

Package ‘racir’

July 23, 2025

Type Package

Title Rapid A/Ci Response (RACiR) Data Analysis

Version 2.0.0

Date 2020-07-29

Maintainer Joseph Stinziano <josephstinziano@gmail.com>

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](https://doi.org/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>

License MIT + file LICENSE

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

Author Joseph Stinziano [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-7628-4201>>)

Repository CRAN

Date/Publication 2020-08-03 11:30:03 UTC

Contents

racircal	2
racircalbatch	3
racircalbatch_advanced	4
racircalcheck	5
racircalcheck_advanced	6
racircal_advanced	7
read_6800	9
Index	10

racircal	<i>Corrects rapid A/Ci response (RACiR) data from leaves using empty chamber data.</i>
----------	--

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	<i>Corrects a batch of rapid A/Ci response (RACiR) data</i>
---------------	---

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

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

<code>data</code>	Data frame with the calibration (empty chamber) rapid A/Ci response
<code>mincut</code>	Minimum cutoff value for reference CO ₂ (CO _{2_r}). Used to cut out the data from the initial chamber mixing. Default value is set to the minimum COR_r value.
<code>maxcut</code>	Maximum cutoff value for reference CO ₂ (CO _{2_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.
<code>varnames</code>	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 CO ₂ (CO _{2_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 CO ₂ (CO _{2_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 CO ₂).
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	<i>Corrects rapid A/Ci response (RACiR) data from leaves using empty chamber data.</i>
-------------------	--

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

[illegible]

read_6800	<i>Reads files from the Li-Cor 6800</i>
-----------	---

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

Index

racircal, [2](#)
racircal_advanced, [7](#)
racircalbatch, [3](#)
racircalbatch_advanced, [4](#)
racircalcheck, [5](#)
racircalcheck_advanced, [6](#)
read_6800, [9](#)