Package ‘seedr’

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Type Package

Title Hydro and Thermal Time Seed Germination Models in R

Version 0.3.0

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Description Analysis of seed germination data
using the physiological time modelling approach. Includes functions
to fit hydrotime and thermal-time models with the traditional approaches
of Bradford (1990) <doi:10.1104/pp.94.2.840>
and Garcia-Huidobro (1982) <doi:10.1093/jxb/33.2.288>.
Allows to fit models to grouped datasets,
i.e. datasets containing multiple species, seedlots or experiments.

URL `https://github.com/efernandezpascual/seedr`

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Depends R (>= 4.0.0)

Imports data.table (>= 1.13), binom (>= 1.1), graphics, grDevices,
stats

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Contents

`bradford` *Fits Bradford's hydrotime model*

Description

`bradford` fits a hydrotime seed germination model using the method of Bradford (Gummerson 1986, Bradford 1990, Bewley et al. 2013). This function can be used only with one-group dataset, i.e. one seed lot of one species. To fit models to grouped datasets (multi-seedlots, multi-species) use the function `physiotime` instead.

Usage

```
bradford(d)
```

Arguments

`d`	a data.table within a "physiodata" object, containing the cumulative germination proportion at each scoring time and water potential treatment.

Value

`bradford` returns a S3 object of class "bradford" with the results of fitting the hydrotime model. The generic functions `summary` and `plot` are used to obtain and visualize the model results.

References

Bewley, J. D., Bradford, K. J., Hilhorst, H. W., & Nonogaki, H. (2013). Hydrotime Model of Germination. In Seeds: Physiology of Development, Germination and Dormancy, 3rd Edition (pp. 303-307). Springer, New York, NY.

Bradford, K. J. (1990). A water relations analysis of seed germination rates. Plant Physiology, 94(2), 840-849.

Gummerson, R. J. (1986). The effect of constant temperatures and osmotic potentials on the germination of sugar beet. Journal of Experimental Botany, 37(6), 729-741.

Examples

```
# format dataset with physiodata
anisantha <- physiodata(subset(grasses, species == "Anisantha rubens"), x = "psi")
# bradford() uses the $proportions element within the physiodata object
b <- bradford(anisantha$proportions)
b # prints the main hydrotime variables
summary(b) # returns the main hydrotime variables as a data.table
plot(b) # plots the fitted model
```

`centaury` *Temperature example dataset*

Description

This is a dataset containing information from a germination temperature experiment with centaury seeds. It is used to give examples of the functions dealing with thermal time germination models. It also gives and idea of the format in which germination data should be provided to seedr.

Usage

```
centaury
```

Format

A data frame with 896 rows and 7 variables

species	Name or code for the species to which the data refers
population	Name or code for the seedlot
temperature	Temperature treatment (in ºC) of the experiment
dish	Code for the Petri dish, container, replicate, etc.
times	Time of germination scoring since the start of the experiment, in days
germinated	Number of germinated seeds recorded at that time
germinable	Total number of viable seeds in the replicate

Source

Own data from a laboratory experiment.

`grasses` *Water potential example dataset*

Description

This is a dataset containing information from a water potential experiment with grass seeds. It is used to give examples of the functions dealing with hydrotime germination models. It also gives and idea of the format in which germination data should be provided to seedr.

Usage

```
grasses
```

Format

A data frame with 1605 rows and 7 variables

species Name or code for the species to which the data refers

temperature Temperature treatment (in ºC) of the experiment

psi Water potential treatment (in MPa) of the experiment

dish Code for the Petri dish, container, replicate, etc.

times Time of germination scoring since the start of the experiment, in days

germinated Number of germinated seeds recorded at that time

germinable Total number of viable seeds in the replicate

Source

Own data from a laboratory experiment.

`huidobro` *Fits Garcia-Huidobro's thermal time model*

Description

`huidobro` fits a thermal time seed germination model using the method of Garcia-Huidobro (Garcia-Huidobro et al. 1982, Gummerson 1986, Bewley et al. 2013). This function can be used only with one-group dataset, i.e. one seed lot of one species. To fit models to grouped datasets (multi-seedlots, multi-species) use the function `physiotime` instead.

Usage

```
huidobro(d, min.ptos = 3, tops = c("Max R2","Max value"), fractions =
  (1:9)/10)
```

Arguments

`d`	a data.table within a "physiodata" object, containing the cumulative germination proportion at each scoring time and temperature treatment.
`min.ptos`	minimal number of data points (i.e. different temperature treatments) needed to fit the suboptimal and supraoptimal germination models. If the number of points available in the dataset is less than `min.ptos`, then the suboptimal or the supraoptimal models are not fitted.
`tops`	method used to divide the dataset in suboptimal and supraoptimal sections. "Max value" splits the data by the temperature that produces the highest seed germination rate. "Max R2" splits the data by the temperature that maximises the R2 of the suboptimal and supraoptimal linear regressions.
`fractions`	percentiles into which the seed population is split to fit the thermal time model. The default is the 9 deciles (i.e. t10, t20.. t90) as used by Garcia-Huidobro.

Value

`huidobro` returns a S3 object of class "huidobro" with the results of fitting the thermal time model. The generic functions `summary` and `plot` are used to obtain and visualize the model results.

References

Bewley, J. D., Bradford, K. J., Hilhorst, H. W., & Nonogaki, H. (2013). Thermal Time Models. In Seeds: Physiology of Development, Germination and Dormancy, 3rd Edition (pp. 312-317). Springer, New York, NY. Bradford, K. J. (1990). A water relations analysis of seed germination rates. Plant Physiology, 94(2), 840-849.

Garcia-Huidobro, J., Monteith, J. L., & Squire, G. R. (1982). Time, temperature and germination of pearl millet (Pennisetum typhoides S. & H.) I. Constant temperature. Journal of Experimental Botany, 33(2), 288-296.

Gummerson, R. J. (1986). The effect of constant temperatures and osmotic potentials on the germination of sugar beet. Journal of Experimental Botany, 37(6), 729-741.

Examples

```
# format dataset with physiodata
malva <- physiodata(subset(centaury, population == "La Malva"), x = "temperature")
# huidobro() uses the $proportions element within the physiodata object
h <- huidobro(malva$proportions)
h # prints the main thermal time variables
summary(h) # returns the main thermal time variables as a data.table
plot(h) # plots the fitted model
```

`physiodata` *Transforms dataset to physiodata format*

Description

`physiodata` takes the user's dataset and transforms it to an object of class "physiodata". This object will be used by the model-fitting functions, and it can also be used to explore the data.

Usage

```
physiodata(d, t = "times", g = "germinated", pg = "germinable", x =
  "treatment", groups = NULL)
```

Arguments

`d`	a data.frame containing the results of a germination experiment. The data frame should include columns with scoring times, germination counts (not cumulative), number of potentially germinable seeds, and the environmental variable of interest. (e.g. temperature or water potential) (see `grasses` example dataset for appropriate structure).
`t`	the name of a column in `d` containing a vector of numeric scoring times.
`g`	the name of a column in `d` containing a vector of integer germination counts (non cumulative).
`pg`	the name of a column in `d` containing a vector of integer numbers of potentially germinable seeds.
`x`	the name of a column in `d` containing a vector of numeric values for the environmental variable of interest (e.g. temperature, water potential).
`groups`	optional, the names of columns in `d` containing grouping variables for the experiment that have to be analysed separately (e.g. different species or populations, different temperatures in a water potential experiment, different treatments to break seed dormancy).

Value

`physiodata` returns a S3 object of class "physiodata". The object is a list containing, for each group, treatment and scoring time: the cumulative germination count; the cumulative germination proportion; and the lower and upper bounds of the 95 calculated with the Wilson method as implemented in the package `binom`. The object can be used to explore the data using the generic functions `summary`, `barplot` and `plot`.

Examples

```
cent <- physiodata(centaury, x = "temperature")
cent
summary(cent) # average final germination proportions and germination rates per treatment
barplot(cent) # bar plots for the final germination proportions and germination rates
```

```
plot(cent) # cumulative germination curves
physiodata(grasses, x = "psi", groups = "species") # grouping dataset by species
```

`physiotime` *Fits physiological time seed germination models*

Description

`physiotime` fits physiological time models (thermal time, hydrotime) to seed germination data. It is a wrapper function that transforms data to class "physiodata" and allows to specify the physiological time model to be fitted (i.e. Bradford's hydrotime model or Garcia-Huidobro's thermal time model).

Usage

```
physiotime(d, t = "times", g = "germinated", pg = "germinable", x =
  "treatment", groups = NULL, method = "bradford", min.ptos = 3, tops =
  c("Max R2","Max value"), fractions = (1:9)/10)
```

Arguments

`d`	a data.frame containing the results of a germination experiment. The data frame should include columns with scoring times, germination counts (not cumulative), number of potentially germinable seeds, and the environmental variable of interest. (e.g. temperature or water potential) (see `grasses` example dataset for appropriate structure).
`t`	the name of a column in `d` containing a vector of numeric scoring times.
`g`	the name of a column in `d` containing a vector of integer germination counts (non cumulative).
`pg`	the name of a column in `d` containing a vector of integer numbers of potentially germinable seeds.
`x`	the name of a column in `d` containing a vector of numeric values for the environmental variable of interest (e.g. temperature, water potential).
`groups`	optional, the names of columns in `d` containing grouping variables for the experiment that have to be analysed separately (e.g. different species or populations, different temperatures in a water potential experiment, different treatments to break seed dormancy).
`method`	the method to be used to fit the models, can be "bradford" to fit a hydrotime model or "huidobro" to fit a thermal time model.
`min.ptos`	minimal number of data points (i.e. different temperature treatments) needed to fit the suboptimal and supraoptimal germination models if fitting a thermal time model. If the number of points available in the dataset is less than `min.ptos`, then the suboptimal or the supraoptimal models are not fitted.

`tops`	method used to divide the dataset in suboptimal and supraoptimal sections if fitting a thermal time model. "Max value" splits the data by the temperature that produces the highest seed germination rate. "Max R2" splits the data by the temperature that maximises the R2 of the suboptimal and supraoptimal linear regressions.
`fractions`	percentiles into which the seed population is split if fitting a thermal time model. The default is the 9 deciles (i.e. t10, t20.. t90) as used by Garcia-Huidobro.

Value

`physiotime` returns a S3 object of class "physiotime". The object is a list containing, for each group (seedlot, species, etc.) the results of fitting the physiological time models. The generic functions `summary` and `plot` are used to obtain and visualize the model results.

Examples

```
m <- physiotime(centaury, x = "temperature",
                method = "huidobro", groups = c("species", "population"))
m
summary(m)
plot(m)
```

`seedr` *seedr: Hydro and Thermal Time Seed Germination Models in R*

Description

The `seedr` package provides functions to fit hydro and thermal time germination models. These models characterize seed lots by two sets of parameters: (i) the physiological thresholds (water, temperature) between which the seed lot can germinate, and (ii) the physiological-time units that the seed lot needs to accumulate before it can germinate. `seedr` allows to fit the hydro time model of Bradford (Gummerson 1986, Bradford 1990, Bewley et al. 2013) and the thermal time model of Garcia-Huidobro (Garcia-Huidobro et al. 1982, Gummerson 1986, Bewley et al. 2013). `seedr` also allows to quickly fit models to multi-seedlot or multi-species datasets.

References

Bewley, J. D., Bradford, K. J., Hilhorst, H. W., & Nonogaki, H. (2013). Environmental Control of Germination. In Seeds: Physiology of Development, Germination and Dormancy, 3rd Edition (pp. 302-317). Springer, New York, NY.

Bradford, K. J. (1990). A water relations analysis of seed germination rates. Plant Physiology, 94(2), 840-849.

Garcia-Huidobro, J., Monteith, J. L., & Squire, G. R. (1982). Time, temperature and germination of pearl millet (Pennisetum typhoides S. & H.) I. Constant temperature. Journal of Experimental Botany, 33(2), 288-296.

Gummerson, R. J. (1986). The effect of constant temperatures and osmotic potentials on the germination of sugar beet. Journal of Experimental Botany, 37(6), 729-741.

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