

Package ‘GGIRread’

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Type Package

Title Wearable Accelerometer Data File Readers

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Description Reads data collected from wearable accelerometers as used in sleep and physical activity research. Currently supports file formats: binary data from 'GENEAActiv' <<https://activinsights.com/>>, .bin-format from GENEActiv devices (not for sale), and .cwa-format from 'Axivity' <<https://axivity.com>>. Primarily designed to complement R package GGIR <<https://CRAN.R-project.org/package=GGIR>>.

URL <https://github.com/wadpac/GGIRread/>

BugReports <https://github.com/wadpac/GGIRread/issues>

License Apache License (== 2.0)

Suggests testthat

Imports matlab, bitops, Rcpp (>= 0.12.10)

Depends stats, utils, R (>= 3.5.0)

NeedsCompilation yes

LinkingTo Rcpp

ByteCompile yes

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GGIRread-package	<i>A package to read data files from wearable accelerometers</i>
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Description

This package offers a collection of functions to read data files from wearable accelerometers. Some functions were migrated from R package GGIR to make GGIR more modular and to reduce its complexity, while other functions such as readGENEActiv (R) and GENEActivReader (C++) are newly written.

Details

Package: GGIRread
 Type: Package
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 Date: 2024-03-27
 License: LGPL (>= 2.0, < 3)

Author(s)

- Vincent T van Hees <v.vanhees@accelting.com> main creator and developer
- Patrick Bos developed function [GENEActivReader](#)
- Jing Hua Zhao <jinghua.zhao@mrc-epid.cam.ac.uk> co-developed function [readGenea](#)
- Evgeny Mirkes created function [readAxivity](#)
- Dan Jackson helped improve function [readAxivity](#)

GENEActivReader	<i>Function (C++) to read binary files as produced by the GENEActiv accelerometer</i>
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Description

Function to read binary files as produced by the GENEActiv accelerometer by ActivInsights Ltd
<https://activinsights.com/>

Usage

```
GENEActivReader(filename, start = 0L, end = 0L, progress_bar = FALSE)
```

Arguments

filename	filename (required)
start	start page for reading data
end	end page for reading data
progress_bar	Boolean

Details

If only start page is defined then all data is read beyond start until the end of the file is reached

Value

info	List with ReadOK (good=0 or error=1), ReadErrors (Count of pages with read errors), SampleRate (Hertz), numBlocksTotal
time	Numeric vector with time in milliseconds since start page
x	Numeric vector with x-axis acceleration in gravitational units
y	Numeric vector with y-axis acceleration in gravitational units
z	Numeric vector with z-axis acceleration in gravitational units
temperature	matrix with battery voltage and corresponding timestamps
lux	Numeric vector with lux values in Volts

Author(s)

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readAxivity	<i>Function to read .cwa-format files as produced by the accelerometer named 'Axivity'</i>
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Description

For reading .cwa-format data with the Axivity AX3 and AX6 sensors.

Usage

```
readAxivity(filename, start = 0, end = 0, progressBar = FALSE,
            desiredtz = "", configtz = c(), interpolationType=1, loadbattery = FALSE,
            header = NULL, frequency_tol = 0.1, maxAllowedCorruptBlocks = 20)
```

Arguments

filename	filename (required) is name of cwa file to read
start	non-negative integer which is a cwa file block number.
end	non-negative integer which is a cwa file block number. End must be not be less than start. If end is less or equal to start, then there is no data read.
progressBar	Is trigger to switch on/off the text progress bar. If progressBar is TRUE then the function displays the progress bar but it works slightly slower
desiredtz	Desired timezone, a character with timezone database name.
configtz	Only functional for AX3 cwa data at the moment. Timezone in which the accelerometer was configured. Only use this argument if the timezone of configuration and timezone in which recording took place are different.
interpolationType	Integer to indicate type of interpolation to be used, 1=linear, 2=nearest neighbour.
loadbattery	Boolean to indicate whether battery voltage should be loaded
header	Header to be reused if it was extracted earlier
frequency_tol	Numeric value representing the tolerance for frequency bias expressed as a fraction of the expected sampling frequency. For example, 0.10 indicates that we accept the sampling frequency configured at 100 Hertz to vary between 90 and 110 Hertz. If this condition is not met the data will be imputed with a constant value and the start and end time will be logged in the QClog output object. Regardless of the setting the function will always log instances when frequency differs by more than 5%, but if this is less than frequency_tol the block will not be imputed.
maxAllowedCorruptBlocks	Max number of consecutive blocks with a failed checksum that we'll tolerate.

Value

- data dataframe with data from start inclusive till end exclusive. If start == end then data section of final structure is empty.
 - timestamp in numeric format
 - gx gyroscope x-axis (only available in AX6)
 - gy gyroscope y-axis (only available in AX6)
 - gz gyroscope z-axis (only available in AX6)
 - x accelerometer x-axis
 - y accelerometer y-axis
 - z accelerometer z-axis
 - temperature in Celsius (only recorded once per block)
 - battery one value per block (only recorded once per block)
 - light in LUX on (only recorded once per block)
- header file header. list of header information:
 - uniqueSerialCode is unique serial code of used device
 - frequency is measurement frequency. All data will be resampled for this frequency
 - start is timestamp in numeric form. To get text representation it is enough to use as.POSIXct(start, origin = "1970-01-01", tz=desiredtz)
 - device is "Axivity"
 - firmwareVersion
 - blocks is number of datablocks with 80 or 120 raw observations in each.
- QClog dataframe with log of integrity checks on each block including:
 - checksum_pass Boolean to indicate whether checksum was zero.
 - blockID_previous ID for previous block
 - blockID_current ID for current block
 - start_previous numeric start time of previous block
 - start_current numeric start time of current block
 - blockLengthSeconds length of previous block
 - frequency_blockheader frequency derived from block header
 - frequency_observed frequency as observed
 - imputed Boolean to indicate whether this block was imputed

Author(s)

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Examples

```
cwafire = system.file("testfiles/ax3_testfile.cwa", package = "GGIRread")[1]
AX3 = readAxivity(filename = cwafire, desiredtz = "Europe/Berlin", start = 1, end = 2)
```

readGenea	<i>Function to read binary files as produced by the accelerometer named 'Genea', not to be confused with the 'GENEActiv' (see package GENEActive for this)</i>
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Description

For reading the binary data as collected with a Genea accelerometer (Unilever Discover, UK). For reading GENEActive binary data, see package GENEActive.

Usage

```
readGenea(filename, start = 0, end = 0)
```

Arguments

filename	filename (required)
start	start point for reading data, this can either be a timestamp in POSIXct format "year-month-day hr:min:sec" or a page number (optional)
end	end point for reading data, this can either be a timestamp in POSIXct format "year-month-day hr:min:sec" or a page number (optional)

Details

If only start is defined then readGenea will read all data beyond start until the end of the file is reached

Value

rawxyz	matrix with raw x, y, and, z acceleration values
header	file header
timestamps1	timestamps for rawxyz in seconds since 1970-01-01 00:00
timestamps2	timestamps for rawxyz in day time format
batt.voltage	matrix with battery voltage and corresponding timestamps

Author(s)

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Examples

```
geneafile = system.file("testfiles/genea_testfile.bin", package = "GGIRread")[1]
GENEA = readGenea(filename = geneafile, start = 0, end = 2)
```

readGENEActiv	<i>Function (R) to read binary files as produced by the GENEActiv accelerometer</i>
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Description

R function wrapper around [GENEActivReader](#) to read binary files as produced by the GENEActiv accelerometer by ActivInsights Ltd <https://activinsights.com/>

Usage

```
readGENEActiv(filename, start = 0L, end = 0L, progress_bar = FALSE,
              desiredtz = "", configtz = NULL)
```

Arguments

filename	filename (required)
start	start page for reading data
end	end page for reading data
progress_bar	Boolean
desiredtz	Character, timezone database name of the timezone where the accelerometer was worn.
configtz	Character, timezone database name of the timezone where the accelerometer was configured. Leave NULL if equal to timezone where experiment took place.

Details

If only start page is defined then all data is read beyond start until the end of the file is reached

Value

header:

serial_number	Device serial number as extracted from file header
firmware	Firmware version
tzzone	Time zone as extracted from file header
ReadOK	see GENEActivReader
SampleRate	matrix with battery voltage and corresponding timestamps
ReadErrors	matrix with battery voltage and corresponding timestamps
numBlocksTotal	matrix with battery voltage and corresponding timestamps
StartTime	Start time as extracted from file header

data.out:

time	Unix time in seconds with decimal places for milliseconds
x	see GENEActivReader
y	see GENEActivReader
z	see GENEActivReader
light	Ligth values express in lux units
temperature	Temperature in Celsius

Author(s)

Patrick Bos <egpbos@gmail.com> Vincent T van Hees <v.vanhees@accelting.com>

Examples

```
binfile = system.file("testfiles/GENEActiv_testfile.bin", package = "GGIRread")[1]
rdata = readGENEActiv(filename = binfile, start = 1, end = 1, desiredtz = "Europe/London")
```

readWav	<i>Deprecated function to read .wav files as can be stored with OMGUI software by Axivity Ltd</i>
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Description

Originally designed to read the wav accelerometer data format as stored with the OMGUI software by Axivity Ltd and documented [here](#).

This function has been deprecated as wav files are hardly used, their formatting is not consistent causing ongoing challenges with keeping the keep functional, wav format not well facilitated for AX6 recording.

Usage

```
readWav(filename, start = 1, end = 100,units="minutes")
```

Arguments

filename	filename (required)
start	start point for reading data, see also units
end	end point for reading data, see also units
units	units used for defining start and end

Details

If only start is defined then `g.binread` will read all data beyond start until the end of the file is reached

Value

rawxyz	matrix with raw x, y, and, z acceleration values
header	file header
timestamps	local timestamps for rawxyz

Author(s)

Vincent T van Hees <v.vanhees@accelting.com>

resample	<i>Resample timeseries</i>
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Description

Resample single- or multi-variate time series using linear or nearest neighbour interpolation

Usage

```
resample(raw, rawTime, time, stop, type = 1)
```

Arguments

raw	stop-by-3 matrix with raw values of x, y and z.
rawTime	vector with stop elements of raw time.
time	array with required time points.
stop	Number of rows in raw
type	integer to indicate type of interpolation, 1=linear, 2=nearest neighbour

Examples

```
raw = cbind(1:10, 1:10, 1:10)
rawTime = seq(0.1, 1, by = 0.1)
time = seq(0.15001, 1.05001, by = 0.1)
stop = 10
dat_lin = resample(raw, rawTime, time, stop, type = 1)
```

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