, germination percentages may also be used for computation of speed of germination.</p>	% time ⁻¹	Mixed	Bradbeer (1988) ; Wardle et al. (1991) ; Haugland and Brandsaeter (1996) ; Santana and Ranal (2004)
Corrected germination rate index	GermSpeedCorrected	<p>It is computed as follows.</p> $S_{corrected} = \frac{S}{FGP}$ <p>Where, 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>		Mixed	Reddy et al. (1985) ; Reddy (1978)

Germination index	Function	Details	Unit	Measures	Reference
Mean germination percentage per unit time (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 k th 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 \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.		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 $j = i - 1$.		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 Unger (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.		Mixed	George (1961) ; Tucker and Wright (1965) ; Nichols and Heydecker (1968)
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.		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.		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.		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>		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>		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>		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>		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 <i>DGS</i> 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>		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 the mean germination time, T_i is the time from the start of the experiment to the <i>i</i>th interval (day for the example), N_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>		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>		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> $Z = \frac{\sum_{i=1}^k C_{N_i,2}}{C_{\Sigma N_i,2}}$ <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 $C_{\Sigma N_i,2}$ 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.</p>		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)
```

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

```
GermPercent()
```

```
[1] 80
```

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

```
[1] 80
```

```
# 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] 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
```

```
# 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)
```

```
EmergenceRateIndex()
```

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 292
```

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

```
[1] 292
```

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

```
[1] 7.3
```

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

```
[1] 5.970149
```

```
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE,
                    total.seeds = 50, 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
3	34	3	34	17.0
4	40	4	74	37.0
5	21	5	95	47.5
6	10	6	105	52.5
7	4	7	109	54.5
8	5	8	114	57.0
9	3	9	117	58.5
10	5	10	122	61.0
11	8	11	130	65.0
12	7	12	137	68.5
13	7	13	144	72.0
14	6	14	150	75.0
15	6	15	156	78.0
16	4	16	160	80.0
17	0	17	160	80.0
18	2	18	162	81.0
19	0	19	162	81.0
20	2	20	164	82.0


```

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

	DGS	SumDGSbyN	GV
3	5.666667	5.666667	9.633333
4	9.250000	7.458333	27.595833
5	9.500000	8.138889	38.659722
6	8.750000	8.291667	43.531250
7	7.785714	8.190476	44.638095
8	7.125000	8.012897	45.673512
9	6.500000	7.796769	45.611097
10	6.100000	7.584673	46.266503

```

11 5.909091 7.398497 48.090230
12 5.708333 7.229481 49.521942
13 5.538462 7.075752 50.945411
14 5.357143 6.932534 51.994006
15 5.200000 6.799262 53.034246
16 5.000000 6.670744 53.365948
17 4.705882 6.539753 52.318022
18 4.500000 6.412268 51.939373
19 4.263158 6.285850 50.915385
20 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
1	0	1	0	0.0
2	0	2	0	0.0
3	34	3	34	17.0
4	40	4	74	37.0
5	21	5	95	47.5
6	10	6	105	52.5
7	4	7	109	54.5
8	5	8	114	57.0
9	3	9	117	58.5
10	5	10	122	61.0
11	8	11	130	65.0
12	7	12	137	68.5
13	7	13	144	72.0
14	6	14	150	75.0
15	6	15	156	78.0
16	4	16	160	80.0
17	0	17	160	80.0
18	2	18	162	81.0
19	0	19	162	81.0
20	2	20	164	82.0

```
DGS
```

```

1 0.000000
2 0.000000
3 5.666667
4 9.250000
5 9.500000
6 8.750000
7 7.785714
8 7.125000
9 6.500000
10 6.100000
11 5.909091
12 5.708333

```

```

13 5.538462
14 5.357143
15 5.200000
16 5.000000
17 4.705882
18 4.500000
19 4.263158
20 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
1	0	1	0	0.0
2	0	2	0	0.0
3	34	3	34	17.0
4	40	4	74	37.0
5	21	5	95	47.5
6	10	6	105	52.5
7	4	7	109	54.5
8	5	8	114	57.0
9	3	9	117	58.5
10	5	10	122	61.0
11	8	11	130	65.0
12	7	12	137	68.5
13	7	13	144	72.0
14	6	14	150	75.0
15	6	15	156	78.0
16	4	16	160	80.0
17	0	17	160	80.0
18	2	18	162	81.0
19	0	19	162	81.0
20	2	20	164	82.0

	DGS	SumDGSbyN	GV
1	0.000000	0.000000	0.000000
2	0.000000	0.000000	0.000000
3	5.666667	1.888889	3.211111
4	9.250000	3.729167	13.797917
5	9.500000	4.883333	23.195833
6	8.750000	5.527778	29.020833
7	7.785714	5.850340	31.884354
8	7.125000	6.009673	34.255134
9	6.500000	6.064153	35.475298
10	6.100000	6.067738	37.013202
11	5.909091	6.053316	39.346552
12	5.708333	6.024567	41.268285
13	5.538462	5.987174	43.107655
14	5.357143	5.942172	44.566291
15	5.200000	5.892694	45.963013
16	5.000000	5.836901	46.695205
17	4.705882	5.770370	46.162961

```
18 4.500000 5.699794 46.168331
19 4.263158 5.624182 45.555871
20 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
3	34	3	34	17.0
4	40	4	74	37.0
5	21	5	95	47.5
6	10	6	105	52.5
7	4	7	109	54.5
8	5	8	114	57.0
9	3	9	117	58.5
10	5	10	122	61.0
11	8	11	130	65.0
12	7	12	137	68.5
13	7	13	144	72.0
14	6	14	150	75.0
15	6	15	156	78.0
16	4	16	160	80.0
17	0	17	160	80.0
18	2	18	162	81.0
19	0	19	162	81.0
20	2	20	164	82.0

```
DGS
3 5.666667
4 9.250000
5 9.500000
6 8.750000
7 7.785714
8 7.125000
9 6.500000
10 6.100000
11 5.909091
12 5.708333
13 5.538462
14 5.357143
15 5.200000
16 5.000000
```

```
17 4.705882
18 4.500000
19 4.263158
20 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
3	34	3	34	17.0
4	40	4	74	37.0
5	21	5	95	47.5
6	10	6	105	52.5
7	4	7	109	54.5
8	5	8	114	57.0
9	3	9	117	58.5
10	5	10	122	61.0
11	8	11	130	65.0
12	7	12	137	68.5
13	7	13	144	72.0
14	6	14	150	75.0
15	6	15	156	78.0
16	4	16	160	80.0
17	0	17	160	80.0
18	2	18	162	81.0
19	0	19	162	81.0
20	2	20	164	82.0

	DGS	SumDGSbyN	GV
3	5.666667	5.666667	9.633333
4	9.250000	7.458333	27.595833
5	9.500000	8.138889	38.659722
6	8.750000	8.291667	43.531250
7	7.785714	8.190476	44.638095
8	7.125000	8.012897	45.673512
9	6.500000	7.796769	45.611097
10	6.100000	7.584673	46.266503
11	5.909091	7.398497	48.090230
12	5.708333	7.229481	49.521942
13	5.538462	7.075752	50.945411
14	5.357143	6.932534	51.994006
15	5.200000	6.799262	53.034246
16	5.000000	6.670744	53.365948
17	4.705882	6.539753	52.318022
18	4.500000	6.412268	51.939373
19	4.263158	6.285850	50.915385
20	4.100000	6.164414	50.548194

```
$testend
[1] 16
```

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

```
$`Germination Value`
```

```
[1] 38.95
```

```
[[2]]
```

	germ.counts	intervals	Cumulative.germ.counts	Cumulative.germ.percent
1	0	1	0	0.0
2	0	2	0	0.0
3	34	3	34	17.0
4	40	4	74	37.0
5	21	5	95	47.5
6	10	6	105	52.5
7	4	7	109	54.5
8	5	8	114	57.0
9	3	9	117	58.5
10	5	10	122	61.0
11	8	11	130	65.0
12	7	12	137	68.5
13	7	13	144	72.0
14	6	14	150	75.0
15	6	15	156	78.0
16	4	16	160	80.0
17	0	17	160	80.0
18	2	18	162	81.0
19	0	19	162	81.0
20	2	20	164	82.0

```
DGS
```

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

	DGS	SumDGSbyN	GV
1	0.000000	0.000000	0.000000
2	0.000000	0.000000	0.000000
3	5.666667	1.888889	3.211111
4	9.250000	3.729167	13.797917
5	9.500000	4.883333	23.195833
6	8.750000	5.527778	29.020833
7	7.785714	5.850340	31.884354
8	7.125000	6.009673	34.255134
9	6.500000	6.064153	35.475298
10	6.100000	6.067738	37.013202
11	5.909091	6.053316	39.346552
12	5.708333	6.024567	41.268285
13	5.538462	5.987174	43.107655
14	5.357143	5.942172	44.566291
15	5.200000	5.892694	45.963013
16	5.000000	5.836901	46.695205
17	4.705882	5.770370	46.162961
18	4.500000	5.699794	46.168331
19	4.263158	5.624182	45.555871
20	4.100000	5.547972	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, 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] 0.05267935

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
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."

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
$lag = b \sqrt{\frac{-y_0 c^b}{a + y_0}}$			
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>umax</code> 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.	time	Germination time
$s = \frac{\partial y}{\partial x} = \frac{abc^b x^{b-1}}{(c^b + x^b)^2}$			
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.			

Germination parameters	Details	Unit	Measures
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 <code>tmax</code> .		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, 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
1	1.769385	TRUE	1.490116e-08	-25.49868	60.99736	64.19265	31.30723	10

```
nobs
1  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
1 1.769385  TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723         10
  nobs
1  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

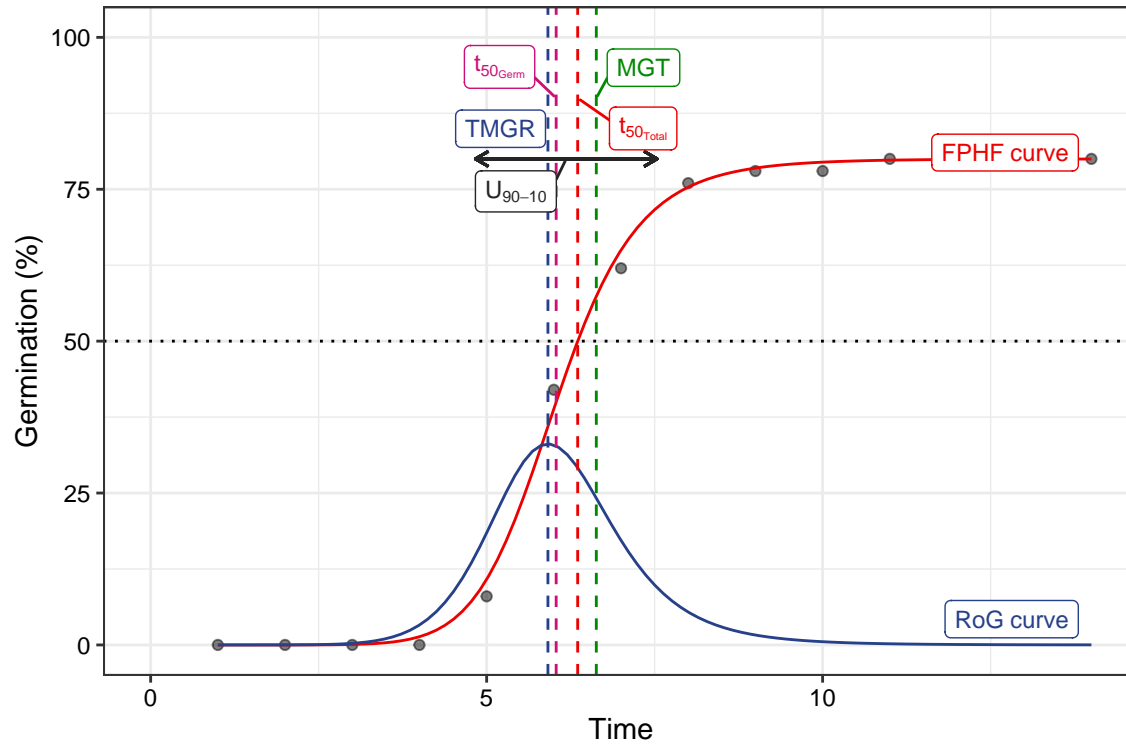
```

```

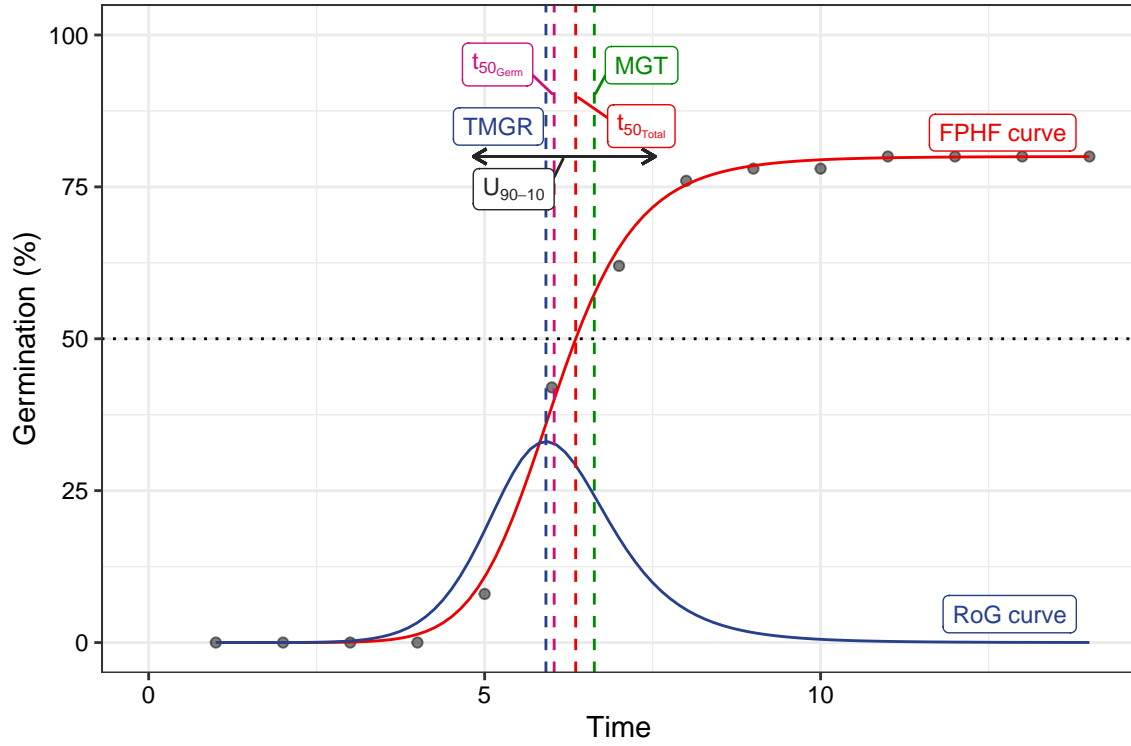
#-----
fit2 <- FourPHFfit(germ.counts = y, intervals = int,
                  total.seeds = 50, tmax = 20, partial = FALSE)

# Default plots
plot(fit1)

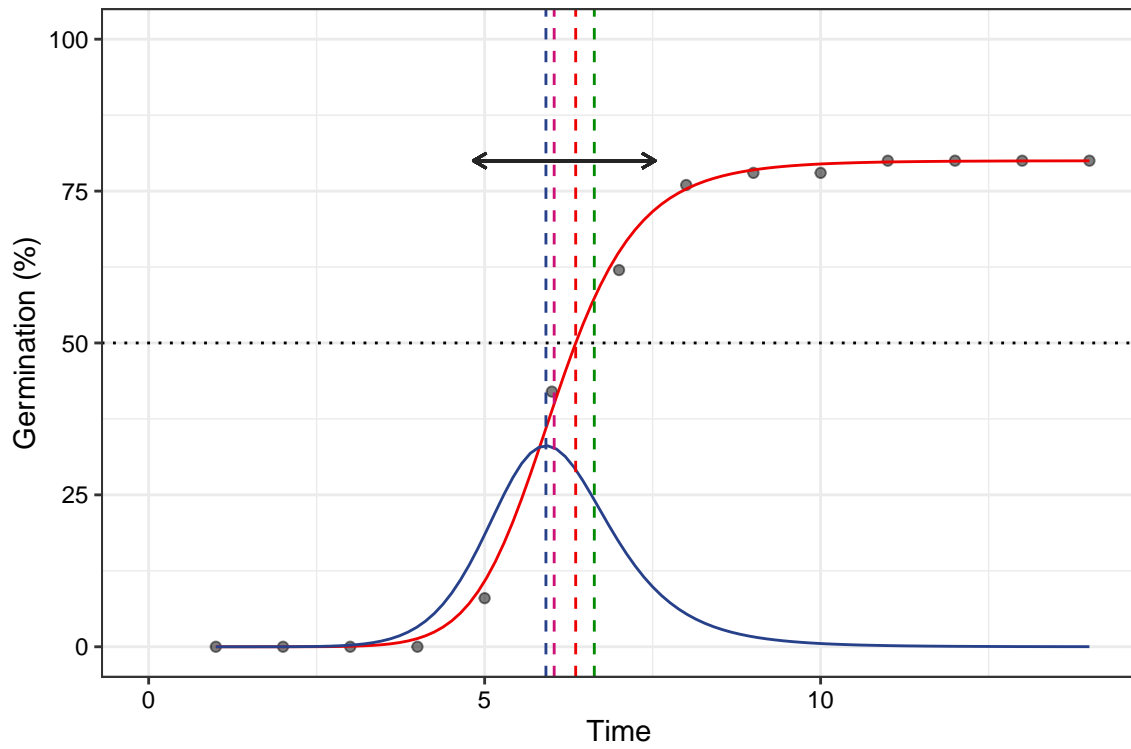
```



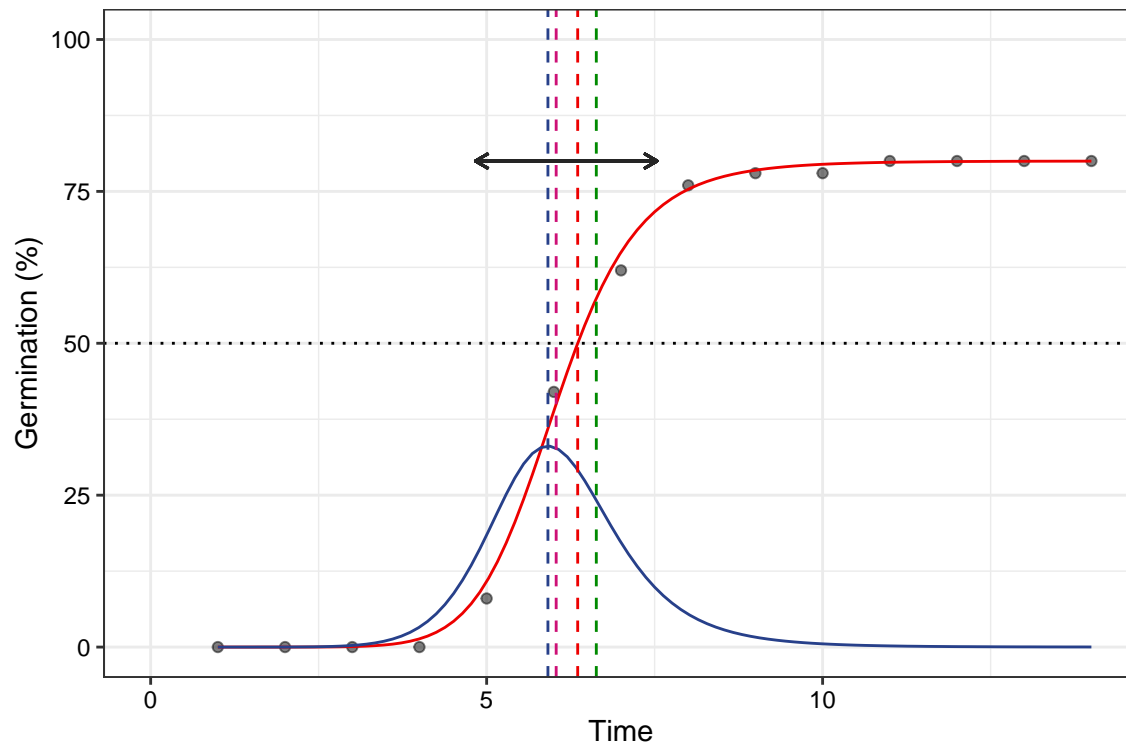
```
plot(fit2)
```



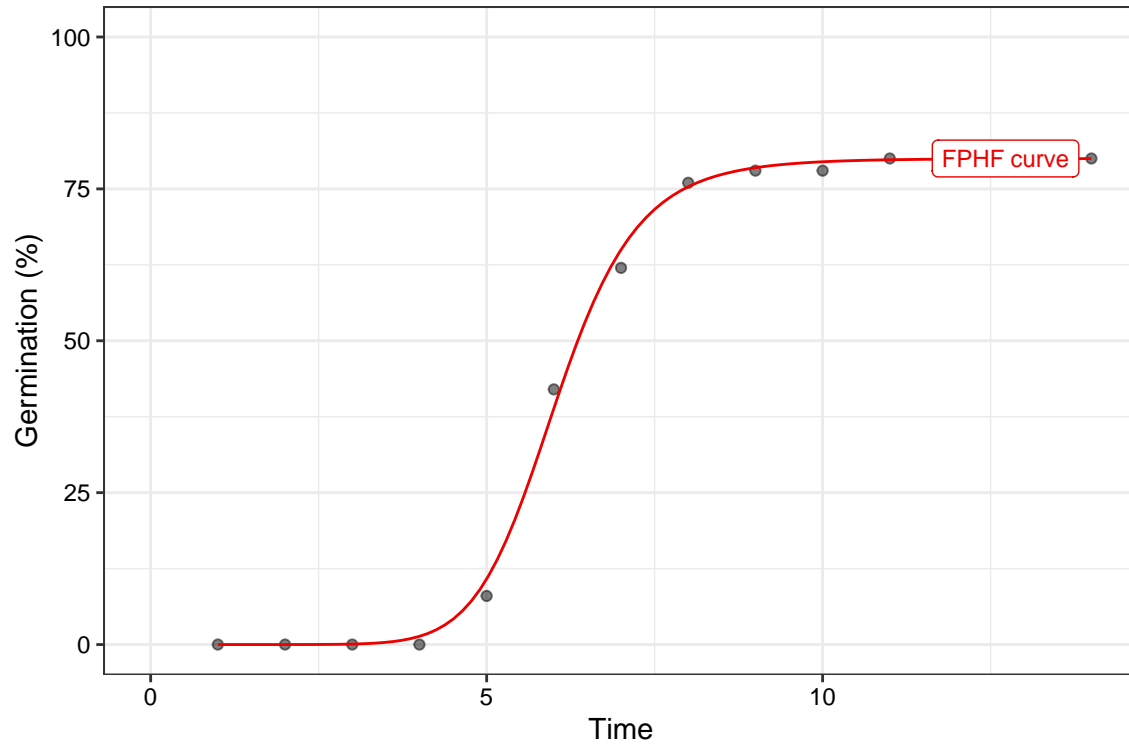
```
# No labels
plot(fit1, plotlabels = FALSE)
```



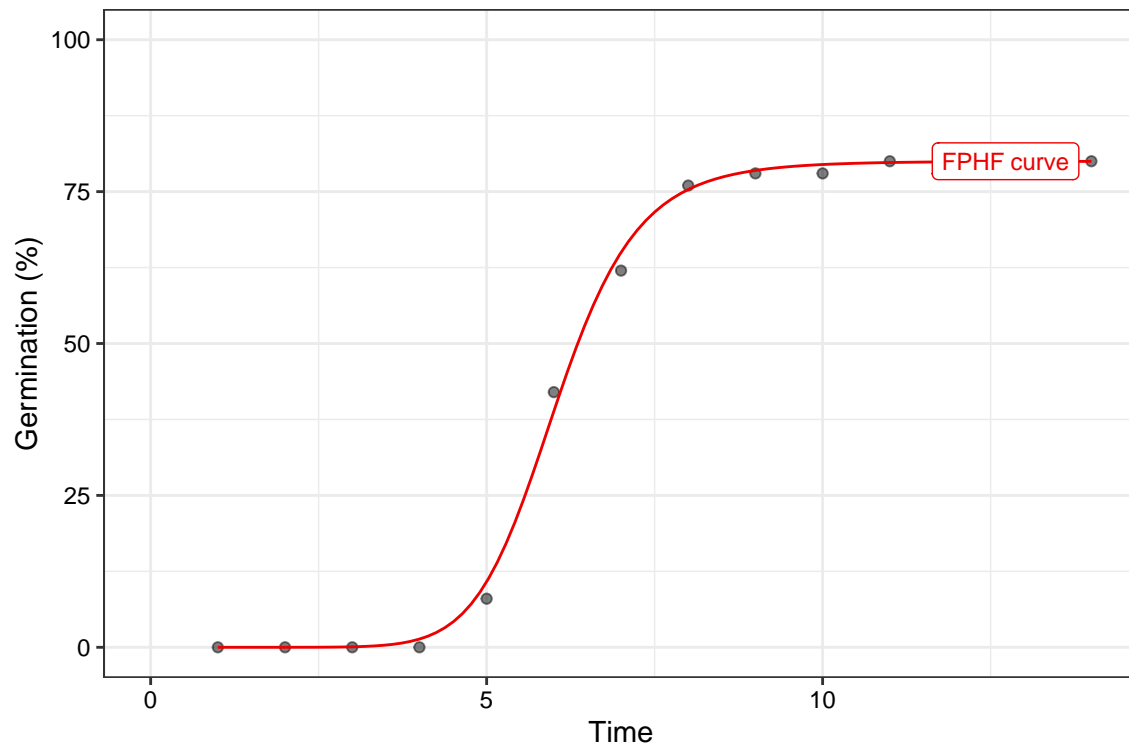
```
plot(fit2, plotlabels = FALSE)
```



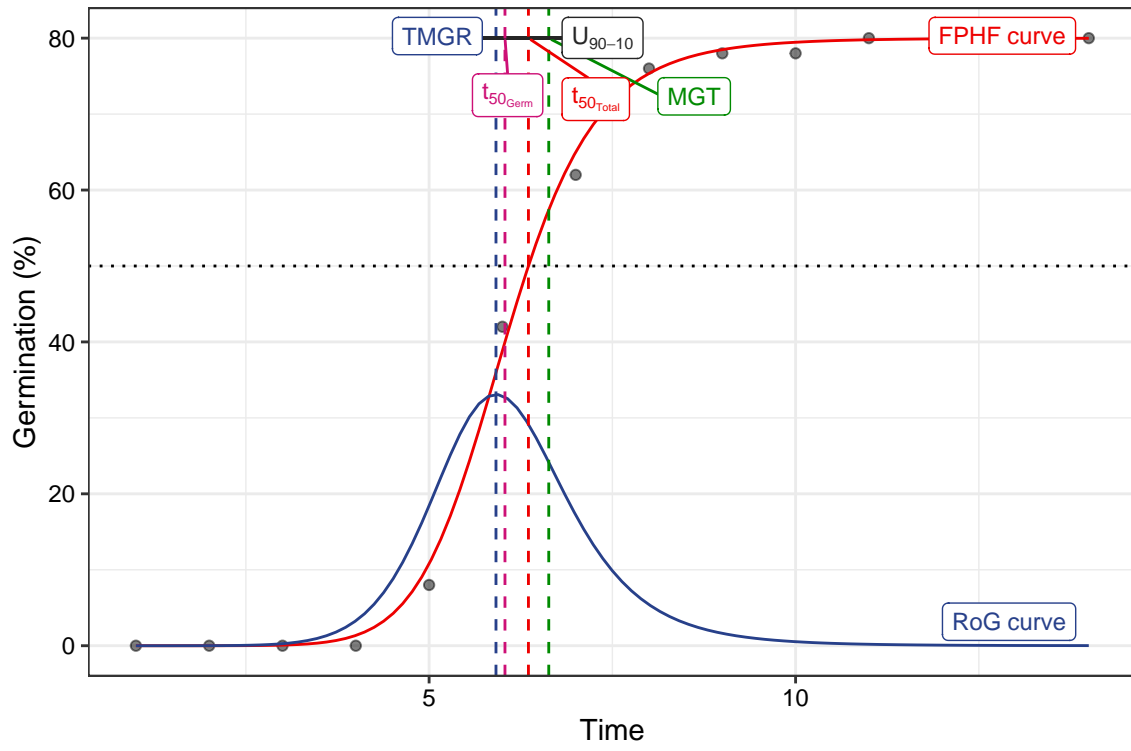
```
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```

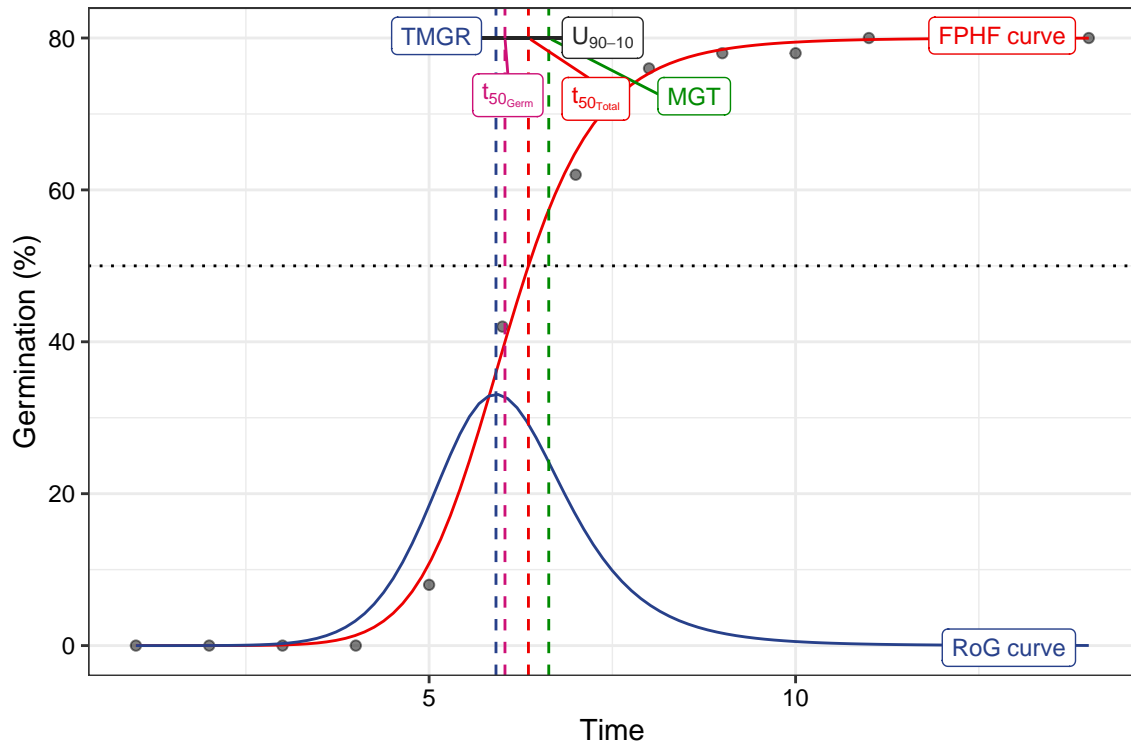
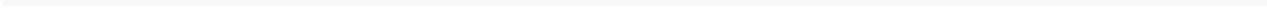
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,  
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



```
# 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.

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

	Day11	Day12	Day13	Day14	Total Seeds	GermPercent	FirstGermTime	LastGermTime
1	1	0	0	0	50	80.00000	5	11
2	0	1	0	0	51	82.35294	4	12
3	1	1	0	0	48	93.75000	4	12
4	1	1	0	0	51	90.19608	5	12
5	0	1	1	0	50	96.00000	5	13
6	1	1	0	0	49	93.87755	5	12
7	1	0	0	0	48	87.50000	5	11
8	0	1	0	0	47	85.10638	4	12
9	1	1	0	0	52	86.53846	4	12
10	0	1	0	0	50	90.00000	5	12
11	0	1	1	0	51	94.11765	5	13
12	1	1	0	0	51	86.27451	5	12
13	0	1	1	0	49	95.91837	5	13
14	1	1	0	0	48	91.66667	5	12
15	1	0	0	0	48	87.50000	5	11

	PeakGermTime	TimeSpreadGerm	t50_Coolbear	t50_Farooq	MeanGermTime	VarGermTime	
1	6		6	5.970588	5.941176	6.700000	1.446154
2	6		8	6.192308	6.153846	6.857143	2.027875
3	6		8	6.000000	5.972222	6.866667	2.572727
4	6		7	6.041667	6.000000	6.891304	2.187923

5	6	8	5.975000	5.950000	6.812500	2.368351
6	6	7	5.976190	5.952381	6.869565	2.071498
7	6	6	5.972222	5.944444	6.690476	1.389663
8	6	8	6.208333	6.166667	6.875000	2.112179
9	6	8	6.000000	5.973684	6.866667	2.300000
10	6	7	6.076923	6.038462	6.822222	1.831313
11	6	8	5.928571	5.904762	6.791667	2.381206
12	6	7	5.975000	5.950000	6.886364	2.149577
13	6	8	6.083333	6.041667	6.936170	2.539315
14	6	7	5.928571	5.904762	6.772727	1.900634
15	6	6	6.050000	6.000000	6.809524	1.670151

	SEGermTime	CVGermTime	MeanGermRate	VarGermRate	SEGermRate	CVG
1	0.1901416	0.1794868	0.1492537	0.0007176543	0.004235724	14.92537
2	0.2197333	0.2076717	0.1458333	0.0009172090	0.004673148	14.58333
3	0.2391061	0.2335882	0.1456311	0.0011572039	0.005071059	14.56311
4	0.2180907	0.2146419	0.1451104	0.0009701218	0.004592342	14.51104
5	0.2221275	0.2259002	0.1467890	0.0010995627	0.004786184	14.67890
6	0.2122088	0.2095140	0.1455696	0.0009301809	0.004496813	14.55696
7	0.1818989	0.1761967	0.1494662	0.0006935558	0.004063648	14.94662
8	0.2297923	0.2113940	0.1454545	0.0009454531	0.004861721	14.54545
9	0.2260777	0.2208604	0.1456311	0.0010345321	0.004794747	14.56311
10	0.2017321	0.1983606	0.1465798	0.0008453940	0.004334343	14.65798
11	0.2227295	0.2272072	0.1472393	0.0011191581	0.004828643	14.72393
12	0.2210295	0.2129053	0.1452145	0.0009558577	0.004660905	14.52145
13	0.2324392	0.2297410	0.1441718	0.0010970785	0.004831366	14.41718
14	0.2078370	0.2035568	0.1476510	0.0009033254	0.004531018	14.76510
15	0.1994129	0.1897847	0.1468531	0.0007767634	0.004300508	14.68531

	GermRateRecip_Coolbear	GermRateRecip_Farooq	GermSpeed_Count
1	0.1674877	0.1683168	6.138925
2	0.1614907	0.1625000	6.362698
3	0.1666667	0.1674419	6.882179
4	0.1655172	0.1666667	6.927417
5	0.1673640	0.1680672	7.318987
6	0.1673307	0.1680000	6.931782
7	0.1674419	0.1682243	6.448449
8	0.1610738	0.1621622	6.053175
9	0.1666667	0.1674009	6.830592
10	0.1645570	0.1656051	6.812698
11	0.1686747	0.1693548	7.342796
12	0.1673640	0.1680672	6.622258
13	0.1643836	0.1655172	7.052320
14	0.1686747	0.1693548	6.706782
15	0.1652893	0.1666667	6.363925

	GermSpeed_Percent	GermSpeedAccumulated_Count	GermSpeedAccumulated_Percent
1	12.27785	34.61567	69.23134
2	12.47588	35.54058	69.68741
3	14.33787	38.29725	79.78594
4	13.58317	38.68453	75.85202
5	14.63797	41.00786	82.01571
6	14.14649	38.77620	79.13509
7	13.43427	36.38546	75.80304
8	12.87909	33.77079	71.85275
9	13.13575	38.11511	73.29829
10	13.62540	38.19527	76.39054

11	14.39764	41.17452	80.73436	
12	12.98482	37.00640	72.56158	
13	14.39249	39.29399	80.19182	
14	13.97246	37.69490	78.53103	
15	13.25818	35.69697	74.36868	
	GermSpeedCorrected_Normal	GermSpeedCorrected_Accumulated	WeightGermPercent	
1	0.07673656	0.4326958	47.42857	
2	0.07726134	0.4315642	47.89916	
3	0.07340991	0.4085040	54.46429	
4	0.07680397	0.4288937	52.24090	
5	0.07623944	0.4271652	56.14286	
6	0.07383855	0.4130508	54.51895	
7	0.07369656	0.4158338	51.93452	
8	0.07112480	0.3968068	49.39210	
9	0.07893128	0.4404413	50.27473	
10	0.07569665	0.4243919	52.57143	
11	0.07801721	0.4374793	55.18207	
12	0.07675799	0.4289379	50.00000	
13	0.07352419	0.4096608	55.24781	
14	0.07316490	0.4112171	53.86905	
15	0.07273057	0.4079653	51.19048	
	MeanGermPercent	MeanGermNumber	TimsonsIndex	TimsonsIndex_Labouriau
1	5.714286	2.857143	8.000000	1.00
2	5.882353	3.000000	9.803922	1.25
3	6.696429	3.214286	14.583333	1.40
4	6.442577	3.285714	7.843137	1.00
5	6.857143	3.428571	10.000000	1.00
6	6.705539	3.285714	6.122449	1.00
7	6.250000	3.000000	8.333333	1.00
8	6.079027	2.857143	10.638298	1.25
9	6.181319	3.214286	9.615385	1.25
10	6.428571	3.214286	8.000000	1.00
11	6.722689	3.428571	9.803922	1.00
12	6.162465	3.142857	5.882353	1.00
13	6.851312	3.357143	8.163265	1.00
14	6.547619	3.142857	6.250000	1.00
15	6.250000	3.000000	8.333333	1.00
	TimsonsIndex_KhanUngar	GermRateGeorge	GermIndex	GermIndex_mod
1	0.5714286	4	5.840000	7.300000
2	0.7002801	5	5.882353	7.142857
3	1.0416667	7	6.687500	7.133333
4	0.5602241	4	6.411765	7.108696
5	0.7142857	5	6.900000	7.187500
6	0.4373178	3	6.693878	7.130435
7	0.5952381	4	6.395833	7.309524
8	0.7598784	5	6.063830	7.125000
9	0.6868132	5	6.173077	7.133333
10	0.5714286	4	6.460000	7.177778
11	0.7002801	5	6.784314	7.208333
12	0.4201681	3	6.137255	7.113636
13	0.5830904	4	6.775510	7.063830
14	0.4464286	3	6.625000	7.227273
15	0.5952381	4	6.291667	7.190476
	EmergenceRateIndex_Melville	EmergenceRateIndex_Melville_mod		

1	292	7.300000		
2	300	7.142857		
3	321	7.133333		
4	327	7.108696		
5	345	7.187500		
6	328	7.130435		
7	307	7.309524		
8	285	7.125000		
9	321	7.133333		
10	323	7.177778		
11	346	7.208333		
12	313	7.113636		
13	332	7.063830		
14	318	7.227273		
15	302	7.190476		
	EmergenceRateIndex_BilbroWanjura	EmergenceRateIndex_Fakorede	PeakValue	
1	5.970149	8.375000	9.500000	
2	6.125000	8.326531	9.313725	
3	6.553398	7.324444	10.416667	
4	6.675079	7.640359	10.049020	
5	7.045872	7.096354	11.250000	
6	6.696203	7.317580	10.714286	
7	6.277580	7.646259	10.416667	
8	5.818182	8.078125	9.574468	
9	6.553398	7.934815	9.855769	
10	6.596091	7.580247	10.250000	
11	7.067485	7.216146	11.029412	
12	6.389439	7.981921	9.803922	
13	6.776074	7.231326	10.969388	
14	6.496644	7.388430	10.677083	
15	6.167832	7.782313	10.156250	
	GermValue_Czabator	GermValue_DP	GermValue_Czabator_mod	GermValue_DP_mod
1	54.28571	57.93890	54.28571	39.56076
2	54.78662	52.58713	54.78662	40.99260
3	69.75446	68.62289	69.75446	53.42809
4	64.74158	70.43331	64.74158	48.86825
5	77.14286	80.16914	77.14286	56.23935
6	71.84506	76.51983	71.84506	53.06435
7	65.10417	69.41325	65.10417	47.37690
8	58.20345	56.00669	58.20345	43.67948
9	60.92165	58.13477	60.92165	45.30801
10	65.89286	70.91875	65.89286	49.10820
11	74.14731	77.39782	74.14731	54.27520
12	60.41632	64.44988	60.41632	44.71582
13	75.15470	78.16335	75.15470	54.94192
14	69.90947	74.40140	69.90947	51.41913
15	63.47656	67.62031	63.47656	46.48043
	CUGerm	GermSynchrony	GermUncertainty	
1	0.7092199	0.2666667	2.062987	
2	0.5051546	0.2346109	2.321514	
3	0.3975265	0.2242424	2.462012	
4	0.4672113	0.2502415	2.279215	
5	0.4312184	0.2606383	2.146051	
6	0.4934701	0.2792271	2.160545	

```

7 0.7371500      0.2729384      2.040796
8 0.4855842      0.2256410      2.357249
9 0.4446640      0.2494949      2.321080
10 0.5584666     0.2555556     2.187983
11 0.4288905     0.2686170     2.128670
12 0.4760266     0.2737844     2.185245
13 0.4023679     0.2506938     2.241181
14 0.5383760     0.2991543     2.037680
15 0.6133519     0.2497096     2.185028

```

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

```

data(gcdata)

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

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

```

	Genotype	Rep	Day01	Day02	Day03	Day04	Day05	Day06	Day07	Day08	Day09	Day10
1	G1	1	0	0	0	0	4	17	10	7	1	0
2	G2	1	0	0	0	1	3	15	13	6	2	1
3	G3	1	0	0	0	2	3	18	9	8	2	1
4	G4	1	0	0	0	0	4	19	12	6	2	1
5	G5	1	0	0	0	0	5	20	12	8	1	0
6	G1	2	0	0	0	0	3	21	11	7	1	1
7	G2	2	0	0	0	0	4	18	11	7	1	0
8	G3	2	0	0	0	1	3	14	12	6	2	1
9	G4	2	0	0	0	1	3	19	10	8	1	1
10	G5	2	0	0	0	0	4	18	13	6	2	1
11	G1	3	0	0	0	0	5	21	11	8	1	0
12	G2	3	0	0	0	0	3	20	10	7	1	1
13	G3	3	0	0	0	0	4	19	12	8	1	1
14	G4	3	0	0	0	0	3	21	11	6	1	0
15	G5	3	0	0	0	0	4	17	10	8	1	1

	Day11	Day12	Day13	Day14	Total Seeds	a	b	c	y0	lag
1	1	0	0	0	50	80.00000	9.881947	6.034954	0	0
2	0	1	0	0	51	82.35294	9.227667	6.175193	0	0
3	1	1	0	0	48	93.75000	7.793055	6.138110	0	0
4	1	1	0	0	51	90.19608	8.925668	6.125172	0	0
5	0	1	1	0	50	96.00000	9.419194	6.049641	0	0
6	1	1	0	0	49	93.87755	9.450187	6.097412	0	0
7	1	0	0	0	48	87.50000	10.172466	6.029851	0	0
8	0	1	0	0	47	85.10638	8.940702	6.189774	0	0
9	1	1	0	0	52	86.53846	8.617395	6.125121	0	0
10	0	1	0	0	50	90.00000	9.608849	6.109503	0	0
11	0	1	1	0	51	94.11765	9.400248	6.018759	0	0
12	1	1	0	0	51	86.27451	9.162558	6.108449	0	0
13	0	1	1	0	49	95.91837	8.995233	6.149011	0	0

```

14      1      1      0      0          48 91.66667 10.391898 6.015907 0 0
15      1      0      0      0          48 87.50000  9.136762 6.121580 0 0
      Dlag50 t50.total t50.Germinated      TMGR      AUC      MGT Skewness
1  6.034954  6.355122      6.034954 5.912195 1108.975 6.632252 1.098973
2  6.175193  6.473490      6.175193 6.031282 1128.559 6.784407 1.098655
3  6.138110  6.244190      6.138110 5.938179 1283.693 6.772742 1.103392
4  6.125172  6.276793      6.125172 5.972686 1239.887 6.739665 1.100323
5  6.049641  6.103433      6.049641 5.914289 1328.328 6.654980 1.100062
6  6.097412  6.182276      6.097412 5.961877 1294.463 6.702470 1.099232
7  6.029851  6.202812      6.029851 5.914057 1213.908 6.622417 1.098272
8  6.189774  6.439510      6.189774 6.036193 1164.346 6.804000 1.099232
9  6.125121  6.352172      6.125121 5.961631 1188.793 6.745241 1.101242
10 6.109503  6.253042      6.109503 5.978115 1240.227 6.711899 1.098600
11 6.018759  6.099434      6.018759 5.883558 1305.200 6.624247 1.100600
12 6.108449  6.326181      6.108449 5.964079 1188.021 6.718636 1.099892
13 6.149011  6.207500      6.149011 5.998270 1316.407 6.762272 1.099733
14 6.015907  6.122385      6.015907 5.905179 1273.386 6.604963 1.097916
15 6.121580  6.317392      6.121580 5.976088 1203.664 6.732267 1.099760
      msg isConv
1 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
2 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
3 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
4 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
5 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
6 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
7 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
8 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
9 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
10 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
11 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
12 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
13 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
14 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
15 #1. Relative error in the sum of squares is at most `ftol'.  TRUE
      txp.total_10 txp.total_60 Uniformity_90 Uniformity_10 Uniformity
1  4.956266  6.744598  7.537688  4.831809  2.705880
2  4.983236  6.872603  7.835407  4.866755  2.968652
3  4.673022  6.608437  8.137340  4.630062  3.507277
4  4.850876  6.614967  7.834806  4.788598  3.046208
5  4.814126  6.386788  7.639025  4.790947  2.848078
6  4.868635  6.477594  7.693458  4.832474  2.860984
7  4.930423  6.510495  7.483642  4.858477  2.625165
8  4.940058  6.823299  7.914162  4.841106  3.073056
9  4.836659  6.733275  7.904040  4.746574  3.157466
10 4.920629  6.566505  7.679176  4.860681  2.818494
11 4.798630  6.391288  7.603603  4.764249  2.839354
12 4.893597  6.684521  7.763844  4.806015  2.957830
13 4.841310  6.509952  7.850339  4.816395  3.033943
14 4.915143  6.397486  7.432360  4.869401  2.562960
15 4.892505  6.667247  7.785804  4.813086  2.972718

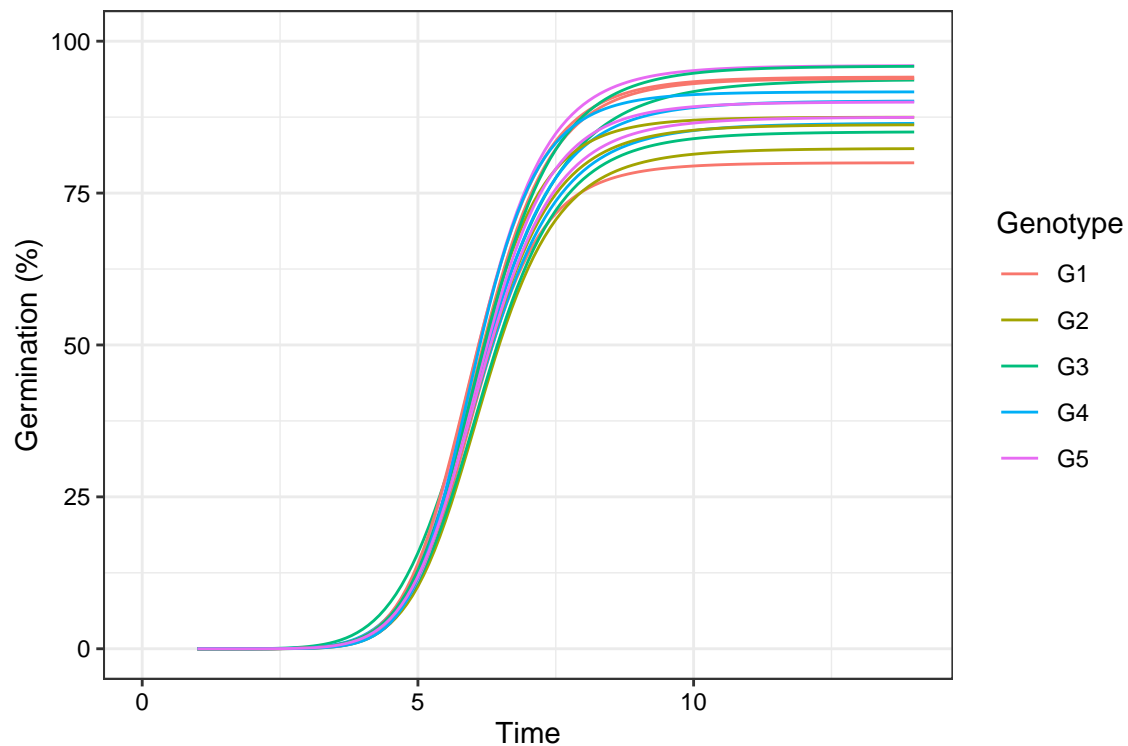
```

Multiple fitted curves generated in batch can also be plotted.

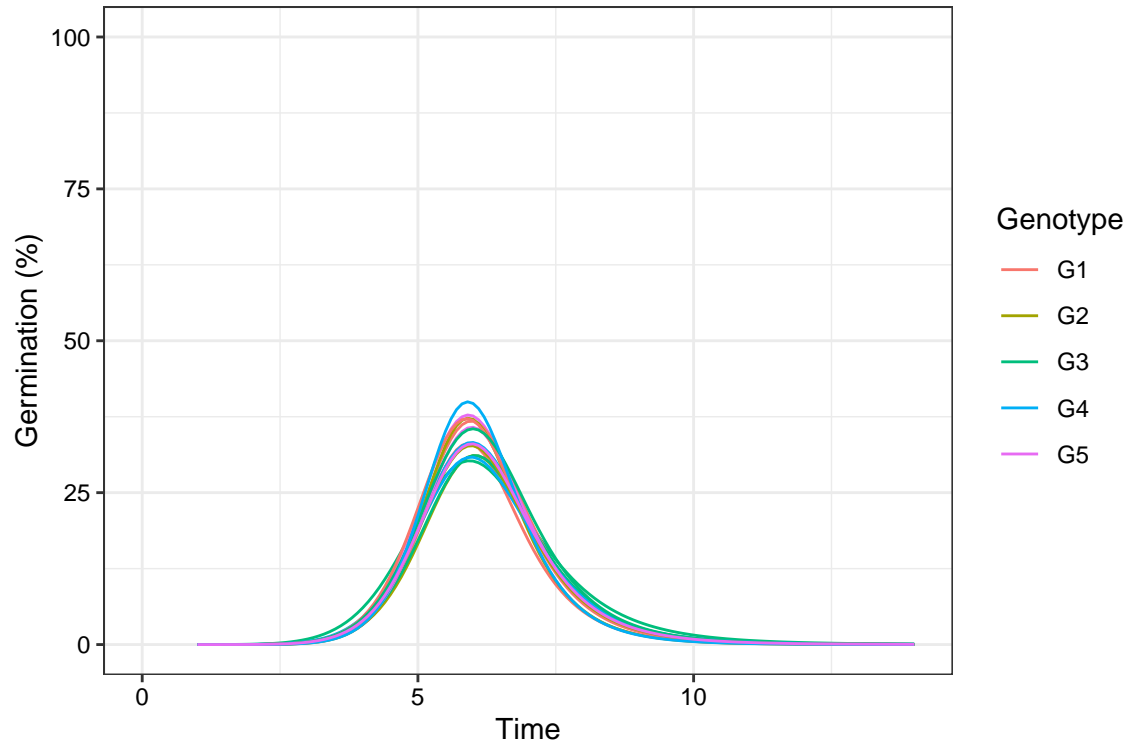
```
data(gcdata)
```



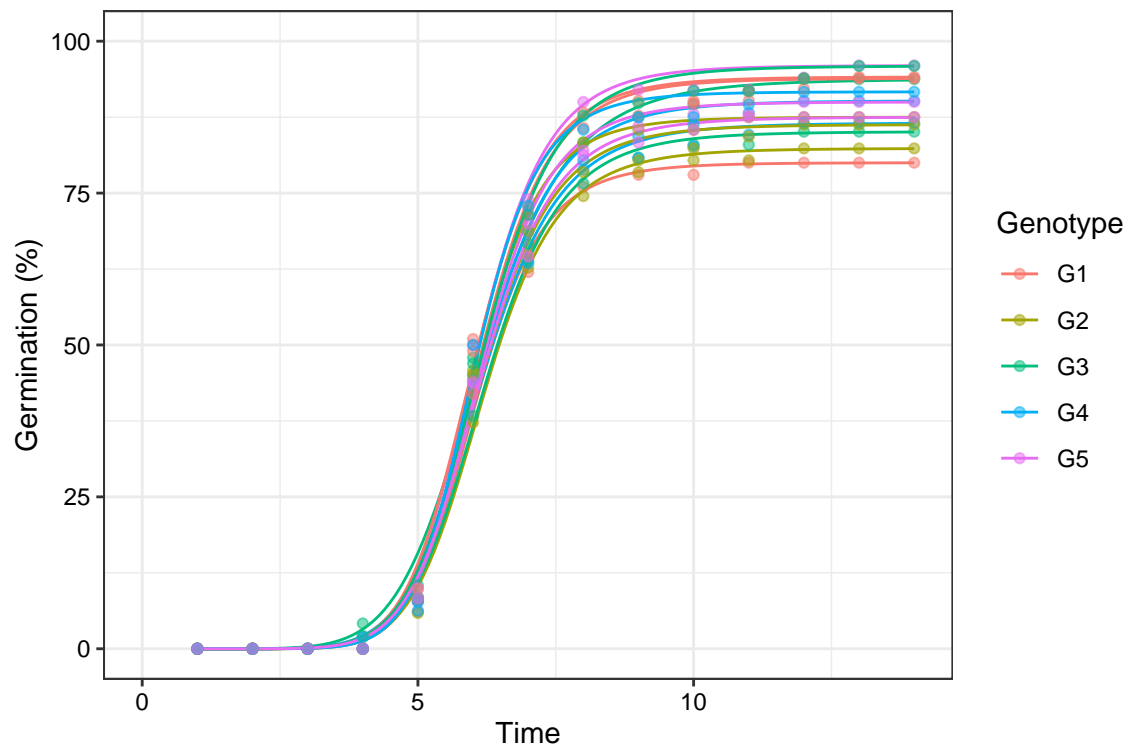
```
counts.per.intervals <- c("Day01", "Day02", "Day03", "Day04", "Day05",  
                          "Day06", "Day07", "Day08", "Day09", "Day10",  
                          "Day11", "Day12", "Day13", "Day14")  
  
fits <- FourPHFfit.bulk(gcdata, total.seeds.col = "Total Seeds",  
                       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")
```



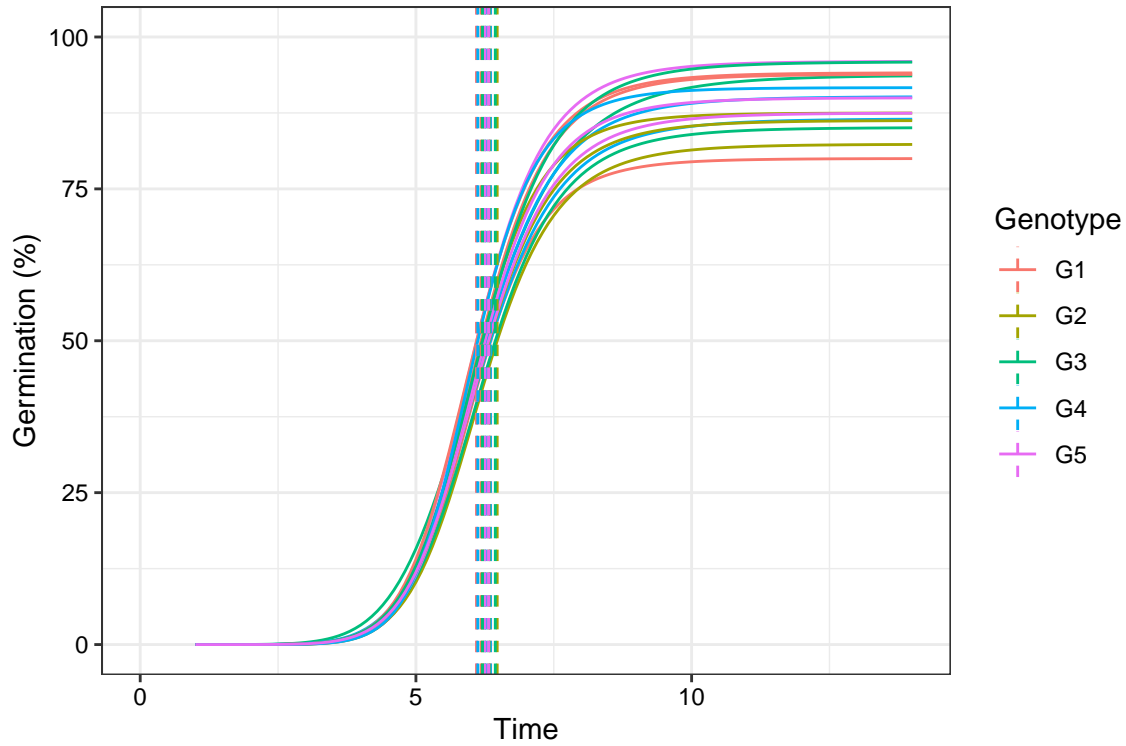
```
# Plot ROG curves  
plot(fits, rog = TRUE, group.col = "Genotype")
```



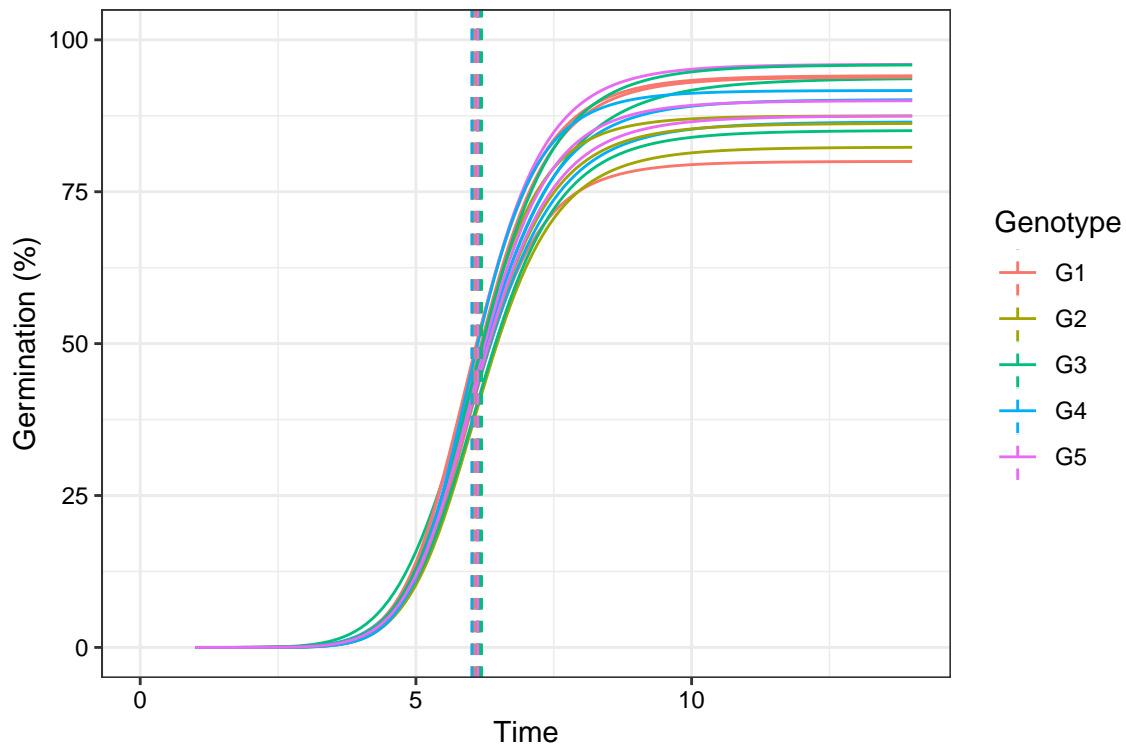
```
# Plot FPHF curves with points
plot(fits, group.col = "Genotype", show.points = TRUE)
```



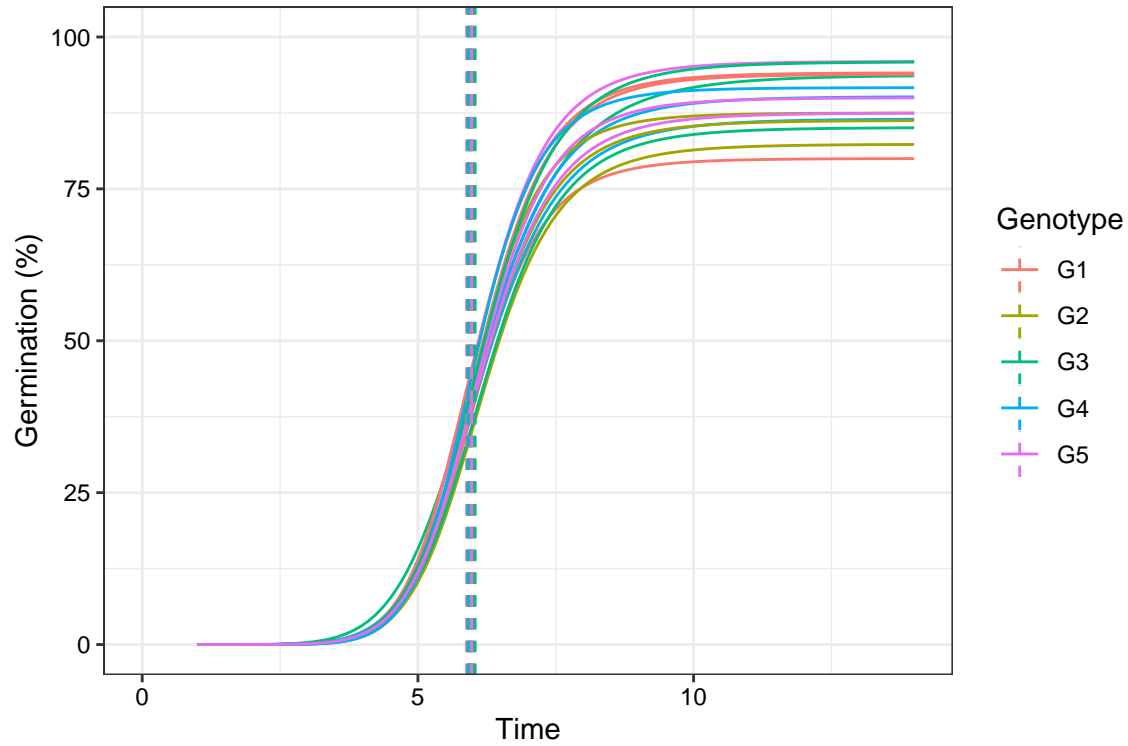
```
# Plot FPHF curves with annotations
plot(fits, group.col = "Genotype", annotate = "t50.total")
```



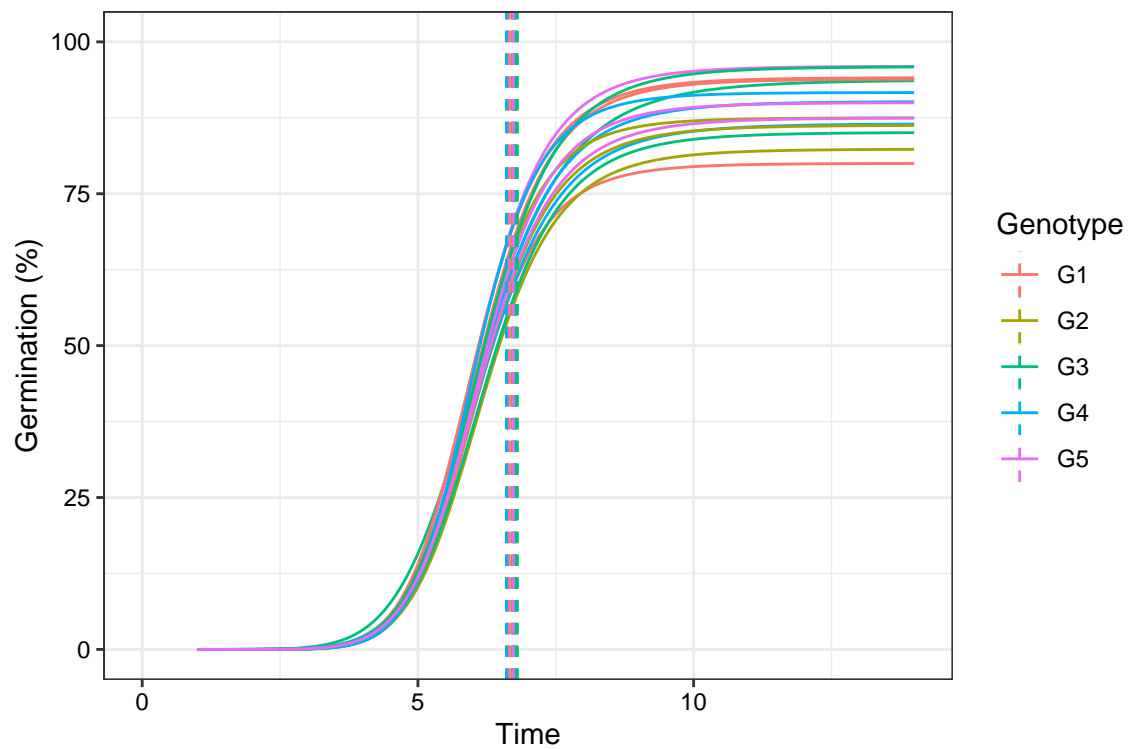
```
plot(fits, group.col = "Genotype", annotate = "t50.germ")
```



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



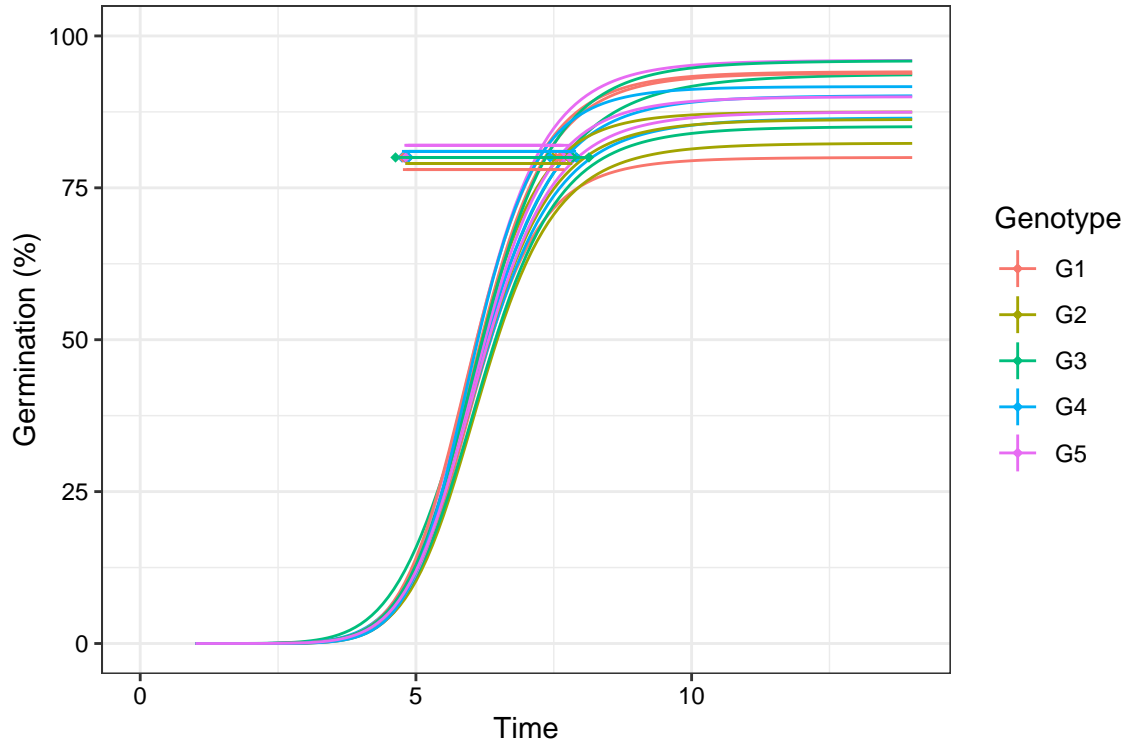
```
plot(fits, group.col = "Genotype", annotate = "mgt")
```



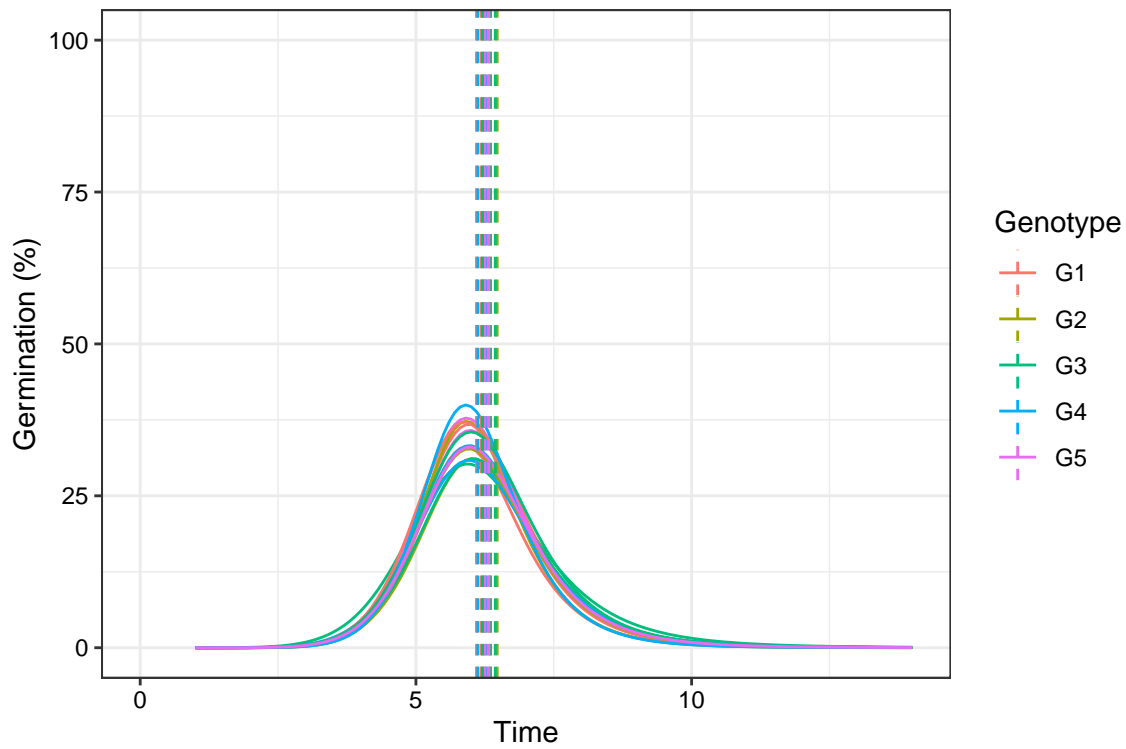
```
plot(fits, group.col = "Genotype", annotate = "uniformity")
```

Warning: position_dodge requires non-overlapping x intervals

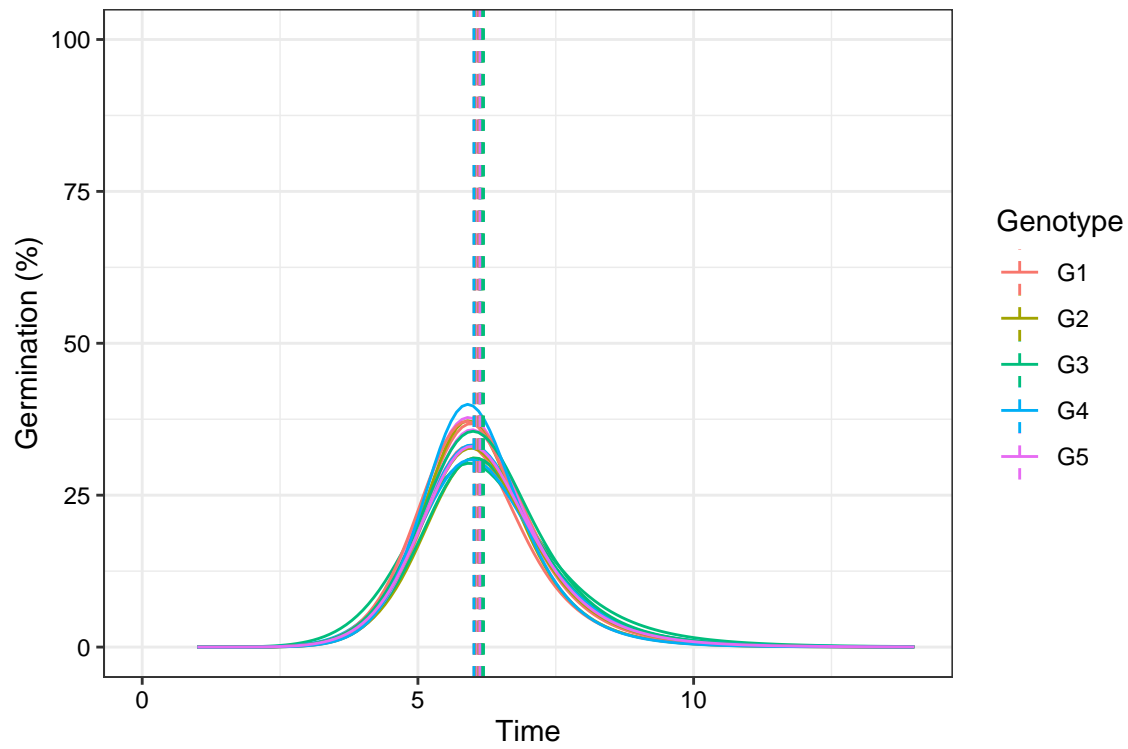
Warning: position_dodge requires non-overlapping x intervals



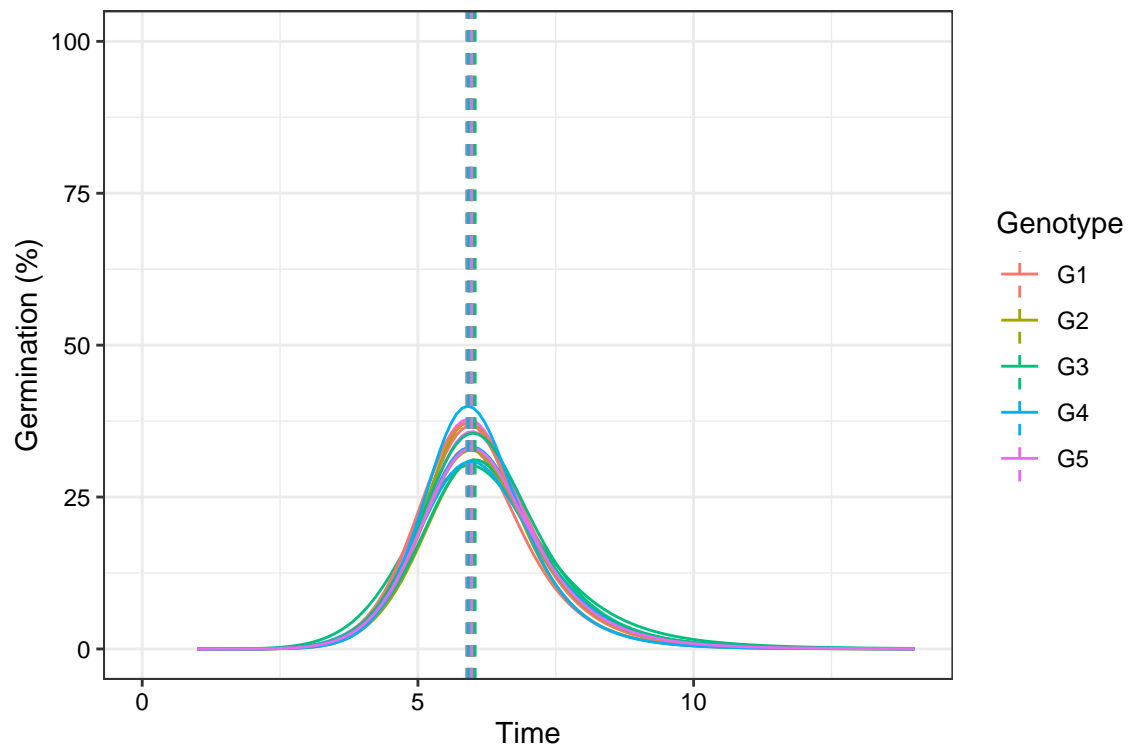
```
# Plot ROG curves with annotations  
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.total")
```



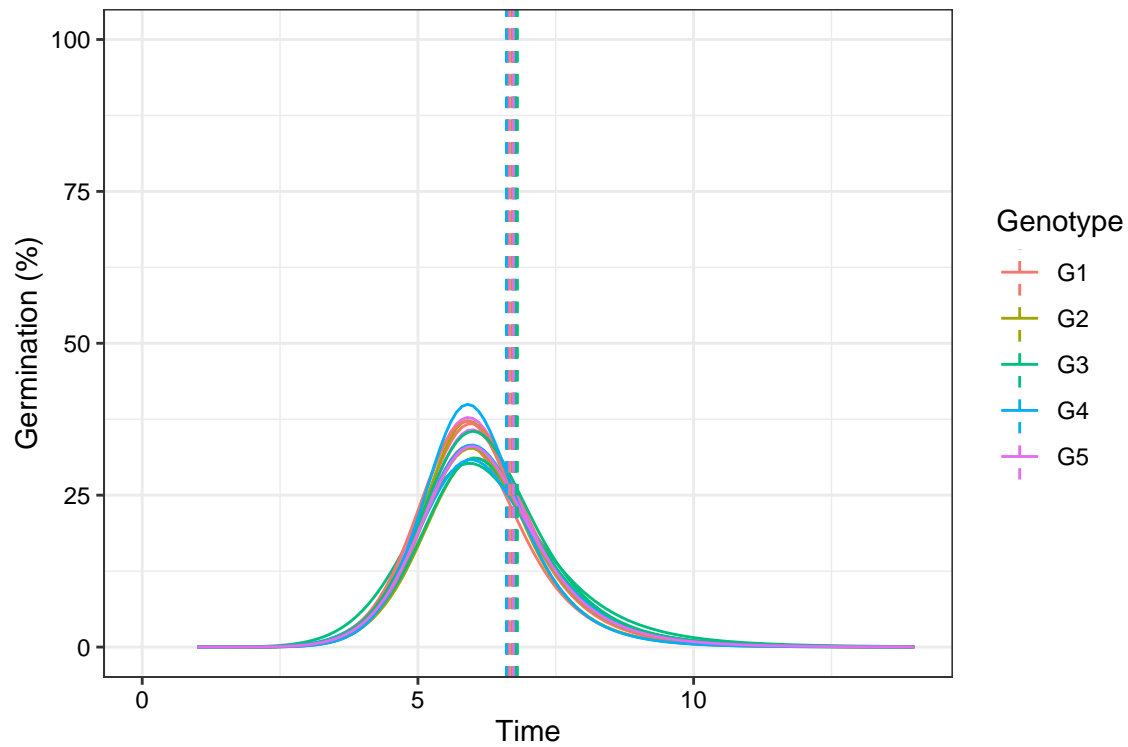
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "t50.germ")
```



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



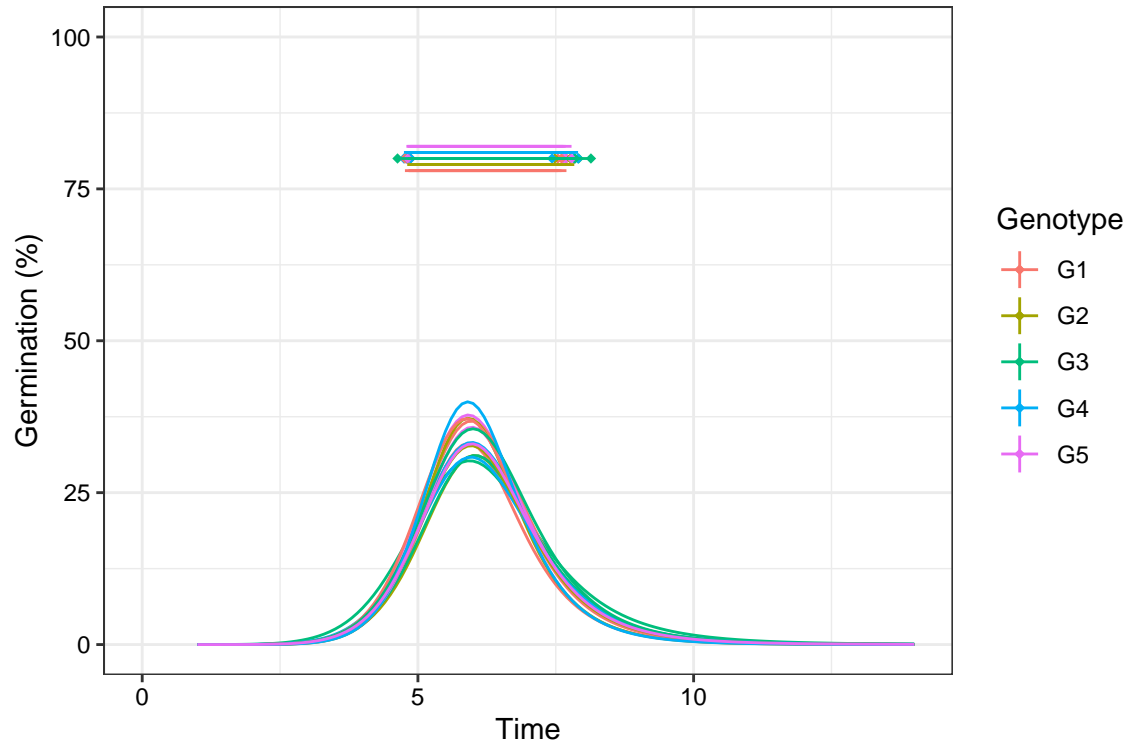
```
plot(fits, rog = TRUE, group.col = "Genotype", annotate = "mgt")
```



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

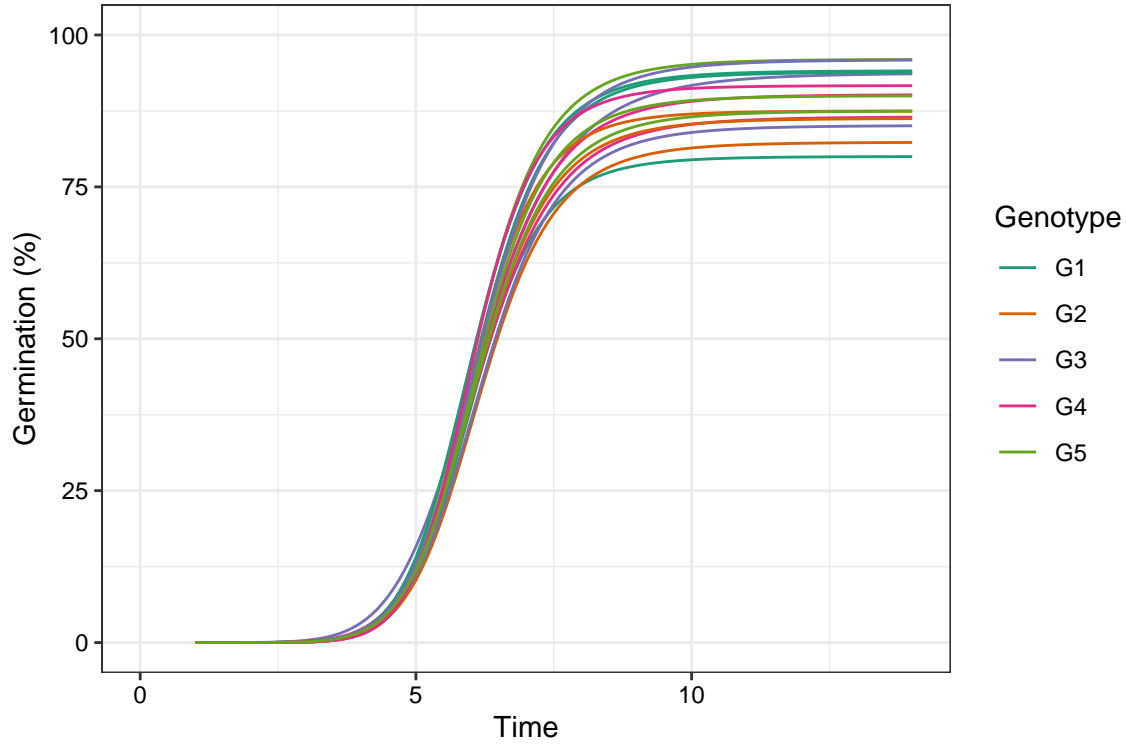
Warning: position_dodge requires non-overlapping x intervals

Warning: position_dodge requires non-overlapping x intervals

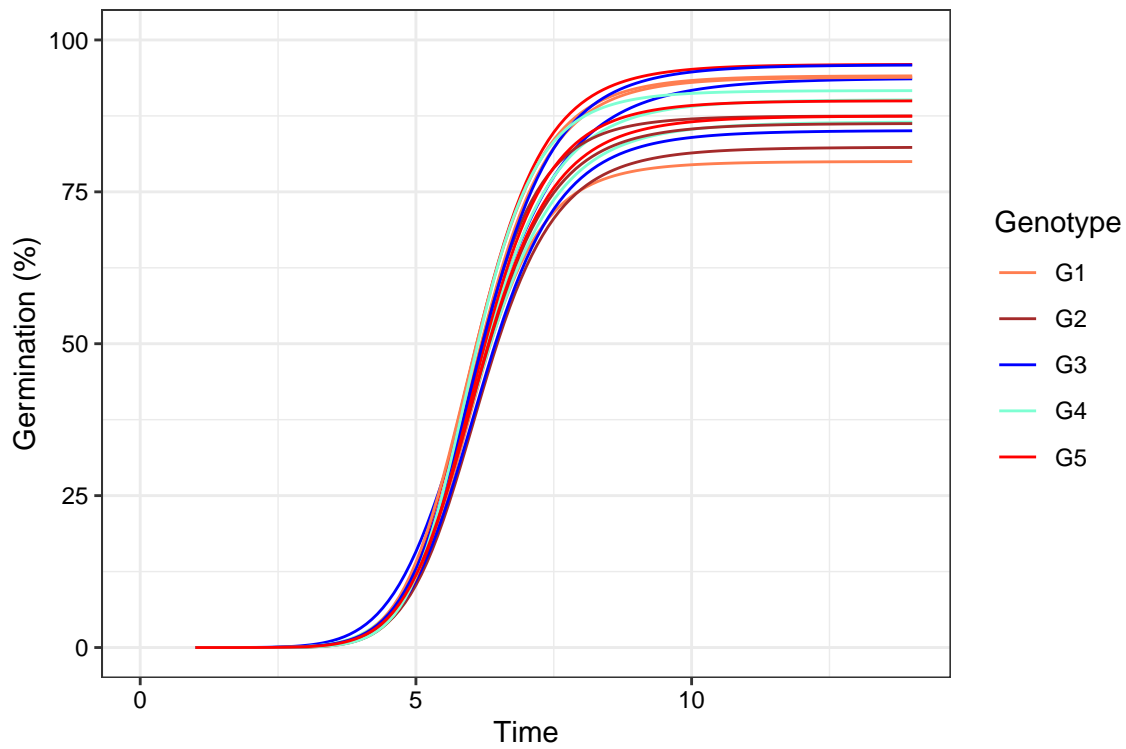


```
# Change colour of curves using ggplot2 options
library(ggplot2)
curvesplot <- plot(fits, group.col = "Genotype")

# '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 (2021). germinationmetrics: Seed Germination Indices and Curve Fitting. R package version 0.1.5, <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},
  year = {2021},
  note = {R package version 0.1.5},
  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 use it, please support the project by citing the package.

Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2021-02-03 r79933)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 19041)
```

```
Matrix products: default
```

```
locale:
 [1] LC_COLLATE=C                LC_CTYPE=English_India.1252
 [3] LC_MONETARY=English_India.1252 LC_NUMERIC=C
 [5] LC_TIME=English_India.1252
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

```
other attached packages:
```

```
[1] germinationmetrics_0.1.5 ggplot2_3.3.3
```

```
loaded via a namespace (and not attached):
```

```
[1] minpack.lm_1.2-1  tidymodels_1.1.0  xfun_0.20         purrr_0.3.4
 [5] pander_0.6.3     reshape2_1.4.4   colorspace_2.0-0 vctrs_0.3.6
 [9] generics_0.1.0  htmltools_0.5.1.1 yaml_2.2.1       XML_3.99-0.5
[13] rlang_0.4.10    pillar_1.4.7     glue_1.4.2       withr_2.4.1
[17] DBI_1.1.1       RColorBrewer_1.1-2 lifecycle_0.2.0  plyr_1.8.6
[21] stringr_1.4.0   munsell_0.5.0    gtable_0.3.0     evaluate_0.14
[25] labeling_0.4.2  knitr_1.31       gbRd_0.4-11      curl_4.3
[29] highr_0.8       broom_0.7.4      Rcpp_1.0.6       scales_1.1.1
```

[33] <code>backports_1.2.1</code>	<code>farver_2.0.3</code>	<code>digest_0.6.27</code>	<code>stringi_1.5.3</code>
[37] <code>dplyr_1.0.4</code>	<code>ggrepel_0.9.1</code>	<code>rbibutils_2.0</code>	<code>grid_4.1.0</code>
[41] <code>mathjaxr_1.2-0</code>	<code>Rdpack_2.1</code>	<code>tools_4.1.0</code>	<code>bitops_1.0-6</code>
[45] <code>magrittr_2.0.1</code>	<code>RCurl_1.98-1.2</code>	<code>tibble_3.0.6</code>	<code>crayon_1.4.0</code>
[49] <code>tidyr_1.1.2</code>	<code>pkgconfig_2.0.3</code>	<code>ellipsis_0.3.1</code>	<code>data.table_1.13.6</code>
[53] <code>assertthat_0.2.1</code>	<code>rmarkdown_2.6</code>	<code>httr_1.4.2</code>	<code>R6_2.5.0</code>
[57] <code>compiler_4.1.0</code>			

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