

Package ‘musclesyneRgies’

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Title Extract Muscle Synergies from Electromyography

Version 1.1.3

Description Provides a framework to factorise electromyography (EMG) data. Tools are provided for raw data pre-processing, non negative matrix factorisation, classification of factorised data and plotting of obtained outcomes. In particular, reading from ASCII files is supported, along with wide-used filtering approaches to process EMG data. All steps include one or more sensible defaults that aim at simplifying the workflow. Yet, all functions are largely tunable at need. Example data sets are included.

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URL <https://github.com/alesantuz/musclesyneRgies>

BugReports <https://github.com/alesantuz/musclesyneRgies/issues>

Depends R (>= 4.1.0)

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classify_kmeans	<i>Muscle synergy classification with k-means</i>
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Description

Muscle synergy classification with k-means

Usage

```
classify_kmeans(x, MSE_lim = 0.001, inspect = FALSE, show_plot = FALSE)
```

Arguments

x	A list of musclesyneRgies objects
MSE_lim	Mean squared error threshold for determining the minimum number of clusters
inspect	Logical, ask for interactive re-ordering or go fully automated?
show_plot	Logical, to decide whether plots should be plotted in the active graphic device

Details

This function must be applied to a list with a sufficient amount of trials, otherwise the classification will not work. Typically, at least 10 trials for the same condition are needed for satisfactory classification. If `show_plot` is TRUE (default) plots are also shown in the active graphic device. Plots can then be saved with the preferred export method, such as `ggplot2::ggsave`.

Value

List of `musclesyneRgies` objects, each with elements:

- `syns` factorisation rank or minimum number of synergies
- `M` motor modules (time-invariant coefficients)
- `P` motor primitives (time-dependent coefficients)
- `V` original data
- `Vr` reconstructed data
- `iterations` number of iterations to convergence
- `R2` quality of reconstruction (coefficient of determination)
- `rank_type` was the rank fixed or variable?
- `classification` classification type (k-means)

Examples

```
# Load some data
data(SYNS)
# Classify synergies
SYNS_classified <- classify_kmeans(SYNS)
```

CoA

Centre of activity

Description

Centre of activity

Usage

CoA(x)

Arguments

x A time series (numeric)

Value

The centre of activity of the time series, calculated with circular statistics

References

Martino, G. et al. Locomotor patterns in cerebellar ataxia. *J. Neurophysiol.* 112, 2810–2821 (2014).

Examples

```
# Number of users connected to the Internet through a server every minute
ts <- datasets::WWWusage[1:80]

# Calculate CoA
ts_CoA <- CoA(ts)

# Plot
plot(ts, ty = "l", xlab = "Time", ylab = "Number of users")
graphics::abline(v = ts_CoA, lwd = 2, lty = 2)
```

filtEMG

To filter raw EMG

Description

To filter raw EMG

Usage

```
filtEMG(  
  x,  
  demean = TRUE,  
  rectific = "fullwave",  
  HPf = 50,  
  HPo = 4,  
  LPf = 20,  
  LPo = 4,  
  min_sub = TRUE,  
  ampl_norm = TRUE  
)
```

Arguments

x	Object of class EMG with elements cycles and emg
demean	Logical: should EMG be demeaned?
rectif	Rectification type: "fullwave", "halfwave" or "none"
HPf	High-pass filter cut-off frequency, use 0 to exclude high-pass filtering
HPo	High-pass filter order
LPf	Low-pass filter cut-off frequency, use 0 to exclude Low-pass filtering
LPO	Low-pass filter order
min_sub	Logical: should the minimum be subtracted?
ampl_norm	Logical: should amplitude be normalised?

Details

Lists in the correct format can be created with the function `rawdata()`. The first column of each `emg` element must be time in the same units as those used for `cycles` (e.g., [s] or [ms]).

Value

Object of class EMG with elements:

- `cycles` data frame containing cycle timings, with as many columns as many cycle subdivisions are wanted
- `emg` data frame containing filtered EMG data in columns, first column is time

References

Santuz, A., Ekizos, A., Janshen, L., Baltzopoulos, V. & Arampatzis, A. On the Methodological Implications of Extracting Muscle Synergies from Human Locomotion. *Int. J. Neural Syst.* 27, 1750007 (2017).

Examples

```
# Load some data
data("RAW_DATA")
# Filter raw EMG
filtered_EMG <- lapply(
  RAW_DATA,
  function(x) {
    filtEMG(x,
      HPf = 50,
      HPo = 4,
      LPf = 20,
      LPO = 4
    )
  }
)
```

FILT_EMG

Filtered EMG example

Description

A list containing filtered and time-normalised electromyographic (EMG) human data from the right-side lower limb recorded during one walking trial.

Usage

FILT_EMG

Format

A list containing one object of class EMG with elements `cycles` and `emg`, both data frames.

ID0012_TW_01 Object of class EMG containing the two following data frames:

`cycles` Gait cycle-timings, in seconds.

`emg` Filtered and time-normalised EMG, first column is time in points, muscles named as:

ME=gluteus medius
MA=gluteus maximus
FL=tensor fasciae latae
RF=rectus femoris
VM=vastus medialis
VL=vastus lateralis
ST=semitendinosus
BF=biceps femoris
TA=tibialis anterior
PL=peroneus longus
GM=gastrocnemius medialis
GL=gastrocnemius lateralis
SO=soleus

Source

doi: [10.1016/j.isci.2019.100796](https://doi.org/10.1016/j.isci.2019.100796)

FWHM	<i>Full width at half maximum</i>
------	-----------------------------------

Description

Full width at half maximum

Usage

```
FWHM(x, sub_minimum = TRUE)
```

Arguments

x	A time series (numeric)
sub_minimum	Logical; should the minimum be subtracted before amplitude normalisation?

Value

The full width at half maximum of the time series.

References

Martino, G. et al. Locomotor patterns in cerebellar ataxia. *J. Neurophysiol.* 112, 2810–2821 (2014).

Examples

```
# Number of users connected to the Internet through a server every minute
ts <- datasets::WWWusage

# Calculate FWHM
ts_FWHM <- FWHM(ts)

# Half maximum (for the plots)
hm <- min(ts) + (max(ts) - min(ts)) / 2
hm_plot <- ts
hm_plot[which(hm_plot > hm)] <- hm
hm_plot[which(hm_plot < hm)] <- NA

# Plots
plot(ts, ty = "l", xlab = "Time", ylab = "Number of users")
lines(hm_plot, lwd = 3, col = 2)
```

HFD

Higuchi's fractal dimension

Description

Higuchi's fractal dimension

Usage

```
HFD(P, k_max = 10)
```

Arguments

P	A time series (numeric)
k_max	Maximum window length in points

Details

For motor primitives, only the most linear part of the log-log plot should be used, as reported in Santuz, Akay (2020).

Value

A list with elements:

- `loglog` containing the log-log plot from which the HFD is calculated
- `Higuchi` containing the Higuchi's fractal dimension of the time series.

References

Higuchi, T. Approach to an irregular time series on the basis of the fractal theory. *Phys. D Nonlinear Phenom.* 31, 277–283 (1988).

Santuz, A. & Akay, T. Fractal analysis of muscle activity patterns during locomotion: pitfalls and how to avoid them. *J. Neurophysiol.* 124, 1083–1091 (2020).

Examples

```
# Measurements of the annual flow of the river Nile at Aswan
flow <- datasets::Nile

# Calculate HFD
fractal_dimension <- HFD(flow)$Higuchi
message("Higuchi's fractal dimension: ", round(fractal_dimension, 3))

# Thirty-cycle locomotor primitive from Santuz & Akay (2020)
```



```
data(primitive)
fractal_dimension <- HFD(primitive$signal)$Higuchi
message("Higuchi's fractal dimension: ", round(fractal_dimension, 3))
```

Hurst	<i>Hurst exponent</i>
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Description

Hurst exponent

Usage

```
Hurst(P, min_win = 2)
```

Arguments

P	A time series (numeric)
min_win	Minimum window length in points

Details

Hurst calculates the Hurst exponent based on the R/S approach as in Hurst (1951). For motor primitives, the minimum window length should be bigger than the period (i.e., the length of each cycle), as reported in Santuz, Akay (2020).

Value

A list with elements:

- loglog containing the log-log plot from which the HFD is calculated
- Hurst containing the Higuchi's fractal dimension of the time series.

References

Hurst, H. E. Long-term storage capacity of reservoirs. *Trans. Am. Soc. Civ. Eng.* 116, 770-808 (1951).

Santuz, A. & Akay, T. Fractal analysis of muscle activity patterns during locomotion: pitfalls and how to avoid them. *J. Neurophysiol.* 124, 1083-1091 (2020).

Examples

```
# Measurements of the annual flow of the river Nile at Aswan
flow <- datasets::Nile

# Calculate Hurst exponent
H <- Hurst(flow)$Hurst
message("Hurst exponent: ", round(H, 3))

# Thirty-cycle locomotor primitive from Santuz & Akay (2020)
data(primitive)
H <- Hurst(primitive$signal, min_win = max(primitive$time))$Hurst
message("Hurst exponent: ", round(H, 3))
```

normEMG

*To time-normalise filtered EMG***Description**

To time-normalise filtered EMG

Usage

```
normEMG(x, trim = TRUE, cy_max = NA, cycle_div = NA)
```

Arguments

x	Object of class EMG with elements cycles and emg
trim	Logical: should first and last cycle be trimmed to remove filtering effects?
cy_max	Maximum number of cycles to be considered
cycle_div	A vector or one dimensional array with the number of points each cycle should be normalised to

Details

Lists in the correct format can be created with the function `rawdata()`. The first column of each emg element must be time in the same units as those used for cycles (e.g., [s] or [ms]).

Value

Object of class EMG with elements:

- cycles data frame containing cycle timings, with as many columns as many cycle subdivisions are wanted
- emg data frame containing filtered and time-normalised EMG data in columns, first column is time

References

Santuz, A., Ekizos, A., Janshen, L., Baltzopoulos, V. & Arampatzis, A. On the Methodological Implications of Extracting Muscle Synergies from Human Locomotion. *Int. J. Neural Syst.* 27, 1750007 (2017).

Examples

```
# Load some data
data("RAW_DATA")
# Filter raw EMG
filtered_EMG <- lapply(RAW_DATA, function(x) {
  filtEMG(x, HPf = 50, HPo = 4, LPf = 20, LPo = 4)
})
# Time-normalise filtered EMG, including three cycles and trimming first and last
norm_EMG <- lapply(filtered_EMG, function(x) {
  normEMG(
    x,
    cy_max = 3,
    cycle_div = c(100, 100))
})
```

plot_classified_syms *Plot muscle synergies*

Description

Plot muscle synergies

Usage

```
plot_classified_syms(
  x,
  dark_mode = FALSE,
  line_size = 0.9,
  dot_size = 0.1,
  line_col = "black",
  sd_col = "grey80",
  condition = NA,
  show_plot = TRUE
)
```

Arguments

x	List of objects of class <code>musclesyneRgies</code> (must be classified)
dark_mode	To enable dark mode
line_size	Line thickness
dot_size	Dot size on motor modules

line_col	Line colour
sd_col	Standard deviation ribbon colour
condition	Character: the condition that is being analysed, for archiving purposes
show_plot	Logical, to decide whether plots should be plotted in the active graphic device

Details

If show_plot is TRUE (default) plots are also shown in the active graphic device. Plots can then be saved with the preferred export method, such as ggplot2: :ggsave.

Value

Global plot containing the average classified muscle synergies and individual trials (motor modules) or standard deviations (motor primitives)

Examples

```
# Load some data
data(SYNS)

# Classify synergies with k-means
SYNS_classified <- classify_kmeans(SYNS)

# Save plot of classified synergies
pp <- plot_classified_syms(SYNS_classified,
  dark_mode = TRUE,
  line_col = "tomato1",
  sd_col = "tomato4",
  condition = "TW",
  show_plot = FALSE
)
```

plot_classified_syms_UMAP

Plot 2D UMAP of muscle synergies

Description

Plot 2D UMAP of muscle synergies

Usage

```
plot_classified_syms_UMAP(x, condition, show_plot = TRUE)
```

Arguments

x	List of objects of class musclesyneRgies (must be classified)
condition	Character: the condition that is being analysed, for archiving purposes
show_plot	Logical, to decide whether plots should be plotted in the active graphic device

Details

If `show_plot` is `TRUE` (default) plots are also shown in the active graphic device. Plots can then be saved with the preferred export method, such as `ggplot2::ggsave`.

Value

2D UMAP plot of classified synergies.

Examples

```
# Load some data
data(SYNS)

# Classify synergies with k-means
SYNS_classified <- classify_kmeans(SYNS)

# Save plot
pp <- plot_classified_syms_UMAP(SYNS_classified,
  condition = "TW",
  show_plot = FALSE
)
```

plot_meanEMG

Plot EMG averaged across all cycles

Description

Plot EMG averaged across all cycles

Usage

```
plot_meanEMG(
  x,
  trial,
  row_number = NA,
  col_number = 1,
  dark_mode = FALSE,
  line_size = 0.6,
  line_col = "black",
  show_plot = TRUE
)
```

Arguments

<code>x</code>	A data frame containing filtered EMG organised in columns
<code>trial</code>	Character: the name of the considered trial, for archiving purposes
<code>row_number</code>	How many rows should the final plot be divided into?

col_number	How many columns should the final plot be divided into?
dark_mode	To enable dark mode
line_size	Line thickness
line_col	Line colour
show_plot	Logical, to decide whether plots should be plotted in the active graphic device

Details

If show_plot is TRUE (default) plots are also shown in the active graphic device. Plots can then be saved with the preferred export method, such as ggplot2::ggsave.

Value

Exports average filtered and normalised EMG.

Examples

```
# Load some data
data(FILT_EMG)

# Save a plot of the only present trial with the average filtered and time-normalised EMG
pp <- plot_meanEMG(FILT_EMG[[1]],
  trial = names(FILT_EMG)[1],
  row_number = 4,
  col_number = 4,
  dark_mode = TRUE,
  line_col = "tomato3",
  show_plot = FALSE
)
```

plot_rawEMG

Plot raw EMG

Description

Plot raw EMG

Usage

```
plot_rawEMG(
  x,
  trial,
  plot_time = 3,
  start = 1,
  row_number = NA,
  col_number = 1,
  dark_mode = FALSE,
```

```
    line_size = 0.3,  
    line_col = "black",  
    show_plot = TRUE  
  )
```

Arguments

x	Object of class EMG with elements cycles and emg
trial	Character: the name of the considered trial, for archiving purposes
plot_time	How many seconds of data should be plotted?
start	At which data point should the plot start?
row_number	How many rows should the final plot be divided into?
col_number	How many columns should the final plot be divided into?
dark_mode	To enable dark mode
line_size	Line thickness
line_col	Line colour
show_plot	Logical, to decide whether plots should be plotted in the active graphic device

Details

If show_plot is TRUE (default) plots are also shown in the active graphic device. Plots can then be saved with the preferred export method, such as ggplot2: :ggsave.

Value

Plots raw EMG trials of the specified length.

Examples

```
# Load some data  
data(RAW_DATA)  
  
# Save a plot with the first (and only) trial in RAW_DATA, first three seconds, in dark mode  
plot_rawEMG(RAW_DATA[[1]],  
  trial = names(RAW_DATA)[1],  
  row_number = 4,  
  col_number = 4,  
  dark_mode = TRUE,  
  line_col = "tomato3",  
  show_plot = FALSE  
)
```

plot_syn_trials *Plot muscle synergies (individual trials)*

Description

Plot muscle synergies (individual trials)

Usage

```
plot_syn_trials(  
  x,  
  max_syms,  
  trial,  
  dark_mode = FALSE,  
  line_size = 0.6,  
  line_col = "black",  
  sd_col = "grey80",  
  show_plot = TRUE  
)
```

Arguments

x	Object of class <code>musclesyneRgies</code>
max_syms	Number of synergies to be plotted or how many rows should the final panel be divided into
trial	Character: the name of the considered trial, for archiving purposes
dark_mode	To enable dark mode
line_size	Line thickness
line_col	Line colour
sd_col	Standard deviation ribbon colour
show_plot	Logical, to decide whether plots should be plotted in the active graphic device

Details

If `show_plot` is `TRUE` (default) plots are also shown in the active graphic device. Plots can then be saved with the preferred export method, such as `ggplot2::ggsave`.

Value

Plots of the unclassified synergies, trial by trial.

Examples

```
# Load some data
data(SYNS)

# Find maximum number of synergies
max_syms <- max(unlist(lapply(SYNS, function(x) x$syms)))

# Save a plot with the first (and only, in this case) trial in the list
pp <- plot_syn_trials(SYNS[[1]],
  max_syms = max_syms,
  trial = names(SYNS)[1],
  dark_mode = TRUE,
  line_size = 0.8,
  line_col = "tomato1",
  sd_col = "tomato4",
  show_plot = FALSE
)
```

primitive

Single motor primitive example (30 cycles)

Description

A data frame containing one motor primitive extracted from one wild type mouse walking on a treadmill.

Usage

```
primitive
```

Format

A data frame of two columns:

time Normalised time in points.

signal Motor primitive

Source

doi: [10.1152/jn.00360.2020](https://doi.org/10.1152/jn.00360.2020)

primitives	<i>All motor primitives of one synergy example (30 cycles)</i>
------------	--

Description

A demo and incomplete `musclesyneRgies` object containing time info and three motor primitives extracted from one wild type mouse walking on a treadmill.

Usage

```
primitives
```

Format

A data frame of four columns:

`time` Normalised time in points.

`Syn1` Motor primitive of synergy 1

`Syn2` Motor primitive of synergy 2

`Syn3` Motor primitive of synergy 3

Source

doi: [10.1152/jn.00360.2020](https://doi.org/10.1152/jn.00360.2020)

rawdata	<i>Import ASCII data into R</i>
---------	---------------------------------

Description

Import ASCII data into R

Usage

```
rawdata(path_cycles = NA, path_emg = NA, header_cycles, header_emg = TRUE)
```

Arguments

`path_cycles` Optional, path where cycle timing files are located

`path_emg` Optional, path where raw EMG files are located

`header_cycles` Logical, are the cycle-ASCII files containing a named header (optional)?

`header_emg` Logical, are the raw EMG-ASCII files containing a named header (they should)?

Details

Supported are tab- or comma-separated files readable through `read.table()` or `read.csv()`. The first column of each raw emg file must be time in the same units as those used for the cycle timings (e.g., [s] or [ms]).

Value

List of objects of class EMG, each with elements:

- cycles data frame containing cycle timings, with as many columns as many cycle subdivisions are wanted
- emg data frame containing raw EMG data in columns, first column must be time in the same units as in the cycle timings

Examples

```
# Load built-in data set
data("RAW_DATA")

# Get current working directory
data_path <- getwd()
data_path <- paste0(data_path, .Platform$file.sep)

# Create two conveniently-named subfolders if they don't already exist
# (if they exist, please make sure they're empty!)
dir.create("cycles", showWarnings = FALSE)
dir.create("emg", showWarnings = FALSE)

# Export ASCII data from built-in data set to the new subfolders
write.table(RAW_DATA[[1]]$cycles,
  file = paste0(data_path, "cycles", .Platform$file.sep, names(RAW_DATA)[1], ".txt"),
  sep = "\t", row.names = FALSE
)
write.table(RAW_DATA[[1]]$emg,
  file = paste0(data_path, "emg", .Platform$file.sep, names(RAW_DATA)[1], ".txt"),
  sep = "\t", row.names = FALSE
)

# Run the function to parse ASCII files into objects of class `EMG`
raw_data_from_files <- rawdata(
  path_cycles = paste0(data_path, "/cycles/"),
  path_emg = paste0(data_path, "/emg/"),
  header_cycles = FALSE
)

# Check data in the new folders if needed before running the following (will delete!)

# Delete folders
unlink("cycles", recursive = TRUE)
```

```
unlink("emg", recursive = TRUE)
```

RAW_DATA

Raw EMG example

Description

A list containing electromyographic (EMG) human data from the right-side lower limb recorded during one walking trial.

Usage

```
RAW_DATA
```

Format

A list containing one object of class EMG with elements `cycles` and `emg`, both data frames.

ID0012_TW_01 Object of class EMG containing the two following data frames:

`cycles` Gait cycle-timings, in seconds.

`emg` Raw EMG, first column is time in seconds, muscles named as:

- ME=gluteus medius
- MA=gluteus maximus
- FL=tensor fasciae latae
- RF=rectus femoris
- VM=vastus medialis
- VL=vastus lateralis
- ST=semitendinosus
- BF=biceps femoris
- TA=tibialis anterior
- PL=peroneus longus
- GM=gastrocnemius medialis
- GL=gastrocnemius lateralis
- SO=soleus

Source

doi: [10.1016/j.isci.2019.100796](https://doi.org/10.1016/j.isci.2019.100796)

sMLE *Short-term maximum Lyapunov exponents*

Description

Short-term maximum Lyapunov exponents

Usage

```
sMLE(synergies, mean_period, future_pts, norm, pts, R2_threshold = 0.9)
```

Arguments

synergies	A musclesyneRgies object
mean_period	To locate the nearest neighbour of each point on the state space trajectory
future_pts	To limit the number of points "in the future" that are being searched
norm	Type of normalisation ("u" for minimum subtraction and normalisation to the maximum, "z" for subtracting the mean and then divide by the standard deviation)
pts	Minimum number of points needed to linearly approximate the first part of the divergence curve
R2_threshold	Threshold for calculating the slope of the divergence curve

Details

The mean period is intended to exclude temporally close points. In gait, values are usually plus/minus half gait cycle. Future points usually correspond in gait to one to two gait cycles. Please consider that a sufficient amount of cycles in order to compute meaningful sMLE. For locomotor primitives, 30 gait cycles have been shown to be sensitive to perturbations (Santuz et al. 2020). However, in the more classical and widespread use on kinematic data, more are usually needed (Kang and Dingwell, 2006).

Value

A list with elements:

- divergences containing the average logarithmic divergence curve
- sMLE the short-term Maximum Lyapunov exponent
- R2 the goodness of fit of the most linear part of the divergence curve

References

Rosenstein, M.T., Collins, J.J., and De Luca, C.J. (1993). A practical method for calculating largest Lyapunov exponents from small data sets. *Phys. D* 65, 117–134.

Santuz A, Brüll L, Ekizos A, Schroll A, Eckardt N, Kibele A, et al. Neuromotor Dynamics of Human Locomotion in Challenging Settings. *iScience*. 2020;23: 100796.

Kang H.G., and Dingwell J.B. (2006). Intra-session reliability of local dynamic stability of walking. *Gait Posture*. 24(3) 386-390.

Examples

```
# Load some primitives
data("primitives")
# Calculate sMLE of motor primitives in the muscle synergy space
short_term_MLE <- sMLE(primitives,
  mean_period = 80,
  future_pts = 200,
  norm = "z",
  pts = 30
)
```

subsetEMG

Subset raw EMG

Description

Subset raw EMG

Usage

```
subsetEMG(x, cy_max, cy_start = 1)
```

Arguments

x	Objects of class EMG with elements <code>cycles</code> and <code>emg</code>
cy_max	Maximum number of cycles to be considered
cy_start	From which cycle should the subset begin?

Details

Lists in the correct format can be created with the function `rawdata()`. The first column of each `emg` element must be time in the same units as those used for `cycles` (e.g., [s] or [ms]). For locomotion, thirty cycles are enough for proper synergy extraction (Oliveira et al. 2014).

Value

Object of class EMG with elements:

- cycles data frame containing cycle timings, with as many columns as many cycle subdivisions are wanted
- emg data frame containing raw EMG data in columns, first column is time

References

Oliveira, A. S. C., Gizzi, L., Farina, D. & Kersting, U. G. Motor modules of human locomotion: influence of EMG averaging, concatenation, and number of step cycles. *Front. Hum. Neurosci.* 8, 335 (2014).

Examples

```
# Load some data
data("RAW_DATA")
# Subset example raw data to the first 3 cycles
RAW_DATA_sub <- lapply(
  RAW_DATA,
  function(x) {
    subsetEMG(x,
      cy_max = 3,
      cy_start = 1
    )
  }
)
```

 SYNS

Muscle synergies example

Description

A list created by `synsNMF` containing muscle synergies extracted from 15 humans walking on a treadmill.

Usage

```
SYNS
```

Format

A list containing 15 objects of class `musclesyneRgies`, each of which represents a walking trial from a different person.

```
ID0012_TW_01 ID0001_TW_01 ID0002_TW_01 ID0003_TW_01 ID0004_TW_01 ID0005_TW_01 ID0006_TW_01 ID0007_TW_01
```

Objects of class `musclesyneRgies` containing the following items:

syns Factorisation rank or minimum number of synergies.

M Motor modules (time-invariant coefficients)

P Motor primitives (time-dependent coefficients)

V Original data, muscles named as:

ME=gluteus medius
 MA=gluteus maximus
 FL=tensor fasciae latae
 RF=rectus femoris
 VM=vastus medialis
 VL=vastus lateralis
 ST=semitendinosus
 BF=biceps femoris
 TA=tibialis anterior
 PL=peroneus longus
 GM=gastrocnemius medialis
 GL=gastrocnemius lateralis
 SO=soleus

Vr Reconstructed data, muscles named as in Vr

iterations Number of iterations to convergence

R2 Quality of reconstruction (coefficient of determination)

classification Classification type (e.g., none, k-means, NMF, etc.)

Source

doi: [10.1016/j.isci.2019.100796](https://doi.org/10.1016/j.isci.2019.100796)

synsNMF

Non-negative matrix factorisation

Description

Non-negative matrix factorisation

Usage

```
synsNMF(  
  V,  
  R2_target = 0.01,  
  runs = 5,  
  max_iter = 1000,  
  last_iter = 20,  
  MSE_min = 1e-04,  
  fixed_syms = NA  
)
```


Arguments

V	EMG data frame to be reconstructed, usually filtered and time-normalised
R2_target	Threshold to stop iterations for a certain factorisation rank
runs	Number of repetitions for each rank to avoid local minima
max_iter	Maximum number of iterations allowed for each rank
last_iter	How many of the last iterations should be checked before stopping?
MSE_min	Threshold on the mean squared error to choose the factorisation rank or minimum number of synergies
fixed_syms	To impose the factorisation rank or number of synergies

Details

The first column of V must always contain time information.

Value

Object of class `musclesynergies` with elements:

- `syms` factorisation rank or minimum number of synergies
- `M` motor modules (time-invariant coefficients)
- `P` motor primitives (time-dependent coefficients)
- `V` original data
- `Vr` reconstructed data
- `iterations` number of iterations to convergence
- `R2` quality of reconstruction (coefficient of determination)
- `rank_type` was the rank fixed or variable?
- `classification` classification type (e.g., none, k-means, NMF, etc.)

References

Lee, D. D. & Seung, H. S. Learning the parts of objects by non-negative matrix factorization. *Nature* 401, 788-91 (1999).

Santuz, A., Ekizos, A., Janshen, L., Baltzopoulos, V. & Arampatzis, A. On the Methodological Implications of Extracting Muscle Synergies from Human Locomotion. *Int. J. Neural Syst.* 27, 1750007 (2017).

Févotte, C., Idier, J. Algorithms for Nonnegative Matrix Factorization with the Beta-Divergence
Neural Computation 23, 9 (2011).

Examples

```
# Note that for bigger data sets one might want to run computation in parallel
# Load some data
data(FILT_EMG)
# Extract synergies (careful, rank is imposed here!)
SYNS <- lapply(FILT_EMG, synsNMF, fixed_syms = 4)
```

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