

# Package ‘GGIRread’

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**Type** Package

**Title** Wearable Accelerometer Data File Readers

**Version** 0.2.2

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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/>>, binary data from GENEActiv devices (not for sale), and .cwa-format data 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** LGPL (>= 2.0, < 3)

**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  
 Version: 0.2.2  
 Date: 2022-08-31  
 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](#)

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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)**

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

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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)
```

**Arguments**

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

**Value**

data	dataframe with timestamp, raw x, -y, and, -z acceleration values, temperature, battery and light
header	file header

**Author(s)**

Evgeny Mirkes <em322@leicester.ac.uk> Vincent van Hees <v.vanhees@accelting.com>

**Examples**

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

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readGenea	<i>Function to read binary files as produced by the accelerometer named 'Genea', not to be confused with the 'GENEActiv' (see package GENEAREad 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 GENEAREad.

**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)**

Vincent T van Hees <v.vanhees@accelting.com> Jing Hua Zhao <jinghua.zhao@mrc-epid.cam.ac.uk>

**Examples**

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

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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 <a href="#">GENEActivReader</a>
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 <a href="#">GENEActivReader</a>
y	see <a href="#">GENEActivReader</a>
z	see <a href="#">GENEActivReader</a>
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")
```

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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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