Package ‘CardiacDP’

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Title Automated Cardiac Data Processing via ACF, GA & Tracking Index

Version 0.4.2

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Description An algorithm developed to efficiently and accurately process complex and variable cardiac data with three key features: 1. employing autocorrelation to identify recurrent heartbeats and use their periods to compute heart rates; 2. incorporating a genetic algorithm framework to minimize data loss due to noise interference and accommodate within-sequence variations; and 3. introducing a tracking index as a moving reference to reduce errors. Lau, Wong, & Gu (2026) <`https://ssrn.com/abstract=5153081`>.

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Encoding UTF-8

RoxygenNote 7.3.3

Depends R (>= 4.3.0)

Imports data.table, doParallel, dplyr, foreach, ggplot2, purrr, RColorBrewer, stringr

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

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Contents

`collatedata` *CardiacDP - collatedata()*

Description

Automatically read and collate separate .csv files in chronological order as inferred by the file names and in hierarchy.

Usage

```
collatedata(file_path, output_file = NULL, verbose = FALSE)
```

Arguments

`file_path`	Designate the path to your file, must be a .zip file
`output_file`	Optional path to write the collated data table as a CSV file. May be either a full file path (e.g. `/path/to/out.csv`) or an output directory (e.g. `/path/to/outdir`). If a directory (or a path without a file extension) is provided, a file named `<input_stem>_collated.csv` is written inside it. Default NULL (no file written).
`verbose`	Logical; if TRUE, emit progress messages. Default FALSE.

Value

A single collated data table

Examples

```
zip_path <- system.file("extdata", "example.zip", package = "CardiacDP")
collated <- collatedata(zip_path)
```

`computeHR` *CardiacDP - computeHR()*

Description

Employing the autocorrelation function (ACF) with a genetic algorithm framework to locate periodic sub-sequences within each sequence. From the candidate heart rates of these sub-sequences, the final results are either evaluated based on the autocorrelation value or a tracking index (TI).

Usage

```
computeHR(
  file_path,
  reduce_res = 0.01,
  pop_size = 10L,
  max_gen = 20L,
  patience = 2L,
  an_in = 1,
  acf_thres = 0.5,
  lr_thres = 0.7,
  ncore = NULL,
  output_dir = NULL,
  save_outputs = FALSE,
  verbose = FALSE
)
```

Arguments

`file_path`	Designate the path to your file, must be a .zip or .csv file
`reduce_res`	Time interval of reduced resolution (seconds), by default 0.01
`pop_size`	Number of populations used in the genetic algorithm, by default 10L
`max_gen`	Maximum number of generations in the genetic algorithm, by default 20L
`patience`	Patience threshold (maximum number of generations with no further changes) in the genetic algorithm, by default 2L
`an_in`	Analysis interval (length of a sequence; in minute), by default 1
`acf_thres`	Threshold used in ACF to classify periodic oscillations from aperiodic noises, by default 0.5
`lr_thres`	Linear regression r-sq threshold in extrapolating the tracking index, by default 0.7
`ncore`	Integer; number of CPU cores to use for the genetic algorithm. If NULL (default), uses `parallel::detectCores() - 1`. During `R CMD check`, cores are clamped to a small number to satisfy check limits.
`output_dir`	Optional directory to write CSV/PNG outputs when `save_outputs = TRUE`. If NULL, defaults to `tempdir()`.
`save_outputs`	Logical; if TRUE, write CSV/PNG outputs to `output_dir`. Default FALSE.
`verbose`	Logical; if TRUE, emit progress messages. Default FALSE.

Value

The positions (in indices) and durations of the sub-sequences (finalsubseq) and the corresponding candidate HR (candidateHR) obtained from the genetic algorithm, and the final results evaluating the candidates by autocorrelation values (results_ACF) or the tracking index (results_TI), which contains the details of the subsequences after checking for resolution (subseqHR with Time_min column), the weighted heart rate per sequence (weightedHR with Time_min column) and a plot (plot). If `save_outputs = TRUE`, file paths are recorded in `output$files`.

Examples

```
# use the default parameters to analyse a zip file
# the collatedata function will be called automatically
zip_path <- system.file("extdata", "example.zip", package = "CardiacDP")
computeHR(file_path = zip_path, save_outputs = FALSE)



# use the default parameters to analyse a csv file
csv_path <- system.file("extdata", "example.csv", package = "CardiacDP")
computeHR(file_path = csv_path, reduce_res = 0.1,
          save_outputs = FALSE)



# use customized parameters to analyse a zip file
zip_path <- system.file("extdata", "example.zip", package = "CardiacDP")
computeHR(zip_path, reduce_res = 0.1, max_gen = 30L,
          lr_thres = 0.8, save_outputs = FALSE)



# use custom parameters to analyse a csv file
csv_path <- system.file("extdata", "example.csv", package = "CardiacDP")
computeHR(csv_path, reduce_res = 0.1, pop_size = 20L,
          an_in = 1, acf_thres = 0.6, save_outputs = FALSE)
```

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