Package 'plantecowrap'

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Type Package

Title Enhancing Capabilities of 'plantecophys'

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Description Provides wrapping functions to add to capabilities to 'plantecophys' (Duursma, 2015, <doi:10.1371/journal.pone.0143346>). Key added capabilities include temperature responses of mesophyll conductance (gm, gmeso), apparent Michaelis-Menten constant for rubisco carboxylation in air (Km, Kcair),and photorespiratory CO2 compensation point (GammaStar) for fitting A-Ci or A-Cc curves for C3 plants (for temperature responses of gm, Km, & GammaStar, see Bernacchi et al., 2002, <doi:10.1104/pp.008250>; for theory on fitting A-Ci or A-Cc curves, see Farquhar et al., 1980; <doi:10.1007/BF00386231>, von Caemmerer, 2000, ISBN:064306379X; Ethier & Livingston, 2004 <doi:10.1111/j.1365-3040.2004.01140.x>; and Gu et al., 2010, <doi:10.1111/j.1365-3040.2010.02192.x>). Includes the ability to fit the Arrhenius and modified Arrhenius temperature response functions (see Medlyn et al., 2002, <doi:10.1046/j.1365-3040.2002.00891.x>) for maximum rubisco carboxylation rates (Vcmax) and maximum electron transport rates (Jmax) (see Farquhar et al., 1980; <doi:10.1007/BF00386231>).

URL https://github.com/jstinzi/plantecowrap

BugReports https://github.com/jstinzi/plantecowrap/issues

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Depends R (>= 3.5.0), ggplot2 (>= 3.2.1), minpack.lm (>= 1.2-1), plantecophys (>= 1.4-4), tidyr (>= 1.0.0)

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

`acisummary` *Extracts coefficients from fitacis2*

Description

Extracts coefficients from fitacis2

Usage

```
acisummary(data, group1, group2 = NA, group3 = NA, fits)
```

Arguments

`data`	data frame with A/Ci curve data
`group1`	grouping variable 1, must match fitacis2
`group2`	grouping variable 2, must match fitacis2
`group3`	grouping variable 3, must match fitacis2
`fits`	list output from fitacis2

Value

acisummary produces a data frame with A-Ci coefficients. If the input data have failed curve fits, these need to be removed before running acisummary().

Examples

```
#Read in data
data <- read.csv(system.file("extdata", "example_2.csv",
package = "plantecowrap"), stringsAsFactors = FALSE)
#Run ACi curve fitting
fits <- fitacis2(data, group1 = "Grouping",
varnames = list(ALEAF = "A",
                Tleaf = "Tleaf",
                Ci = "Ci",
                PPFD = "PPFD",
                Rd = "Rd",
                Press = "Press"),
fitmethod = "bilinear", fitTPU = TRUE, Tcorrect = FALSE)
#Extract coefficients
outputs <- acisummary(data, group1 = "Grouping", fits = fits)
```

---

arrhenius *The Arrhenius temperature response equation*

Description

The Arrhenius temperature response equation

Usage

```
arrhenius(Ea, Tleaf)
```

Arguments

Ea	activation energy in kJ mol-1
Tleaf	leaf temperature in Celsius

Value

arrhenius is an exponential temperature response model. This function automatically converts temperature from Celsius to Kelvin for the calculation. REFERENCE Arrhenius S. 1915. Quantitative laws in biological chemistry. Bell.

`fitacis2` *Fit A-Ci curves with custom kinetics*

Description

Fit A-Ci curves with custom kinetics

Usage

```
fitacis2(
  data,
  group1,
  group2 = NA,
  group3 = NA,
  gm25 = 0.08701,
  Egm = 47.65,
  K25 = 718.4,
  Ek = 65.50828,
  Gstar25 = 42.75,
  Egamma = 37.83,
  fitmethod = "default",
  fitTPU = TRUE,
  Tcorrect = FALSE,
  useRd = FALSE,
  citransition = NULL,
  alphag = 0,
  PPFD = NULL,
  Tleaf = NULL,
  alpha = 0.24,
  theta = 0.85,
 varnames = list(ALEAF = "Photo", Tleaf = "Tleaf", Ci = "Ci", PPFD = "PARi", Rd = "Rd",
    Press = "Press"),
  ...
)
```

Arguments

`data`	data frame with A/Ci curves. Requires net CO2 assimilation (Anet/Photo/ALEAF in umol m-2 s-1), leaf temperature (Tleaf in Celsius), intercellular CO2 concentration (Ci, in umol mol-1), incident irradiance on the leaf (PPFD/PARi in umol m-2 s-1), atmospheric pressure (Patm/Press in kPa), and (optional, set useRd = TRUE for this option) respiration (Rd, in umol m-2 s-1).
`group1`	grouping variable 1, could be species, temperature, ID
`group2`	grouping variable 2
`group3`	grouping variable 3
`gm25`	mesophyll conductance at 25 Celsius in mol m-2 s-1 bar-1

Egm	activation energy of mesophyll conductance in kJ mol-1
K25	Km in 21 in umol mol-1 (equivalent to ubar bar-1)
Ek	activation energy of Kcair in kJ mol-1
Gstar25	photorespiratory CO2 compensation point at 25 Celsius in umol mol-1 (equivalent to ubar bar-1)
Egamma	activation energy of GammaStar in kJ mol-1
fitmethod	Set to either "bilinear" or "default". Default option in this package is "default". See ?fitaci in plantecophys for more details.
fitTPU	Should TPU limitations be fit? Set to TRUE/FALSE. See ?fitaci in plantecophys for more details.
Tcorrect	Should outputs be temperature corrected? Default here is FALSE. See ?fitaci in plantecophys for more details.
useRd	Should respiration be used? Default is FALSE. See ?fitaci in plantecophys for more details.
citransition	Pre-specify Ci transition point? Units in umol mol-1 (ubar bar-1) Default is FALSE. See ?fitaci in plantecophys for more details.
alphag	Fraction of photorespiratory glycolate carbon that is not returned to the chloroplast (von Caemmerer, 2000). If ACi curves show high-CO2 decline, then this value should be > 0. See ?fitaci in plantecophys for more details.
PPFD	Light intensity? Can be retrieved from dataframe. Default is NULL. Units are umol m-2 s-1. See ?fitaci in plantecophys for more details.
Tleaf	Leaf temperature? Can be retrieved from dataframe. Default is NULL. Units are Celsius. See ?fitaci in plantecophys for more details.
alpha	Quantum yield of CO2 assimilation. Default is 0.24. Units are umol CO2 fixed / umol incident photons. See ?fitaci in plantecophys for more details.
theta	Curvature of the photosynthetic light response. Default is 0.85. If light response has sharper transition, increase up to 1. If light response has shallower curves, decrease towards 0. See ?fitaci in plantecophys for more details.
varnames	Variable names in your dataframe. ALEAF is net CO2 assimilation in umol m-2 s-1, Tleaf is leaf temperature in Celsius, Ci is intercellular CO2 concentration in umol mol-1, PPFD is light intensity in umol m-2 s-1, Rd is respiration rate in umol m-2 s-1, and Press is atmospheric pressure in kPa. See ?fitaci in plantecophys for more details.
...	Further arguments for plantecophys::fitaci(). See ?fitaci for details.

Value

fitacis2 allows gmeso, GammaStar, and Km to vary with Tleaf. Output matches the fitacis function from plantecophys. Note that the temperature response function of Km is derived from the temperature responses of Ko and Kc in Bernacchi et al.2001, as is the GammaStar temperature response defaults. The gm defaults are from Bernacchi et al. 2002 fitted between 1and 35 Celsius. Also note that this ALWAYS uses gm. To fit data on a "Ci-basis", set gm25 really high (e.g. 10000 mol m-2 s-1 bar-1) and Egm to 0 kJ mol-1.

In some instances (e.g. very low stomatal conductance), fitacis2 will fail. In these cases, the output for that curve will be "Failed", rather than an A-Ci curve fit object.

REFERENCES Bernacchi CJ, Singsaas EL, Pimentel C, Portis AR, Long SP. 2001. Improved temperature response functions for models of rubisco-limited photosynthesis. Plant Cell Environment 24:253-259. Bernacchi CJ, Portis AR, Nakano H, von Caemmerer S, Long SP. 2002. Temperature response of mesophyll conductance. Implications for the determination of rubisco enzyme kinetics and for limitations to photosynthesis in vivo. Plant Physiology 130:1992-1998. von Caemmerer S. 2000. Biochemical models of leaf photosynthesis. CSIRO Publishing, Collingwood.

Examples

```
#Read in data
data <- read.csv(system.file("extdata", "example_2.csv",
package = "plantecowrap"), stringsAsFactors = FALSE)
#Run ACi curve fitting
fits <- fitacis2(data, group1 = "Grouping",
varnames = list(ALEAF = "A",
                Tleaf = "Tleaf",
                Ci = "Ci",
                PPFD = "PPFD",
                Rd = "Rd",
                Press = "Press"),
fitmethod = "bilinear", fitTPU = TRUE, Tcorrect = FALSE)
```

---

fit_topt_VJ *Fitting the temperature responses of Vcmax and Jmax*

Description

Fitting the temperature responses of Vcmax and Jmax

Usage

```
fit_topt_VJ(
  data,
  varnames = list(Vcmax = "Vcmax", Jmax = "Jmax", Tleaf = "Tleaf"),
  title = NULL,
  limit_jmax = 1e+05,
  limit_vcmax = 1e+05,
  ...
)
```

Arguments

data	Dataframe containing Vcmax (maximum rubisco carboxylation capacity in umol m-2 s-1), Jmax (maximum photosynthetic electron transport to CO2 fixation in umol m-2 s-1), and Tleaf (leaf temperature in Celsius)
varnames	Variable names to account for different spellings of Vcmax, Jmax, and Tleaf.
title	Graph title, usually a group name
limit_jmax	Upper limit to Jmax values for fitting. Defaults to 100,000 umol m-2 s-1 as this is the "nonsense output" from fitaci. Ensures that these points are not fit.
limit_vcmax	Upper limit to Vcmax values for fitting. Defaults to 100,000 umol m-2 s-1.
...	Arguments to be passed on to minpack.lm::nlsLM(). See ?nlsLM for details.

Value

fit_topt_VJ fits the Topt modified Arrhenius function to Vcmax and Jmax data. Note that Hd may max out at 3000 kJ mol-1 for Jmax and 2000 kJ mol-1 for Vcmax. REFERENCE Medlyn BE, Dreyer E, Ellsworth D, Forstreuter M, Harley PC, Kirschbaum MUF, Le Roux X, Montpied P, Strassemeyer J, Walcroft A, Wang K, Loutstau D. 2002. Temperature response of parameters of a biochemically based model of photosynthesis. II. A review of experimental data. Plant Cell Environ 25:1167-1179

Examples

```
#Read in data
data <- read.csv(system.file("extdata", "example_1.csv",
package = "plantecowrap"), stringsAsFactors = FALSE)
#Fit ACi Curves then fit temperature responses
fits <- fitacis2(data = data,
                 varnames = list(ALEAF = "A",
                                 Tleaf = "Tleaf",
                                 Ci = "Ci",
                                 PPFD = "PPFD",
                                 Rd = "Rd",
                                 Press = "Press"),
                 group1 = "Treat",
                 fitTPU = FALSE,
                 fitmethod = "bilinear",
                 gm25 = 10000,
                 Egm = 0)
#Extract coefficients
outputs <- acisummary(data, group1 = "Treat", fits = fits)
#Fit temperature response
tresp <- fit_topt_VJ(outputs)
#View plot
tresp[[3]]
```

`fit_topt_VJs` *Fitting multiple temperature response curves*

Description

Fitting multiple temperature response curves

Usage

```
fit_topt_VJs(
  data,
  group,
  varnames = list(Vcmax = "Vcmax", Jmax = "Jmax", Tleaf = "Tleaf"),
  limit_jmax = 1e+05,
  limit_vcmax = 1e+05,
  ...
)
```

Arguments

`data`	Dataframe with multiple temperature response curves for Vcmax (maximum rubisco carboxylation capacity in umol m-2 s-1) and Jmax (maximum photosynthetic electron transport to CO2 fixation in umol m-2 s-1).
`group`	Grouping variable to use, e.g. Plant ID
`varnames`	Variable names. Reassigns variable names to account for different spellings of Vcmax, Jmax, and Tleaf
`limit_jmax`	Upper limit to Jmax values for fitting. Defaults to 100,000 umol m-2 s-1 as this is the "nonsense output" from fitaci. Ensures that these points are not fit.
`limit_vcmax`	Upper limit to Vcmax values for fitting. Defaults to 100,000 umol m-2 s-1.
`...`	Arguments to be passed on to minpack.lm::nlsLM via fit_topt_VJ(). See ?nlsLM for details.

Value

fit_topt_VJs fits multiple Vcmax and Jmax temperature responses using the optimum temperature response model from Medlyn et al. 2002. REFERENCE Medlyn BE, Dreyer E, Ellsworth D, Forstreuter M, Harley PC, Kirschbaum MUF, Le Roux X, Montpied P, Strassemeyer J, Walcroft A, Wang K, Loutstau D. 2002. Temperature response of parameters of a biochemically based model of photosynthesis. II. A review of experimental data. Plant Cell Environ 25:1167-1179

Examples

```
#Read in data
data <- read.csv(system.file("extdata", "example_2.csv",
package = "plantecowrap"), stringsAsFactors = FALSE)
```

```
#Fit ACi Curves then fit temperature responses
fits <- fitacis2(data = data,
                 varnames = list(ALEAF = "A",
                                 Tleaf = "Tleaf",
                                 Ci = "Ci",
                                 PPFD = "PPFD",
                                 Rd = "Rd",
                                 Press = "Press"),
                 group1 = "Grouping",
                 fitTPU = FALSE,
                 fitmethod = "bilinear",
                 gm25 = 10000,
                 Egm = 0)
#Extract coefficients
outputs <- acisummary(data, group1 = "Grouping", fits = fits)
#Plot curve fits
for (i in 1:length(fits)) {
  plot(fits[[i]])
}
#Separate out grouping variable
outputs <- separate(outputs, col = "ID", c("Treat", "Block"), sep = "_")
#Fit the Topt model from Medlyn et al. 2002 for all individuals
#Output is a list of lists for each individual
#There is also a fit_topt_VJ for single temperature response
#fitting
out <- fit_topt_VJs(data = outputs,
                    group = "Block", #this grouping variable is for
                    #each individual
                    varnames = list(Vcmax = "Vcmax",
                                    Jmax = "Jmax",
                                    Tleaf = "Tleaf"),
                    limit_jmax = 100000,
                    limit_vcmax = 100000)
#Let's get the parameters out into a single data frame
pars <- get_t_pars(out)
#Let's get the graphs out into a list
#You can get a graph using: graph[1]
graphs <- get_t_graphs(out)
```

`get_t_graphs` *Get temperature response graphs*

Description

Get temperature response graphs

Usage

```
get_t_graphs(data)
```

Arguments

data	List of data output from fit_topt_VJs

Value

get_t_graphs returns temperature response graphs for Vcmax and Jmax from the group fitting process. Output is a list of graphs.

Examples

```
#Read in data
data <- read.csv(system.file("extdata", "example_2.csv",
package = "plantecowrap"), stringsAsFactors = FALSE)
#Fit ACi Curves then fit temperature responses
fits <- fitacis2(data = data,
                 varnames = list(ALEAF = "A",
                                 Tleaf = "Tleaf",
                                 Ci = "Ci",
                                 PPFD = "PPFD",
                                 Rd = "Rd",
                                 Press = "Press"),
                 group1 = "Grouping",
                 fitTPU = FALSE,
                 fitmethod = "bilinear",
                 gm25 = 10000,
                 Egm = 0)
#Extract coefficients
outputs <- acisummary(data, group1 = "Grouping", fits = fits)
#Plot curve fits
for (i in 1:length(fits)) {
  plot(fits[[i]])
}
#Separate out grouping variable
outputs <- separate(outputs, col = "ID", c("Treat", "Block"), sep = "_")
#Fit the Topt model from Medlyn et al. 2002 for all individuals
#Output is a list of lists for each individual
#There is also a fit_topt_VJ for single temperature response
#fitting
out <- fit_topt_VJs(data = outputs,
                    group = "Block", #this grouping variable is for
                    #each individual
                    varnames = list(Vcmax = "Vcmax",
                                    Jmax = "Jmax",
                                    Tleaf = "Tleaf"),
                    limit_jmax = 100000,
                    limit_vcmax = 100000)
#Let's get the graphs out into a list
#You can get a graph using: graph[1]
graphs <- get_t_graphs(out)
```

get_t_pars *Get temperature response parameters*

Description

Get temperature response parameters

Usage

```
get_t_pars(data)
```

Arguments

data	List of data output from fit_topt_VJs

Value

get_t_pars returns temperature response parameters for Vcmax and Jmax from the group fitting process. Output is a dataframe.

Examples

```
#Read in data
data <- read.csv(system.file("extdata", "example_2.csv",
package = "plantecowrap"), stringsAsFactors = FALSE)
#Fit ACi Curves then fit temperature responses
fits <- fitacis2(data = data,
                 varnames = list(ALEAF = "A",
                                 Tleaf = "Tleaf",
                                 Ci = "Ci",
                                 PPFD = "PPFD",
                                 Rd = "Rd",
                                 Press = "Press"),
                 group1 = "Grouping",
                 fitTPU = FALSE,
                 fitmethod = "bilinear",
                 gm25 = 10000,
                 Egm = 0)
#Extract coefficients
outputs <- acisummary(data, group1 = "Grouping", fits = fits)
#Plot curve fits
for (i in 1:length(fits)) {
  plot(fits[[i]])
}
#Separate out grouping variable
outputs <- separate(outputs, col = "ID", c("Treat", "Block"), sep = "_")
#Fit the Topt model from Medlyn et al. 2002 for all individuals
#Output is a list of lists for each individual
#There is also a fit_topt_VJ for single temperature response
```

```
#fitting
out <- fit_topt_VJs(data = outputs,
                    group = "Block", #this grouping variable is for
                    #each individual
                    varnames = list(Vcmax = "Vcmax",
                                    Jmax = "Jmax",
                                    Tleaf = "Tleaf"),
                    limit_jmax = 100000,
                    limit_vcmax = 100000)
#Let's get the parameters out into a single data frame
pars <- get_t_pars(out)
```

`modarrhenius` *Fitting the peaked Arrhenius temperature response model*

Description

Fitting the peaked Arrhenius temperature response model

Usage

```
modarrhenius(Ea, Hd, dS, Tleaf)
```

Arguments

`Ea`	activation energy in kJ mol-1
`Hd`	deactivation energy in kJ mol-1
`dS`	entropy of deactivation in kJ mol-1
`Tleaf`	leaf temperature in Celsius

Value

modarrhenius is used to fit a peaked Arrhenius model. REFERENCE Medlyn BE, Dreyer E, Ellsworth D, Forstreuter M, Harley PC, Kirschbaum MUF, Le Roux X, Montpied P, Strassemeyer J, Walcroft A, Wang K, Loutstau D. 2002. Temperature response of parameters of a biochemically based model of photosynthesis. II. A review of experimental data. Plant Cell Environ 25:1167-1179

print_graphs *Printing graphs from a list of graphs*

Description

Printing graphs from a list of graphs

Usage

```
print_graphs(data, path, height = 5, width = 5, res = 600, units = "in", ...)
```

Arguments

data	List of graphs to output as .jpeg files
path	File path for printing out graphs. Use "./" to set to current working directory.
height	Height of output graphs. Defaults to 5.
width	Width of output graphs. Defaults to 5.
res	Resolution of output graphs. Defaults to 600.
units	Units of height and width. Defaults to "in".
...	Further arguments, specifically for jpeg().

Value

print_graphs creates jpeg files from a list of graphs based on the graph names. Used in combination with get_t_graphs. Output is a series of .jpeg files in the working directory.

Examples

```
#Read in data
data <- read.csv(system.file("extdata", "example_2.csv",
package = "plantecowrap"), stringsAsFactors = FALSE)
#Fit ACi Curves then fit temperature responses
fits <- fitacis2(data = data,
                 varnames = list(ALEAF = "A",
                                 Tleaf = "Tleaf",
                                 Ci = "Ci",
                                 PPFD = "PPFD",
                                 Rd = "Rd",
                                 Press = "Press"),
                 group1 = "Grouping",
                 fitTPU = FALSE,
                 fitmethod = "bilinear",
                 gm25 = 10000,
                 Egm = 0)
#Extract coefficients
outputs <- acisummary(data, group1 = "Grouping", fits = fits)
```

```
#Plot curve fits
for (i in 1:length(fits)) {
  plot(fits[[i]])
}
#Separate out grouping variable
outputs <- separate(outputs, col = "ID", c("Treat", "Block"), sep = "_")
#Fit the Topt model from Medlyn et al. 2002 for all individuals
#Output is a list of lists for each individual
#There is also a fit_topt_VJ for single temperature response
#fitting
out <- fit_topt_VJs(data = outputs,
                    group = "Block", #this grouping variable is for
                    #each individual
                    varnames = list(Vcmax = "Vcmax",
                                    Jmax = "Jmax",
                                    Tleaf = "Tleaf"),
                    limit_jmax = 100000,
                    limit_vcmax = 100000)
#Let's get the graphs out into a list
#You can get a graph using: graph[1]
graphs <- get_t_graphs(out)
#Print graphs out as jpegs into folder
print_graphs(graphs, path = tempdir())
```

`toptfit` *Fitting the Topt temperature response model*

Description

Fitting the Topt temperature response model

Usage

```
toptfit(Ea, Hd, kopt, Tleaf, Topt)
```

Arguments

`Ea`	activation energy in kJ mol-1
`Hd`	deactivation energy in kJ mol-1
`kopt`	parameter value at optimum temperature
`Tleaf`	leaf temperature in Celsius
`Topt`	optimum leaf temperature in Celsius

Value

toptfit is the Topt temperature response model. REFERENCE Medlyn BE, Dreyer E, Ellsworth D, Forstreuter M, Harley PC, Kirschbaum MUF, Le Roux X, Montpied P, Strassemeyer J, Walcroft A, Wang K, Loutstau D. 2002. Temperature response of parameters of a biochemically based model of photosynthesis. II. A review of experimental data. Plant Cell Environ 25:1167-1179

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