Package ‘plantecowrap’

Type Package
Title Enhancing Capabilities of ‘plantecophys’
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Version 1.0.4
Maintainer Joseph Stinziano <josephstinziano@gmail.com>
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**

```r
cisisummary(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

The Arrhenius temperature response equation

#### Description

The Arrhenius temperature response equation

#### Usage

```r
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.

### 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)
```
fitacis2  

*Fit A-Ci curves with custom kinetics*

**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"),  
  ...  
)
```

**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
<table>
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<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Egm</td>
<td>activation energy of mesophyll conductance in kJ mol⁻¹</td>
</tr>
<tr>
<td>K25</td>
<td>Km in 21 in umol mol⁻¹ (equivalent to ubar bar⁻¹)</td>
</tr>
<tr>
<td>Ek</td>
<td>activation energy of Kcair in kJ mol⁻¹</td>
</tr>
<tr>
<td>Gstar25</td>
<td>photosynthetic CO₂ compensation point at 25 Celsius in umol mol⁻¹ (equivalent to ubar bar⁻¹)</td>
</tr>
<tr>
<td>Egamma</td>
<td>activation energy of GammaStar in kJ mol⁻¹</td>
</tr>
<tr>
<td>fitmethod</td>
<td>Set to either &quot;bilinear&quot; or &quot;default&quot;. Default option in this package is &quot;default&quot;. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>fitTPU</td>
<td>Should TPU limitations be fit? Set to TRUE/FALSE. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>Tcorrect</td>
<td>Should outputs be temperature corrected? Default here is FALSE. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>useRd</td>
<td>Should respiration be used? Default is FALSE. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>citransition</td>
<td>Pre-specify Ci transition point? Units in umol mol⁻¹ (ubar bar⁻¹) Default is FALSE. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>alphag</td>
<td>Fraction of photosynthetic glycolate carbon that is not returned to the chloroplast (von Caemmerer, 2000). If ACi curves show high-CO₂ decline, then this value should be &gt; 0. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>PPFD</td>
<td>Light intensity? Can be retrieved from dataframe. Default is NULL. Units are umol m⁻² s⁻¹. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>Tleaf</td>
<td>Leaf temperature? Can be retrieved from dataframe. Default is NULL. Units are Celsius. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>alpha</td>
<td>Quantum yield of CO₂ assimilation. Default is 0.24. Units are umol CO₂ fixed / umol incident photons. See ?fitaci in plantecophys for more details.</td>
</tr>
<tr>
<td>theta</td>
<td>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.</td>
</tr>
<tr>
<td>varnames</td>
<td>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.</td>
</tr>
</tbody>
</table>

**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 1 and 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 Ac-I 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**

```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

#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

```r
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

```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 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[i]
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, 
  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

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",
                  fitTPIU = 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
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_vmax = 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())

---

toxtfit

Fitting the Topt temperature response model

Description

Fitting the Topt temperature response model

Usage

toxtfit(Ea, Hd, kopt, Tleaf, Topt)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ea</td>
<td>activation energy in kJ mol-1</td>
</tr>
<tr>
<td>Hd</td>
<td>deactivation energy in kJ mol-1</td>
</tr>
<tr>
<td>kopt</td>
<td>parameter value at optimum temperature</td>
</tr>
<tr>
<td>Tleaf</td>
<td>leaf temperature in Celsius</td>
</tr>
<tr>
<td>Topt</td>
<td>optimum leaf temperature in Celsius</td>
</tr>
</tbody>
</table>

Value

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