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
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().
arrhenius

Examples

```r
# 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.


```r
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

**Description**

Fit A-Ci curves with custom kinetics

**Usage**

```r
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"),  
  ...  
)
```
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.


Examples

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

#Run ACi curve fitting
```

Description

Fitting the temperature responses of Vcmax and Jmax

Usage

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

---

fit_topt_VJ  Fitting the temperature responses of Vcmax and Jmax

---

Description

Fitting the temperature responses of Vcmax and Jmax

Usage

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

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


Examples

```r
# 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


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
                     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)
get_t_graphs

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

###Fit ACi Curves then fit temperature responses
```r
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
```r
outputs <- acisummary(data, group1 = "Grouping", fits = fits)
```

###Plot curve fits
```r
for (i in 1:length(fits)) {
    plot(fits[[i]])
}
```

###Separate out grouping variable
```r
outputs <- separate(outputs, col = "ID", c("Treat", "Block"), sep = ".")
```

###Fit the Topt model from Medlyn et al. 2002 for all individuals
```r
#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
```r
#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

```r
get_t_pars(data)
```

Arguments

- **data**: List of data output from `fit_topt_VJs`

Value

`get_t_pars` returns temperature response parameters for \( V_{cmax} \) and \( J_{max} \) from the group fitting process. Output is a dataframe.

Examples

```r
# 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
```
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

Description

Printing graphs from a list of graphs

Usage

```r
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

```r
# 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())
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