

Package ‘GENEAcore’

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Title Pre-Processing of 'GENEActiv' Data

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Description

Analytics to read in and segment raw 'GENEActiv' accelerometer data into epochs and events.
For more details on the 'GENEActiv' device, see <<https://activinsights.com/resources/geneactiv-support-1-2/>>.

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 7.3.2

Imports changepoint, signal, methods

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GENEAcclassify

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

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aggregateEpochs	<i>Aggregate Epochs</i>
-----------------	-------------------------

Description

Aggregate Epochs

Usage

```
aggregateEpochs(  
  time_series,  
  measure = "AGSA",  
  time = "timestamp",  
  sample_frequency,  
  duration = NA,  
  first_epoch_timestamp = NA,  
  fun = mean  
)
```

Arguments

- time_series Data frame to be aggregated.
- measure Name of the measure columns to be included.
- time Name of the time column.
- sample_frequency Measurement frequency of data.

duration Time duration to aggregate in each epoch.
first_epoch_timestamp Time to start the first epoch, defaults to first record.
fun Function to apply on aggregation, defaults to mean.

Details

Wrapper function that calls aggregatePeriods for epochs (duration of fixed length).

Value

Data frame of aggregated epochs.

Examples

```

timestamp <- c(
  1619424004, 1619424005, 1619424006, 1619424007,
  1619424008, 1619424009, 1619424010, 1619424011,
  1619424012, 1619424013, 1619424014, 1619424015
)
value <- c(
  0.729614366, 1.729115871, 0.804973546, 2.510181118,
  2.23764038, 0.613203747, 0.681953275, 0.089566943,
  0.021042388, 2.4780338, 2.437488989, 2.632635727
)
data <- data.frame(timestamp, value)
aggregated <- aggregateEpochs(data,
  duration = 5,
  measure = "value",
  sample_frequency = 1,
  first_epoch_timestamp = 1619424005,
  time = "timestamp"
)

```

aggregateEvents	<i>Aggregate Events</i>
-----------------	-------------------------

Description

Aggregate Events

Usage

```

aggregateEvents(
  time_series,
  measure = "AGSA",
  time = "timestamp",
  sample_frequency,
  events = NA,

```

```

    start_time = "start",
    end_time = "end",
    fun = mean
  )

```

Arguments

time_series	Data frame to be aggregated.
measure	Name of the measure columns to be included.
time	Name of the time column.
sample_frequency	Measurement frequency of data.
events	Data frame containing the start and end index of each event.
start_time	Name of the column in events containing the start index of the events.
end_time	Name of the column in events containing the end index of the events.
fun	Function to apply on aggregation, defaults to mean.

Details

Wrapper function that calls aggregatePeriods for events (duration of variable length).

Value

Data frame of aggregated events.

Examples

```

timestamp <- c(
  1619424004, 1619424005, 1619424006, 1619424007,
  1619424008, 1619424009, 1619424010, 1619424011,
  1619424012, 1619424013, 1619424014, 1619424015
)
value <- c(
  0.729614366, 1.729115871, 0.804973546, 2.510181118,
  2.23764038, 0.613203747, 0.681953275, 0.089566943,
  0.021042388, 2.4780338, 2.437488989, 2.632635727
)
data <- data.frame(timestamp, value)
event_start <- c(1, 5, 10)
event_end <- c(4, 9, 12)
aggregated_events <- aggregateEvents(data,
  events = data.frame(start = event_start, end = event_end),
  measure = "value",
  time = "timestamp",
  start_time = "start",
  end_time = "end",
  sample_frequency = 1,
  fun = sum
)

```

aggregatePeriods	<i>Aggregate Periods</i>
------------------	--------------------------

Description

Generalised aggregation function generates distinct epochs or events outputs based on the initial parameters provided.

Usage

```
aggregatePeriods(  
  time_series,  
  measure = "AGSA",  
  time = "timestamp",  
  sample_frequency,  
  duration = NA,  
  first_epoch_timestamp = NA,  
  events = NA,  
  start_time = "start",  
  end_time = "end",  
  fun = mean  
)
```

Arguments

time_series	Data frame to be aggregated.
measure	Name of the measure columns to be included.
time	Name of the time column.
sample_frequency	Frequency of data.
duration	Time duration to aggregate in each epoch.
first_epoch_timestamp	Time to start the first epoch, defaults to first record.
events	Data frame containing the start and end index of each event.
start_time	Name of the column in events containing the start index of the events.
end_time	Name of the column in events containing the end index of the events.
fun	Function to apply on aggregation, defaults to mean.

Value

Data frame of aggregated epochs or events.

apply_AGSA	<i>Apply Absolute Gravity-Subtracted Acceleration (AGSA)</i>
------------	--

Description

Apply Absolute Gravity-Subtracted Acceleration (AGSA)

Usage

```
apply_AGSA(x)
```

Arguments

x	Calibrated acceleration data frame.
---	-------------------------------------

Value

Measure column appended to end of calibrated data frame.

Examples

```
x <- c(0.14268, 0.21757, -0.529, -0.36383)
y <- c(0.26385, 0.27295, 0.29220, 0.79510)
z <- c(0.27722, 0.20296, 0.35092, 0.27459)
calibrated <- data.frame(x, y, z)
calibrated <- apply_AGSA(calibrated)
```

apply_calibration	<i>Apply Calibration</i>
-------------------	--------------------------

Description

Apply Calibration

Usage

```
apply_calibration(sensor_data, cal_params, measurement_device, use_temp = TRUE)
```

Arguments

sensor_data	Raw sensor-level data from a bin file in the form (x, y, z, light, button, temp).
cal_params	Calibration parameters for acceleration and light from MPI.
measurement_device	Name of the measurement device used "GENEActiv 1.1" or "GENEActiv 1.2".
use_temp	Allows auto-calibration to be run with and without temperature compensation.

Details

Function to apply calibration to sensor-level data from a bin file.

Value

Data frame of calibrated sensor data.

Examples

```
cal_params <- list(
  scale = c(1.015, 1.017, 1.027),
  offset = c(0.00128, 0.0383, 0.0138),
  temperatureoffset = c(0, 0, 0),
  error = NA,
  lightdenominator = 48,
  lightnumerator = 911
)

rawdata <- data.frame(
  time = c(rep(1726650857, 5)),
  x = c(0.2421875, 0.24609375, 0.25390625, 0.24609375, 0.23828125),
  y = c(-0.04296875, -0.04687500, -0.03515625, -0.03125000, -0.04296875),
  z = c(-0.9453125, -0.9453125, -0.9531250, -0.9531250, -0.9609375),
  light = c(rep(22, 5)),
  button = c(rep(0, 5)),
  temp = c(rep(21.3, 5)),
  volts = c(rep(4.0896, 5))
)

calibrated <- apply_calibration(rawdata, cal_params, "GENEActiv 1.1")
```

apply_degrees	<i>Apply Rotation (degrees)</i>
---------------	---------------------------------

Description

Apply Rotation (degrees)

Usage

```
apply_degrees(x)
```

Arguments

x Calibrated acceleration data frame.

Value

Measure column appended to end of calibrated data frame.

Examples

```
x <- c(0.14268, 0.21757, -0.529, -0.36383)
y <- c(0.26385, 0.27295, 0.29220, 0.79510)
z <- c(0.27722, 0.20296, 0.35092, 0.27459)
calibrated <- data.frame(x, y, z)
calibrated <- apply_degrees(calibrated)
```

apply_ENMO	<i>Apply Euclidean Norm Minus One (ENMO)</i>
------------	--

Description

Apply Euclidean Norm Minus One (ENMO)

Usage

```
apply_ENMO(x)
```

Arguments

x Calibrated acceleration data frame.

Value

Measure column appended to end of calibrated data frame.

Examples

```
x <- c(0.14268, 0.21757, -0.529, -0.36383)
y <- c(0.26385, 0.27295, 0.29220, 0.79510)
z <- c(0.27722, 0.20296, 0.35092, 0.27459)
calibrated <- data.frame(x, y, z)
calibrated <- apply_ENMO(calibrated)
```

apply_radians	<i>Apply Rotation (radians)</i>
---------------	---------------------------------

Description

Apply Rotation (radians)

Usage

```
apply_radians(x)
```

Arguments

x Calibrated acceleration data frame.

Value

Measure column appended to end of calibrated data frame.

Examples

```
x <- c(0.14268, 0.21757, -0.529, -0.36383)
y <- c(0.26385, 0.27295, 0.29220, 0.79510)
z <- c(0.27722, 0.20296, 0.35092, 0.27459)
calibrated <- data.frame(x, y, z)
calibrated <- apply_radians(calibrated)
```

apply_updown	<i>Apply Elevation (updown)</i>
--------------	---------------------------------

Description

Apply Elevation (updown)

Usage

```
apply_updown(x)
```

Arguments

x Calibrated acceleration data frame.

Value

Measure column appended to end of calibrated data frame.

Examples

```
x <- c(0.14268, 0.21757, -0.529, -0.36383)
y <- c(0.26385, 0.27295, 0.29220, 0.79510)
z <- c(0.27722, 0.20296, 0.35092, 0.27459)
calibrated <- data.frame(x, y, z)
calibrated <- apply_updown(calibrated)
```

binfile_summary	<i>Bin File Summary</i>
-----------------	-------------------------

Description

Bin File Summary

Usage

```
binfile_summary(input, recursive = TRUE)
```

Arguments

input	Bin file path.
recursive	TRUE applies the operation to all nested elements.

Details

Wrapper function that calls create_summary for bin files only.

Value

Data frame of bin file or MPI summary.

calc_autocalparams	<i>Calculate Auto-calibration Parameters</i>
--------------------	--

Description

Function to calculate auto-calibration parameters from known still points from a bin file that create a unitary sphere.

Usage

```
calc_autocalparams(
  binfile,
  binfile_path,
  output_folder,
  sphere_points,
  use_temp = TRUE,
  spherecrit = 0.3,
  maxiter = 500,
  tol = 1e-13
)
```

Arguments

binfile	Text lines read from an open connection to a bin file.
binfile_path	Path to the bin file to be processed.
output_folder	Path to the folder containing GENEAcCore run outputs and Measurement Period Information (MPI) files.
sphere_points	List of points that populate a unitary sphere and their associated temperature in the form (x,y,z,temp).
use_temp	Allows auto-calibration to be run with and without temperature compensation.
spherecrit	The minimum required acceleration value for each axis in both directions for auto-calibration to be reliable.
maxiter	The maximum number of sphere fit iterations attempted during auto-calibration.
tol	The limit of incremental sphere fit improvements before auto-calibration is considered complete.

Value

List of auto-calibration parameters within the measurement period information (MPI).

Examples

```
binfile_path <- system.file("inst/extdata/10Hz_calibration_file.bin", package = "GENEAcCore")
output_folder <- "."
con <- file(binfile_path, "r")
binfile <- readLines(con, skipNul = TRUE)
close(con)
MPI <- create_MPI(binfile, binfile_path, output_folder)
nonmovement_list <- detect_nonmovement(binfile, binfile_path, output_folder)
MPI <- calc_autocalparams(binfile, binfile_path, output_folder, nonmovement_list$sphere_points)
```

createEventMapping	<i>Create Event Mapping</i>
--------------------	-----------------------------

Description

Create Event Mapping

Usage

```
createEventMapping(events, start_time, end_time, max_row_number)
```

Arguments

events	Data frame containing the start and end index of each event.
start_time	Name of the column in events containing the start index of the events.
end_time	Name of the column in events containing the end index of the events.
max_row_number	Number of rows in the source vector the events describe

Details

Enumerate a vector to identify which event each measurement belongs to.

Value

List of mapped events.

Examples

```
events <- data.frame(
  "start" = c(1, 5, 10, 15),
  "end" = c(4, 9, 14, 19)
)
time_series <- rnorm(25)
period_number <- createEventMapping(events, "start", "end", length(time_series))
```

create_MPI

Create Measurement Period Information

Description

Create Measurement Period Information

Usage

```
create_MPI(binfile, binfile_path, output_folder, out_rds = TRUE)
```

Arguments

binfile	Text lines read from an open connection to a bin file.
binfile_path	Path to the bin file to be processed.
output_folder	Folder to write MPI file in.
out_rds	Allows RDS output to be saved during MPI creation.

Details

Function to create measurement period information (MPI) from a GENEActiv bin file

Value

List of measurement period information.

Examples

```
binfile_path <- system.file("inst/extdata/20Hz_file.bin", package = "GENEAcore")
con <- file(binfile_path, "r")
binfile <- readLines(con, skipNul = TRUE)
close(con)
MPI <- create_MPI(binfile)
```

create_summary	<i>Create Summary</i>
----------------	-----------------------

Description

Create Summary

Usage

```
create_summary(input, path_type, recursive)
```

Arguments

input	Input type of either a bin file path, MPI path or an MPI object.
path_type	The file type within the folder to create summary for.
recursive	TRUE applies the operation to all nested elements.

Details

Function to create a summary of key information of a bin file or MPI path.

Value

Data frame of bin file or MPI summary.

detect_nonmovement	<i>Detect Non-movement</i>
--------------------	----------------------------

Description

Detect Non-movement

Usage

```
detect_nonmovement(
  binfile,
  binfile_path,
  output_folder,
  still_seconds = 120,
  sd_threshold = 0.011,
  temp_seconds = 240,
  border_seconds = 300,
  long_still_seconds = 120 * 60,
  delta_temp_threshold = -0.7,
  posture_changes_max = 2,
  non_move_duration_max = 12 * 60 * 60
)
```

Arguments

<code>binfile</code>	Text lines read from an open connection to a bin file.
<code>binfile_path</code>	Path to the bin file to be processed.
<code>output_folder</code>	Path to the folder containing GENEAcCore run outputs and Measurement Period Information (MPI) files.
<code>still_seconds</code>	The number of seconds included in the rolling standard deviation calculation for stillness to determine the shortest detection duration.
<code>sd_threshold</code>	The threshold applied to the rolling standard deviation of combined acceleration to determine stillness.
<code>temp_seconds</code>	The number of seconds included in the rolling temperature difference calculation or non-wear which also determines the shortest detection duration.
<code>border_seconds</code>	The minimum number of seconds of a still event to be classed as a new bout.
<code>long_still_seconds</code>	The minimum number of seconds of a still bout that is classed as non-wear.
<code>delta_temp_threshold</code>	The threshold applied to the rolling temperature difference to determine non-wear.
<code>posture_changes_max</code>	The maximum number of adjoining events that make up a single bout.
<code>non_move_duration_max</code>	The maximum number of seconds of a still bout to be classed as non-movement. Still bouts with a duration longer than this number is automatically classed as non-wear.

Details

Function to detect non-movement bouts, non-wear events and points in a 1Hz downsampled bin file.

Value

List of sphere points, non-movement bouts and non-wear events.

Examples

```
binfile_path <- system.file("inst/extdata/20Hz_file.bin", package = "GENEAcCore")
con <- file(binfile_path, "r")
binfile <- readLines(con, skipNul = TRUE)
close(con)
output_folder <- "."
MPI <- create_MPI(binfile, binfile_path, output_folder)
MPI <- detect_nonmovement(binfile, binfile_path, output_folder)
```

detect_transitions	<i>Detect Transitions</i>
--------------------	---------------------------

Description

Detect Transitions

Usage

```
detect_transitions(
  binfile,
  binfile_path,
  output_folder,
  minimum_event_duration = 3,
  x_cpt_penalty = 20,
  y_cpt_penalty = 30,
  z_cpt_penalty = 20,
  CutTime24Hr = "15:00"
)
```

Arguments

binfile	Text lines read from an open connection to a bin file.
binfile_path	Path to the bin file to be processed.
output_folder	Path to the folder containing GENEAcCore run outputs and Measurement Period Information (MPI) files.
minimum_event_duration	The minimum interval between changepoint transitions.
x_cpt_penalty	The manual penalty value applied in the PELT changepoint algorithm for the x axis, see cpt.var .
y_cpt_penalty	The manual penalty value applied in the PELT changepoint algorithm for the y axis, see cpt.var .
z_cpt_penalty	The manual penalty value applied in the PELT changepoint algorithm for the z axis, see cpt.var .
CutTime24Hr	Time in 24h to split the days up by.

Details

Function to detect mean and variance changepoints in 1Hz acceleration data from a bin file.

Value

List of time, index and day number of each transition within the measurement period information.

Examples

```
binfile_path <- system.file("inst/extdata/20Hz_file.bin", package = "GENEAcore")
con <- file(binfile_path, "r")
binfile <- readLines(con, skipNul = TRUE)
close(con)
output_folder <- "."
MPI <- create_MPI(binfile, binfile_path, output_folder)
MPI <- detect_transitions(binfile, binfile_path, output_folder)
```

geneacore

Main GENEAcCore Function

Description

Main GENEAcCore Function

Usage

```
geneacore(
  data_folder = data_folder,
  CutTime24Hr = "15:00",
  output_epochs = TRUE,
  epoch_duration = 1,
  output_events = TRUE,
  output_steps = FALSE,
  output_csv = FALSE,
  timer = FALSE
)
```

Arguments

<code>data_folder</code>	Folder that contains raw data bin files to process.
<code>CutTime24Hr</code>	Time in 24h to split the days up by.
<code>output_epochs</code>	Create epoch outputs.
<code>epoch_duration</code>	Specify duration of fixed epochs.
<code>output_events</code>	Create event outputs.
<code>output_steps</code>	Include step counts and stepping rate outputs.
<code>output_csv</code>	Allows CSV output to be saved during epoch and event processing.
<code>timer</code>	Print elapsed times of each process.

Value

RDS and CSV of Measurement Period Information, Epoch measures and Event measures.

get_decimal_places	<i>Get Decimal Places</i>
--------------------	---------------------------

Description

Get Decimal Places

Usage

```
get_decimal_places(column)
```

Arguments

column	Aggregated data frame column.
--------	-------------------------------

Details

Function to determine the number of decimal places based on column name.

Value

Decimal place integer.

Examples

```
epochs_df <- data.frame(  
  "x.mean" = c(0.1111, 0.1222, 0.1333, 0.1444),  
  "y.mean" = c(0.2111, 0.2222, 0.2333, 0.2444),  
  "light.mean" = c(1.25, 1.73, 1.99, 2.02)  
)  
dp <- get_decimal_places(epochs_df[1])
```

get_UniqueBinFileIdentifier	<i>Generate Unique Bin File Identifier</i>
-----------------------------	--

Description

Generate Unique Bin File Identifier

Usage

```
get_UniqueBinFileIdentifier(binfile)
```

Arguments

binfile	Text lines read from an open connection to a bin file.
---------	--

Details

Function to create a UniqueBinFileIdentifier from a GENEActiv bin file.

Value

Single string identifier.

Examples

```
binfile_path <- system.file("inst/extdata/20Hz_file.bin", package = "GENEAcore")
con <- file(binfile_path, "r")
binfile <- readLines(con, skipNul = TRUE)
close(con)
UniqueBinFileIdentifier <- get_UniqueBinFileIdentifier(binfile)
```

MPI_summary	<i>MPI Summary</i>
-------------	--------------------

Description

MPI Summary

Usage

```
MPI_summary(input, recursive = TRUE)
```

Arguments

- input MPI path.
- recursive TRUE applies the operation to all nested elements.

Details

Wrapper function that calls create_summary for MPI only.

Value

Data frame of MPI summary.

new_cut_times	<i>New Cut Times</i>
---------------	----------------------

Description

New Cut Times

Usage

```
new_cut_times(df)
```

Arguments

df Cut Times data frame.

Details

Add the timestamps, indexes and day numbers of the cut times and their ends.

Value

Data frame with added cut times.

Examples

```
CutTimes_df <- data.frame(
  time = c(1731421000, 1731421100, 1731421362, 1731421480, 1731421525),
  index = c(56, 1, 230, 1, 400), day = c(1, 2, 2, 3, 3)
)
CutTimes_df <- new_cut_times(CutTimes_df)
```

sample_binfile	<i>Sample Bin File</i>
----------------	------------------------

Description

Sample Bin File

Usage

```
sample_binfile(
  binfile,
  binfile_path,
  output_folder,
  start_time = NULL,
  end_time = NULL,
  downsample = TRUE,
  output_csv = FALSE
)
```

Arguments

binfile	Text lines read from an open connection to a bin file.
binfile_path	Path to the bin file to be processed.
output_folder	Path to the folder containing GENEAcCore run outputs and Measurement Period Information (MPI) files.
start_time	Time stamp to start the read from, default start of file.
end_time	Time stamp to end the read from, default end of file.
downsample	Logical to determine whether to downsample the file, default TRUE.
output_csv	Allow outputs of bin file sampling to be saved as CSV.

Details

Function to read in a GENEActiv bin file with option to downsample to 1Hz.

Value

List of 1Hz downsampled data or raw sample data.

Examples

```
binfile_path <- system.file("inst/extdata/20Hz_file.bin", package = "GENEAcCore")
output_folder <- "."
con <- file(binfile_path, "r")
binfile <- readLines(con, skipNul = TRUE)
close(con)
measurements <- sample_binfile(binfile, binfile_path, output_folder)
```

stepCounter

Step Counter

Description

Function to calculate the number and variance of the steps in the data.

Usage

```
stepCounter(
  StepData,
  samplefreq = 100,
  filterorder = 2,
  boundaries = c(0.5, 5),
  Rp = 3,
  hysteresis = 0.05,
  fun = c("GENEAcCount", "mean", "sd")
)
```

Arguments

StepData	The data to use for calculating the steps. This should either an AccData object or a vector.
samplefreq	The sampling frequency of the data, in hertz, when calculating the step number (default 100).
filterorder	single integer, order of the Chebyshev bandpass filter, passed to argument n of cheby1 .
boundaries	length 2 numeric vector specifying lower and upper bounds of Chebychev filter (default c(0.5, 5) Hz), passed to argument W of butter or cheby1 .
Rp	the decibel level that the cheby filter takes, see cheby1 .
hysteresis	The hysteresis applied after zero crossing. (default 100mg)
fun	character vector naming functions by which to summarize steps. "count" is an internally implemented summarizing function that returns step count.

Value

Returns a vector with length fun.

Examples

```
d1 <- sin(seq(0.1, 100, 0.1))/2 + rnorm(1000)/10 + 1
Steps4 = stepCounter(d1)
length(Steps4)
mean(Steps4)
sd(Steps4)
plot(Steps4)
```

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