The **germinationmetrics** Package: A Brief Introduction


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Contents

Overview .......................................................... 1
Installation ......................................................... 1
Version History ................................................... 3
Germination count data ......................................... 3
Single-value germination indices ............................... 4
Non-linear regression analysis ................................ 32
  Four-parameter hill function ................................. 32
Wrapper functions .............................................. 38
Citing **germinationmetrics** .................................. 39
Session Info ......................................................... 39
References ......................................................... 40

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:

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

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

Then the package can be loaded using the function

```r
library(germinationmetrics)
```
Welcome to germinationmetrics version 0.1.4

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

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

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

# To suppress this message use:
suppressPackageStartupMessages(library(germinationmetrics))
The *germinationmetrics* Package: A Brief Introduction

**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.

<table>
<thead>
<tr>
<th>intervals</th>
<th>counts</th>
<th>cumulative.counts</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>6</td>
<td>17</td>
<td>21</td>
</tr>
<tr>
<td>7</td>
<td>10</td>
<td>31</td>
</tr>
<tr>
<td>8</td>
<td>7</td>
<td>38</td>
</tr>
<tr>
<td>9</td>
<td>1</td>
<td>39</td>
</tr>
<tr>
<td>10</td>
<td>0</td>
<td>39</td>
</tr>
<tr>
<td>11</td>
<td>1</td>
<td>40</td>
</tr>
<tr>
<td>12</td>
<td>0</td>
<td>40</td>
</tr>
<tr>
<td>13</td>
<td>0</td>
<td>40</td>
</tr>
<tr>
<td>14</td>
<td>0</td>
<td>40</td>
</tr>
</tbody>
</table>

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

```r
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`.

<table>
<thead>
<tr>
<th>Germination index</th>
<th>Function</th>
<th>Details</th>
<th>Unit</th>
<th>Measures</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Germination percentage or Final germination percentage or Germinability (GP)</td>
<td>GermPercent</td>
<td>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.</td>
<td>Percentage (%)</td>
<td>Germination capacity</td>
<td>ISTA (2015)</td>
</tr>
<tr>
<td>Time for the first germination or Germination time lag (t₀)</td>
<td>FirstGermTime</td>
<td>It is the time for first germination to occur (e.g. First day of germination)</td>
<td>time</td>
<td>Germination time</td>
<td>Edwards (1932); Czabator (1962); Goloff and Bazzaz (1975); Labouriau (1983a); Ranal (1999); Quintanilla et al. (2000)</td>
</tr>
<tr>
<td>Time for the last germination (t₉)</td>
<td>LastGermTime</td>
<td>It is the time for last germination to occur (e.g. Last day of germination)</td>
<td>time</td>
<td>Germination time</td>
<td>Edwards (1932)</td>
</tr>
<tr>
<td>Time spread of germination or Germination distribution</td>
<td>TimeSpreadGerm</td>
<td>It is the difference between time for last germination (t₉) and time for first germination (t₀). [ Time\ spread\ of\ germination = t_9 - t_0 ]</td>
<td>time</td>
<td>Germination time</td>
<td>Al-Mudaris (1998); Schrader and Graves (2000); Kader (2005)</td>
</tr>
<tr>
<td>Peak period of germination or Modal time of germination</td>
<td>PeakGermTime</td>
<td>It is the time in which highest frequency of germinated seeds are observed and need not be unique.</td>
<td>time</td>
<td>Germination time</td>
<td>Ranal and Santana (2006)</td>
</tr>
<tr>
<td>Median germination time (t₅₀) (Coolbear)</td>
<td>t₅₀</td>
<td>It is the time to reach 50% of final/maximum germination. With argument <code>method</code> specified as &quot;coolbear&quot;, it is computed as follows. [ t_{50} = T_i + \frac{(N + \frac{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 &lt; \frac{N + \frac{1}{2}}{2} &lt; N_j ).</td>
<td>time</td>
<td>Germination time</td>
<td>Coolbear et al. (1984)</td>
</tr>
<tr>
<td>Median germination time (t₅₀) (Farooq)</td>
<td>t₅₀</td>
<td>With argument <code>method</code> specified as &quot;farooq&quot;, it is computed as follows. [ t_{50} = T_i + \frac{(N - 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 &lt; \frac{N - 1}{2} &lt; N_j ).</td>
<td>time</td>
<td>Germination time</td>
<td>Farooq et al. (2005)</td>
</tr>
</tbody>
</table>
## Germination index details

<table>
<thead>
<tr>
<th>Germination index</th>
<th>Function</th>
<th>Details</th>
<th>Unit</th>
<th>Measures</th>
<th>Reference</th>
</tr>
</thead>
</table>
| Mean germination time or Mean length of incubation time ($\bar{T}$) or Germination resistance (GR) or Sprouting index (SI) or Emergence index (EI) | **MeanGermTime** | It is the average length of time required for maximum germination of a seed lot and is estimated according to the following formula.  
$$\bar{T} = \frac{\sum_{i=1}^{k} N_i T_i}{\sum_{i=1}^{k} N_i}$$  
Where, $T_i$ is the time from the start of the experiment to the $i$th interval, $N_i$ is the number of seeds germinated in the $i$th time interval (not the accumulated number, but the number corresponding to the $i$th interval), and $k$ is the total number of time intervals.  
It is the inverse of mean germination rate ($\bar{V}$).  
$$\bar{T} = \frac{1}{\bar{V}}$$ | time | Germination time | Edmond and Drapala (1958); Czabator (1962); Smith and Millet (1964); Gordon (1969); Gordon (1971); Mock and Eberhart (1972); Ellis and Roberts (1980) Labouriau (1983a); Ranal and Santana (2006) |
| Variance of germination time ($s_T^2$) | **VarGermTime** | It is computed according to the following formula.  
$$s_T^2 = \frac{\sum_{i=1}^{k} N_i (T_i - \bar{T})^2}{\sum_{i=1}^{k} N_i - 1}$$  
Where, $T_i$ is the time from the start of the experiment to the $i$th interval, $N_i$ is the number of seeds germinated in the $i$th time interval (not the accumulated number, but the number corresponding to the $i$th interval), and $k$ is the total number of time intervals. | time | Germination time | Labouriau (1983a); Ranal and Santana (2006) |
| Standard error of germination time ($s_T$) | **SEGermTime** | It signifies the accuracy of the calculation of the mean germination time.  
It is estimated according to the following formula:  
$$s_T = \sqrt{\frac{s_T^2}{\sum_{i=1}^{k} N_i}}$$  
Where, $N_i$ is the number of seeds germinated in the $i$th time interval (not the accumulated number, but the number corresponding to the $i$th interval) and $k$ is the total number of time intervals. | time | Germination time | Labouriau (1983a); Ranal and Santana (2006) |
<table>
<thead>
<tr>
<th>Germination index</th>
<th>Function</th>
<th>Details</th>
<th>Unit</th>
<th>Measures</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean germination rate (M)</td>
<td>MeanGermRate</td>
<td>It is computed according to the following formula:</td>
<td>time⁻¹</td>
<td>Germination rate</td>
<td>Labouriau and Valadares (1976); Labouriau (1983b); Ranal and Santana (2006)</td>
</tr>
</tbody>
</table>
|                   |                  | \[
M = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i}
\]
|                   |                  | Where, \(T_i\) is the time from the start of the experiment to the \(i\)th interval, \(N_i\) is the number of seeds germinated in the \(i\)th time interval (not the accumulated number, but the number corresponding to the \(i\)th interval), and \(k\) is the total number of time intervals.
|                   |                  | It is the inverse of mean germination time (\(T\)).                                                                                                                                                     | time⁻¹    | Germination rate | Labouriau and Valadares (1976); Labouriau (1983b); Ranal and Santana (2006) |
|                   | CVG              | It is estimated according to the following formula.                                                                                                                                                     | % day⁻¹   | Germination rate | Kotowski (1926), Nichols and Heydecker (1968); Bewley and Black (1994); Labouriau (1983b); Scott et al. (1984) |
|                   |                  | \[CVG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} N_i T_i} \times 100\]
|                   |                  | \[CVG = \frac{V}{100}\]
|                   |                  | Where, \(T_i\) is the time from the start of the experiment to the \(i\)th interval, \(N_i\) is the number of seeds germinated in the \(i\)th time interval (not the accumulated number, but the number corresponding to the \(i\)th interval), and \(k\) is the total number of time intervals.
|                   | VarGermRate      | It is calculated according to the following formula.                                                                                                                                                     | time⁻²    | Germination rate | Labouriau (1983b); Ranal and Santana (2006) |
|                   |                  | \[s_{V}^2 = \frac{V^4}{\sum_{i=1}^{k} N_i} \times s_{T}^2\]
|                   |                  | Where, \(s_{T}^2\) is the variance of germination time.                                                                                                                                                  | time⁻¹    | Germination rate | Labouriau (1983b); Ranal and Santana (2006) |
|                   | SEGermRate       | It is estimated according to the following formula.                                                                                                                                                     | time⁻¹    | Germination rate | Labouriau (1983b); Ranal and Santana (2006) |
|                   |                  | \[s_{T} = \sqrt{\frac{s_{V}^2}{\sum_{i=1}^{k} N_i}}\]
|                   |                  | Where, \(N_i\) is the number of seeds germinated in the \(i\)th time interval (not the accumulated number, but the number corresponding to the \(i\)th interval), and \(k\) is the total number of time intervals.
|                   | GermRateRecip    | It is the reciprocal of the median germination time (\(t_{50}\)).                                                                                                                                       | time⁻¹    | Germination rate | Went (1957); Labouriau (1983b); Ranal and Santana (2006) |
|                   |                  | \[v_{50} = \frac{1}{t_{50}}\]
<table>
<thead>
<tr>
<th>Germination index</th>
<th>Function</th>
<th>Details</th>
<th>Unit</th>
<th>Measures</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Speed of germination or Germination rate Index or index of velocity of germination or Emergence rate index (Allan, Vogel and Peterson; Erbach; Hsu and Nelson) or Germination index (AOSA)</td>
<td>GermSpeed</td>
<td>It is the rate of germination in terms of the total number of seeds that germinate in a time interval. It is estimated as follows. $S = \sum_{i=1}^{k} \frac{N_i}{T_i}$ Where, $T_i$ is the time from the start of the experiment to the $i$th interval, $N_i$ is the number of seeds germinated in the $i$th time interval (not the accumulated number, but the number corresponding to the $i$th interval), and $k$ is the total number of time intervals. Instead of germination counts, germination percentages may also be used for computation of speed of germination.</td>
<td>% time$^{-1}$</td>
<td>Mixed</td>
<td>Throneberry and Smith (1955); Maguire (1962); Allan et al. (1962); Kendrick and Frankland (1969); Bouton et al. (1976); Erbach (1982); AOSA (1983); Khandakar and Bradbeer (1988); Hsu and Nelson (1986); Bradbeer (1988); Wardle et al. (1991)</td>
</tr>
<tr>
<td>Speed of accumulated germination</td>
<td>GermSpeedAccumulated</td>
<td>It is the rate of germination in terms of the accumulated/cumulative total number of seeds that germinate in a time interval. It is estimated as follows. $S_{accumulated} = \sum_{i=1}^{k} \frac{\sum_{j=1}^{i} N_j}{T_i}$ Where, $T_i$ is the time from the start of the experiment to the $i$th interval, $\sum_{j=1}^{i} N_j$ is the cumulative/accumulated number of seeds germinated in the $i$th interval, and $k$ is the total number of time intervals. Instead of germination counts, germination percentages may also be used for computation of speed of germination.</td>
<td>% time$^{-1}$</td>
<td>Mixed</td>
<td>Bradbeer (1988); Wardle et al. (1991); Haugland and Brandaæter (1996); Santana and Ranal (2004)</td>
</tr>
<tr>
<td>Corrected germination rate index</td>
<td>GermSpeedCorrected</td>
<td>It is computed as follows. $S_{corrected} = \frac{S}{FGP}$ Where, $FGP$ is the final germination percentage or germinability.</td>
<td>time$^{-1}$</td>
<td>Mixed</td>
<td>Evetts and Burnside (1972)</td>
</tr>
<tr>
<td>Weighted germination percentage ($WGP$)</td>
<td>WeightGermPercent</td>
<td>It is estimated as follows. $WGP = \frac{\sum_{i=1}^{k}(k - i + 1)N_i}{k \times N} \times 100$ Where, $N_i$ is the number of seeds that germinated in the time interval $i$ (not cumulative, but partial count), $N$ is the total number of seeds tested, and $k$ is the total number of time intervals.</td>
<td>Mixed</td>
<td>Reddy et al. (1985); Reddy (1978)</td>
<td></td>
</tr>
<tr>
<td>Germination metric</td>
<td>Function</td>
<td>Details</td>
<td>Unit</td>
<td>Measures</td>
<td>Reference</td>
</tr>
<tr>
<td>-------------------</td>
<td>----------</td>
<td>---------</td>
<td>------</td>
<td>----------</td>
<td>-----------</td>
</tr>
</tbody>
</table>
| Mean germination percentage per unit time (GP) | MeanGermPercent | It is estimated as follows. \[
\bar{GP} = \frac{GP}{T_k}
\] Where, GP is the final germination percentage, T_k is the time at the kth time interval, and k is the total number of time intervals required for final germination. | Mixed | Czabator (1962) |
| Number of seeds germinated per unit time \(N\) | MeanGermNumber | It is estimated as follows. \[
N = \frac{N_g}{T_k}
\] Where, \(N_g\) is the number of germinated seeds at the end of the germination test, \(T_k\) is the time at the kth time interval, and k is the total number of time intervals required for final germination. | Mixed | Khamassi et al. (2013) |
| Timson’s index \(\sum k\) (Ten summation), \(\sum 5\) or \(\sum 20\) or Germination energy index \((GEI)\) | TimsonsIndex | It is the progressive total of cumulative germination percentage recorded at specific intervals for a set period of time and is estimated in terms of cumulative germination percentage \((G_i)\) as follows. \[
\Sigma k = \sum_{i=1}^{k} G_i
\] Where, \(G_i\) is the cumulative germination percentage in time interval \(i\), and \(k\) is the total number of time intervals. It also estimated in terms of partial germination percentage as follows. \[
\Sigma k = \sum_{i=1}^{k} g_i(k - j)
\] Where, \(g_i\) is the germination (not cumulative, but partial germination) in time interval \(i\) \((i\) varying from 0 to \(k\)), \(k\) is the total number of time intervals, and \(j = i - 1\). | Mixed | Grose and Zimmer (1958); Timson (1965); Lyon and Coffelt (1966); Chaudhary and Ghildyal (1970); Negm and Smith (1978); Brown and Mayer (1988); Baskin and Baskin (1998); Goodchild and Walker (1971) |
| Modified Timson’s index \(\Sigma k_{mod}\) (Labouriau) | TimsonsIndex | It is estimated as Timson’s index \(\Sigma k\) divided by the sum of partial germination percentages. \[
\Sigma k_{mod} = \frac{\Sigma k}{\sum_{i=1}^{k} g_i}
\] | Mixed | Ranal and Santana (2006) |
<table>
<thead>
<tr>
<th>Germination index</th>
<th>Function</th>
<th>Details</th>
<th>Unit</th>
<th>Measures</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Modified Timson’s index ((\Sigma k_{mod})) (Khan and Unger)</td>
<td><strong>TimsonsIndex</strong></td>
<td>It is estimated as Timson’s index ((\Sigma k)) divided by the total time period of germination ((T_k)). [\Sigma k_{mod} = \frac{\Sigma k}{T_k}]</td>
<td>Mixed</td>
<td></td>
<td>Khan and Ungar (1984)</td>
</tr>
<tr>
<td>George’s index ((GR))</td>
<td><strong>GermRateGeorge</strong></td>
<td>It is estimated as follows. [GR = \sum_{i=1}^{k} N_i K_i] Where (N_i) is the number of seeds germinated by (i^{th}) interval and (K_i) is the number of intervals (eg. days) until the end of the test, and (k) is the total number of time intervals.</td>
<td>Mixed</td>
<td></td>
<td>George (1961); Tucker and Wright (1965); Nichols and Heydecker (1968)</td>
</tr>
<tr>
<td>Germination Index ((GI)) (Melville)</td>
<td><strong>GermIndex</strong></td>
<td>It is estimated as follows. [GI = \sum_{i=1}^{k} \left</td>
<td>\frac{(T_k - T_i) N_i}{N_t} \right</td>
<td>] Where, (T_i) is the time from the start of the experiment to the (i^{th}) interval (day for the example), (N_i) is the number of seeds germinated in the (i^{th}) time interval (not the accumulated number, but the number corresponding to the (i^{th}) interval), (N_t) is the total number of seeds used in the test, and (k) is the total number of time intervals.</td>
<td>Mixed</td>
</tr>
<tr>
<td>Germination Index ((GI_{mod})) (Melville; Santana and Ranal)</td>
<td><strong>GermIndex</strong></td>
<td>It is estimated as follows. [GI_{mod} = \sum_{i=1}^{k} \left</td>
<td>\frac{(T_k - T_i) N_i}{N_g} \right</td>
<td>] Where, (T_i) is the time from the start of the experiment to the (i^{th}) interval (day for the example), (N_i) is the number of seeds germinated in the (i^{th}) time interval (not the accumulated number, but the number corresponding to the (i^{th}) interval), (N_g) is the total number of germinated seeds at the end of the test, and (k) is the total number of time intervals.</td>
<td>Mixed</td>
</tr>
<tr>
<td>Germination index (ERI) or Germination Rate Index (Shmueli and Goldberg)</td>
<td>Function</td>
<td>Details</td>
<td>Unit</td>
<td>Measures</td>
<td>Reference</td>
</tr>
<tr>
<td>---</td>
<td>---</td>
<td>---</td>
<td>---</td>
<td>---</td>
<td>---</td>
</tr>
<tr>
<td><strong>Emergence Rate Index (ERI)</strong> or Germination Rate Index (Shmueli and Goldberg)</td>
<td><strong>EmergenceRateInde</strong></td>
<td>It is estimated as follows.</td>
<td>Mixed</td>
<td>Shmueli and Goldberg (1971)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>[ ERI = \sum_{i=i_0}^{k-1} N_i (k - i) ]</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Where, ( N_i ) is the number of seeds germinated in the ( i )th time interval (not the accumulated number, but the number corresponding to the ( i )th interval), ( i_0 ) is the time interval when emergence/germination started, and ( k ) is the total number of time intervals.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modified Emergence Rate Index (ERI_{mod}) or Modified Germination Rate Index (Shmueli and Goldberg; Santana and Ranal)</td>
<td><strong>EmergenceRateInde</strong></td>
<td>It is estimated by dividing Emergence rate index (ERI) by total number of emerged seedlings (or germinated seeds).</td>
<td>Mixed</td>
<td>Shmueli and Goldberg (1971); Santana and Ranal (2004); Ranal and Santana (2006)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>[ ERI_{mod} = \frac{\sum_{i=i_0}^{k-1} N_i (k - i)}{N_g} = \frac{ERI}{N_g} ]</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Where, ( N_g ) is the total number of germinated seeds at the end of the test, ( N_i ) is the number of seeds germinated in the ( i )th time interval (not the accumulated number, but the number corresponding to the ( i )th interval), ( i_0 ) is the time interval when emergence/germination started, and ( k ) is the total number of time intervals.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Emergence Rate Index (ERI) or Germination Rate Index (Bilbro &amp; Wanjura)</td>
<td><strong>EmergenceRateInde</strong></td>
<td>It is the estimated as follows.</td>
<td>Mixed</td>
<td>Bilbro and Wanjura (1982)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>[ ERI = \frac{\sum_{i=1}^{k} N_i}{T} = \frac{N_g}{T} ]</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Where, ( N_g ) is the total number of germinated seeds at the end of the test, ( N_i ) is the number of seeds germinated in the ( i )th time interval (not the accumulated number, but the number corresponding to the ( i )th interval), and ( T ) is the mean germination time or mean emergence time.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Emergence Rate Index (ERI) or Germination Rate Index (Fakorede)</td>
<td><strong>EmergenceRateInde</strong></td>
<td>It is estimated as follows.</td>
<td>Mixed</td>
<td>Fakorede and Ayoola (1980); Fakorede and Ojo (1981); Fakorede and Agbana (1983)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>[ ERI = \frac{T}{FGP/100} ]</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Where, ( T ) is the Mean germination time and ( FGP ) is the final germination time.</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### Germination index

<table>
<thead>
<tr>
<th>Function</th>
<th>Details</th>
<th>Unit</th>
<th>Measures</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Peak Value ($PV$)</td>
<td>It is the accumulated number of seeds germinated at the point on the germination curve at which the rate of germination starts to decrease. It is computed as the maximum quotient obtained by dividing successive cumulative germination values by the relevant incubation time.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>$PV = \max \left( \frac{G_1}{T_1}, \frac{G_2}{T_2}, \ldots, \frac{G_k}{T_k} \right)$</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Where, $T_i$ is the time from the start of the experiment to the $i$th interval, $G_i$ is the cumulative germination percentage in the $i$th time interval, and $k$ is the total number of time intervals.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Mixed</td>
<td>% time$^{-1}$</td>
<td>Czabator (1962); Bonner (1967)</td>
<td></td>
</tr>
<tr>
<td>GermValue</td>
<td>It is computed as follows.</td>
<td>Mixed</td>
<td>Czabator (1962); Brown and Mayer (1988)</td>
<td></td>
</tr>
<tr>
<td>GermValue</td>
<td>$GV = PV \times MDG$</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Where, $PV$ is the peak value and $MDG$ is the mean daily germination percentage from the onset of germination.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>It can also be computed for other time intervals of successive germination counts, by replacing $MDG$ with the mean germination percentage per unit time ($GP$).</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>$GV$ value can be modified ($GV_{mod}$), to consider the entire duration from the beginning of the test instead of just from the onset of germination.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GermValue</td>
<td>It is computed as follows.</td>
<td>Mixed</td>
<td>Djavanshir and Pourbeik (1976); Brown and Mayer (1988)</td>
<td></td>
</tr>
<tr>
<td>GermValue</td>
<td>$GV = \frac{\sum DGS}{N} \times GP \times c$</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Where, $DGS$ is the daily germination speed computed by dividing cumulative germination percentage by the number of days since the since the onset of germination, $N$ is the frequency or number of DGS calculated during the test, $GP$ is the germination percentage expressed over 100, and $c$ is a constant. The value of $c$ is decided on the basis of average daily speed of germination (average $\frac{DGS}{N}$). If it is less than 10, then $c$ value of 10 can be used and if it is more than 10, then value of 7 or 8 can be used for $c$.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>$GV$ value can be modified ($GV_{mod}$), to consider the entire duration from the beginning of the test instead of just from the onset of germination.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Germination index</td>
<td>Function</td>
<td>Details</td>
<td>Unit</td>
<td>Measures</td>
</tr>
<tr>
<td>------------------------------------------------------</td>
<td>---------------</td>
<td>-------------------------------------------------------------------------</td>
<td>---------------</td>
<td>------------------------</td>
</tr>
<tr>
<td>Coefficient of uniformity of germination <em>(CUG)</em></td>
<td>CUGerm</td>
<td>It is computed as follows.</td>
<td>Unit</td>
<td>Germination uniformity</td>
</tr>
<tr>
<td></td>
<td></td>
<td>[ CUG = \frac{\sum_{i=1}^{k} N_i}{\sum_{i=1}^{k} (T - T_i)^2 N_i} ]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Where, ( T ) is the mean germination time, ( T_i ) is the time from the start of the experiment to the ( i )th interval (day for the example), ( N_i ) is the number of seeds germinated in the ( i )th time interval (not the accumulated number, but the number corresponding to the ( i )th interval), and ( k ) is the total number of time intervals.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Coefficient of variation of the germination time <em>(CV</em>)</td>
<td>CVGermTime</td>
<td>It is estimated as follows.</td>
<td></td>
<td>Germination uniformity</td>
</tr>
<tr>
<td></td>
<td></td>
<td>[ CV_T = \sqrt{\frac{s_T^2}{T}} ]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Where, ( s_T^2 ) is the variance of germination time and ( T ) is the mean germination time.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Synchronization index <em>(E)</em> or Uncertainty of the germination process <em>(U)</em> or informational entropy <em>(H)</em></td>
<td>GermUncertainty</td>
<td>It is estimated as follows.</td>
<td>bit</td>
<td>Germination synchrony</td>
</tr>
<tr>
<td></td>
<td></td>
<td>[ E = - \sum_{i=1}^{k} f_i \log_2 f_i ]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>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 ( i )th time interval, and ( k ) is the total number of time intervals.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Synchrony of germination <em>(Z)</em> index</td>
<td>GermSynchrony</td>
<td>It is computed as follows.</td>
<td></td>
<td>Germination synchrony</td>
</tr>
<tr>
<td></td>
<td></td>
<td>[ Z = \frac{\sum_{i=1}^{k} C_{N_i,2}}{C_{\Sigma N_i,2}} ]</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>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 ( i )th time interval (estimated as ( C_{N_i,2} = \frac{N_i(N_i-1)}{2} )), and ( C_{\Sigma N_i,2} ) is the partial combination of the two germinated seeds from among the total number of seeds germinated at the final count, assuming that all seeds that germinated did so simultaneously.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Examples

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

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

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

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

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, 40, 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)
```
The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

[1] 5

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

[1] 11

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

[1] 6

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

[1] 6

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

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

[1] 5 6

```
x <- c(0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0)
y <- c(0, 0, 0, 4, 21, 31, 38, 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, 4, 17, 10, 7, 1, 0, 1, 0, 0)
y <- c(0, 0, 0, 4, 21, 31, 38, 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
The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

```
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, 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
```
The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

# 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
```

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

# From partial germination counts
#______________________________________________________________________________

`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
```
The `germinationmetrics` Package: A Brief Introduction

### Single-value germination indices

- **GermSpeedAccumulated**
  ```r
  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")
The `germinationmetrics` Package: A Brief Introduction

### Single-value germination indices

[1] 0.4326958

# From partial germination counts (with percentages instead of counts)

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

[1] 12.27785

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

[1] 69.23134

# From cumulative germination counts

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

[1] 6.138925

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

[1] 34.61567

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

[1] 0.07673656

```r
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)

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

[1] 12.27785

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

[1] 69.23134

```r
x <- c(0, 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, 40, 40, 40, 40, 40, 40)
int <- 1:length(x)
```

# From partial germination counts

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

WeightGermPercent()

[1] 47.42857

# From cumulative germination counts

```r
```
The `germinationmetrics` Package: A Brief Introduction

### Single-value germination indices

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

```
[1] 47.42857
```

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

```r
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
```

```r
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
```

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

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

TimsonsIndex(), GermRateGeorge()

```

```
[1] 664
```

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

```

```
[1] 664
```

```r
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50, modification = "labouriau")
```
The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

[1] 8.3
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
            modification = "khanungar")

[1] 47.42857
GermRateGeorge(germ.counts = x, intervals = int)

[1] 332
# With max specified
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50, max = 10)

[1] 344
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
            max = 10, modification = "none")

[1] 344
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
            max = 10, modification = "labouriau")

[1] 4.410256
TimsonsIndex(germ.counts = x, intervals = int, total.seeds = 50,
            max = 10, modification = "khanungar")

[1] 24.57143
GermRateGeorge(germ.counts = x, intervals = int, max = 10)

[1] 172
GermRateGeorge(germ.counts = x, intervals = int, max = 14)

[1] 332
# From cumulative germination counts
#-----------------------------------------------
# Without max specified
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
            total.seeds = 50)

[1] 664
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
            total.seeds = 50,
            modification = "none")

[1] 664
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
            total.seeds = 50,
            modification = "labouriau")

[1] 8.3
TimsonsIndex(germ.counts = y, intervals = int, partial = FALSE,
            total.seeds = 50,
            modification = "khanungar")
The `germinationmetrics` Package: A Brief Introduction

**Single-value germination indices**

```
[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
```
The `germinationmetrics` Package: A Brief Introduction

### Single-value germination indices

#### From cumulative germination counts

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

[1] 5.84

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

[1] 5.84

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

[1] 7.3

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

#### From partial germination counts

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

```r
EmergenceRateIndex()
```

[1] 292

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

[1] 292

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

[1] 7.3

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

[1] 5.970149

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

[1] 8.375

#### From cumulative germination counts

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

[1] 292

```r
EmergenceRateIndex(germ.counts = y, intervals = int, partial = FALSE, method = "melville")
```
The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

[1] 292

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

[1] 7.3

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

[1] 5.970149

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

[1] 8.375

```r
x <- c(0, 0, 34, 40, 21, 10, 4, 5, 3, 5, 8, 7, 6, 6, 4, 0, 2, 0, 2)
y <- c(0, 0, 34, 74, 95, 105, 109, 114, 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

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

Germination Value

[1] 38.95

[[2]]

<table>
<thead>
<tr>
<th>germ.counts</th>
<th>intervals</th>
<th>Cumulative.germ.counts</th>
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The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

```
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
```
The `germinationmetrics` Package: A Brief Introduction

### Single-value germination indices

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```r
$testend
[1] 16

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

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

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**DGS**

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</tr>
<tr>
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<td>5.708333</td>
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</table>
The germinationmetrics Package: A Brief Introduction

Single-value germination indices

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

`Germination Value`
[1] 46.6952

[[2]]

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

DGS SumDGSbyN GV
1 0.000000 0.000000 0.000000
2 0.000000 0.000000 0.000000
3 5.666667 1.888889 3.211111
4 9.250000 3.729167 13.797917
5 9.500000 4.883333 23.195833
6 8.750000 5.850340 31.884354
7 7.785714 5.805340 31.894354
8 7.125000 6.009673 34.255134
9 6.500000 6.064153 35.475298
10 6.100000 6.067738 37.013202
11 5.909091 6.053316 39.346552
12 5.708333 6.024567 41.268285
13 5.538462 5.987174 43.107655
14 5.357143 5.942172 44.566291
15 5.200000 5.892694 45.963013
16 5.000000 5.836901 46.695205
17 4.705882 5.770370 46.162961
The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

$\text{testend}$

[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")
```

$'\text{Germination Value}'$

[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
```
The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

```r
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]]

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<th>intervals</th>
<th>Cumulative.germ.counts</th>
<th>Cumulative.germ.percent</th>
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$testend
[1] 16
The \texttt{germinationmetrics} Package: A Brief Introduction

Single-value germination indices

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

```r
'$\text{Germination Value}$'

[1] 38.95

[[2]]

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\texttt{DGS}

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

```r
'$\text{Germination Value}$'

30
The `germinationmetrics` Package: A Brief Introduction

Single-value germination indices

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<th>intervals</th>
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DGS SumDGSbyN GV

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

<table>
<thead>
<tr>
<th>Germination parameters</th>
<th>Details</th>
<th>Unit</th>
<th>Measures</th>
</tr>
</thead>
<tbody>
<tr>
<td>y intercept ($y_0$)</td>
<td>The intercept on the y axis.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asymptote ($a$)</td>
<td>It is the maximum cumulative germination percentage, which is equivalent to germination capacity.</td>
<td>%</td>
<td>Germination capacity</td>
</tr>
<tr>
<td>Shape and steepness ($b$)</td>
<td>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.</td>
<td></td>
<td>Germination rate</td>
</tr>
<tr>
<td>Half-maximal activation level ($c$)</td>
<td>Time required for 50% of viable seeds to germinate.</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td>lag</td>
<td>It is the time at germination onset and is computed by solving four-parameter hill function after setting $y$ to 0 as follows.</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td></td>
<td>$lag = b \sqrt{\frac{-2y_0c^b}{a + y_0}}$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$D_{lag-50}$</td>
<td>The duration between the time at germination onset ($lag$) and that at 50% germination ($c$).</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td>$t_{50total}$</td>
<td>Time required for 50% of total seeds to germinate.</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td>$t_{50germinated}$</td>
<td>Time required for 50% of viable/germinated seeds to germinate</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td>$t_{xtotal}$</td>
<td>Time required for $x%$ of total seeds to germinate.</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td>$t_{xgerminated}$</td>
<td>Time required for $x%$ of viable/germinated seeds to germinate</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td>Uniformity ($U_{t_{max}-t_{min}}$)</td>
<td>It is the time interval between the percentages of viable seeds specified in the arguments $umin$ and $umin$ to germinate.</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td>Time at maximum germination rate ($TMGR$)</td>
<td>The partial derivative of the four-parameter hill function gives the instantaneous rate of germination ($s$) as follows.</td>
<td>time</td>
<td>Germination time</td>
</tr>
<tr>
<td></td>
<td>$s = \frac{\partial y}{\partial x} = \frac{abc^b x^{b-1}}{(c^b + x^b)^2}$</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>From this function for instantaneous rate of germination, $TMGR$ can be estimated as follows.</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>$TMGR = b \sqrt{\frac{c^b(b - 1)}{b + 1}}$</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>It represents the point in time when the instantaneous rate of germination starts to decline.</td>
<td></td>
<td></td>
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</table>
The `germinationmetrics` Package: A Brief Introduction

Non-linear regression analysis

<table>
<thead>
<tr>
<th>Germination parameters</th>
<th>Details</th>
<th>Unit</th>
<th>Measures</th>
</tr>
</thead>
<tbody>
<tr>
<td>Area under the curve</td>
<td>It is obtained by integration of the fitted curve between time 0 and</td>
<td></td>
<td>Mixed</td>
</tr>
<tr>
<td>( (AUC) )</td>
<td>time specified in the argument ( t_{\text{max}} ).</td>
<td></td>
<td></td>
</tr>
<tr>
<td>( MGT )</td>
<td>Calculated by integration of the fitted curve and proper normalisation.</td>
<td></td>
<td>time</td>
</tr>
<tr>
<td>( Skewness )</td>
<td>It is computed as follows.</td>
<td></td>
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<tr>
<td></td>
<td>[ \frac{MGT}{t_{50_{\text{germinated}}}} ]</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Examples

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

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

$fit
  sigma isConv finTol logLik AIC BIC deviance df.residual
```
The `germinationmetrics` Package: A Brief Introduction

Non-linear regression analysis

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
The `germinationmetrics` Package: A Brief Introduction

Non-linear regression analysis

```r
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

36
The `germinationmetrics` Package: A Brief Introduction

Non-linear regression analysis

$$t50\text{.total}$$

[1] 6.355121

$$txp\text{.total}$$

10 60
4.956263 6.744599

$$t50\text{.Germinated}$$

[1] 6.034953

$$txp\text{.Germinated}$$

10 60
4.831806 6.287723

$$\text{Uniformity}$$

90 10 uniformity
7.537691 4.831806 2.705885

$$\text{TMGR}$$

[1] 5.912194

$$\text{AUC}$$

[1] 1108.976

$$\text{MGT}$$

[1] 6.632252

$$\text{Skewness}$$

[1] 1.098973

$$\text{msg}$$

[1] "#1. Relative error in the sum of squares is at most \texttt{ftol}'."

$$\text{isConv}$$

[1] TRUE

attr(,"class")

[1] "FourPHFfit"

## No test:

##D x <- c(0, 0, 0, 0, 4, 17, 10, 7, 1, 0, 1, 0, 0, 0)
##D y <- c(0, 0, 0, 0, 4, 21, 31, 38, 39, 39, 40, 40, 40, 40)
##D int <- 1:length(x)
##D total.seeds = 50
##D
##D # From partial germination counts
##D #----------------------------------------------------------------------------
##D fit1 <- FourPHFfit(germ.counts = x, intervals = int,
##D                   total.seeds = 50, tmax = 20)
##D
##D # From cumulative germination counts
##D #----------------------------------------------------------------------------
##D fit2 <- FourPHFfit(germ.counts = y, intervals = int,
Wrapper functions

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

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

```r
## No test:
##D data(gcdata)
##D
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)
## End(No test)
```

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

```r
## No test:
##D data(gcdata)
##D
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,
```
Citing germinationmetrics

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


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 Srinivasan}},
  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 use it, please support the project by citing the package.

Session Info

sessionInfo()

R Under development (unstable) (2020-05-06 r78376)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 18362)

Matrix products: default

locale:
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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] Rcpp_1.0.4.6 highr_0.8 plyr_1.8.6 compiler_4.1.0
[5] pillar_1.4.4 mathjaxr_1.0-0 bitops_1.0-6 tools_4.1.0
The germinationmetrics Package: A Brief Introduction

Session Info

```
[9] digest_0.6.25  lattice_0.20-41  nlm_3.1-147  evaluate_0.14
[13] lifecycle_0.2.0  tibble_3.0.1  gtable_0.3.0  pkgconfig_2.0.3
[17] rlang_0.4.6  bibtex_0.4.2.2  curl_4.3  ggrepel_0.8.2
[21] yaml_2.2.1  xfun_0.14  http_1.4.1  stringr_1.4.0
[25] dplyr_0.8.5  knitr_1.28  generics_0.0.2  vctrs_0.2.4
[29] gbRd_0.4-11  grid_4.1.0  tidyselect_1.1.0  glue_1.4.1
[33] data.table_1.12.8  R_6.2.4.1  Rdpack_0.11-2  XML_3.99-0.3
[37] minpack.lm_1.2-1  grid_4.1.0  tidyselect_1.1.0  glue_1.4.1
[41] ggplot2_3.3.1  purrr_0.3.4  magrittr_1.5  backports_1.1.7
[45] scales_1.1.1  ellipsis_0.3.1  htmltools_0.4.0  assertthat_0.2.1
[49] colorspace_1.4-1  stringi_1.4.6  RCurl_1.98-1.2  munsell_0.5.0
[53] broom_0.5.6  crayon_1.3.4
```

References


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Reddy, L. V. (1978). Effect of temperature on seed dormancy and alpha-amylase activity during kernel maturation and germination in wheat (*Triticum aestivum* L.) Cultivars. Available at: [https://ir.library. oregonstate.edu/concern/graduate_thesis_or_dissertations/1j92gb854](https://ir.library.oregonstate.edu/concern/graduate_thesis_or_dissertations/1j92gb854).


