# Package: racir (via r-universe)

October 31, 2024

**Type** Package

**Title** Rapid A/Ci Response (RACiR) Data Analysis

**Version** 2.0.0

**Date** 2020-07-29

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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

**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

**Repository** https://jstinzi.r-universe.dev

**RemoteUrl** https://github.com/jstinzi/racir

**RemoteRef** HEAD

**RemoteSha** 3850ebf0fa0e475c25b3798fbb8fe7da1fb37839

# Contents



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`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

# Index