The `germinationmetrics` Package: A Brief Introduction

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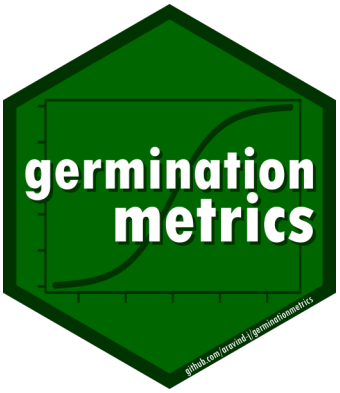
Overview



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

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

Installation

The package can be installed using the following functions:

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

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

Then the package can be loaded using the function

```
library(germinationmetrics)
```

Version History

The current version of the package is 0.1.4. 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

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

Germination count data

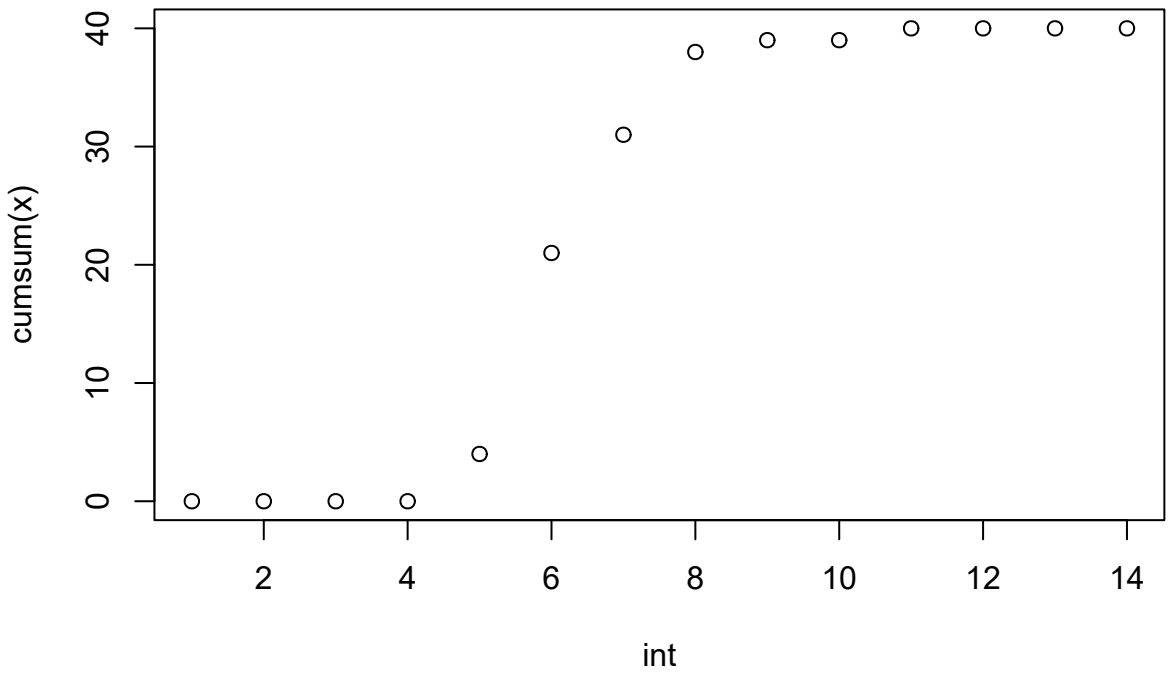
Typically in a germination test, the germination count data of a fixed number of seeds is recorded at regular intervals for a definite period of time or until all the seeds have germinated. These germination count data can be either partial or cumulative (Table 2).

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.

```
[1] "Package 'pander' and pandoc are required to generate this table"
```

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 germi
```

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

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

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

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

$testend
[1] 16
```

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

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

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

```
17           0        17                   160                  80.0 4.705882
18           2        18                   162                  81.0 4.500000
19           0        19                   162                  81.0 4.263158
20           2        20                   164                  82.0 4.100000
```

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

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

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

$testend
[1] 16
```

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

```
[1] 9.5
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
3           34         3                    34                    17.0 5.666667
4           40         4                    74                    37.0 9.250000
5           21         5                    95                    47.5 9.500000
6           10         6                   105                    52.5 8.750000
```

```
7           4         7                   109                    54.5 7.785714
8           5         8                   114                    57.0 7.125000
9           3         9                   117                    58.5 6.500000
10          5        10                   122                    61.0 6.100000
11          8        11                   130                    65.0 5.909091
12          7        12                   137                    68.5 5.708333
13          7        13                   144                    72.0 5.538462
14          6        14                   150                    75.0 5.357143
15          6        15                   156                    78.0 5.200000
16          4        16                   160                    80.0 5.000000
17          0        17                   160                    80.0 4.705882
18          2        18                   162                    81.0 4.500000
19          0        19                   162                    81.0 4.263158
20          2        20                   164                    82.0 4.100000
```

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

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

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

$testend
[1] 16
```

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

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

[[2]]
   germ.counts intervals Cumulative.germ.counts Cumulative.germ.percent      DGS
1           0         1                     0                     0.0 0.000000
2           0         2                     0                     0.0 0.000000
```

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

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

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

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

$testend
[1] 16
```

```
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.

```
[1] "Package 'pander' and pandoc are required to generate this table"
```

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

$a
[1] 80

$b
```

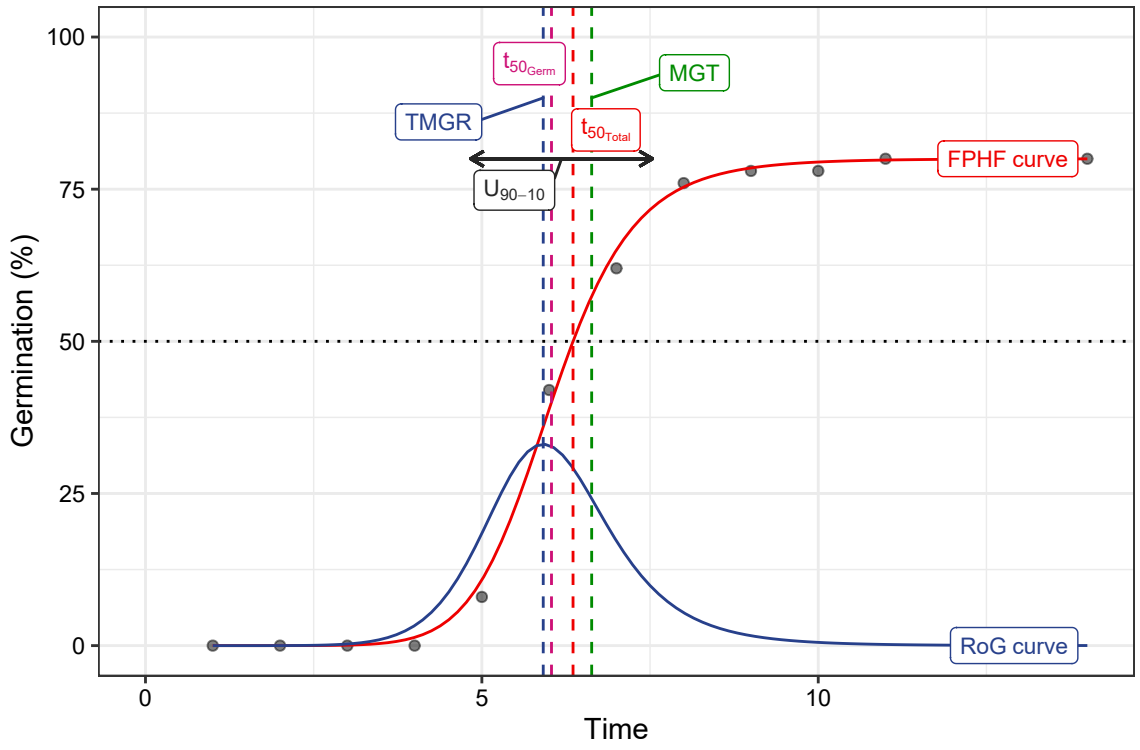
```
[1] 9.881947

$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"
```

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

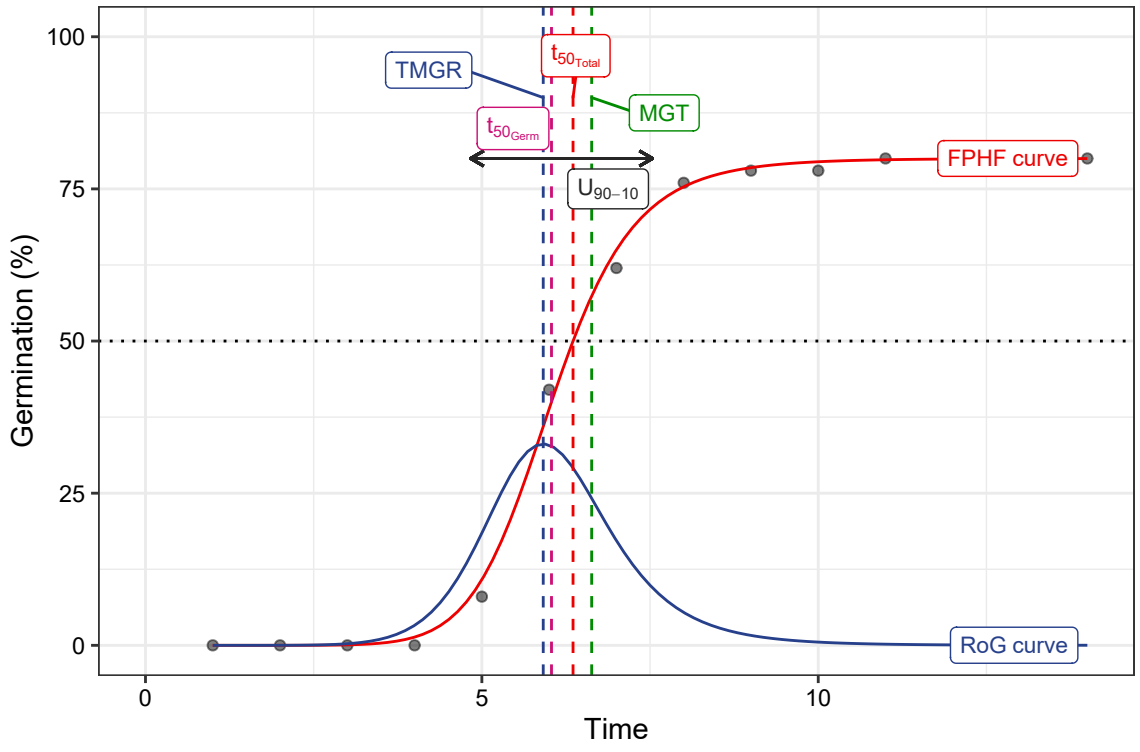
```
$data
   gp csgp intervals
1   0    0         1
2   0    0         2
3   0    0         3
4   0    0         4
5   8    8         5
6  34   42         6
7  20   62         7
8  14   76         8
9   2   78         9
10  0   78        10
11  2   80        11
12  0   80        12
13  0   80       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

$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"
```

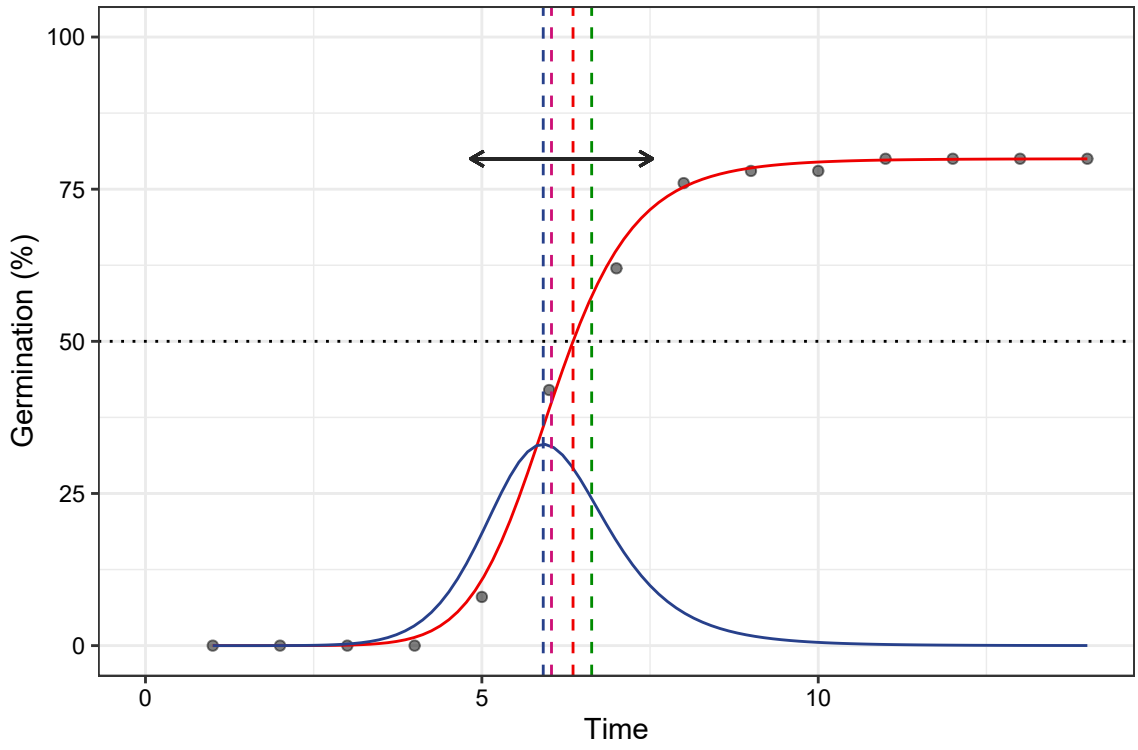
```
x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
int <- 1:length(x)
total.seeds = 50

# 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)
```



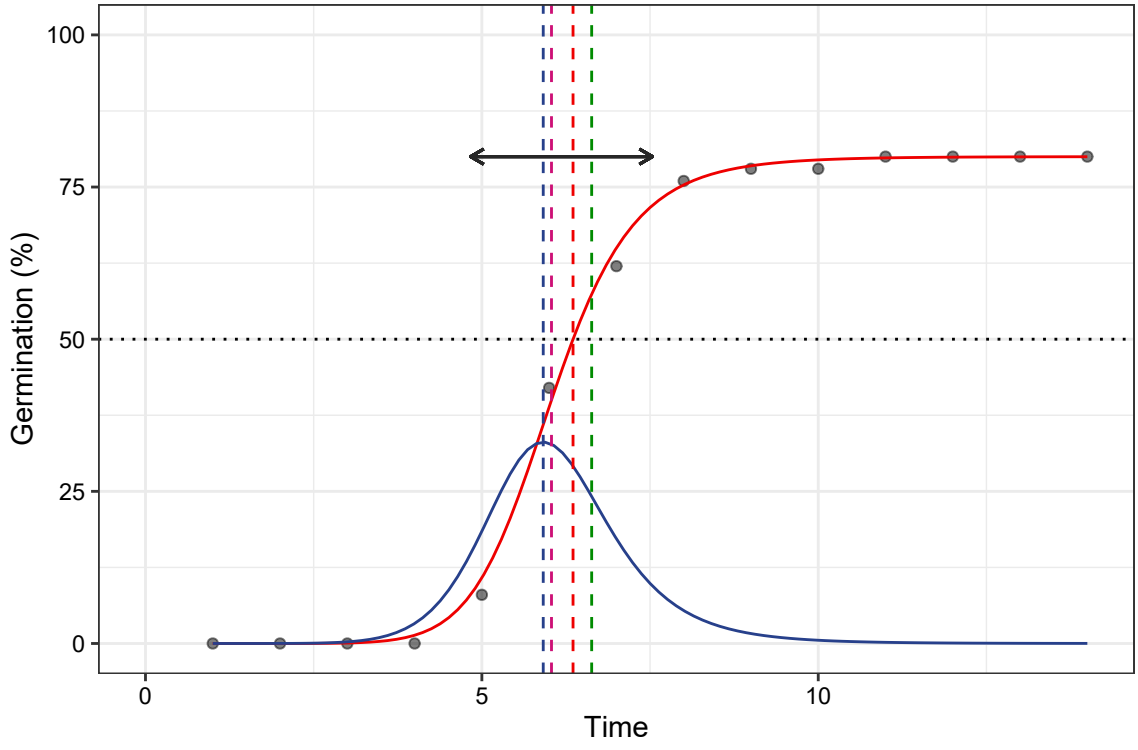

```
plot(fit2)
```



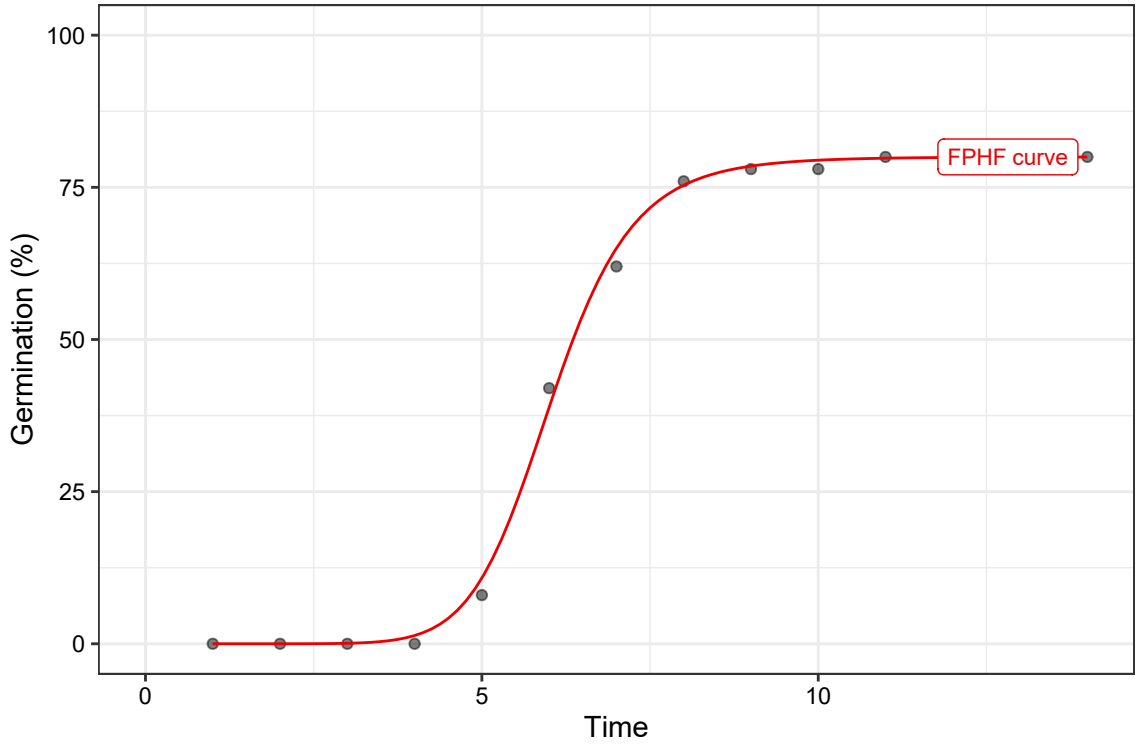

```
# No labels
plot(fit1, plotlabels = FALSE)
```



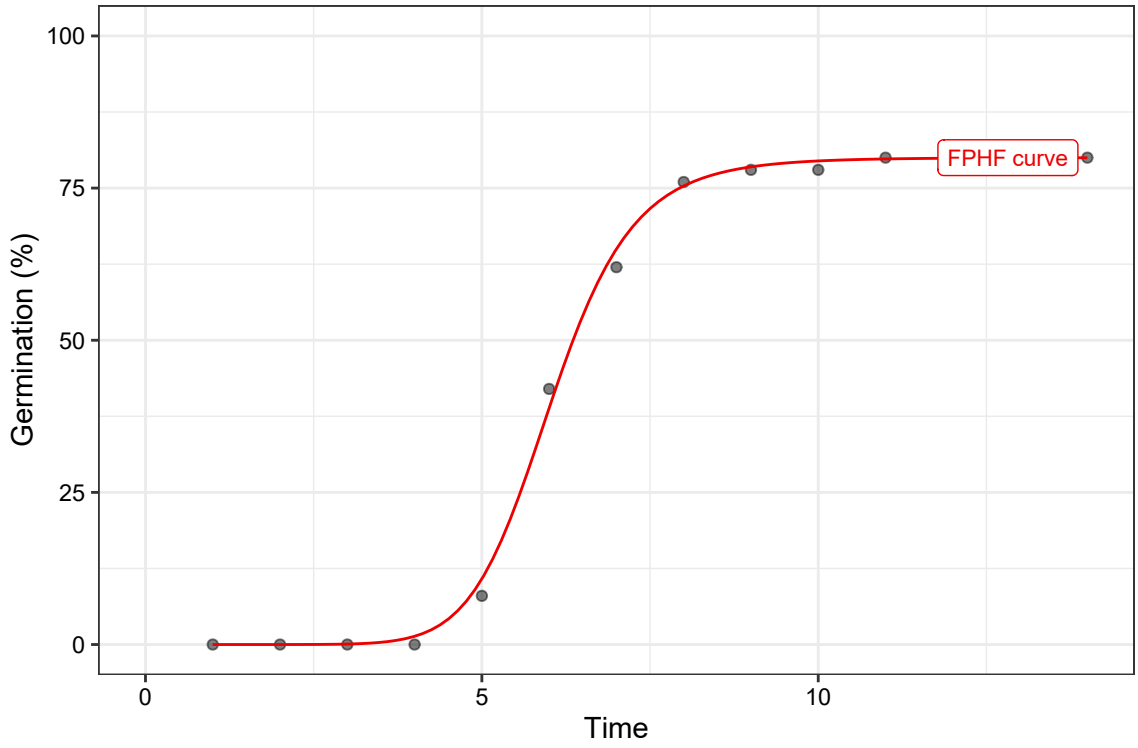

```
plot(fit2, plotlabels = FALSE)
```



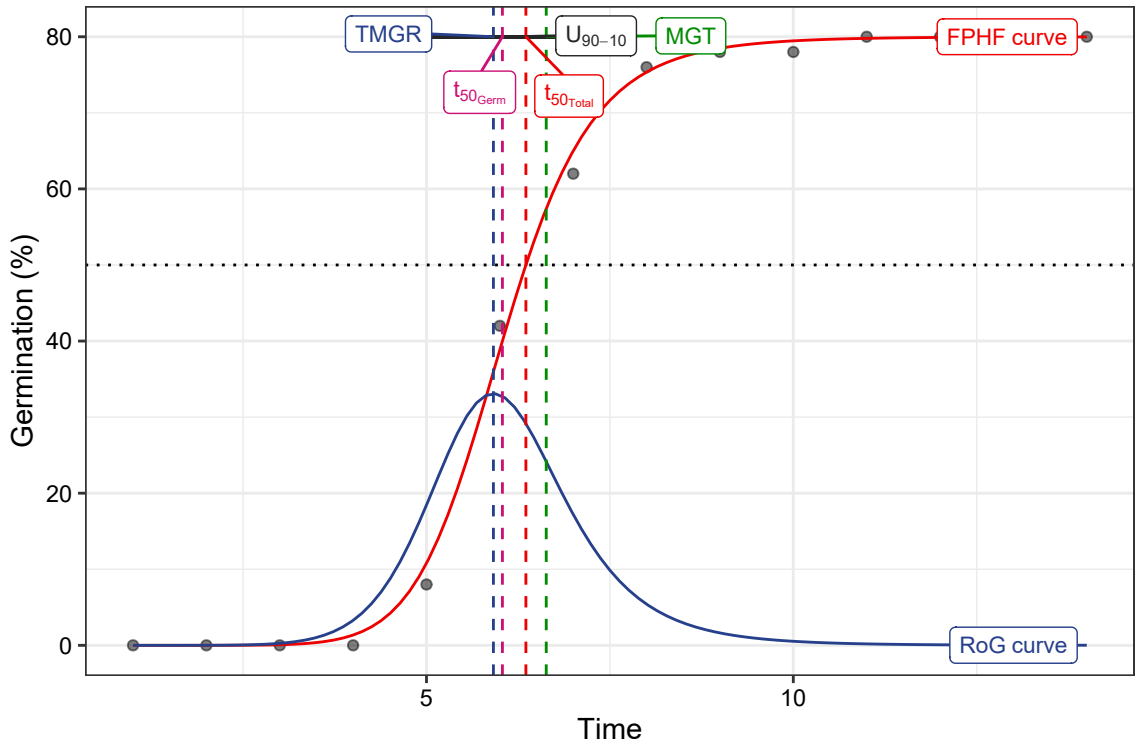

```
# Only the FPHF curve
plot(fit1, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



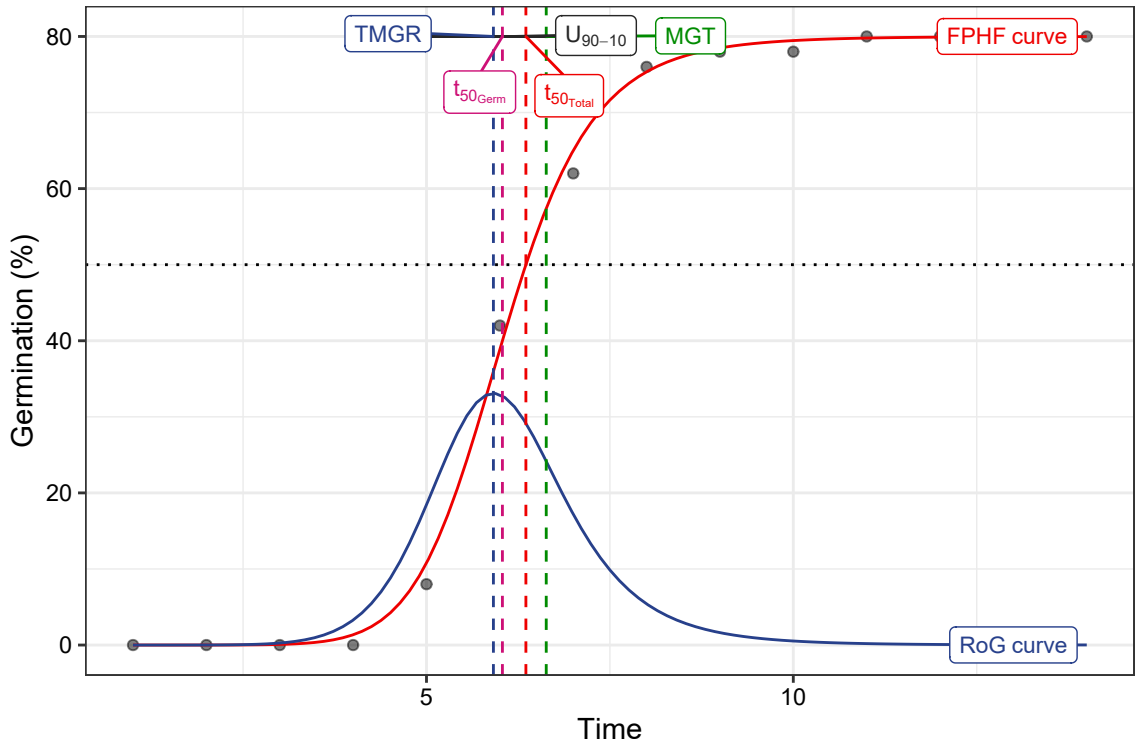

```
plot(fit2, rog = FALSE, t50.total = FALSE, t50.germ = FALSE,
     tmgr = FALSE, mgt = FALSE, uniformity = FALSE)
```



```
# 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 Day11 Day12 Day13 Day14 Tota
1        G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
2        G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
3        G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
4        G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
5        G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
6        G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0     0
7        G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0     0
8        G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0     0
9        G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0     0
10       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0     0
11       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1     0
12       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0     0
13       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1     0
14       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0     0
15       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0     0
   FirstGermTime LastGermTime PeakGermTime TimeSpreadGerm t50_Coolbear t50_Farooq MeanGermTime VarGermTi
1              5           11            6              6     5.970588   5.941176     6.700000    1.446
2              4           12            6              8     6.192308   6.153846     6.857143    2.027
3              4           12            6              8     6.000000   5.972222     6.866667    2.572
4              5           12            6              7     6.041667   6.000000     6.891304    2.187
5              5           13            6              8     5.975000   5.950000     6.812500    2.368
6              5           12            6              7     5.976190   5.952381     6.869565    2.071
7              5           11            6              6     5.972222   5.944444     6.690476    1.389
8              4           12            6              8     6.208333   6.166667     6.875000    2.112
9              4           12            6              8     6.000000   5.973684     6.866667    2.300
10             5           12            6              7     6.076923   6.038462     6.822222    1.831
11             5           13            6              8     5.928571   5.904762     6.791667    2.381
12             5           12            6              7     5.975000   5.950000     6.886364    2.149
13             5           13            6              8     6.083333   6.041667     6.936170    2.539
14             5           12            6              7     5.928571   5.904762     6.772727    1.900
15             5           11            6              6     6.050000   6.000000     6.809524    1.670
   MeanGermRate  VarGermRate  SEGermRate      CVG GermRateRecip_Coolbear GermRateRecip_Farooq GermSpeed_
1     0.1492537 0.0007176543 0.004235724 14.92537              0.1674877           0.1683168        6.
2     0.1458333 0.0009172090 0.004673148 14.58333              0.1614907           0.1625000        6.
3     0.1456311 0.0011572039 0.005071059 14.56311              0.1666667           0.1674419        6.
4     0.1451104 0.0009701218 0.004592342 14.51104              0.1655172           0.1666667        6.
```

```
5     0.1467890 0.0010995627 0.004786184 14.67890             0.1673640            0.1680672       7.3
6     0.1455696 0.0009301809 0.004496813 14.55696             0.1673307            0.1680000       6.9
7     0.1494662 0.0006935558 0.004063648 14.94662             0.1674419            0.1682243       6.4
8     0.1454545 0.0009454531 0.004861721 14.54545             0.1610738            0.1621622       6.0
9     0.1456311 0.0010345321 0.004794747 14.56311             0.1666667            0.1674009       6.8
10    0.1465798 0.0008453940 0.004334343 14.65798             0.1645570            0.1656051       6.8
11    0.1472393 0.0011191581 0.004828643 14.72393             0.1686747            0.1693548       7.3
12    0.1452145 0.0009558577 0.004660905 14.52145             0.1673640            0.1680672       6.0
13    0.1441718 0.0010970785 0.004831366 14.41718             0.1643836            0.1655172       7.0
14    0.1476510 0.0009033254 0.004531018 14.76510             0.1686747            0.1693548       6.7
15    0.1468531 0.0007767634 0.004300508 14.68531             0.1652893            0.1666667       6.3
   GermSpeedAccumulated_Count GermSpeedAccumulated_Percent GermSpeedCorrected_Normal GermSpeedCorrected_
1                    34.61567                    69.23134               0.07673656
2                    35.54058                    69.68741               0.07726134
3                    38.29725                    79.78594               0.07340991
4                    38.68453                    75.85202               0.07680397
5                    41.00786                    82.01571               0.07623944
6                    38.77620                    79.13509               0.07383855
7                    36.38546                    75.80304               0.07369656
8                    33.77079                    71.85275               0.07112480
9                    38.11511                    73.29829               0.07893128
10                   38.19527                    76.39054               0.07569665
11                   41.17452                    80.73436               0.07801721
12                   37.00640                    72.56158               0.07675799
13                   39.29399                    80.19182               0.07352419
14                   37.69490                    78.53103               0.07316490
15                   35.69697                    74.36868               0.07273057
   WeightGermPercent MeanGermPercent MeanGermNumber TimsonsIndex TimsonsIndex_Labouriau TimsonsIndex_Kha
1           47.42857        5.714286       2.857143     8.000000                  1.00              0.5
2           47.89916        5.882353       3.000000     9.803922                  1.25              0.7
3           54.46429        6.696429       3.214286    14.583333                  1.40              1.0
4           52.24090        6.442577       3.285714     7.843137                  1.00              0.5
5           56.14286        6.857143       3.428571    10.000000                  1.00              0.7
6           54.51895        6.705539       3.285714     6.122449                  1.00              0.4
7           51.93452        6.250000       3.000000     8.333333                  1.00              0.5
8           49.39210        6.079027       2.857143    10.638298                  1.25              0.7
9           50.27473        6.181319       3.214286     9.615385                  1.25              0.0
10          52.57143        6.428571       3.214286     8.000000                  1.00              0.5
11          55.18207        6.722689       3.428571     9.803922                  1.00              0.7
12          50.00000        6.162465       3.142857     5.882353                  1.00              0.4
13          55.24781        6.851312       3.357143     8.163265                  1.00              0.5
14          53.86905        6.547619       3.142857     6.250000                  1.00              0.4
15          51.19048        6.250000       3.000000     8.333333                  1.00              0.5
   GermIndex GermIndex_mod EmergenceRateIndex_Melville EmergenceRateIndex_Melville_mod EmergenceRateInd
1   5.840000      7.300000                         292                        7.300000
2   5.882353      7.142857                         300                        7.142857
3   6.687500      7.133333                         321                        7.133333
4   6.411765      7.108696                         327                        7.108696
5   6.900000      7.187500                         345                        7.187500
6   6.693878      7.130435                         328                        7.130435
7   6.395833      7.309524                         307                        7.309524
8   6.063830      7.125000                         285                        7.125000
9   6.173077      7.133333                         321                        7.133333
10  6.460000      7.177778                         323                        7.177778
```

```
11  6.784314      7.208333                       346                       7.208333
12  6.137255      7.113636                       313                       7.113636
13  6.775510      7.063830                       332                       7.063830
14  6.625000      7.227273                       318                       7.227273
15  6.291667      7.190476                       302                       7.190476
   EmergenceRateIndex_Fakorede PeakValue GermValue_Czabator GermValue_DP GermValue_Czabator_mod GermValu
1                     8.375000  9.500000           54.28571     57.93890                54.28571
2                     8.326531  9.313725           54.78662     52.58713                54.78662
3                     7.324444 10.416667           69.75446     68.62289                69.75446
4                     7.640359 10.049020           64.74158     70.43331                64.74158
5                     7.096354 11.250000           77.14286     80.16914                77.14286
6                     7.317580 10.714286           71.84506     76.51983                71.84506
7                     7.646259 10.416667           65.10417     69.41325                65.10417
8                     8.078125  9.574468           58.20345     56.00669                58.20345
9                     7.934815  9.855769           60.92165     58.13477                60.92165
10                    7.580247 10.250000           65.89286     70.91875                65.89286
11                    7.216146 11.029412           74.14731     77.39782                74.14731
12                    7.981921  9.803922           60.41632     64.44988                60.41632
13                    7.231326 10.969388           75.15470     78.16335                75.15470
14                    7.388430 10.677083           69.90947     74.40140                69.90947
15                    7.782313 10.156250           63.47656     67.62031                63.47656
   GermSynchrony GermUncertainty
1      0.2666667        2.062987
2      0.2346109        2.321514
3      0.2242424        2.462012
4      0.2502415        2.279215
5      0.2606383        2.146051
6      0.2792271        2.160545
7      0.2729384        2.040796
8      0.2256410        2.357249
9      0.2494949        2.321080
10     0.2555556        2.187983
11     0.2686170        2.128670
12     0.2737844        2.185245
13     0.2506938        2.241181
14     0.2991543        2.037680
15     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 Day11 Day12 Day13 Day14 To
 1:       G1   1     0     0     0     0     4    17    10     7     1     0     1     0     0     0
```

```
 2:       G2   1     0     0     0     1     3    15    13     6     2     1     0     1     0     0
 3:       G3   1     0     0     0     2     3    18     9     8     2     1     1     1     0     0
 4:       G4   1     0     0     0     0     4    19    12     6     2     1     1     1     0     0
 5:       G5   1     0     0     0     0     5    20    12     8     1     0     0     1     1     0
 6:       G1   2     0     0     0     0     3    21    11     7     1     1     1     1     0     0
 7:       G2   2     0     0     0     0     4    18    11     7     1     0     1     0     0     0
 8:       G3   2     0     0     0     1     3    14    12     6     2     1     0     1     0     0
 9:       G4   2     0     0     0     1     3    19    10     8     1     1     1     1     0     0
10:       G5   2     0     0     0     0     4    18    13     6     2     1     0     1     0     0
11:       G1   3     0     0     0     0     5    21    11     8     1     0     0     1     1     0
12:       G2   3     0     0     0     0     3    20    10     7     1     1     1     1     0     0
13:       G3   3     0     0     0     0     4    19    12     8     1     1     0     1     1     0
14:       G4   3     0     0     0     0     3    21    11     6     1     0     1     1     0     0
15:       G5   3     0     0     0     0     4    17    10     8     1     1     1     0     0     0
           b        c y0 lag   Dlag50 t50.total t50.Germinated     TMGR      AUC      MGT Skewness
 1:  9.881947 6.034954  0   0 6.034954  6.355122       6.034954 5.912195 1108.975 6.632252 1.098973
 2:  9.227667 6.175193  0   0 6.175193  6.473490       6.175193 6.031282 1128.559 6.784407 1.098655
 3:  7.793055 6.138110  0   0 6.138110  6.244190       6.138110 5.938179 1283.693 6.772742 1.103392
 4:  8.925668 6.125172  0   0 6.125172  6.276793       6.125172 5.972686 1239.887 6.739665 1.100323
 5:  9.419194 6.049641  0   0 6.049641  6.103433       6.049641 5.914289 1328.328 6.654980 1.100062
 6:  9.450187 6.097412  0   0 6.097412  6.182276       6.097412 5.961877 1294.463 6.702470 1.099232
 7: 10.172466 6.029851  0   0 6.029851  6.202812       6.029851 5.914057 1213.908 6.622417 1.098272
 8:  8.940702 6.189774  0   0 6.189774  6.439510       6.189774 6.036193 1164.346 6.804000 1.099232
 9:  8.617395 6.125121  0   0 6.125121  6.352172       6.125121 5.961631 1188.793 6.745241 1.101242
10:  9.608849 6.109503  0   0 6.109503  6.253042       6.109503 5.978115 1240.227 6.711899 1.098600
11:  9.400248 6.018759  0   0 6.018759  6.099434       6.018759 5.883558 1305.200 6.624247 1.100600
12:  9.162558 6.108449  0   0 6.108449  6.326181       6.108449 5.964079 1188.021 6.718636 1.099892
13:  8.995233 6.149011  0   0 6.149011  6.207500       6.149011 5.998270 1316.407 6.762272 1.099733
14: 10.391898 6.015907  0   0 6.015907  6.122385       6.015907 5.905179 1273.386 6.604963 1.097916
15:  9.136762 6.121580  0   0 6.121580  6.317392       6.121580 5.976088 1203.664 6.732267 1.099760
                                                      msg isConv txp.total_10 txp.total_60 Unifo
 1: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.956266     6.744598      
 2: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.983236     6.872603      
 3: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.673022     6.608437      
 4: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.850876     6.614967      
 5: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.814126     6.386788      
 6: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.868635     6.477594      
 7: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.930423     6.510495      
 8: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.940058     6.823299      
 9: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.836659     6.733275      
10: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.920629     6.566505      
11: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.798630     6.391288      
12: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.893597     6.684521      
13: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.841310     6.509952      
14: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.915143     6.397486      
15: #1. Relative error in the sum of squares is at most `ftol'.    TRUE     4.892505     6.667247      
    Uniformity
 1:   2.705880
 2:   2.968652
 3:   3.507277
 4:   3.046208
 5:   2.848078
 6:   2.860984
 7:   2.625165
```

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

Citing germinationmetrics

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

  Aravind, J., Vimala Devi, S., Radhamani, J., Jacob, S. R., and Kalyani Srinivasan (2020).  germinatio
  Seed Germination Indices and Curve Fitting. R package version 0.1.4,
  https://github.com/aravind-j/germinationmetricshttps://cran.r-project.org/package=germinationmetrics.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {germinationmetrics: Seed Germination Indices and Curve Fitting},
    author = {J. Aravind and S. {Vimala Devi} and J. Radhamani and Sherry Rachel Jacob and {Kalyani Sri
    year = {2020},
    note = {R package version 0.1.4},
    note = {https://github.com/aravind-j/germinationmetrics},
    note = {https://cran.r-project.org/package=germinationmetrics},
  }

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

Session Info

```
sessionInfo()
```

```
R version 4.0.0 (2020-04-24)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 17763)

Matrix products: default

locale:
[1] LC_COLLATE=English_United States.1252  LC_CTYPE=English_United States.1252    LC_MONETARY=English_U
[4] LC_NUMERIC=C                           LC_TIME=English_United States.1252

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

other attached packages:
[1] germinationmetrics_0.1.4

loaded via a namespace (and not attached):
 [1] minpack.lm_1.2-1  tidyselect_1.1.0  xfun_0.14         pander_0.6.3      purrr_0.3.4       lattice_
```

```
 [7] colorspace_1.4-1  vctrs_0.3.0       generics_0.0.2    testthat_2.3.2    htmltools_0.4.0   yaml_2.2
[13] XML_3.99-0.3      rlang_0.4.6       pillar_1.4.4      glue_1.4.1        withr_2.2.0       lifecycl
[19] plyr_1.8.6        stringr_1.4.0     munsell_0.5.0     gtable_0.3.0      evaluate_0.14     labeling
[25] knitr_1.28        gbRd_0.4-11       curl_4.3          fansi_0.4.1       highr_0.8         broom_0.5
[31] Rcpp_1.0.4.6      scales_1.1.1      backports_1.1.6   desc_1.2.0        pkgload_1.0.2     farver_2
[37] ggplot2_3.3.0     packrat_0.5.0     digest_0.6.25     stringi_1.4.6     dplyr_1.0.0       ggrepel_
[43] grid_4.0.0        rprojroot_1.3-2   bibtex_0.4.2.2    mathjaxr_1.0-0    Rdpack_0.11-2     cli_2.0.
[49] tools_4.0.0       bitops_1.0-6      magrittr_1.5      RCurl_1.98-1.2    tibble_3.0.1      crayon_1
[55] tidyr_1.1.0       pkgconfig_2.0.3   ellipsis_0.3.1    data.table_1.12.8 assertthat_0.2.1  rmarkdow
[61] httr_1.4.1        rstudioapi_0.11   R6_2.4.1          nlme_3.1-147      compiler_4.0.0
```

References

El-Kassaby, Y. A., Moss, I., Kolotelo, D., and Stoehr, M. (2008). Seed germination: Mathematical representation and parameters extraction. *Forest Science* 54, 220–227. doi:10.1093/forestscience/54.2.220.