Package ‘MFO’

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> and Chenevière et al. (2009) <doi:10.1249/MSS.0b013e31819e2f91>.
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**basal_df**

**R topics documented:**

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- VO2max_df

**Description**

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

**Usage**

```r
data(basal_df)
```

**Format**

A data frame with 88 rows and 8 variables:

- **Time**  time test, in minutes
- **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**

**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`: database with MFO test
- `VO2max`: maximum oxygen uptake
- `author`: either "Frayn" or "Jeukendrup"
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

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
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.
## Not run:

```r
# Get old working directory
oldwd <- getwd()

# Set temporary directory
setwd(tempdir())

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

# 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)
```

### Description

Maximal Fat Oxidation calculation of multiple databases

### Usage

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

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

```r
## 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**
**MFO_kinetics**

**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 minutes
- **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 carbon dioxide 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

```r
## 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 direction
setwd(oldwd)

## End(Not run)
```

---

read_MFO_databases  Read databases for MFO package

Description

Read databases for MFO package

Usage

```r
read_MFO_databases(
  from = c("folder", "files"),
  path,
  db_basal_name,
  db_MFO_name,
  db_graded_name,
)```
VO2max_df

    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.

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 minutes
- **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 carbon dioxide pressure, in mmHg
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