Package 'MFO'

October 12, 2022

Title Maximal Fat Oxidation and Kinetics Calculation

Version 0.1.0

Description Calculate the maximal fat oxidation, the exercise intensity that elicits the
maximal fat oxidation and the SIN model to represent the fat oxidation kinetics.
Three variables can be obtained from the SIN model: dilatation, symmetry and translation.
Examples of these meth-
ods can be found in Montes de Oca et al (2021) <doi:10.1080/17461391.2020.1788650>
and Chenevière et al. (2009) <doi:10.1249/MSS.0b013e31819e2f91>.

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LazyData true

RoxygenNote 7.1.1

URL https://github.com/JorgeDelro/MFO

BugReports https://github.com/JorgeDelro/MFO/issues

Imports stats, dplyr, ggplot2, magrittr, tibble, minpack.lm, openxlsx,
readxl, stringr, tidyr

Depends R (>= 2.10)

Suggests covr, testthat (>= 3.0.0)

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R topics documented:

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basal_df *Basal test dataframe*

Description

A dataframe with the results of a test to assess basal metabolism

Usage

```
data(basal_df)
```

Format

A data frame with 88 rows and 8 variables:

Time time test, in minutess

HR heart rate, in beats/min

VO2 volume of oxygen consumption, in ml/min

VCO2 volume of exhaled carbon dioxide, in ml/min

RER respiratory exchange ratio

BF breathe frequency, in breaths/min

VE ventilation, in l/min

PETCO2 end-tidal carbondioxide pressure, in mmHg

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calculate_steps *Calculate steps*

Description

Calculate steps

Usage

```
calculate_steps(step_time, db, db_type)
```

Arguments

step_time	how often the data was collected (in seconds).
db	a database
db_type	either "basal" or "MFO"

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calculate_vars *Calculation of CHO, FAT and Kcal*

Description

Calculation of CHO, FAT and Kcal

Usage

```
calculate_vars(step_time, db_MFO, VO2max, author)
```

Arguments

step_time	how often the data was collected (in seconds).
db_MFO	dtabase with MFO test
VO2max	maximum oxygen uptake
author	eithe "Frayn" or "Jeukendrup"

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get_5min   *Get a 5 minutes database*

Description

Get a 5 minutes database

Usage

```
get_5min(db, cv_var, n_row)
```

Arguments

db	a database
cv_var	variable to calculate coefficient of variation
n_row	number of rows

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met_basal   *Basal metabolic rate*

Description

Basal metabolic rate

Usage

```
met_basal(step_time, db, cv_var)
```

Arguments

step_time	how often the data was collected (in seconds).
db	a database
cv_var	variable to calculate coefficient of variation

MFO *Maximal Fat Oxidation & Fat Max Function*

Description

Maximal Fat Oxidation & Fat Max Function

Usage

```
MFO(
  step_time,
  db_MFO,
  db_basal,
  db_graded = NULL,
  cv_var,
  author,
  VO2max = NULL
)
```

Arguments

step_time	how often the data was collected (in seconds).
db_MFO	database containing MFO test.
db_basal	database containing basal test.
db_graded	database containing incremental exercise test.
cv_var	variable to estimate coefficient of variation. Can be: VO2, VCO2 or RER.
author	author to estimate MFO. Can be: Frayn or Jeukendrup.
VO2max	VO2max can be passed directly using this argument instead of use db_graded argument.

Value

Returns a list which contains:

- MFO_db: database used to create the MFO plot.
- MFO_plot: ggplot object with the MFO plot.
- MFO: Maximal fat oxidation.
- FAT_MAX: Intensity that elicits MFO.
- x_CHO: carbohydrates in basal metabolism.
- x_FAT: fat in basal metabolism.
- x_Kcal: Kcal in basal metabolism.

Examples

```
## Not run:
# Get old working directory
oldwd <- getwd()

# Set temporary directory
setwd(tempdir())

# Read dfs
data(list = c("basal_df", "MFO_df", "VO2max_df"), package = "MFO")

# Convert to data.frame
basal_df <- data.frame(basal_df)
MFO_df <- data.frame(MFO_df)
VO2max_df <- data.frame(VO2max_df)

# Calculate MFO and Fatmax
result_MFO <- MFO(step_time = 20,
                  db_MFO = MFO_df,
                  db_basal = basal_df,
                  db_graded = VO2max_df,
                  cv_var = "RER",
                  author = "Frayn",
                  VO2max = NULL)

# set user working directory
setwd(oldwd)

## End(Not run)
```

MFOs   *Maximal Fat Oxidation calculation of multiple databases*

Description

Maximal Fat Oxidation calculation of multiple databases

Usage

```
MFOs(
  from = c("folder", "files"),
  path,
  db_basal_name,
  db_MFO_name,
  db_graded_name,
  step_time,
  cv_var,
```

```
    author,
    VO2max = NULL,
    remove_rows = NULL,
    col_name_VO2 = "VO2",
    col_name_VCO2 = "VCO2",
    col_name_RER = "RER",
    col_name_HR = "HR",
    save_plot = TRUE,
    save_result = TRUE
)
```

Arguments

`from`	select or folder (basal, MFO and graded databases of the same participant are store in different files but in the same folder) or files (basal, MFO and graded databases of the same participant are store in one file but in different sheets)
`path`	path to the folder with the databases
`db_basal_name`	name given to the basal database, eg: basal_df
`db_MFO_name`	name given to the MFO database, eg: MFO_df
`db_graded_name`	name given to the graded database, eg: VO2max_df
`step_time`	how often the data was collected (in seconds).
`cv_var`	variable to estimate coefficient of variation. Can be: VO2, VCO2 or RER.
`author`	author to estimate MFO. Can be: Frayn or Jeukendrup.
`VO2max`	VO2max can be passed directly using this argument instead of use db_graded argument. Default set to NULL.
`remove_rows`	An integer (or a vector of integers) representing the position of the rows to delete
`col_name_VO2`	name given to the variable VO2 in the databases. Must be the same for all databases. Default set to "VO2"
`col_name_VCO2`	name given to the variable VCO2 in the databases. Must be the same for all databases. Default set to "VCO2"
`col_name_RER`	name given to the variable RER in the databases. Must be the same for all databases. Default set to "RER"
`col_name_HR`	name given to the variable HR in the databases. Must be the same for all databases. Default set to "HR"
`save_plot`	to save the plot or not. Default set to True.
`save_result`	to save the results in a .xlsx file or not. Default set to True.

Value

This function creates an .xlsx file in the working directory with the following variables:

- MFO_db: database used to create the MFO plot.
- MFO_plot: ggplot object with the MFO plot.
- MFO: Maximal fat oxidation.

- FAT_MAX: Intensity that elicits MFO.

- x_CHO: carbohydrates in basal metabolism.

- x_FAT: fat in basal metabolism.

- x_Kcal: Kcal in basal metabolism.

Examples

```
## Not run:
# Get old working directory
oldwd <- getwd()

# Set temporary directory
setwd(tempdir())

# Create path to store databases
dir.create(paste(getwd(),"/MFO_databases", sep = ""))
# Get path to databases
path <- paste(getwd(),"/MFO_databases", sep = "")

# MFOs function
# "path" is the path to the databases
MFOs <- function(from = "folder",
                 path = path,
                 db_basal_name = "basal_df",
                 db_MFO_name = "MFO_df",
                 db_graded_name = "graded_df",
                 step_time = 20,
                 cv_var = "RER",
                 author = "Frayn",
                 VO2max = NULL,
                 remove_rows = NULL,
                 col_name_VO2 = "VO2",
                 col_name_VCO2 = "VCO2",
                 col_name_RER = "RER",
                 col_name_HR = "HR",
                 save_plot = TRUE,
                 save_result = TRUE)

# set user working directory
setwd(oldwd)

## End(Not run)
```

MFO_df   *MFO test dataframe*

Description

A dataframe with the results of a test to assess MFO metabolism

Usage

```
data(MFO_df)
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 45 rows and 8 columns.

Variables

Time time test, in minutess

HR heart rate, in beats/min

VO2 volume of oxygen consumption, in ml/min

VCO2 volume of exhaled carbon dioxide, in ml/min

RER respiratory exchange ratio

VE ventilation, in l/min

PETCO2 end-tidal carbondioxide pressure, in mmHg

MFO_kinetics	*Maximal Fat Oxidation Kinetics*

Description

Maximal Fat Oxidation Kinetics

Usage

```
MFO_kinetics(MFO_data)
```

Arguments

`MFO_data`   a data frame obtained from MFO function

Value

Returns a list which contains:

- MFO_kinetics_data: database used to create the MFO kinetics plot.
- MFO_kinetics_plot: ggplot object with the MFO kinetics plot.
- d: dilatation.
- t: translation.
- s: symmetry.

Examples

```
## Not run:
# Get old working directory
oldwd <- getwd()

# Set temporary directory
setwd(tempdir())

# Read dfs
data(list = c("basal_df", "MFO_df", "VO2max_df"), package = "MFO")

# Convert to data.frame
basal_df <- data.frame(basal_df)
MFO_df <- data.frame(MFO_df)
VO2max_df <- data.frame(VO2max_df)

# Calculate MFO and Fatmax
result_MFO <- MFO(step_time = 20,
                db_MFO = MFO_df,
                db_basal = basal_df,
                db_graded = VO2max_df,
                cv_var = "RER",
                author = "Frayn",
                VO2max = NULL)

# Calculate MFO Kinetics
result_MFO_kinetics <- MFO_kinetics(result_MFO$MFO_db)

# set user working directory
setwd(oldwd)

## End(Not run)
```

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read_MFO_databases   *Read databases for MFO package*

Description

Read databases for MFO package

Usage

```
read_MFO_databases(
  from = c("folder", "files"),
  path,
  db_basal_name,
  db_MFO_name,
  db_graded_name,
```

```
    col_name_VO2,
    col_name_VCO2,
    col_name_RER,
    col_name_HR,
    remove_rows = NULL
)
```

Arguments

from	select either from folder or files
path	path to the the databases
db_basal_name	name of the database with the basal metabolic rate test
db_MFO_name	name of the database of MFO test
db_graded_name	name of the database of the graded exercise test
col_name_VO2	name given to the variable VO2 in the databases. Must be the same for all databases. Default set to "VO2"
col_name_VCO2	name given to the variable VCO2 in the databases. Must be the same for all databases. Default set to "VCO2"
col_name_RER	name given to the variable RER in the databases. Must be the same for all databases. Default set to "RER"
col_name_HR	name given to the variable HR in the databases. Must be the same for all databases. Default set to "HR"
remove_rows	An integer (or a vector of integers) representing the position of the rows to delete

Value

Returns 3 databases:

- participant_db_basal: database with basal metabolism.
- participant_db_MFO: database with MFO test.
- participant_db_graded: graded exercise test.

VO2max_df	*Graded exercise test dataframe*

Description

A dataframe with the results of a graded exercise test

Usage

```
data(VO2max_df)
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 30 rows and 9 columns.

Variables

Time time test, in minutess

HR heart rate, in beats/min

Load Load of the test, in watts

VO2 volume of oxygen consumption, in ml/min

VCO2 volume of exhaled carbon dioxide, in ml/min

RER respiratory exchange ratio

VE ventilation, in l/min

PETCO2 end-tidal carbondioxide pressure, in mmHg

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