Package 'racir'

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Type Package

Title Rapid A/Ci Response (RACiR) Data Analysis

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Description Contains functions useful for reading in Licor 6800 files, correcting and analyzing rapid A/Ci response (RACiR) data. Requires some user interaction to adjust the calibration (empty chamber) data file to a useable range. Calibration uses a 1st to 5th order polynomial as suggested in Stinziano et al. (2017) <doi:10.1111/pce.12911>. Data can be processed individually or batch processed for all files paired with a given calibration file. RACiR is a trademark of LI-COR Biosciences, and used with permission.

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

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

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Depends R (>= 4.0.0)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Imports utils, stats, graphics

NeedsCompilation no

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R topics documented:

`racircal` *Corrects rapid A/Ci response (RACiR) data from leaves using empty chamber data.*

Description

`racircal` Corrects your RACiR data based on calibration data. Produces corrected A vs. Ci graph. Output is a data frame with corrected RACiR data using variable names Acor and Cicor for the corrected A and Ci values.

Usage

```
racircal(
  data,
  caldata,
  mincut,
  maxcut,
  title,
  varnames = list(A = "A", Ca = "Ca", CO2_r = "CO2_r", E = "E", gtc = "gtc")
)
```

Arguments

`data`	Data frame with the RACiR response data
`caldata`	Data frame with the calibration data
`mincut`	Minimum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the initial chamber mixing. Default value is set to the minimum COR_r value.
`maxcut`	Maximum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the end of the response. Not needed in all cases. Default value is set to the maximum COR_r value.
`title`	Title of output graph - useful for batch RACiR corrections.
`varnames`	Variable names - this allows for the use of this code with other machines and setups where variable names may differ.

Value

racircal returns a data frame with corrected RACiR data

Examples

```
#Read in data
data <- read_6800(system.file("extdata", "poplar_2", package = "racir"))
caldata <- read_6800(system.file("extdata", "cal", package = "racir"))
#Correct data
data_corrected <- racircal(data = data, caldata = caldata,
                           mincut = 350, maxcut = 780, title = "Test")
```

---

racircalbatch *Corrects a batch of rapid A/Ci response (RACiR) data*

Description

racircalbatch Corrects your RACiR data files based on a calibration file. Produces diagnostic graphs of A vs. Ci for quality control. Output includes a list of data frames with corrected data.

Usage

```
racircalbatch(
  caldata,
  data,
  mincut,
  maxcut,
  title,
  varnames = list(A = "A", Ca = "Ca", CO2_r = "CO2_r", E = "E", gtc = "gtc")
)
```

Arguments

caldata	Data frame with the calibration data
data	List of data frames with the RACiR response data
mincut	Minimum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the initial chamber mixing. Default value is set to the minimum COR_r value.
maxcut	Maximum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the end of the response. Not needed in all cases. Default value is set to the maximum COR_r value.
title	Vector for titles of output graph - useful for batch RACiR corrections. Length must be equal to data list length
varnames	Variable names - this allows for the use of this code with other machines and setups where variable names may differ.

Value

racircalbatch calibrates a batch of RACiR data

Examples

```
#Create a list of files
files <- c(system.file("extdata", "poplar_1", package = "racir"),
          system.file("extdata", "poplar_2", package = "racir"))
data <- vector("list", length(files))
for(i in seq_along(files)){
 data[[i]] <- read_6800(files[i])
 names(data)[i] <- files[i]
}

caldata <- read_6800(system.file("extdata", "cal", package = "racir"))
output <- racircalbatch(caldata = caldata, data = data,
                        mincut = 300, maxcut = 780, title = files)
```

---

racircalbatch_advanced

Corrects a batch of rapid A/Ci response (RACiR) data

Description

racircalbatch_advanced Corrects your RACiR data files based on a calibration file. Produces diagnostic graphs of A vs. Ci for quality control. Output includes a list of data frames with corrected data.

Usage

```
racircalbatch_advanced(
  caldata,
  data,
  mincut,
  maxcut,
  digits,
  title,
  varnames = list(A = "A", Ca = "Ca", CO2_r = "CO2_r", E = "E", gtc = "gtc")
)
```

Arguments

caldata	Data frame with the calibration data
data	List of data frames with the RACiR response data

mincut	Minimum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the initial chamber mixing. Default value is set to the minimum COR_r value.
maxcut	Maximum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the end of the response. Not needed in all cases. Default value is set to the maximum COR_r value.
digits	Specifies rounding for groups. Defaults to -2 (100s). Effectively uses 100 ppm intervals (e.g. data matching >50 ppm to 150 ppm would be assigned to an interval centered around 100 ppm for reference CO2).
title	Vector for titles of output graph - useful for batch RACiR corrections. Length must be equal to data list length
varnames	Variable names - this allows for the use of this code with other machines and setups where variable names may differ.

Value

racircalbatch_advanced uses racircal_advanced on many files

Examples

```
#Create a list of files
files <- c(system.file("extdata", "poplar_1", package = "racir"),
          system.file("extdata", "poplar_2", package = "racir"))
data <- vector("list", length(files))
for(i in seq_along(files)){
 data[[i]] <- read_6800(files[i])
 names(data)[i] <- files[i]
}

caldata <- read_6800(system.file("extdata", "cal", package = "racir"))
output <- racircalbatch_advanced(caldata = caldata, data = data,
                                 mincut = 300, maxcut = 780, title = files)
```

---

racircalcheck *Allows visual checking of rapid A/Ci response (RACiR) calibration data using empty chamber data.*

Description

racircalcheck Used to check range of calibration file. Produces diagnostic graphs of A vs. Ci for quality control. Output includes plots for checking and confirming cutoff values, and a plot with the fit, as well as information as to which polynomial fit the data best.

Usage

```
racircalcheck(
  data,
  mincut,
  maxcut,
  varnames = list(A = "A", Ca = "Ca", CO2_r = "CO2_r", E = "E", gtc = "gtc")
)
```

Arguments

data	Data frame with the calibration (empty chamber) rapid A/Ci response
mincut	Minimum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the initial chamber mixing. Default value is set to the minimum COR_r value.
maxcut	Maximum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the end of the response. Not needed in all cases. Default value is set to the maximum COR_r value.
varnames	Variable names - this allows for the use of this code with other machines and setups where variable names may differ.

Value

racircalcheck allows visual checking of RACiR calibration data

Examples

```
#Read in the file
data <- read_6800(system.file("extdata", "cal", package = "racir"))
#Run calibration check
racircalcheck(data = data,
              mincut = 350,
              maxcut = 780)
```

---

racircalcheck_advanced

Allows visual checking of rapid A/Ci response (RACiR) calibration data using empty chamber data.

Description

racircalcheck_advanced Used to check range of calibration file. Produces diagnostic graphs of A vs. Ci for quality control.

Usage

```
racircalcheck_advanced(
  data,
  mincut,
  maxcut,
  digits,
  varnames = list(A = "A", Ca = "Ca", CO2_r = "CO2_r", E = "E", gtc = "gtc")
)
```

Arguments

data	Data frame with the calibration (empty chamber) rapid A/Ci response
mincut	Minimum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the initial chamber mixing. Default value is set to the minimum COR_r value.
maxcut	Maximum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the end of the response. Not needed in all cases. Default value is set to the maximum COR_r value.
digits	Specifies rounding for groups. Defaults to -2 (100s). Effectively uses 100 ppm intervals (e.g. data matching >50 ppm to 150 ppm would be assigned to an interval centered around 100 ppm for reference CO2).
varnames	Variable names - this allows for the use of this code with other machines and setups where variable names may differ.

Value

racircalcheck_advanced returns a data frame with corrected RACiR data

Examples

```
#Read in data
data <- read_6800(system.file("extdata", "poplar_2", package = "racir"))
caldata <- read_6800(system.file("extdata", "cal", package = "racir"))
#Correct data
racircalcheck_advanced(data = data, mincut = 350, maxcut = 780)
```

---

racircal_advanced *Corrects rapid A/Ci response (RACiR) data from leaves using empty chamber data.*

Description

racircal_advanced Interval correction for RACiR data.

Usage

```
racircal_advanced(
  data,
  caldata,
  mincut,
  maxcut,
  title,
  digits,
  varnames = list(A = "A", Ca = "Ca", CO2_r = "CO2_r", E = "E", gtc = "gtc")
)
```

Arguments

data	Data frame with the RACiR response data
caldata	Data frame with the calibration data
mincut	Minimum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the initial chamber mixing. Default value is set to the minimum COR_r value.
maxcut	Maximum cutoff value for reference CO2 (CO2_r). Used to cut out the data from the end of the response. Not needed in all cases. Default value is set to the maximum COR_r value.
title	Title of output graph - useful for batch RACiR corrections.
digits	Specifies rounding for groups. Defaults to -2 (100s). Effectively uses 100 ppm intervals (e.g. data matching >50 ppm to 150 ppm would be assigned to an interval centered around 100 ppm for reference CO2).
varnames	Variable names - this allows for the use of this code with other machines and setups where variable names may differ.

Value

racircal_advanced racircalcheck allows visual checking of RACiR calibration data

Examples

```
#Read in data
data <- read_6800(system.file("extdata", "poplar_2", package = "racir"))
caldata <- read_6800(system.file("extdata", "cal", package = "racir"))
#Correct data
data_corrected <- racircal_advanced(data = data, caldata = caldata,
                                    mincut = 350, maxcut = 780,
                                    digits = -2, title = "Test")
```

read_6800 *Reads files from the Li-Cor 6800*

Description

read_6800 Reads Li-Cor 6800 files, which are delimited by spaces and tabs.

Usage

```
read_6800(x)
```

Arguments

x	A Li-Cor 6800 data file name of the form: "mydata".

Value

read_6800 imports a Li-Cor 6800 file as a data frame

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