

Package ‘MFO’

January 20, 2025

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 methods can be found in Montes de Oca et al (2021) <[doi:10.1080/17461391.2020.1788650](https://doi.org/10.1080/17461391.2020.1788650)> and Chenevière et al. (2009) <[doi:10.1249/MSS.0b013e31819e2f91](https://doi.org/10.1249/MSS.0b013e31819e2f91)>.

License MIT + file LICENSE

Encoding UTF-8

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)

Config/testthat/edition 3

NeedsCompilation no

Author Jorge R Fernandez-Santos [aut, cre]
(<<https://orcid.org/0000-0002-5047-2976>>),
Jesus G Ponce-Gonzalez [ctb] (<<https://orcid.org/0000-0002-5982-7761>>),
Cristina Casals [ctb] (<<https://orcid.org/0000-0002-6992-0492>>),
Jose L Gonzalez-Montesinos [ctb]
(<<https://orcid.org/0000-0002-6867-7718>>),
Juan Corral-Perez [ctb] (<<https://orcid.org/0000-0002-6574-9827>>),
Alejandro Perez-Bey [ctb] (<<https://orcid.org/0000-0002-9849-5544>>)

Maintainer Jorge R Fernandez-Santos <jorgedelrosario.fernandez@uca.es>

Repository CRAN

Date/Publication 2022-02-11 19:00:13 UTC

Contents

| | |
|------------------------------|-----------|
| basal_df | 2 |
| calculate_steps | 3 |
| calculate_vars | 3 |
| get_5min | 4 |
| met_basal | 4 |
| MFO | 5 |
| MFOs | 6 |
| MFO_df | 8 |
| MFO_kinetics | 9 |
| read_MFO_databases | 10 |
| VO2max_df | 11 |
| Index | 13 |

| | |
|----------|-----------------------------|
| basal_df | <i>Basal test dataframe</i> |
|----------|-----------------------------|

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

| | |
|-----------------|------------------------|
| calculate_steps | <i>Calculate steps</i> |
|-----------------|------------------------|

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" |

| | |
|----------------|---|
| calculate_vars | <i>Calculation of CHO, FAT and Kcal</i> |
|----------------|---|

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 | database with MFO test |
| VO2max | maximum oxygen uptake |
| author | either "Frayn" or "Jeukendrup" |

| | |
|----------|---------------------------------|
| get_5min | <i>Get a 5 minutes database</i> |
|----------|---------------------------------|

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 |

| | |
|-----------|-----------------------------|
| met_basal | <i>Basal metabolic rate</i> |
|-----------|-----------------------------|

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 |

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", "V02max_df"), package = "MFO")

# Convert to data.frame
basal_df <- data.frame(basal_df)
MFO_df <- data.frame(MFO_df)
V02max_df <- data.frame(V02max_df)

# Calculate MFO and Fatmax
result_MFO <- MFO(step_time = 20,
                  db_MFO = MFO_df,
                  db_basal = basal_df,
                  db_graded = V02max_df,
                  cv_var = "RER",
                  author = "Frayn",
                  V02max = 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",
                 V02max = NULL,
                 remove_rows = NULL,
                 col_name_V02 = "V02",
                 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", "V02max_df"), package = "MFO")

# Convert to data.frame
basal_df <- data.frame(basal_df)
MFO_df <- data.frame(MFO_df)
V02max_df <- data.frame(V02max_df)

# Calculate MFO and Fatmax
result_MFO <- MFO(step_time = 20,
                  db_MFO = MFO_df,
                  db_basal = basal_df,
                  db_graded = V02max_df,
                  cv_var = "RER",
                  author = "Frayn",
                  V02max = NULL)

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

# set user working directory
setwd(oldwd)

## End(Not run)
```

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

Index

* datasets

- basal_df, [2](#)
- MFO_df, [8](#)
- V02max_df, [11](#)

basal_df, [2](#)

calculate_steps, [3](#)

calculate_vars, [3](#)

get_5min, [4](#)

met_basal, [4](#)

MFO, [5](#)

MFO_df, [8](#)

MFO_kinetics, [9](#)

MFOs, [6](#)

read_MFO_databases, [10](#)

V02max_df, [11](#)