

# Package: respirometr (via r-universe)

October 28, 2024

**Type** Package

**Title** An R toolbox for analysing respirometry data

**Version** 0.1.1

**Description** An R toolbox for analysing respirometry data.

**License** MIT + file LICENSE

**URL** <http://www.roald-arboel.com/respirometr/>,  
<https://github.com/roaldarbol/respirometr/>

**BugReports** <https://github.com/roaldarbol/respirometr/issues>

**Encoding** UTF-8

**LazyData** true

**Imports** cli, dplyr, hms, janitor, lifecycle, readr

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0), here, readxl, stringr,  
tinyplo, tinytable, ggplot2, patchwork, performance, see,  
markdown, tidyr, cffr

**Config/testthat/edition** 3

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**VignetteBuilder** knitr

**Repository** <https://roaldarbol.r-universe.dev>

**RemoteUrl** <https://github.com/roaldarbol/respirometr>

**RemoteRef** HEAD

**RemoteSha** 41830c0b90cfc18f3e182c77f055a27a6ff0929d

## Contents

normalise_prepost . . . . .	2
read_licor . . . . .	2

<b>Index</b>	<b>3</b>
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normalise_prepost	<i>Normalise Traces</i>
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**Description****[Experimental]****Usage**

```
normalise_prepost(data, pre, post, method = "means_linear")
```

**Arguments**

data	Data from trial
pre	Pre-trial level. Case be either a single value (if known) or a vector of values, from which the mean is calculated.
post	Post-trial level. Case be either a single value (if known) or a vector of values, from which the mean is calculated.
method	Which method is used to normalise the data

**Value**

Normalised data

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read_licor	<i>Read Licor data</i>
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**Description****[Experimental]**

Read respirometry data from a variety of Licor devices.

**Usage**

```
read_licor(filepath, model)
```

**Arguments**

filepath	Path to file
model	LiCor model

**Value**

Tidy LiCor data

# Index

`normalise_prepost`, [2](#)

`read_licor`, [2](#)