Package 'FishResp'

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Version 1.1.1

Title Analytical Tool for Aquatic Respirometry

Description Calculates metabolic rate of fish and other aquatic organisms measured using an intermittent-flow respirometry approach. The tool is used to run a set of graphical QC tests of raw respirometry data, correct it for background respiration and chamber effect, filter and extract target values of absolute and mass-specific metabolic rate. Experimental design should include background respiration tests and measuring of one or more metabolic rate traits. The R package is ideally integrated with the pump controller 'PumpResp' and the DO meter 'SensResp' (open-source hardware by FishResp). Raw respirometry data can be also imported from 'AquaResp' (free software), 'AutoResp' ('LoligoSystems'), 'OxyView' ('PreSens'), 'Pyro Oxygen Logger' ('PyroScience') and 'Q-box Aqua' ('QubitSystems'). More information about the R package 'FishResp'is available in the publication by Morozov et al. (2019) <doi:10.1093/conphys/coz003>.

URL https://fishresp.org

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License GPL-3

SystemRequirements Display resolution >= 1280x800; RAM >= 4GB

Depends R (>= 3.0.0)

Imports chron, lattice, mclust, rMR, respirometry

LazyData TRUE

RoxygenNote 7.2.1

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R topics documented:

AMR *Active Metabolic Rate: Final Data*

Description

A dataset contains background respiration, absolute and mass-specific active metabolic rate data obtained by using the function `calculate.MR`

Usage

```
AMR
```

Format

A data frame with 12 rows and 16 variables:

Chamber.No the number of a chamber

Ind ID of an animal

Mass wet mass of an animal (g)

Volume the volume of a chamber (mL)

Date.Time date and time of a measurement phase (yyyy/mm/dd hh:mm:ss)

Phase the type of phase and an ordinal number of measurements (e.g. M1)

Temp average temperature over the period of a measurement phase (C^o)

Slope.with.BR slope of animal oxygen consumption with slope of background respiration ($mgO_2\ L^{-1}s^{-1}$)

Slope slope of animal oxygen consumption without background respiration ($mgO_2\ L^{-1}s^{-1}$)

SE standard error of a slope of animal oxygen consumption without background respiration ($mgO_2\ L^{-1}s^{-1}$)

R2 r^2 of a slope of animal oxygen consumption without background respiration

MR.abs.with.BR absolute AMR with background respiration ($mgO_2\ h^{-1}$)

BR percentage rate of background respiration

MR.abs absolute AMR ($mgO_2\ h^{-1}$)

MR.mass mass-specific AMR ($mgO_2\ kg^{-1}h^{-1}$)

DO.unit the measure unit of DO concentration

AMR.clean *Active Metabolic Rate: Corrected Raw Data*

Description

A dataset contains raw data of active metabolic rate measurements corrected for background respiration using the function correct.meas

Usage

```
AMR.clean
```

Format

A data frame with 7200 rows and 17 variables:

Date.Time date and time (yyyy/mm/dd hh:mm:ss)

Date date (yyyy/mm/dd)

Real.Time time (hh:mm:ss)

Time ordinal number of seconds in each measurement phase (1-600)

Phase the type of phase and an ordinal number of measurements (e.g. M1, F3)

Start.Meas the first second of a measurement phase (hh:mm:ss)

End.Meas the last second of a measurement phase (hh:mm:ss)

Chamber.No the number of a chamber

Ind ID of an animal

Mass wet mass of an animal (g)

Volume the volume of a chamber (mL)

Init.O2 initial level of dissolved oxygen (mgO2/L)

Temp temperature at each second (C^o)

O2 actual level of dissolved oxygen at each second (mgO2/L)

BR slope of background respiration ($mgO_2\ L^{-1}s^{-1}$)

O2.correct actual level of dissolved oxygen at each second corrected by slope of background respiration (mgO2/L)

DO.unit the measure unit of DO concentration

AMR.raw *Active Metabolic Rate: Raw Data*

Description

The dataset contains raw data of active metabolic rate measurements obtained by using the function import.meas)

Usage

```
AMR.raw
```

Format

A data frame with 1800 rows and 16 variables:

Date.Time date and time (yyyy/mm/dd hh:mm:ss)

Phase the type of phase and an ordinal number of measurements (e.g. M1, F3)

Temp.1 temperature at each second (C^o)

Ox.1 actual level of dissolved oxygen at each second (mgO2/L)

Real.Time time (hh:mm:ss)

Date date (yyyy/mm/dd)

Time ordinal number of seconds in each measurement phase (1-600)

Start.Meas the first second of a measurement phase (hh:mm:ss)

End.Meas the last second of a measurement phase (hh:mm:ss)

Total.Phases the total number of measurement phases (constant value)

Ox.2 see Ox.1

Ox.3 see Ox.1

Ox.4 see Ox.1

Temp.2 see Temp.1

Temp.3 see Temp.1

Temp.4 see Temp.1

AMR.slope *Active Metabolic Rate: Extracted Slope(s)*

Description

A dataset contains extracted slopes for further AMR calculations and other attributes of active metabolic rate measurements obtained by using the function `extract.slope`

Usage

```
AMR.slope
```

Format

A data frame with 12 rows and 12 variables:

Chamber.No the number of a chamber

Ind ID of an animal

Mass wet mass of an animal (g)

Volume the volume of a chamber (mL)

Date.Time date and time of a measurement phase (yyyy/mm/dd hh:mm:ss)

Phase the type of phase and an ordinal number of measurements (e.g. M1)

Temp average temperature over the period of a measurement phase (C^o)

Slope.with.BR slope of animal oxygen consumption with slope of background respiration ($mgO_2\ L^{-1}s^{-1}$)

Slope slope of animal oxygen consumption without background respiration ($mgO_2\ L^{-1}s^{-1}$)

SE standard error of a slope of animal oxygen consumption without background respiration ($mgO_2\ L^{-1}s^{-1}$)

R2 r^2 of a slope of animal oxygen consumption without background respiration

DO.unit the measure unit of DO concentration

calculate.MR *Calculation of Metabolic Rate*

Description

The function is used to calculate and plot background respiration, absolute and mass-specific metabolic rates.

Usage

```
calculate.MR(slope.data, density = 1000,
             plot.BR = TRUE,
             plot.MR.abs = TRUE,
             plot.MR.mass = TRUE)
```

Arguments

slope.data	a data frame obtained by using the function extract.slope
density	numeric: the density of an animal body (kg/m^3)
plot.BR	logical: if TRUE, the graph of background respiration rate is plotted
plot.MR.abs	logical: if TRUE, the graph of absolute metabolic rate is plotted
plot.MR.mass	logical: if TRUE, the graph of mass-specific metabolic rate is plotted

Value

The function returns a data frame with calculated background respiration, absolute and mass-specific metabolic rates. The data frame is used in the function export.MR.

Examples

```
# if the data have been already loaded to R,
# skip the first two lines of the code:
data(SMR.slope)
data(AMR.slope)

SMR <- calculate.MR(SMR.slope,
                    density = 1000,
                    plot.BR = TRUE,
                    plot.MR.abs = TRUE,
                    plot.MR.mass = TRUE)

AMR <- calculate.MR(AMR.slope,
                    density = 1000,
                    plot.BR = TRUE,
                    plot.MR.abs = TRUE,
                    plot.MR.mass = TRUE)
```

---

convert.respirometry *Convert Raw Respirometry Data (respirometry)*

Description

This function is the modification of the function conv_o2 from the R package **respirometry** allowing to convert raw respirometry data from one DO unit to another obtained in multichannel respirometry systems.

Usage

```
convert.respirometry(import.file, export.file,
                     n.chamber = c(1,2,3,4,5,6,7,8),
                     logger = c("AutoResp", "FishResp", "QboxAqua"),
                     from, to, sal = 0, atm_pres = 1013.25)
```

Arguments

import.file	the name of a file with raw respirometry data which should be imported to convert DO units
export.file	the name of a file with results of the DO unit conversion
n.chamber	integer: the number of chambers used in an experiment (including empty ones)
logger	string: the name of a logger software used for intermittent-flow respirometry. Note, that both 'OxyView' and 'Pyro Oxygen Logger' used in couple with the 'AquaResp' software should be converted to the 'FishResp' format before running this function (see the functions presens.aquaresp or pyroscience.aquaresp, respectively).
from	string: dissolved oxygen unit in an imported file (more information can be found in the documentation of the function conv_o2, R package **respirometry**)
to	string: dissolved oxygen unit in an exported file (more information can be found in the documentation of the function conv_o2, R package **respirometry**)
sal	string: salinity is measured in ppm (more information can be found in the documentation of the function conv_o2, R package **respirometry**)
atm_pres	string: ambient atmospheric pressure value (more information can be found in the documentation of the function conv_o2, R package **respirometry**)

Value

The function exports a data frame with converted DO units.

Examples

```
## Not run:
# Import raw data for standard metabolic rate
SMR.path = system.file("extdata/stickleback/SMR_raw.txt.xz", package = "FishResp")

convert.respirometry(import.file = SMR.path,
                     export.file = "converted_SMR_raw.txt",
                     n.chamber = 1, logger = "AutoResp",
                     from = "mg_per_l", to = "mmol_per_l",
                     sal = 0, atm_pres = 1013.25)

## End(Not run)
```

---

convert.rMR *Convert Raw Respirometry Data (rMR)*

Description

This function is the modification of the function DO.unit.convert from the R package **rMR** allowing to convert raw respirometry data from one DO unit to another obtained in multichannel respirometry systems.

Usage

```
convert.rMR(import.file, export.file,
            n.chamber = c(1,2,3,4,5,6,7,8),
            logger = c("AutoResp", "FishResp", "QboxAqua"),
            DO.units.in, DO.units.out, salinity = 0,
            bar.press = 101.325, bar.units.in = "kpa")
```

Arguments

import.file	the name of a file with raw respirometry data which should be imported to convert DO units
export.file	the name of a file with results of the DO unit conversion
n.chamber	integer: the number of chambers used in an experiment (including empty ones)
logger	string: the name of a logger software used for intermittent-flow respirometry. Note, that both 'OxyView' and 'Pyro Oxygen Logger' used in couple with the 'AquaResp' software should be converted to the 'FishResp' format before running this function (see the functions presens.aquaresp or pyroscience.aquaresp, respectively).
DO.units.in	string: dissolved oxygen unit in an imported file (more information can be found in the documentation of the function DO.unit.convert, R package **rMR**)
DO.units.out	string: dissolved oxygen unit in an exported file (more information can be found in the documentation of the function DO.unit.convert, R package **rMR**)
salinity	string: salinity is measured in ppm (more information can be found in the documentation of the function DO.unit.convert, R package **rMR**)
bar.press	string: ambient barometric pressure value (more information can be found in the documentation of the function DO.unit.convert, R package **rMR**)
bar.units.in	string: barometric pressure unit (more information can be found in the documentation of the function DO.unit.convert, R package **rMR**)

Value

The function exports a data frame with converted DO units.

Examples

```
## Not run:
# Import raw data for active metabolic rate
AMR.path = system.file("extdata/stickleback/AMR_raw.txt.xz", package = "FishResp")

convert.rMR(import.file = AMR.path,
            export.file = "converted_AMR_raw.txt",
            n.chamber = 2, logger = "AutoResp", salinity = 0,
            DO.units.in = "mg/L", DO.units.out = "PP",
            bar.press = 101.325, bar.units.in = "kpa")

## End(Not run)
```

`correct.meas` *Correction of Metabolic Rate Measurements*

Description

The function is used to correct metabolic rate measurements for background respiration. To this end, oxygen consumption is estimated as the slope of the linear regression of measured O_2 concentration over time, and is extracted for background respiration test and for each measurement phase. The correction is based on subtraction of oxygen consumption obtained during background respiration test from oxygen consumption obtained during metabolic rate measurements.

Usage

```
correct.meas(info.data, pre.data, post.data, meas.data,
             method = c("pre.test", "post.test", "average",
                        "linear", "exponential", "parallel"),
             empty.chamber = c("CH1", "CH2", "CH3", "CH4",
                               "CH5", "CH6", "CH7", "CH8"))
```

Arguments

`info.data`	a data frame obtained by using the function `input.info`
`pre.data`	a data frame obtained by using the function `import.test` for a blank test before actual metabolic rate measurements
`post.data`	a data frame obtained by using the function `import.test` for a blank test after actual metabolic rate measurements
`meas.data`	a data frame obtained by using the function `import.meas` for actual metabolic rate measurements
`method`	string: the name of the method used for background respiration correction: • "pre.test" - subtracts oxygen consumption of pre.data from oxygen consumptions of meas.data • "post.test" - subtracts oxygen consumption of post.data from oxygen consumptions of meas.data • "average" - subtracts an averaged oxygen consumption of pre.data and post.data from oxygen consumptions of meas.data • "linear" - subtracts a vector of progressively changing microbial consumptions from oxygen consumptions of meas.data. The values of oxygen consumption are linearly predicted from two reference points: oxygen consumption of pre.data and oxygen consumption of post.data. • "exponential" - subtracts a vector of progressively changing microbial consumptions from oxygen consumptions of meas.data. The values of oxygen consumption are exponentially predicted from two reference points: oxygen consumption of pre.data and oxygen consumption of post.data. • "parallel" - subtracts oxygen consumption in an empty chamber from oxygen consumptions of meas.data for each chamber
`empty.chamber`	string: the name of an empty chamber used only for the method 'parallel'

Value

The function returns a data frame containing data of metabolic rate measurements corrected for background respiration. The data frame is used in the functions QC.meas, QC.activity, extract.slope and QC.slope.

References

Svendsen, M. B. S., Bushnell, P. G., & Steffensen, J. F. (2016). Design and setup of intermittent-flow respirometry system for aquatic organisms. Journal of Fish Biology, 88(1), 26-50.

Examples

```
# if the data have been already loaded to R,
# skip the first five lines of the code:
data(info)
data(pre)
data(post)
data(AMR.raw)
## Not run:
data(SMR.raw)
SMR.clean <- correct.meas(info.data = info,
                          pre.data = pre,
                          meas.data = SMR.raw,
                          method = "pre.test")

## End(Not run)

AMR.clean <- correct.meas(info.data = info,
                          post.data = post,
                          meas.data = AMR.raw,
                          method = "post.test")
```

---

export.MR *Export Metabolic Rate*

Description

The function is used to export final dataset with information about background respiration, absolute and mass-specific metabolic rates into a .txt or .csv file. If two traits (MR.data.1, MR.data.2) are used, the datasets might be merged. Additionally, absolute, mass-specific and factorial metabolic scope might be calculated, where MR.data.1 is standard or resting metabolic rate and MR.data.2 is active or maximum metabolic rate.

Usage

```
export.MR(MR.data.1, MR.data.2, file = "",
          simplify = TRUE, MS = TRUE,
```

```
            plot.MS.abs = TRUE,
            plot.MS.mass = TRUE,
            plot.MS.fact = TRUE)
```

Arguments

MR.data.1	a data frame obtained by using the function extract.slope
MR.data.2	a data frame obtained by using the function extract.slope
file	the name of an exported file with results of the analysis
simplify	logical: if TRUE, the number of columns in the extracted data frame is reduced
MS	logical: if TRUE, metabolic scope is calculated and attached to the exported dataset
plot.MS.abs	logical: if TRUE, the graph of absolute metabolic scope is plotted (x-axis shows measurement phases for MR.data.2)
plot.MS.mass	logical: if TRUE, the graph of mass-specific metabolic scope is plotted (x-axis shows measurement phases for MR.data.2)
plot.MS.fact	logical: if TRUE, the graph of factorial metabolic scope is plotted (x-axis shows measurement phases of for MR.data.2)

Value

If only one traits exists, the function exports a data frame with full or simplified structure. If both traits are used, the function returns and exports 'MR.data.1' and 'MR.data.2' with metabolic scope parameters (optionally).

Examples

```
## Not run:
# if the data have been already loaded to R,
# skip the first two lines of the code:
data(SMR)
data(AMR)

results <- export.MR(SMR, AMR,
                     file = "results.txt",
                     simplify = TRUE,
                     MS = TRUE,
                     plot.MS.abs = TRUE,
                     plot.MS.mass = TRUE,
                     plot.MS.fact = TRUE)

## End(Not run)
```

`extract.slope` *Extraction of Slope(s)*

Description

The function extracts the slopes of the linear regression of corrected O_2 concentration over time with defined parameters (see Arguments).

Usage

```
extract.slope(clean.data,
              method = c("all", "min", "max",
                         "lower.tail", "upper.tail",
                         "calcSMR.mlnd", "calcSMR.quant",
                         "calcSMR.low10", "calcSMR.low10pc"),
              r2=0.95, length = 999999, n.slope = 1000,
              percent = 10, p = 0.25, G = 1:4)
```

Arguments

`clean.data`	a data frame obtained by using the function `correct.meas`
`method`	string: the method of extracting slopes: • 'all' all slopes • 'min' extracts lowest absolute slopes, specify the number of extracted slopes (parameter: n.slope) • 'max' extracts highest absolute slopes, specify the number of extracted slopes (parameter: n.slope) • 'lower.tail' extracts slopes from a lower tail of absolute slope distribution, specify percentage of a lower tail (parameter: percent) • 'upper.tail' extracts slopes from an upper tail of absolute slope distribution, specify percentage of an upper tail (parameter: percent) • 'calcSMR.mlnd' calculates the mean of the lowest normal distribution (MLND) using the parameter G (see Appendix S1 in Chabot et al, 2016) • 'calcSMR.quant' calculates quantile value of slope distribution using the parameter p (see Appendix S1 in Chabot et al, 2016) • 'calcSMR.low10' calculates the mean of the 10 lowest absolute slopes (see Appendix S1 in Chabot et al, 2016) • 'calcSMR.low10pc' calculates the mean of the lowest 10
`r2`	numeric: minimal coefficient of determination (r^2) for extracted slopes. Coefficient of determination is used as a threshold of quality to be determined by the user (by default r^2 = 0.95)
`length`	integer: length of a measurement period for slope calculations (in seconds; by default - full length)

n.slope	integer: the number of extracted slopes, only one slope is calculated for each measurement phase (used in the methods "min" and "max"; by default - all slopes)
percent	integer: percentage of lower or upper tail (used in the methods "lower.tail" and "upper.tail", respectively; by default percent = 10)
p	integer: p-value of quantile used in the method "calcSMR.quant" (by default p = 0.25)
G	integer: G value is used in the method "calcSMR.mlnd" (by default G = 1:4)

Value

The function returns a data frame with the information about extracted slopes. The data frame is used in the functions QC.slope and calculate.MR.

References

1. Chabot, D., Steffensen, J. F., & Farrell, A. P. (2016). The determination of standard metabolic rate in fishes. Journal of Fish Biology, 88(1), 81-121.
2. Herrmann, J. P., & Enders, E. C. (2000). Effect of body size on the standard metabolism of horse mackerel. Journal of Fish Biology, 57(3), 746-760.

Examples

```
# if the data have been already loaded to R,
# skip the first two lines of the code:
data(SMR.clean)
data(AMR.clean)

SMR.slope <- extract.slope(SMR.clean,
                           method = "min",
                           n.slope = 3,
                           r2=0.95,
                           length = 1200)

AMR.slope <- extract.slope(AMR.clean,
                           method = "all",
                           r2=0.95,
                           length = 300)
```

Description

Calculates metabolic rate of fish and other aquatic organisms measured using an intermittent-flow respirometry approach. The tool is used to run a set of graphical QC tests of raw respirometry data, correct it for background respiration and chamber effect, filter and extract target values of absolute and mass-specific metabolic rate. Experimental design should include background respiration tests and measuring of one or more metabolic rate traits. The R package is ideally integrated with the pump controller 'PumpResp' and the DO meter 'SensResp' (open-source hardware by FishResp). Raw respirometry data can be also imported from 'AquaResp' (free software), 'AutoResp', ('LoligoSystems'), 'OxyView' ('PreSens'), 'Pyro Oxygen Logger' ('PyroScience'), and 'Q-box Aqua' ('QubitSystems').

Author(s)

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References

Before using the R package 'FishResp', we recommend reading the publication describing this software and two keystone reviews devoted to metabolic rate measurements of fish using an intermittent-flow approach:

1. Morozov, S., McCairns, R. J. S., Merila, J. (2019). FishResp: R package and GUI application for analysis of aquatic respirometry data. Conservation Physiology, 7(1), coz003.
2. Clark, T. D., Sandblom, E., Jutfelt, F. (2013). Aerobic scope measurements of fishes in an era of climate change: respirometry, relevance and recommendations. Journal of Experimental Biology, 216(15), 2771-2782.
3. Svendsen, M. B. S., Bushnell, P. G., Steffensen, J. F. (2016). Design and setup of intermittent-flow respirometry system for aquatic organisms. Journal of Fish Biology, 88(1), 26-50.

`import.meas` *Import Raw Data of Metabolic Rate Measurements*

Description

The function is used to import raw data of metabolic rate measurements to R environment.

Usage

```
import.meas(file, info.data,
            n.chamber = c(1,2,3,4,5,6,7,8),
            logger = c("AutoResp", "FishResp", "QboxAqua"),
            date.format = c("DMY", "MDY", "YMD"),
            start.measure = "00:00:00",
            stop.measure = "23:59:59",
            start.measure.date = NA,
            stop.measure.date = NA,
            set.date.time = NA,
```

```
meas.to.wait = 0,
meas.to.flush = 0,
plot.temperature = TRUE,
plot.oxygen = TRUE)
```

Arguments

file	the name of a file which raw data of metabolic rate measurements are to be read from
info.data	a data frame obtained by using the function input.info
n.chamber	integer: the number of chambers used in an experiment (including empty ones)
logger	string: the name of a logger software used for intermittent-flow respirometry • 'AutoResp' if you use commercial software by 'Loligo Systems' • 'FishResp' if you use free software 'AquaResp' in combination with equipment produced by 'PreSens' or 'Pyroscience', please convert data to the 'FishResp' format using the functions presens.aquaresp or pyroscience.aquaresp, respectively. If you do not use commercial software or 'AquaResp' for running intermittent-flow respirometry, adjust raw data manually to the 'FishResp' format (see Details below). • 'QboxAqua' if you use commercial software by 'Qubit Systems'
date.format	string: date format (DMY, MDY or YMD)
start.measure	chron: time when metabolic rate measurements are started
stop.measure	chron: time when metabolic rate measurements are finished
start.measure.date	chron: date when metabolic rate measurements are started
stop.measure.date	chron: date when metabolic rate measurements are finished
set.date.time	chron: this parameter is turned off by default and needed to be specified only if raw data were recorded by 'Q-box Aqua' logger software. Specifically, input the date and time when .cmbl file was built in one of the following formats: "dd/mm/yyyy/hh:mm:ss", "mm/dd/yyyy/hh:mm:ss", or "yyyy/mm/dd/hh:mm:ss" (in accordance to the chosen date.format parameter).
meas.to.wait	integer: the number of first rows for each measurement phase (M) which should be reassigned to the wait phase (W). The parameter should be used when the wait phase (W) is absent (e.g. in 'Q-box Aqua' logger software) or not long enough to eliminate non-linear change in DO concentration over time from the measurement phase (M) after shutting off water supply from the ambient water source.
meas.to.flush	integer: the number of last rows for each measurement phase (M) which should be reassigned to the flush phase (F). The parameter should be used to eliminate non-linear change in DO concentration over time from the measurement phase (M) after untimely shutting on water supply from the ambient water source.
plot.temperature	logical: if TRUE then the graph of raw temperature data is plotted
plot.oxygen	logical: if TRUE then the graph of raw oxygen data is plotted

Details

If you use closed respirometry approach, please standardize raw data. The example of "FishResp" format for 4-channel respirometry system is shown here:

Date&Time	Phase	Temp.1	Ox.1	Temp.2	Ox.2	Temp.3	Ox.3	Temp.4	Ox.4
19/08/2016/18:47:20	F1	24.49	7.78	24.56	7.73	24.49	7.78	24.56	7.73
19/08/2016/18:47:21	F1	24.49	7.78	24.56	7.73	24.49	7.78	24.56	7.73
19/08/2016/18:47:22	M1	24.49	7.77	24.56	7.72	24.49	7.78	24.56	7.73
19/08/2016/18:47:23	M1	24.49	7.76	24.56	7.72	24.49	7.78	24.56	7.73

where the items are:

- Date&Time should be represented in one of the following formats: "dd/mm/yyyy/hh:mm:ss", "mm/dd/yyyy/hh:mm:ss", or "yyyy/mm/dd/hh:mm:ss". Time step-interval is one second: one row of data per second.
- Phase should have at least two levels: M (measurement) and F (flush). The ordinal number of a phase should be attached to the level of a phase: F1, M1, F2, M2 ...
- Temp.1 contains values of water temperature in Celsius (C^o) for Chamber 1
- Ox.1 contains values of dissolved oxygen measured in 'mg/L', 'mmol/L' or 'ml/L' for Chamber 1. If other measurement units were used, convert them to 'mg/L', 'mmol/L' or 'ml/L' using the function `convert.respirometry` or `convert.rMR`.
- ...

Value

The function returns a data frame containing standardized raw data of metabolic rate measurements. The data frame should be used in the function `correct.meas` to correct metabolic rate measurements for background respiration.

Examples

```
# Import raw data for standard and active metabolic
# rate measurements (SMR and AMR, respectively)

# if the data have been already loaded to R,
# skip the first line of the code:
data(info)
## Not run:
SMR.path = system.file("extdata/stickleback/SMR_raw.txt.xz", package = "FishResp")
SMR.raw <- import.meas(file = SMR.path,
                       info.data = info,
                       logger = "AutoResp",
                       n.chamber = 4,
                       date.format = "DMY",
                       start.measure = "22:00:00",
                       stop.measure = "06:00:00",
                       plot.temperature = TRUE,
                       plot.oxygen = TRUE)
```

```
AMR.path = system.file("extdata/stickleback/AMR_raw.txt.xz", package = "FishResp")
AMR.raw <- import.meas(file = AMR.path,
                       info.data = info,
                       logger = "AutoResp",
                       n.chamber = 4,
                       date.format = "DMY",
                       plot.temperature = TRUE,
                       plot.oxygen = TRUE)

# an example for importing raw data recorded by 'Q-box Aqua'
qbox.path = system.file("extdata/qboxaqua/qboxaqua.csv", package = "FishResp")
RMR.raw <- import.meas(file = qbox.path,
                        info.data = info,
                        logger = "QboxAqua",
                        n.chamber = 1,
                        date.format = "DMY",
                        start.measure = "23:30:00",
                        stop.measure = "01:00:00",
                        set.date.time = "23/02/2014/23:30:22",
                        meas.to.wait = 200,
                        plot.temperature = TRUE,
                        plot.oxygen = TRUE)

## End(Not run)
```

`import.test` *Import Background Respiration Data*

Description

The function is used to import raw data of background respiration to R environment. The test should be done immediately before and/or after the actual metabolic rate measurements (pre-test and post-test, respectively).

Usage

```
import.test(file, info.data,
            n.chamber = c(1,2,3,4,5,6,7,8),
            logger = c("AutoResp", "FishResp", "QboxAqua"),
            meas.to.wait = 0,
            plot.temperature = TRUE,
            plot.oxygen = TRUE)
```

Arguments

`file`	the name of a file which the pre- or post-test data are to be read from. Note, if the file contains more than one measurement phase (e.g. M1 and M2), only the first one (M1) will be imported in R.

`info.data` a data frame obtained by using the function `input.info`

`n.chamber` integer: the number of chambers used in an experiment (including empty ones)

`logger` string: the name of a logger software used for intermittent-flow respirometry:

- 'AutoResp' if you use commercial software by 'Loligo Systems'
- 'FishResp' if you use free software 'AquaResp' in combination with equipment produced by 'PreSens' or 'Pyroscience', please convert data to the 'FishResp' format using the functions `presens.aquaresp` or `pyroscience.aquaresp`, respectively.
  If you do not use commercial software or 'AquaResp' for running intermittent-flow respirometry, adjust raw data manually to the 'FishResp' format (see Details below).
- 'QboxAqua' if you use commercial software by 'Qubit Systems'

`meas.to.wait` integer: the number of first rows for each measurement phase (M) which should be reassigned to the wait phase (W). The parameter should be used when the wait phase (W) is absent (e.g. in 'Q-box Aqua' logger software) or not long enough to eliminate non-linear change in DO concentration over time from the measurement phase (M) after shutting off water supply from the ambient water source.

`plot.temperature`
logical: if TRUE then the graph of raw temperature data is plotted

`plot.oxygen` logical: if TRUE then the graph of raw oxygen data is plotted

Details

Do not use this function if an empty chamber is used for controlling background respiration in parallel with actual metabolic rate measurements. See about application of 'parallel' method in the function `correct.meas`
If you use closed respirometry approach, please standardize raw data. The example of "FishResp" format for 4-channel respirometry system is shown here:

Date&Time	Phase	Temp.1	Ox.1	Temp.2	Ox.2	Temp.3	Ox.3	Temp.4	Ox.4
19/08/2016/18:47:20	F1	24.49	7.78	24.56	7.73	24.49	7.78	24.56	7.73
19/08/2016/18:47:21	F1	24.49	7.78	24.56	7.73	24.49	7.78	24.56	7.73
19/08/2016/18:47:22	M1	24.49	7.77	24.56	7.72	24.49	7.78	24.56	7.73
19/08/2016/18:47:23	M1	24.49	7.76	24.56	7.72	24.49	7.78	24.56	7.73

where the items are:

- Date&Time should be represented in one of the following formats: "dd/mm/yyyy/hh:mm:ss", "mm/dd/yyyy/hh:mm:ss", or "yyyy/mm/dd/hh:mm:ss". Time step-interval is one second: one row of data per second.
- Phase should have at least two levels: M (measurement) and F (flush). The ordinal number of a phase should be attached to the level of a phase: F1, M1, F2, M2 ...
- Temp.1 contains values of water temperature in Celsius (C^o) for Chamber 1

- Ox.1 contains values of dissolved oxygen measured in 'mg/L', 'mmol/L' or 'ml/L' for Chamber 1. If other measurement units were used, convert them to 'mg/L', 'mmol/L' or 'ml/L' using the function convert.respirometry or convert.rMR.
- ...

Value

The function returns a data frame containing standardized raw data of a background respiration test. The data frame should be used in the function correct.meas to correct metabolic rate measurements for background respiration.

Examples

```
# Import raw data for pre- and post-tests

# if the data have been already loaded to R,
# skip the first line of the code:
data(info)

pre.path = system.file("extdata/stickleback/pre_raw.txt.xz", package = "FishResp")
pre <- import.test(pre.path,
                   info.data = info,
                   logger = "AutoResp",
                   n.chamber = 4,
                   plot.temperature = TRUE,
                   plot.oxygen = TRUE)

post.path = system.file("extdata/stickleback/post_raw.txt.xz", package = "FishResp")
post <- import.test(post.path,
                    info.data = info,
                    logger = "AutoResp",
                    n.chamber = 4,
                    plot.temperature = TRUE,
                    plot.oxygen = TRUE)
```

---

info *Info about Individuals and Chambers*

Description

A dataset contains the information about individuals (three-spined sticklebacks) and chambers (Blazka-type, 250 mL) which were input manually in the function input.info)

Usage

```
info
```

Format

A data frame with 4 rows and 4 variables:

ID ID of an animal

Mass wet mass of an animal (g)

Volume the volume of a chamber (mL)

DO.unit the measure unit of DO concentration

`input.info` *Input the Information about Individuals and Chambers*

Description

The function is used to input manually the information required for metabolic rate calculations: ID and wet mass of individuals, volume of chambers. Values of those parameters should be filled in the same order in a vector format replacing default NA values in the template. In addition, specify which unit has been used to measure dissolved oxygen concentration.

Usage

```
input.info(ID = c(NA, NA, NA, NA, NA, NA, NA, NA),
           Mass = c(NA, NA, NA, NA, NA, NA, NA, NA),
           Volume = c(NA, NA, NA, NA, NA, NA, NA, NA),
           DO.unit = c("mg/L", "mmol/L", "ml/L"))
```

Arguments

`ID`	string: ID of fish or another aquatic organism
`Mass`	numeric: wet mass of an individual in grams (g)
`Volume`	numeric: the volume of a chamber in milliliters (mL) or the whole respirometry loop (if measured)
`DO.unit`	character: dissolved oxygen used in raw data should be measured in 'mg/L', 'mmol/L' or 'ml/L'. If other measurement units were used, convert them to 'mg/L', 'mmol/L' or 'ml/L' using the function `convert.respirometry` or `convert.rMR`.

Details

It is especially important to keep such format of vectors when not the full number of individuals is in a multi-channel respirometry system. E.g.: if you use a 4-channel respirometry system with three fish and only Chamber 1 is empty, but data are still collected from there, do not remove NA values for that chamber to prevent the shift of actual data between the chambers.

Value

The function returns a data frame with four columns: "ID", "Mass", "Volume", "DO.unit". The data frame is used in the functions `import.test`, `import.meas`, and `correct.meas`.

Examples

```
# Four sticklebacks in a 4-channel respirometry system
info <- input.info(ID = c("Stickleback_1", "Stickleback_2",
                          "Stickleback_3", "Stickleback_4"),
                   Mass = c(1.86, 1.92, 2.23, 1.80),
                   Volume = c(250, 250, 250, 250),
                   DO.unit = "mg/L")
```

`post` *Post Raw Data*

Description

A dataset contains raw data of a background test conducted before metabolic rate measurements (post-test), obtained by using the function `import.test`.

Usage

```
post
```

Format

A data frame with 2400 rows and 7 variables:

Chamber.No the number of a chamber

Test a constant string "test"

Time ordinal number of seconds in each measurement phase (1-600)

Init.O2 initial level of dissolved oxygen (mgO2/L)

Temp temperature at each second (C^o)

O2 actual level of dissolved oxygen at each second (mgO2/L)

delta.O2 the difference between actual and initial O_2

`pre` *Pre Raw Data*

Description

A dataset contains raw data of a background test conducted before metabolic rate measurements (pre-test), obtained by using the function `import.test`.

Usage

```
pre
```

Format

A data frame with 4800 rows and 7 variables:

Chamber.No the number of a chamber

Test a constant string "test"

Time ordinal number of seconds in each measurement phase (1-1200)

Init.O2 initial level of dissolved oxygen (mgO2/L)

Temp temperature at each second (C^o)

O2 actual level of dissolved oxygen at each second (mgO2/L)

delta.O2 the difference between actual and initial O_2

---

prepare.data *Prepare Raw Respirometry Data*

Description

This function is used for preparation of raw data in the FishResp format before the actual respirometry analysis. As namely, the function will create measurement points for each second (the required FishResp format) if the time interval between two measurement points is more than one second. In addition, low and high thresold for both dissolved oxygen and water temperature might be applied here. The measurement points beyond the threshold(s) will be transformed to NA (be careful if use the 'parallel' method for background respiration correction as it might transform DO or Temp to NA as well).

Usage

```
prepare.data(import.file, export.file,
             date.format = c("DMY", "MDY", "YMD"),
             DO.low = NA, DO.high = NA,
             Temp.low = NA, Temp.high = NA)
```

Arguments

`import.file`	the name of a file with raw respirometry data which should be imported for raw data preparation
`export.file`	the name of a file with results of raw data preparation
`date.format`	string: date format (DMY, MDY or YMD), where D = day, M = month, Y - year.
`DO.low`	numeric: the low threshold defining a minimum accepted value for dissolved oxygen (DO)
`DO.high`	numeric: the high threshold defining a maximum accepted value for dissolved oxygen (DO)
`Temp.low`	numeric: the low threshold defining a minimum accepted value for water temperature (Temp)
`Temp.high`	numeric: the high threshold defining a maximum accepted value for water temperature (Temp)

Value

The function exports a data file with one second interval between measurement points and excluded data beyond the defined threshold(s)

Examples

```
## Not run:
amphipod.path = system.file("extdata/amphipod/amphipod.txt",
                 package = "FishResp")

prepare.data(import.file = amphipod.path,
             export.file = "amphipod_corrected.txt",
             date.format = "DMY",
             DO.low = 0.5,
             DO.high = 12)

## End(Not run)
```

`presens.aquaresp` *Convert Respirometry Data from PreSens and AquaResp Software to the FishResp Format*

Description

The function is used to convert raw data from 'OxyView' (PreSens) and a summary file from 'AquaResp' (free software) to 'FishResp' format. This function should be applied before usage of the functions `import.test` and `import.meas`. The output is a file containing raw respirometry data in the 'FishResp' format (see Details in `import.test` to read more information about the 'FishResp' format)

Usage

```
presens.aquaresp(presens.file,
                 aquaresp.file,
                 fishresp.file,
                 n.chamber = c(1,2,3,4),
                 date.format = c("DMY", "MDY", "YMD"),
                 wait.phase = NA, measure.phase = NA)
```

Arguments

`presens.file`	the name of a file which contains raw data obtained from the 'OxyView' software (PreSens)
`aquaresp.file`	the name of a file which contains summary data obtained from the 'AquaResp' software (free software)
`fishresp.file`	the name of an exported file containing raw data in the 'FishResp' format
`n.chamber`	integer: the number of chambers used in an experiment (including empty ones)

date.format	string: date format (DMY, MDY or YMD) used in raw data obtained from the 'OxyView' software
wait.phase	integer: duration of the wait phase (in seconds), see the 'AquaResp' summary file (row #5)
measure.phase	integer: duration of the measure phase (in seconds), see the 'AquaResp' summary file (row #6)

Value

The function exports a file containing raw data in the 'FishResp' format

Examples

```
## Not run:
presens.path.1 = system.file("extdata/presens/presens-ch1.txt",
                 package = "FishResp")
presens.path.2 = system.file("extdata/presens/presens-ch2.txt",
                 package = "FishResp")
presens.path.3 = system.file("extdata/presens/presens-ch3.txt",
                 package = "FishResp")
presens.path.4 = system.file("extdata/presens/presens-ch4.txt",
                 package = "FishResp")
aquaresp.path = system.file("extdata/presens/presens-aquaresp.txt",
                 package = "FishResp")

presens.aquaresp(presens.file = c(presens.path.1, presens.path.2,
                                  presens.path.3, presens.path.4),
                 aquaresp.file = aquaresp.path,
                 fishresp.file = "fishresp.txt",
                 date.format = "DMY",
                 n.chamber = 4,
                 wait.phase = 60,
                 measure.phase = 240)

## End(Not run)
```

---

pyroscience.aquaresp *Convert Respirometry Data from PyroScience and AquaResp Software to the FishResp Format*

Description

The function is used to convert raw data from 'Pyro Oxygen Logger' (PyroScience) and a summary file from 'AquaResp' (free software) to 'FishResp' format. This function should be applied before usage of the functions import.test and import.meas. The output is a file containing raw respirometry data in the 'FishResp' format (see Details in import.test to read more information about the 'FishResp' format)

Usage

```
pyroscience.aquaresp(pyroscience.file,
                     aquaresp.file,
                     fishresp.file,
                     n.chamber = c(1,2,3,4),
                     date.format = c("DMY", "MDY", "YMD"),
                     wait.phase = NA, measure.phase = NA)
```

Arguments

pyroscience.file	the name of a file which contains raw data obtained from the 'Pyro Oxygen Logger' software (PyroScience)
aquaresp.file	the name of a file which contains summary data obtained from the 'AquaResp' software (free software)
fishresp.file	the name of an exported file containing raw data in the 'FishResp' format
n.chamber	integer: the number of chambers used in an experiment (including empty ones)
date.format	string: date format (DMY, MDY or YMD) used in raw data obtained from the 'Pyro Oxygen Logger' software
wait.phase	integer: duration of the wait phase (in seconds), see the 'AquaResp' summary file (row #5)
measure.phase	integer: duration of the measure phase (in seconds), see the 'AquaResp' summary file (row #6)

Value

The function exports a file containing raw data in the 'FishResp' format

Examples

```
## Not run:
pyroscience.path = system.file("extdata/pyroscience/pyroscience.txt",
                 package = "FishResp")
aquaresp.path = system.file("extdata/pyroscience/pyroscience-aquaresp.txt",
                 package = "FishResp")

pyroscience.aquaresp(pyroscience.file = pyroscience.path,
                     aquaresp.file = aquaresp.path,
                     fishresp.file = "fishresp.txt",
                     date.format = "MDY",
                     n.chamber = 1,
                     wait.phase = 120,
                     measure.phase = 600)

## End(Not run)
```

`pyroscience.pumpresp` *Convert Respirometry Data from PyroScience and the pump controller PumpResp to the FishResp Format*

Description

The function is used to convert raw data from 'Pyro Oxygen Logger' (PyroScience) and a logger file of the pump controller PumpResp to the 'FishResp' format. This function should be applied before usage of the functions `import.test` and `import.meas`. The output is a file containing raw respirometry data in the 'FishResp' format (see Details in `import.test` to read more information about the 'FishResp' format)

Usage

```
pyroscience.pumpresp(pyroscience.file,
                     pumpresp.file,
                     fishresp.file,
                     n.chamber = c(1,2,3,4),
                     date.format = c("DMY", "MDY", "YMD"))
```

Arguments

`pyroscience.file`	the name of a file which contains raw data obtained from the 'Pyro Oxygen Logger' software (PyroScience)
`pumpresp.file`	the name of a file which contains logger data obtained from the pump conroller PumpResp
`fishresp.file`	the name of an exported file containing raw data in the 'FishResp' format
`n.chamber`	integer: the number of chambers used in an experiment (including empty ones)
`date.format`	string: date format (DMY, MDY or YMD) used in raw data obtained from the 'Pyro Oxygen Logger' software

Value

The function exports a file containing raw data in the 'FishResp' format

Examples

```
## Not run:
pyroscience.path = system.file("extdata/salmon/salmon_pyroscience.txt",
                 package = "FishResp")

pumpresp.path = system.file("extdata/salmon/salmon_pumpresp.txt",
                 package = "FishResp")

pyroscience.pumpresp(pyroscience.path,
                     pumpresp.path,
```

```
                    "fishresp.txt",
                    n.chamber = 4,
                    date.format = "DMY")

## End(Not run)
```

QC.activity *Quality Control of Animal Activity*

Description

Graphical quality control tests for animal activity in chambers over the period of measurements defined in the function correct.meas. The function is used for determination of time period for calculation of standard or resting metabolic rate. Note, that mass-specific metabolic rate is calculated for each period of measurements (not raw data).

Usage

```
QC.activity(clean.data, compare = TRUE, output = FALSE)
```

Arguments

clean.data	a data frame obtained by using the function correct.meas
compare	logical: if TRUE then two graphs are plotted to compare mass-specific metabolic rate before and after correction for background respiration
output	logical: if TRUE then the functions return output or print it

Details

QC.activity uses functions extract.slope and calculate.MR with default parameters (excluding $r^2 = 0$) to plot a graph of animal activity

Examples

```
# if the data have been already loaded to R,
# skip the first line of the code:
data(SMR.clean)

QC.activity(SMR.clean, compare = TRUE)
```

QC.meas *Quality Control of Raw Data*

Description

Graphical quality control tests of temperature and oxygen raw data before and after correction for background respiration

Usage

```
QC.meas(clean.data,
        QC = c("Temperature",
               "Total.O2.phases",
               "Corrected.O2.phases",
               "Total.O2.chambers",
               "Corrected.O2.chambers"))
```

Arguments

clean.data	a data frame obtained by using the function correct.meas
QC	string: the name of a visual QC test. Five options are available:

- "Temperature": a graph of temperature vs. time ordered by chambers
- "Total.O2.chambers": a graph of dissolved oxygen vs. time ordered by chambers
- "Total.O2.phases": a graph of dissolved oxygen vs. time ordered by chambers and phases
- "Corrected.O2.chambers": a graph of dissolved oxygen corrected for background respiration vs. time ordered by chambers
- "Corrected.O2.phases": a graph of dissolved oxygen corrected for background respiration vs. time ordered by chambers and phases

Examples

```
## Not run:
# if the data have been already loaded to R,
# skip the first line of the code:
data(SMR.clean)

QC.meas(SMR.clean, "Temperature")
QC.meas(SMR.clean, "Total.O2.phases")
QC.meas(SMR.clean, "Corrected.O2.phases")
QC.meas(SMR.clean, "Total.O2.chambers")
QC.meas(SMR.clean, "Corrected.O2.chambers")

## End(Not run)
```

QC.slope *Quality Control of Slope(s)*

Description

Graphical quality control test of extracted slopes represents a visual comparison of linear regression of corrected O_2 concentration over time with current and alternative length of measurements.

Usage

```
QC.slope(slope.data, clean.data,
         chamber = c("CH1", "CH2", "CH3", "CH4",
                     "CH5", "CH6", "CH7", "CH8"),
         current = 999999, alter = 999999, residuals = FALSE)
```

Arguments

slope.data	a data frame obtained by using the function extract.slope
clean.data	a data frame obtained by using the function correct.meas
chamber	string: the chamber chosen for the QC test
current	integer: current length of measurements for slope estimation (in seconds, black line)
alter	integer: alternative length of measurements for slope estimation (in seconds, red line)
residuals	logical: if TRUE then regression diagnostic graphs are plotted for each slope estimation (black graphs: for current slope estimation; red graphs: for alternative slope estimation). More information on diagnostic graphs can be found in the documentation of the function plot.lm.

Examples

```
# if the data have been already loaded to R,
# skip the first four lines of the code:
data(SMR.clean)
data(SMR.slope)
data(AMR.clean)
data(AMR.slope)

QC.slope(SMR.slope, SMR.clean, chamber = "CH1",
         current = 1200, alter = 600)

QC.slope(AMR.slope, AMR.clean, chamber = "CH4",
         current = 600, alter = 300, residuals = TRUE)
```

`results` *Results of Analysis: SMR, AMR and MS*

Description

A final dataset containing information about both standard and active metabolic rates, and metabolic scope obtained by using the function `export.MR`.

Usage

```
results
```

Format

A data frame with 36 rows and 18 variables:

Chamber.No The number of a chamber

Ind ID of an animal

Mass wet mass of an animal (g)

Volume the volume of a chamber (mL)

DO.unit the measure unit of DO concentration

SMR_Temp Average temperature over a period of a measurement phase (C^o)

SMR_R2 $r^2 = 0$ of a slope of animal oxygen consumption without background respiration

SMR_BR Percentage rate of background respiration

SMR_MR.abs Absolute SMR ($mgO_2\ h^{-1}$)

SMR_MR.mass Mass-specific SMR ($mgO_2\ kg^{-1}h^{-1}$)

AMR_Temp Average temperature over a period of a measurement phase (C^o)

AMR_R2 $r^2 = 0$ of a slope of animal oxygen consumption without background respiration

AMR_BR Percentage rate of background respiration

AMR_MR.abs Absolute AMR ($mgO_2\ h^{-1}$)

AMR_MR.mass Mass-specific AMR ($mgO_2\ kg^{-1}h^{-1}$)

MS.abs Absolute metabolic scope: the difference between absolute AMR and SMR ($mgO_2\ h^{-1}$)

MS.mass Mass-specific metabolic scope: the difference between mass-specific AMR and SMR ($mgO_2\ kg^{-1}h^{-1}$)

MS.fact Factorial metabolic scope: the ratio between AMR and SMR

`rm.data` *Remove Poor Quality Data*

Description

The function nulls values of the column 'O2.correct' for specified measurement phase(s) of a specified chamber in a data frame generated by the function `correct.meas`. As a result, those nulled data will not be available for futher steps of the analysis, particularly for the function `extract.slope`.

Usage

```
rm.data(clean.data,
        chamber = c("CH1", "CH2", "CH3", "CH4",
                    "CH5", "CH6", "CH7", "CH8"),
        M.phase = "M0")
```

Arguments

`clean.data`	a data frame obtained by using the function `correct.meas`
`chamber`	string: the chamber where poor quality data were observed (must not contain multiple elements in a vector)
`M.phase`	string: the measurement phase(s) which should be eliminated from further steps of the analysis.

Value

The function returns a data frame containing data of metabolic rate measurements corrected for background respiration, where values of the column 'O2.correct' for exluded measurement phases were nulled. The data frame is used in the functions `extract.slope` and `QC.slope`.

Examples

```
# if the data have been already loaded to R,
# skip the first line of the code:
data(AMR.clean)
AMR.clean.modified <- rm.data(AMR.clean,
                              chamber = "CH3",
                              M.phase = c("M1","M2"))
```

SMR *Standard Metabolic Rate: Final Data*

Description

A dataset contains background respiration, absolute and mass-specific standard metabolic rate data obtained by using the function `calculate.MR`

Usage

```
SMR
```

Format

A data frame with 12 rows and 16 variables:

Chamber.No the number of a chamber

Ind ID of an animal

Mass wet mass of an animal (g)

Volume the volume of a chamber (mL)

Date.Time date and time of a measurement phase (yyyy/mm/dd hh:mm:ss)

Phase the type of phase and an ordinal number of measurements (e.g. M1)

Temp average temperature over the period of a measurement phase (C^o)

Slope.with.BR slope of animal oxygen consumption with slope of background respiration ($mgO_2\ L^{-1}s^{-1}$)

Slope slope of animal oxygen consumption without background respiration ($mgO_2\ L^{-1}s^{-1}$)

SE standard error of a slope of animal oxygen consumption without background respiration ($mgO_2\ L^{-1}s^{-1}$)

R2 r^2 of a slope of animal oxygen consumption without background respiration

MR.abs.with.BR absolute SMR with background respiration ($mgO_2\ h^{-1}$)

BR percentage rate of background respiration

MR.abs absolute SMR ($mgO_2\ h^{-1}$)

MR.mass mass-specific SMR ($mgO_2\ kg^{-1}h^{-1}$)

DO.unit the measure unit of DO concentration

SMR.clean *Standard Metabolic Rate: Corrected Raw Data*

Description

A dataset contains raw data of standard metabolic rate measurements corrected for background respiration using the function correct.meas

Usage

```
SMR.clean
```

Format

A data frame with 76800 rows and 17 variables:

Date.Time date and time (yyyy/mm/dd hh:mm:ss)

Date date (yyyy/mm/dd)

Real.Time time (hh:mm:ss)

Time ordinal number of seconds in each measurement phase (1-1200)

Phase the type of phase and an ordinal number of measurements (e.g. M1, F3)

Start.Meas the first second of a measurement phase (hh:mm:ss)

End.Meas the last second of a measurement phase (hh:mm:ss)

Chamber.No the number of a chamber

Ind ID of an animal

Mass wet mass of an animal (g)

Volume the volume of a chamber (mL)

Init.O2 initial level of dissolved oxygen (mgO2/L)

Temp temperature at each second (C^o)

O2 actual level of dissolved oxygen at each second (mgO2/L)

BR slope of background respiration ($mgO_2\ L^{-1}s^{-1}$)

O2.correct actual level of dissolved oxygen at each second corrected by slope of background respiration (mgO2/L)

DO.unit the measure unit of DO concentration

SMR.raw *Standard Metabolic Rate: Raw Data*

Description

The dataset containing raw data of standard metabolic rate measurements obtained by using the function import.meas)

Usage

```
SMR.raw
```

Format

A data frame with 19200 rows and 16 variables:

Date.Time date and time (yyyy/mm/dd hh:mm:ss)

Phase the type of phase and an ordinal number of measurements (e.g. M1, F3)

Temp.1 temperature at each second (C^o)

Ox.1 actual level of dissolved oxygen at each second (mgO2/L)

Real.Time time (hh:mm:ss)

Date date (yyyy/mm/dd)

Time ordinal number of seconds in each measurement phase (1-1200)

Start.Meas the first second of a measurement phase (hh:mm:ss)

End.Meas the last second of a measurement phase (hh:mm:ss)

Total.Phases the total number of measurement phases (constant value)

Ox.2 see Ox.1

Ox.3 see Ox.1

Ox.4 see Ox.1

Temp.2 see Temp.1

Temp.3 see Temp.1

Temp.4 see Temp.1

SMR.slope *Standard Metabolic Rate: Extracted Slope(s)*

Description

A dataset containing extracted slopes for further SMR calculations and other attributes of standard metabolic rate measurements obtained by using the function `extract.slope`

Usage

```
SMR.slope
```

Format

A data frame with 12 rows and 12 variables:

Chamber.No the number of a chamber

Ind ID of an animal

Mass wet mass of an animal (g)

Volume the volume of a chamber (mL)

Date.Time date and time of a measurement phase (yyyy/mm/dd hh:mm:ss)

Phase the type of phase and an ordinal number of measurements (e.g. M1)

Temp average temperature over the period of a measurement phase (C^o)

Slope.with.BR slope of animal oxygen consumption with slope of background respiration ($mgO_2\ L^{-1}s^{-1}$)

Slope slope of animal oxygen consumption without background respiration ($mgO_2\ L^{-1}s^{-1}$)

SE standard error of a slope of animal oxygen consumption without background respiration ($mgO_2\ L^{-1}s^{-1}$)

R2 r^2 of a slope of animal oxygen consumption without background respiration

DO.unit the measure unit of DO concentration

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