

The **germinationmetrics** package: A brief introduction

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Contents

Overview	1
Installation	1
Germination count data	2
Single-value germination indices	3
Curve fitting	22
Four-parameter hill function	22
Citing germinationmetrics	32
Session Info	32
References	33

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)
```

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 1).

Table 1 : A typical germination count data.

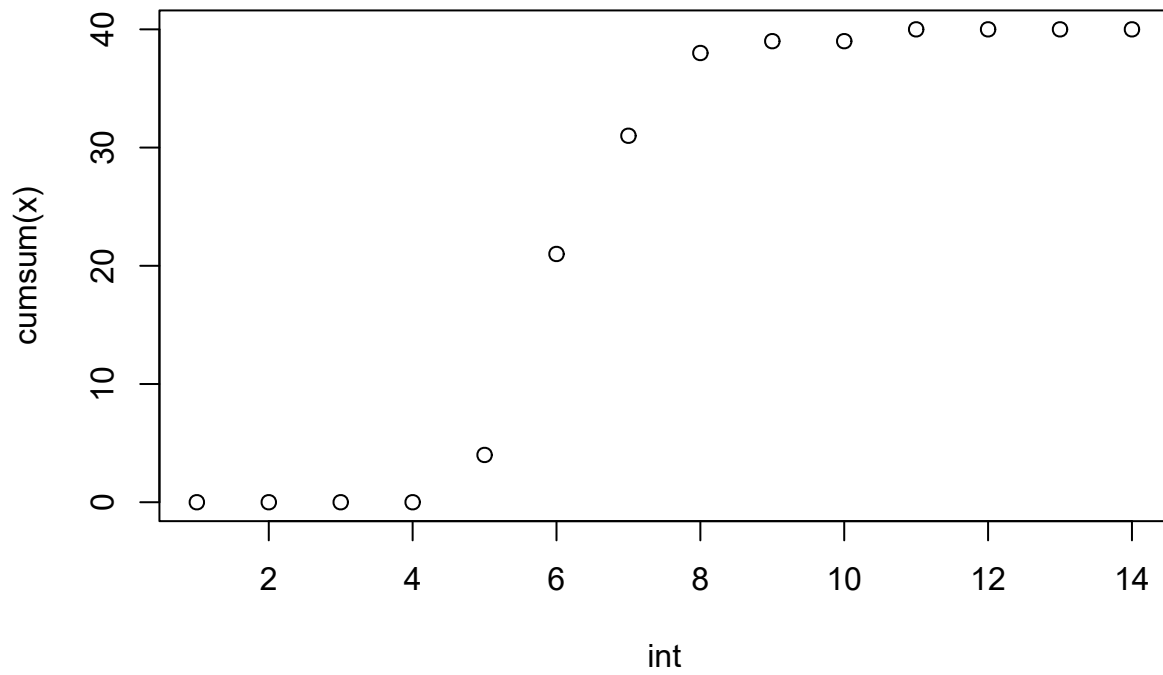
intervals	counts	cumulative.counts
1	0	0
2	0	0
3	0	0
4	0	0
5	4	4
6	17	21
7	10	31
8	7	38
9	1	39
10	0	39
11	1	40
12	0	40
13	0	40
14	0	40

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 2.

Table 2 : Single-value germination indices implemented in `germinationmetrics`.

Germination index	function	Details	Unit	Measures	Reference
Germination percentage or Germinability (<i>GP</i>)	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	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); 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 (Coolbear)	t50	It is the time to reach 50% of final/maximum germination. With argument method specified as " coolbear ", it is computed according to the formula by (Coolbear et al., 1984) 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 (Farooq)	t50	With argument method specified as " farooq ", it is computed according to the formula by (Coolbear et al., 1984) 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})	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 observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.</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); 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 observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.</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 (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.</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 observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.</p> <p>It is the inverse of mean germination rate (\bar{V}).</p> $\bar{V} = \frac{1}{\bar{T}}$	time ⁻¹	Germination rate	Labouriau and Valadares (1976); Labouriau (1983b); Ranal and Santana (2006)
Coefficient of velocity/rate of germination or Kotowski's coefficient of velocity (CVG)	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 observation, N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.</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 (not the accumulated number, but the number correspondent to the ith observation) and k is the last time of germination.</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 (Germination Index according to AOSA)	GermSpeed	<p>It is the rate of germination in terms of the total number of seeds that germinate in a time interval.</p> <p>It is estimated as follows:</p> $S = \frac{N_1}{T_1} + \frac{N_2}{T_2} + \frac{N_3}{T_3} + \dots + \frac{N_n}{T_n}$ <p>Where, $N_1, N_2, N_3, \dots, N_n$ are the number of germinated seeds observed at time (days or hours) $T_1, T_2, T_3, \dots, T_n$ after sowing. (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time).</p>	% time ⁻¹	Mixed	Throneberry and Smith (1955); Maguire (1962); Kendrick and Frankland (1969); AOSA (1983); Khandakar and Bradbeer (1983); Bradbeer (1988); Wardle et al. (1991)
Speed of accumulated germination	GermSpeedAccumulated	<p>It is estimated as follows:</p> $S_{accumulated} = \frac{N_1}{T_1} + \frac{N_1 + N_2}{T_2} + \frac{N_1 + N_2 + N_3}{T_3} + \dots + \frac{N_1 + N_2 + \dots + N_n}{T_n}$ <p>Where, $N_1, N_2, N_3, \dots, N_n$ are the number of germinated seeds observed at time (days or hours) $T_1, T_2, T_3, \dots, T_n$ after sowing. (Not accumulated/cumulative number, but the number of seeds that germinated at the specific time).</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: the final germination percentage or germinability.</p>	time ⁻¹	Mixed	Evetts and Burnside (1972)
Mean germination percentage per unit time \overline{GP}	MeanGermPercent	<p>It is estimated as follows:</p> $\overline{G} = \frac{GP}{T_n}$ <p>Where, GP is the final germination percentage and T_n is the total number of intervals(e.g. days) required for final germination.</p>		Mixed	Czabator (1962)
Number of seeds germinated per unit time \overline{N}	MeanGermNumber	<p>It is estimated as follows:</p> $\overline{N} = \frac{N_g}{T_n}$ <p>Where, N_g is the number of germinated seeds and T_n is the total number of intervals (e.g. days) required for final germination.</p>		Mixed	Khamassi et al. (2013)

Germination index	function	Details	Unit	Measures	Reference
Timson's index ($\sum 10$ (Ten summation), $\sum 5$ or $\sum 20$)	TimsonsIndex	<p>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:</p> $\sum n = \sum_{i=1}^t G_i$ <p>Where, G_i is the cumulative germination percentage in time interval i and t is the total number of time intervals. It also estimated in terms of partial germination percentage as follows:</p> $\sum n = \sum_{i=1}^t g_i(t - j)$ <p>Where, g_i is the germination (not cumulative, but partial germination) in time interval i (i varying from 0 to t) and t is the total number of time intervals and $j = i - 1$.</p>		Mixed	Timson (1965); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971)
Modified Timson's Index (Labouriau)	TimsonsIndex	<p>It is estimated as Timson's index T divided by the sum of partial germination percentages.</p> $T_{mod} = \frac{T}{\sum_{i=1}^t g_i}$		Mixed	Ranal and Santana (2006)
Modified Timson's Index (Khan and Unger)	TimsonsIndex	<p>It is estimated as Timson's index (T) divided by the number of intervals (t).</p> $T_{mod} = \frac{T}{t}$		Mixed	Khan and Ungar (1984)
George's index	GermRateGeorge	<p>It is estimated as follows:</p> $GR = \sum_{i=1}^t N_i K_i$ <p>Where N_i is the number of seeds germinated by ith interval and K_i is the number of intervals(eg. days) until the end of the test.</p>		Mixed	George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968)
Peak value (Czabator)	PeakValue	<p>It is the maximum quotient obtained by dividing successive cumulative germination values by the relevant incubation time.</p>		Mixed	Czabator (1962)

Germination index	function	Details	Unit	Measures	Reference
Germination value (Czabator)	GermValue	<p>It is computed as follows:</p> $GV = PV \times MDG$ <p>Where, PV is the peak value and MDG is the mean daily germination percentage. It can also be computed for other time intervals of successive germination counts, by replacing MDG with the mean germination percentage per unit time (\overline{GP}).</p>		Mixed	Czabator (1962)
Germination value (Diavanshir and Pourbiek)	GermValue	<p>It is computed as follows:</p> $GV = \frac{\sum DGS}{N} \times GP \times k$ <p>Where, DGS is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the beginning of the test, N is the frequency or number of DGS calculated during the test, GP is the germination percentage expressed over 100 and k is a constant. The value of k is decided on the basis of average daily speed of germination ($\frac{\sum DGS}{N}$). If it is less than 10, then k value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for k.</p>		Mixed	Djavanshir and Pourbeik (1976)
Coefficient of uniformity of germination	CUGerm	<p>It is computed as follows:</p> $CUG = \frac{\sum_{i=1}^k N_i}{\sum_{i=1}^k (\bar{T} - T_i)^2 N_i}$ <p>Where, \bar{T} is the the mean germination time, T_i is the time from the start of the experiment to the ith observation (day for the example); N_i is the number of seeds germinated in the ith time (not the accumulated number, but the number correspondent to the ith observation), and k is the last time of germination.</p>		Germinatin unifromity	Heydecker (1972); Bewley and Black (1994)
Coefficient of variation of the germination time	CVSEGermTime	<p>It is estimated as follows:</p> $CV_T = \sqrt{\frac{s_T^2}{\bar{T}}}$ <p>Where, s_T^2 is the variance of germination time and \bar{T} is the mean germination time.</p>		Germinatin unifromity	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 and k is the last day of observation.</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 (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

GermPercent()

```
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)
```

```
[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
```

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

```
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)
```

```
[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
```

```
t50()
```

```
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")
```

```
[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
```

```
MeanGermTime(), VarGermTime(), SEGermTime(), CVSEGermTime()
```

```
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)
```

```
[1] 6.7
```

```

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

[1] 1.446154
SEGermTime(germ.counts = x, intervals = int)

[1] 0.1901416
CVSEGermTime(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
CVSEGermTime(germ.counts = y, intervals = int, partial = FALSE)

[1] 0.6512685

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

[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

GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()
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)

[1] 6.138925
GermSpeedAccumulated(germ.counts = x, intervals = int)

[1] 34.61567
GermSpeedCorrected(germ.counts = x, intervals = int, total.seeds = 50)

[1] 0.07673656
# 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)

```

```
[1] 0.009245369
```

```
GermSpeed(), GermSpeedAccumulated(), GermSpeedCorrected()
```

```
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)
```

```
[1] 6.138925
```

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

```
[1] 34.61567
```

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

```
[1] 0.07673656
```

```
# 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)
```

```
[1] 0.009245369
```

```
MeanGermPercent(), MeanGermNumber()
```

```
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)
```

```
[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
```

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

```
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)
```

```
[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 = "khanunger")
```

```
[1] 47.42857
```

```
# 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 = "khanunger")
```

```
[1] 24.57143
```

```
# Without max specified
```

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



```
[1] 332
```

```
# With max specified
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
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE)
```

```
[1] 332
```

```
# With max specified
GermRateGeorge(germ.counts = x, intervals = int, partial = TRUE, max = 10)
```

```
[1] 172
```

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

```
[1] 332
```

```
PeakValue(), GermValue()

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)
```

```
[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
```

```
# 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

```

```

CUGerm()

```

```

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)

```

```

[1] 0.7092199

```

```

# From cumulative germination counts
#-----

```

```

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

```

```

[1] 0.05267935

```

```

GermSynchrony(), GermUncertainty()

```

```

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)

```

```

[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
```

Curve fitting

Several mathematical functions have been used to fit the cumulative germination count data and describe the germination process 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 3.

Table 3 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

Germination parameters	Details	Unit	Measures
$t_{50_{germinated}}$	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 (<i>TMGR</i>)	<p>The partial derivative of the four-parameter hill function gives the instantaneous rate of germination (s) 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 <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

FourPHFfit()

```
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)

$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
1	1.769385	TRUE	1.490116e-08	-25.49868	60.99736	64.19265	31.30723

df.residual

1	10
---	----

```
$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
```

```
[1] 4.956266 6.744598
```

```
$t50.Germinated
```

```
[1] 6.034954
```



```

$txp.Germinated
[1] 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"

# 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
1 1.769385  TRUE 1.490116e-08 -25.49868 60.99736 64.19265 31.30723
  df.residual
1           10

$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
[1] 4.956263 6.744599

$t50.Germinated
[1] 6.034953

$txp.Germinated
[1] 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'. "

$isOk
[1] TRUE

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

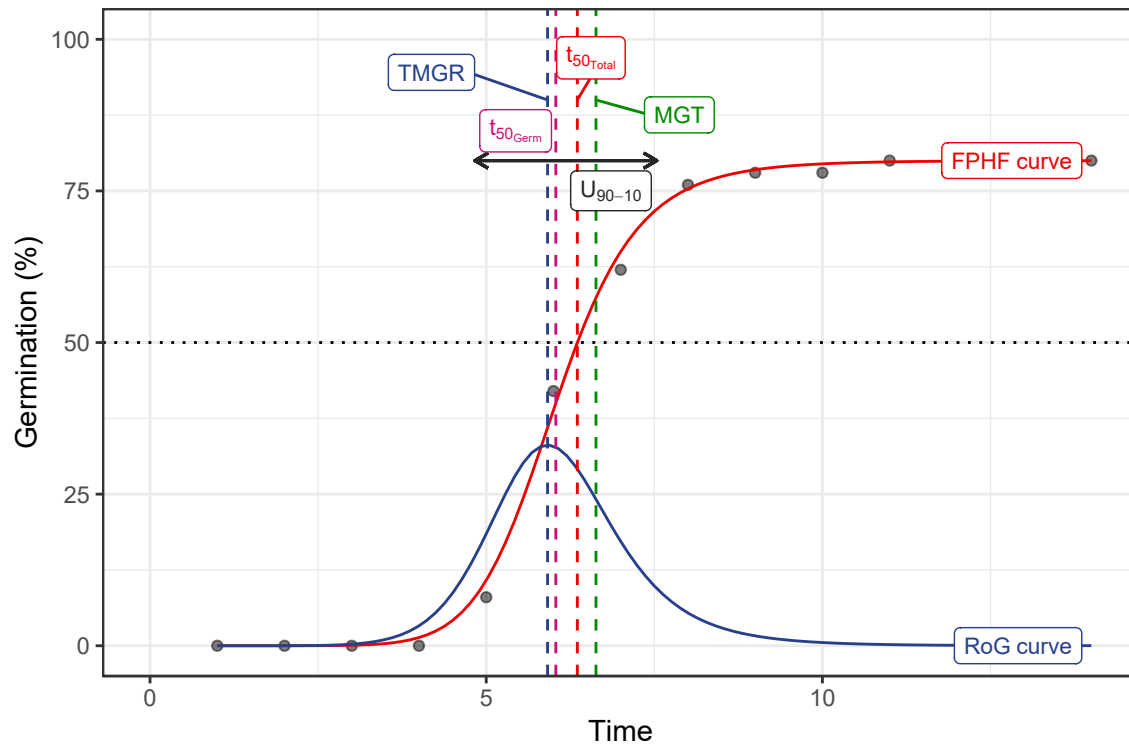
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

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

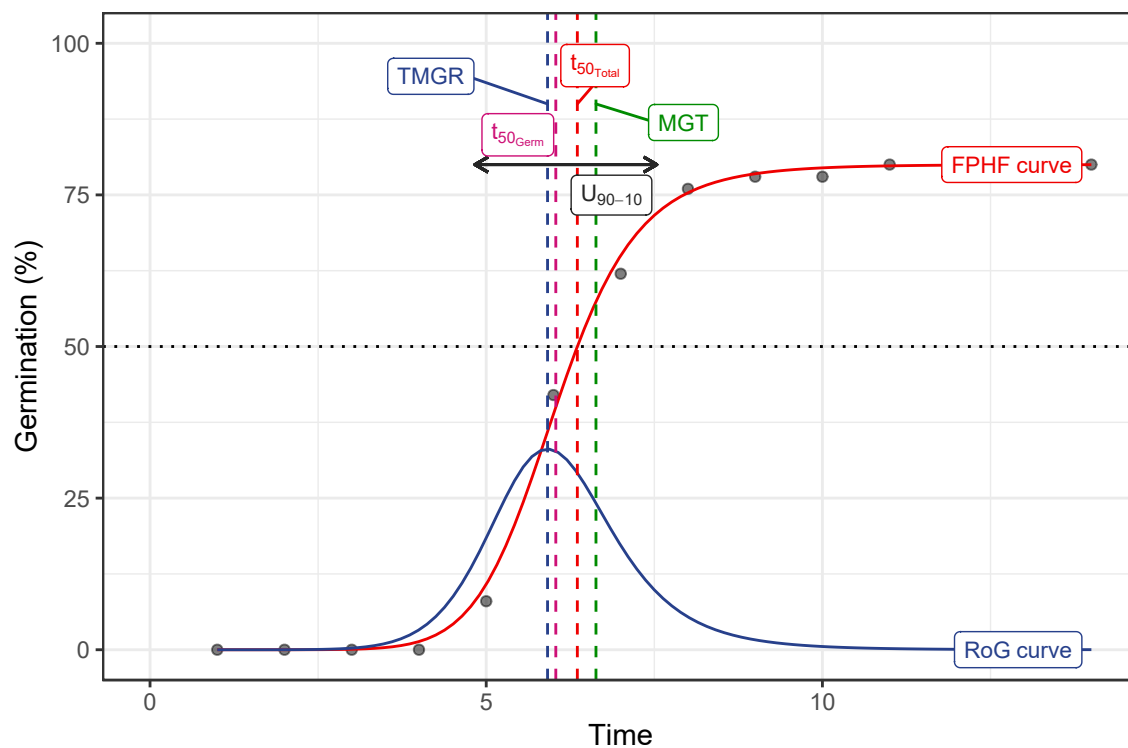
# From cumulative germination counts
#-----
fit2 <- FourPHFfit(germ.counts = y, intervals = int,
                  total.seeds = 50, tmax = 20, partial = FALSE)

# Default plots
plot(fit1)

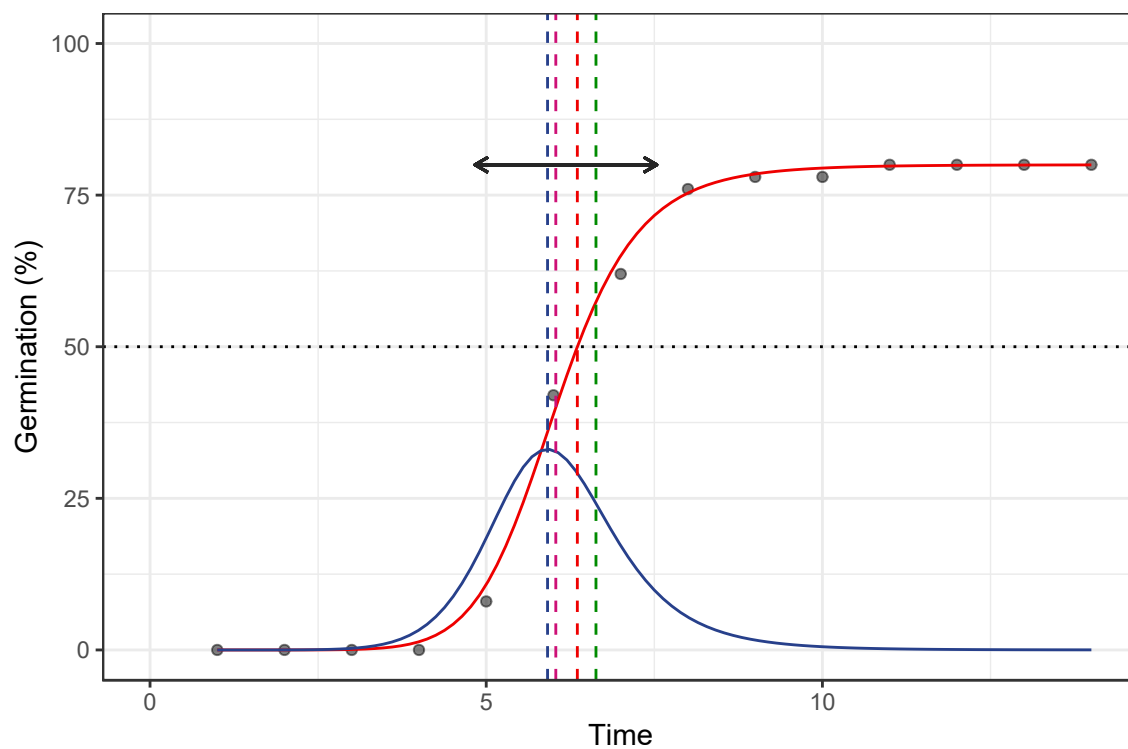
```



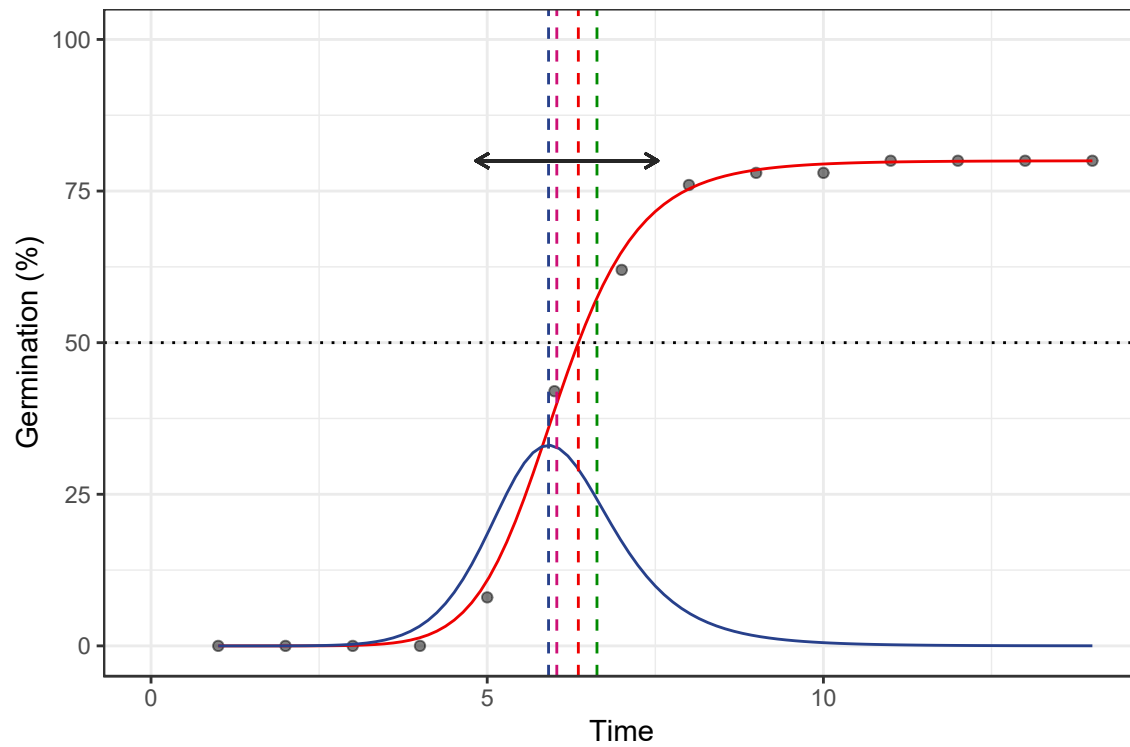
```
plot(fit2)
```



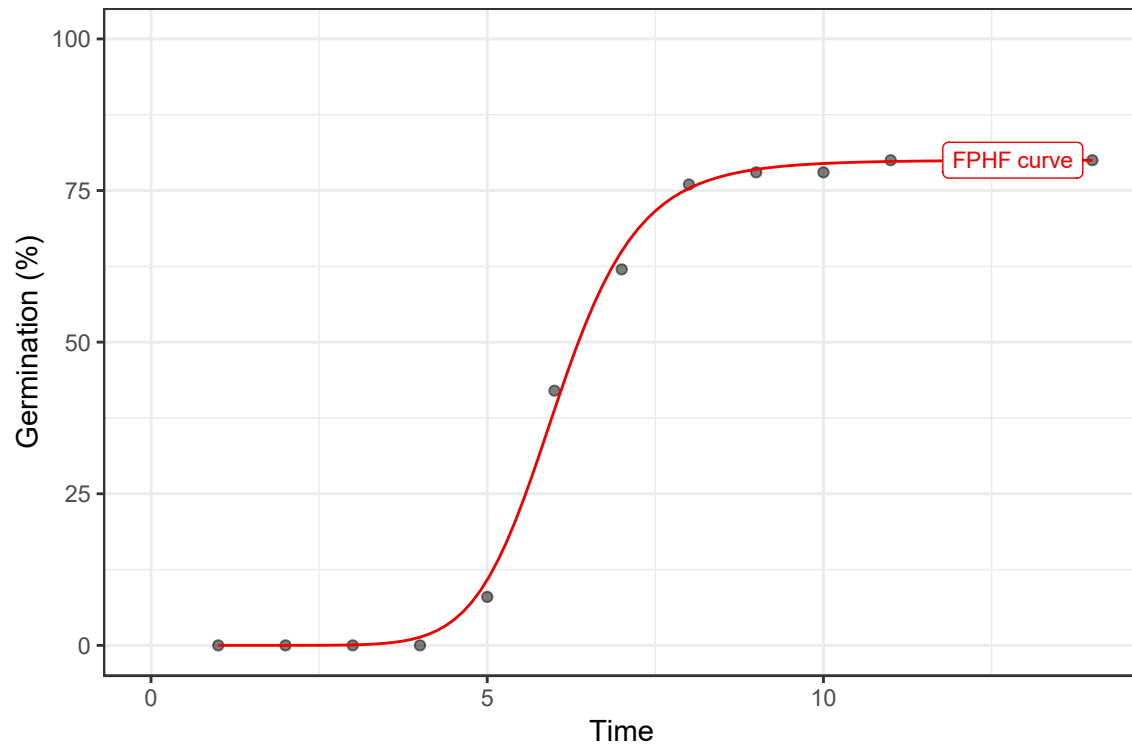
```
# No labels
plot(fit1, plotlabels = FALSE)
```



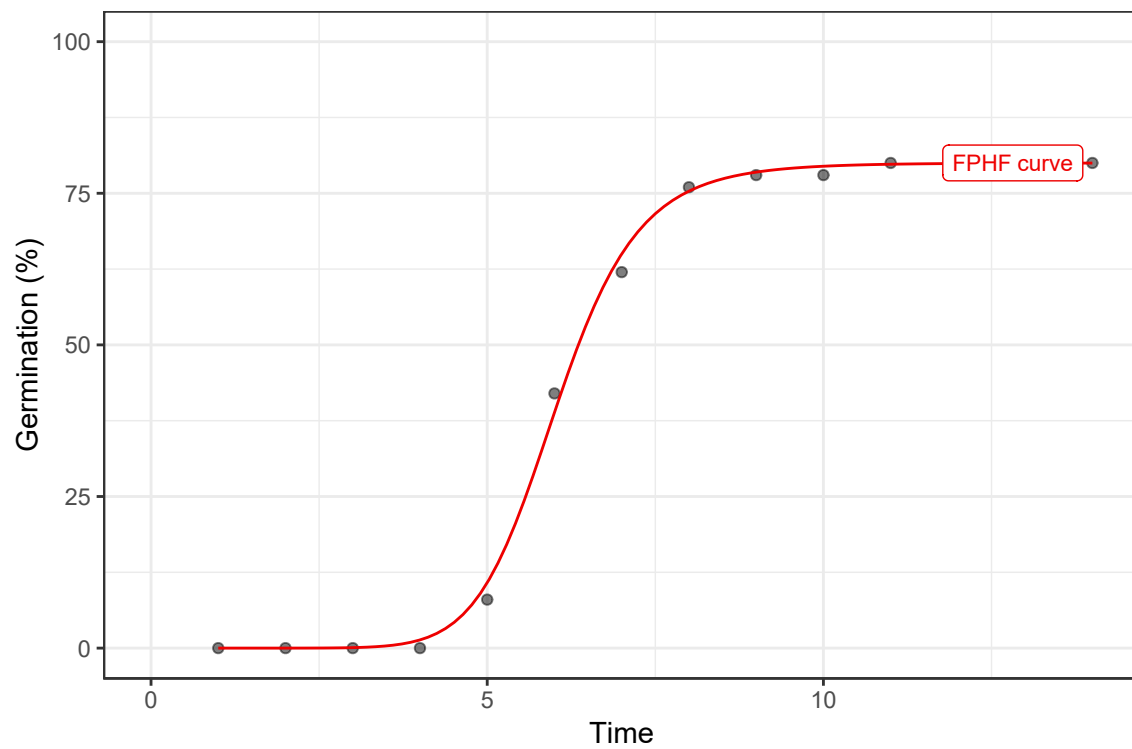
```
plot(fit2, plotlabels = FALSE)
```



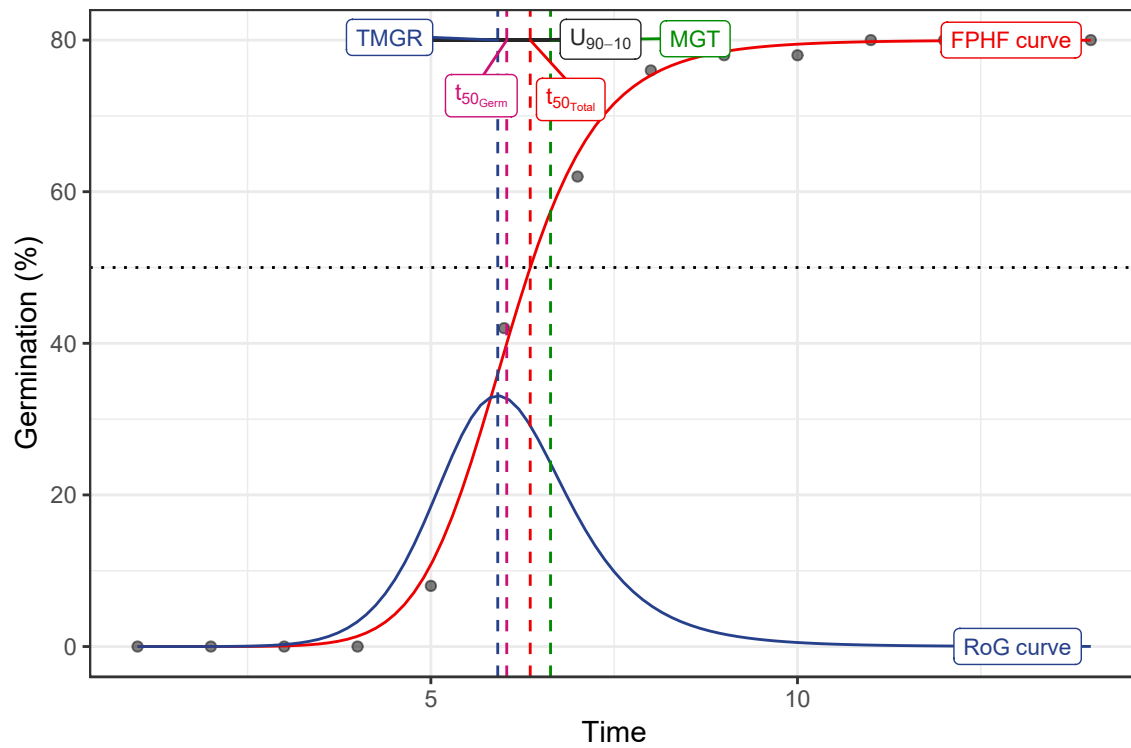
```
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



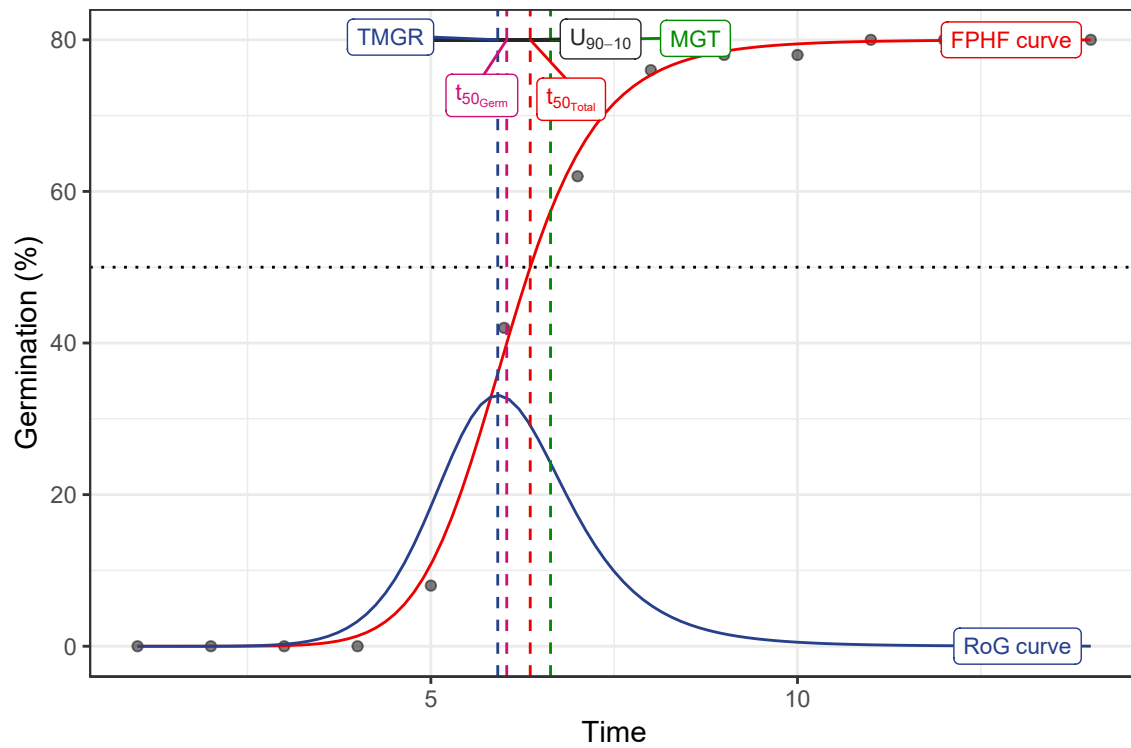
```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



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



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



Citing germinationmetrics

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

J. Aravind, S. Vimala Devi, J. Radhamani, Sherry Rachel Jacob and Kalyani Srinivasan (2018). *germinationmetrics: Seed Germination Indices and Curve Fitting*. R package version 0.1.1, <https://cran.r-project.org/package=germinationmetrics>, <https://doi.org/10.5281/zenodo.1219630>.

A BibTeX entry for LaTeX users is

```
@Manual{,
  title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
  author = {{Aravind J} and {Vimala Devi S} and {Radhamani J} and {Sherry Rachel Jacob} and {Kalyani S}},
  year = {2018},
  note = {R package version 0.1.1},
  note = {https://cran.r-project.org/package=germinationmetrics},
  note = {https://doi.org/10.5281/zenodo.1219630},
}
```

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 version 3.5.1 (2018-07-02)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows >= 8 x64 (build 9200)
```

```
Matrix products: default
```

```
locale:
```

```
[1] LC_COLLATE=English_India.1252 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_0.1.1 stringi_1.2.4
[3] rhub_1.0.2             readxl_1.1.0
```

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

```
[1] ggrepel_0.8.0      Rcpp_0.12.18      whoami_1.1.2
[4] lattice_0.20-35    tidyr_0.8.1       prettyunits_1.0.2
[7] clisymbols_1.2.0   assertthat_0.2.0  rprojroot_1.3-2
[10] digest_0.6.15      R6_2.2.2          cellranger_1.1.0
```


[13] plyr_1.8.4	backports_1.1.2	evaluate_0.11
[16] httr_1.3.1	ggplot2_3.0.0	highr_0.7
[19] pillar_1.3.0	Rdpack_0.8-0	rlang_0.2.1
[22] rematch_1.0.1	lazyeval_0.2.1	rstudioapi_0.7.0-9000
[25] callr_2.0.4	rmarkdown_1.10	labeling_0.3
[28] desc_1.2.0	devtools_1.13.6	pander_0.6.2
[31] stringr_1.3.1	munsell_0.5.0	broom_0.5.0
[34] compiler_3.5.1	pkgconfig_2.0.1	htmltools_0.3.6
[37] tidyselect_0.2.4	tibble_1.4.2	roxygen2_6.0.1
[40] crayon_1.3.4	dplyr_0.7.6	withr_2.1.2
[43] commonmark_1.5	rappdirs_0.3.1	grid_3.5.1
[46] nlme_3.1-137	jsonlite_1.5	gtable_0.2.0
[49] magrittr_1.5	scales_0.5.0	bibtex_0.4.2
[52] debugme_1.1.0	bindrcpp_0.2.2	parsedate_1.1.3
[55] xml2_1.2.0	tools_3.5.1	rcmdcheck_1.2.1
[58] glue_1.3.0	purrr_0.2.5	processx_3.1.0
[61] yaml_2.2.0	colorspace_1.3-2	gbRd_0.4-11
[64] memoise_1.1.0	minpack.lm_1.2-1	knitr_1.20
[67] bindr_0.1.1		

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