The R package `CardiacDP`

The R package `CardiacDP` consists of two functions that can be used to collate separate data files into a single data table for subsequent analyses (function `collatedata`), and to compute heart rate from the cardiac data (function `computeHR`). Depending on the input file format (whether it is a .zip file that requires data collation, or a .csv file that is ready for heart rate computation), function `collatedata` will be automatically called within the function `computeHR`, and the overall workflow is summarized in **Figure 1**.

1 Function `collatedata`: data collation

Some oscilloscope software (e.g. Picoscope) produces small and numerous data files as outputs instead of large, collated data files with all measurements, presumably because large data files are difficult to operate. These numerous files, however, have to be collated into a single data table to facilitate subsequent data analysis procedures. The function `collatedata`, therefore, serves to collate separate data files to generate a single data table of cardiac data (each column represents measurements of one individual; referred to as “channels”) measured across fixed time intervals.

This function automatically reads data files and collates them in chronological order as inferred by the file names. Taking the data files produced from Picoscope (v6, Pico Technology, UK) as an example (**Figure 2**), each ‘page’ as visualized on the software is saved as separate .csv files in one folder. After a defined number of pages, the software will reset, producing another folder with, again, separate .csv files representing different pages. All files are then nested inside one folder which can then be compressed (as a .zip file) for this function. As long as the folders and files are named in chronological order, this function is designed to automatically read them accordingly, and one by one in hierarchy (i.e. collate all files within one folder before moving on to the next folder). After collating all files, time will be rewritten as a sequence increasing from zero at a fixed time interval. As such, only measurements taken across fixed time intervals should be collated as one data table for analyses, or else the data should be analyzed separately.

2 Function `computeHR`: heart rate computation

From the collated data table, the function `computeHR` analyzes channel (i.e. individual) by channel and computes heart rates of each sequence. Users can customize the parameters used in this function (**Table 1**).

To minimize computation time, the cardiac data are first analyzed at a reduced time interval (default to be 0.01s; **Table 1**). As a result of inferring heart rates from time lags in ACF, the time interval used in the analysis determines the resolution of heart rates computed (which is implied by the difference in heart rate across a time lag difference of 1). Taking the time interval of 0.01s as an example (**Table 2** and **Figure 3**), the difference in heart rate decreases with time lag (i.e. the resolution increases with time lag) and such a relationship is not linear: for the same time lag difference of 1, the difference in heart rate computed is large at small time lags (coarse resolution), whereas the difference is small at large time lags (fine resolution). As such, the data are automatically re-analysed at the finest time interval when the corresponding percentage difference is > 2% (**Table 2** and **Figure 3**).

By employing ACF with a genetic algorithm framework, the positions and durations of the final periodic sub-sequences (“`finalsubseq`”) and their candidate heart rates (“`candidateHR`”) are determined from the cardiac data per sequence (**Table 3**; see also **Section 3** for the examples). From these sub-sequences, the final heart rates are computed for each sequence, either with or without implementing the tracking index (i.e. “`results_ACF`” and “`results_TI`” refer to the “ACF + GA” and “ACF + GA + TI” approaches as described in the main manuscript respectively; **Table 3**; see also **Section 3** for the examples).

3 User guidelines

The functions of this package are illustrated with the examples below.

When a .zip file (with the corresponding file path) comprising folders and files named in chorological order is provided:

```
output <- computeHR (file_path = “C:/Users/Documents/20210518A.zip”)
```

The function `collatedata` will be automatically called to read and collate the separate files. The data structure will be analyzed and displayed for the user’s reference, and the progress of collation will be indicated.

```
[[1]]
[1] “Zipped file name: 20210518A”

[[2]]
[1] “Number of files: 6”

[[3]]
              folders pages
1:     20210518A-0001    90
2: 20210518A-0001 (2)    90
3: 20210518A-0001 (3)    90
4: 20210518A-0001 (4)    90
5: 20210518A-0001 (5)    90
6: 20210518A-0001 (6)    61

[[4]]
[1] “Total duration: 170 mins”

[[5]]
[1] “Number of channels: 8”

[[6]]
[1] “Names of channels: Channel A, Channel B, Channel C, Channel D, Chann
el E, Channel F, Channel G, Channel H”
```

```
[1] “Reading data: 17%”
[1] “Reading data: 33%”
[1] “Reading data: 50%”
[1] “Reading data: 67%”
[1] “Reading data: 83%”
[1] “Reading data: 100%”
[1] “Finalizing…”
```

After collation, the structure of the collated data table is displayed and the collated data table is automatically saved to the same file path as the input file.

```
Classes ‘data.table’ and 'data.frame':    69003396 obs. of  9 variables:
 $ Time     : num  0 0.00133 0.00267 0.004 0.00533 ...
 $ Channel A: num  -0.002198 -0.00058 -0.001129 -0.000061 -0.001648 ...
 $ Channel B: num  0.00369 0.00314 0.00424 0.00314 0.00314 ...
 $ Channel C: num  0.00424 0.00479 0.00424 0.00372 0.00479 ...
 $ Channel D: num  -0.000488 -0.000488 -0.001007 -0.001007 -0.001007 ...
 $ Channel E: num  -0.0266 -0.0277 -0.0282 -0.0277 -0.0304 ...
 $ Channel F: num  -0.023 -0.0246 -0.0246 -0.023 -0.0241 ...
 $ Channel G: num  0.00906 0.00906 0.01337 0.00748 0.008 ...
 $ Channel H: num  -0.00534 -0.00375 -0.00641 -0.00693 -0.00693 ...
 - attr(*, ".internal.selfref")=<externalptr>
```

```
[1] "Collated data table saved as 20210518A.csv"
```

With the collated data table, the heart rate computation analyses are conducted channel by channel and the progress will be indicated.

```
[1] "Calculating heart rates: Channel A..."
[1] "Generating output..."
[1] "Calculating heart rates: Channel B..."
…
```

The user can then access the output by the channel name. `finalsubseq` is a list showing the positions and durations of the final sub-sequences determined for each sequence. They are presented as data tables (s = start index of the sub-sequence; e = end index of the sub-sequence; p = which of the initial population the sub-sequence is derived from; and f = duration of the sub-sequence), the rows of which represent separate final sub-sequences. The example below shows the first five sequences (e.g. `[[4]]` indicates at the 4th minute there are three final sub-sequences).

```
# positions (in indices) and durations of the final sub-sequences
output [[“finalsubseq”]] [[“Channel A”]]
```

```
[[1]]
   s    e p    f
1: 1 6430 1 6429

[[2]]
   s    e p    f
1: 1 4387 1 4386

[[3]]
   s    e p    f
```

```
1: 1 5775 1 5774

[[4]]
      s    e p    f
1: 2197 3856 6 1659
2: 3669 6430 8 2761
3: 3570 6363 8 2793

[[5]]
      s    e p    f
1:    1 4977 2 4976
2:  780 5785 9 5005
3: 1028 6430 9 5402


…
```

The corresponding candidate heart rates per sub-sequence can be found in `candidateHR` (ACF = autocorrelation value; lag = time lag; and hr = heart rate). Taking the 4th minute again as an example, there are two candidate heart rates for the first sub-sequence (as shown in `[[4]][[1]]`), and only one candidate heart rate for the other two sub-sequences (as shown in `[[4]][[2]]`and `[[4]][[3]]`).

```
# candidate heart rates of the final sub-sequences
output [[“candidateHR”]] [[“Channel A”]]
```

```

[[1]]
[[1]][[1]]
         ACF lag       hr
1: 0.1438675  88 73.05174
2: 0.5748986 180 35.71418


[[2]]
[[2]][[1]]
         ACF lag       hr
1: 0.5141086 170 37.81502


[[3]]
[[3]][[1]]
         ACF lag       hr
1: 0.5002503 164 39.19849


[[4]]
[[4]][[1]]
         ACF lag       hr
1: 0.4296444 156 41.20867
2: 0.5028381 307 20.93991

[[4]][[2]]
```

```
      ACF lag       hr
1: 0.5149 188 34.19443

[[4]][[3]]
         ACF lag       hr
1: 0.5145251 186 34.56211


[[5]]
[[5]][[1]]
         ACF lag       hr
1: 0.5236133 180 35.71418

[[5]][[2]]
         ACF lag       hr
1: 0.5018653 174 36.94571

[[5]][[3]]
         ACF lag       hr
1: 0.5023476 172 37.37531

…
```

The final results after evaluating the candidate heart rates, checking for resolution and weighting for durations can eventually be obtained from `results_ACF` and `results_TI`. These results refer to evaluating the candidate heart rates by autocorrelation values (i.e. the "ACF + GA" approach) and the tracking index (i.e. the "ACF + GA +TI" approach) respectively. Each of them consists of 1) the details of the sub-sequences (ix = sequence (in minute), res = time interval (resolution) used in the final analysis, and the remaining variables are defined as above; `subseqHR`); 2) the weighted heart rate per sequence (`weightedHR`); and 3) a plot of weighted heart rate against time (`plot`).

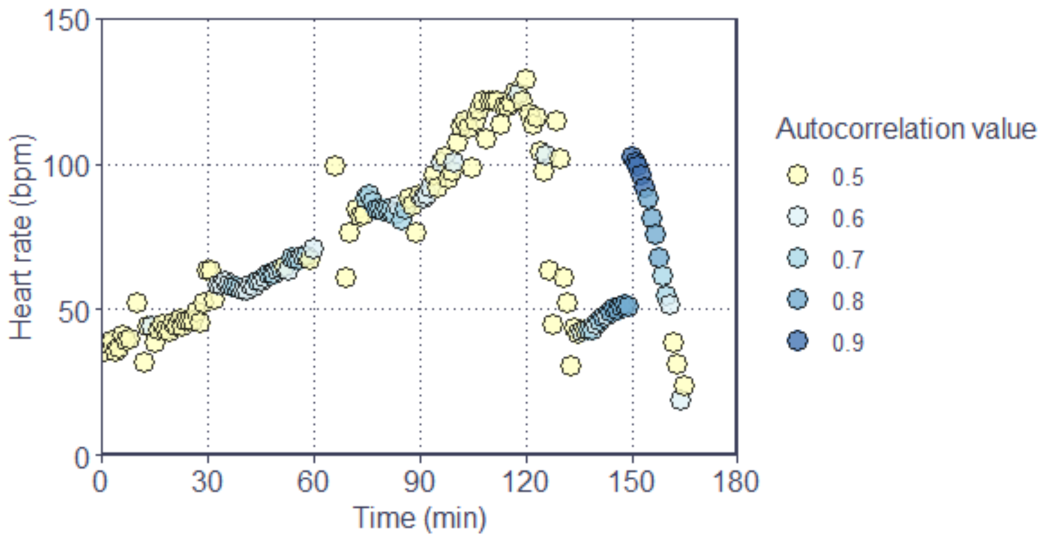
```
# results obtained from evaluating the candidate heart rates by autocorre
lation values
output [["results_ACF"]] [["Channel A"]]
```

```
$subseqHR
      ix win    s    e  p    f       ACF lag       hr        res
  1:   1   1    1 6430 10 6429 0.5748986 180 35.71418 0.00933336
  2:   2   1    1 4201  1 4200 0.5240022 170 37.81502 0.00933336
  3:   3   1    1 5725  1 5724 0.5000011 164 39.19849 0.00933336
  4:   4   1 3215 3856  6  641 0.5241728 156 41.20867 0.00933336
  5:   4   2 3548 6430  8 2882 0.5040846 188 34.19443 0.00933336
 ---
227: 166   1   NA   NA NA   NA        NA  NA       NA 0.00933336
228: 167   1   NA   NA NA   NA        NA  NA       NA 0.00933336
229: 168   1   NA   NA NA   NA        NA  NA       NA 0.00933336
```

```
230: 169   1    NA    NA NA    NA         NA  NA        NA 0.00933336
231: 170   1    NA    NA NA    NA         NA  NA        NA 0.00933336

$weightedHR
      ix      wACF      whr
  1:   1 0.5748986 35.71418
  2:   2 0.5240022 37.81502
  3:   3 0.5000011 39.19849
  4:   4 0.5071297 35.25769
  5:   5 0.5134750 36.53428
 ---
166: 166        NA       NA
167: 167        NA       NA
168: 168        NA       NA
169: 169        NA       NA
170: 170        NA       NA

$plot
```

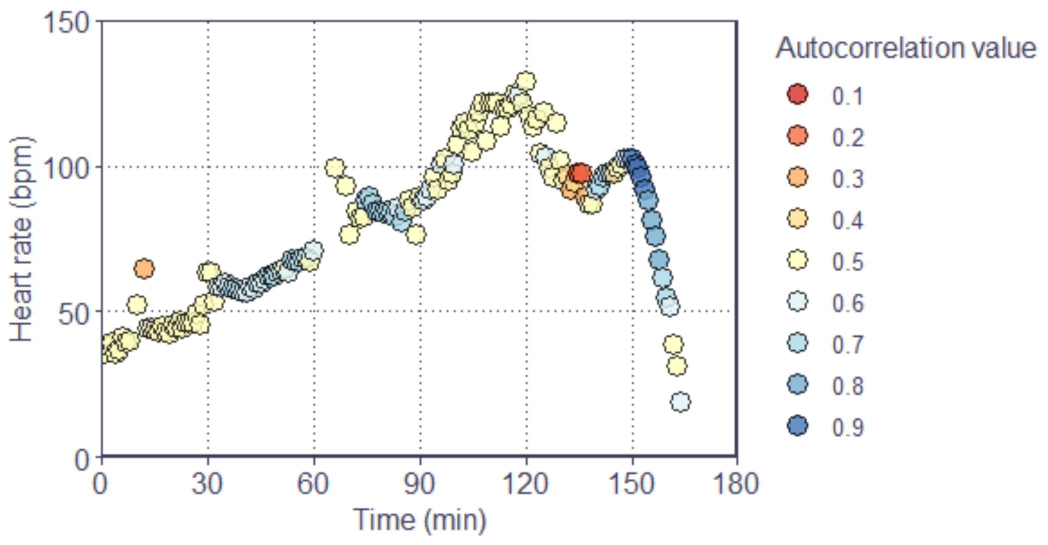


```
# results obtained from evaluating the candidate heart rates by the track
ing index
output [["results_TI"]] [["Channel A"]]
```

```
$subseqHR
      ix win    s    e  p    f       ACF lag       hr        res
  1:   1   1    1 6430 10 6429 0.5748986 180 35.71418 0.00933336
  2:   2   1    1 4201  1 4200 0.5240022 170 37.81502 0.00933336
  3:   3   1    1 5725  1 5724 0.5000011 164 39.19849 0.00933336
  4:   4   1 3215 3856  6  641 0.5241728 156 41.20867 0.00933336
  5:   4   2 3548 6430  8 2882 0.5040846 188 34.19443 0.00933336
 ---
227: 166   1   NA    NA NA    NA        NA  NA       NA 0.00933336
228: 167   1   NA    NA NA    NA        NA  NA       NA 0.00933336
229: 168   1   NA    NA NA    NA        NA  NA       NA 0.00933336
230: 169   1   NA    NA NA    NA        NA  NA       NA 0.00933336
231: 170   1   NA    NA NA    NA        NA  NA       NA 0.00933336
```

```
$weightedHR
      ix      wACF      whr
  1:   1 0.5748986 35.71418
  2:   2 0.5240022 37.81502
  3:   3 0.5000011 39.19849
  4:   4 0.5071297 35.25769
  5:   5 0.5134750 36.53428
 ---
166: 166        NA       NA
167: 167        NA       NA
168: 168        NA       NA
169: 169        NA       NA
170: 170        NA       NA

$plot
```



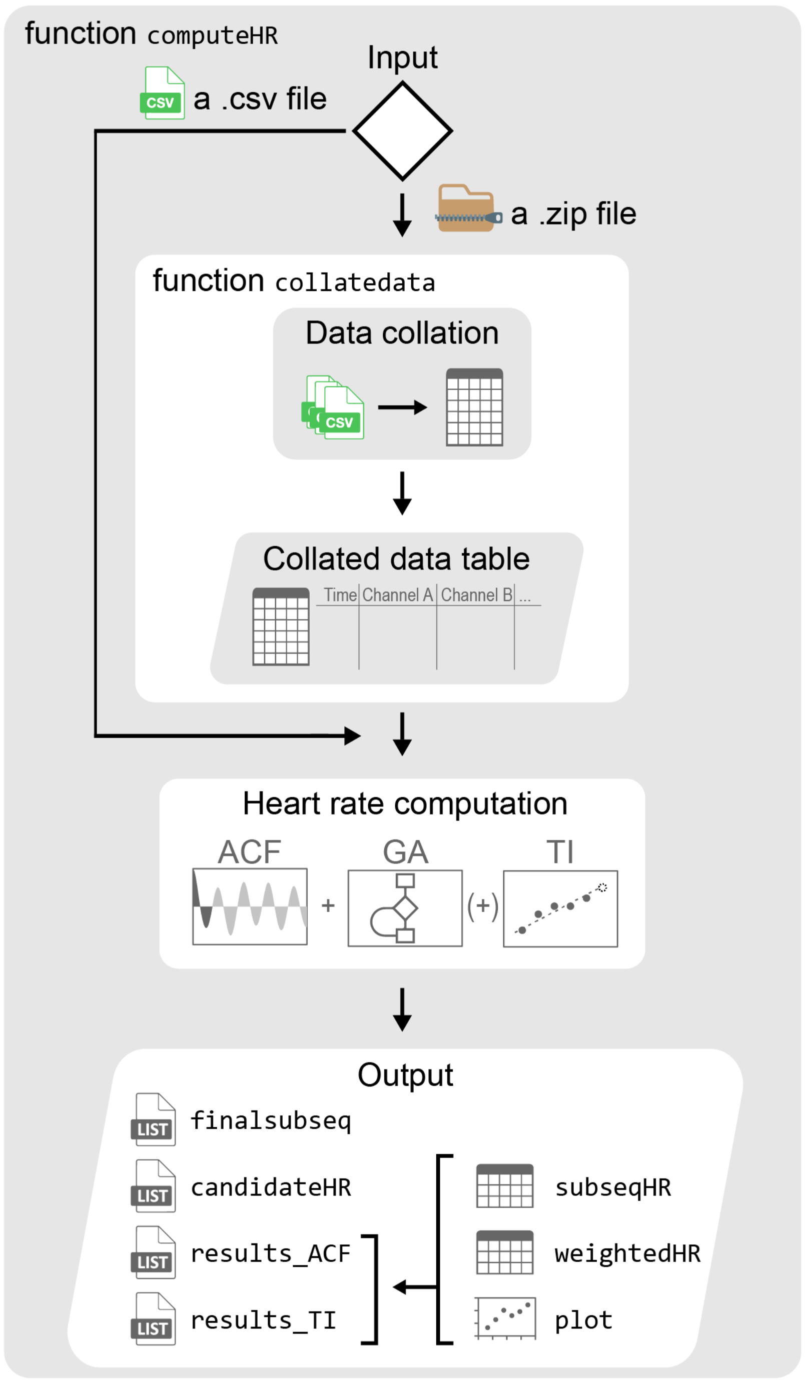


Figure 1 Workflow of the R package `CardiacDP`. In function `computeHR`, depending on the input file format, either the function `collatedata` will be automatically called to read and collate separate files into a single data table in case of a .zip file, or the .csv file will proceed directly to the heart rate computation using autocorrelation function (ACF), genetic algorithm (GA) and tracking index (TI). Details of the output are summarized in **Table 3**.

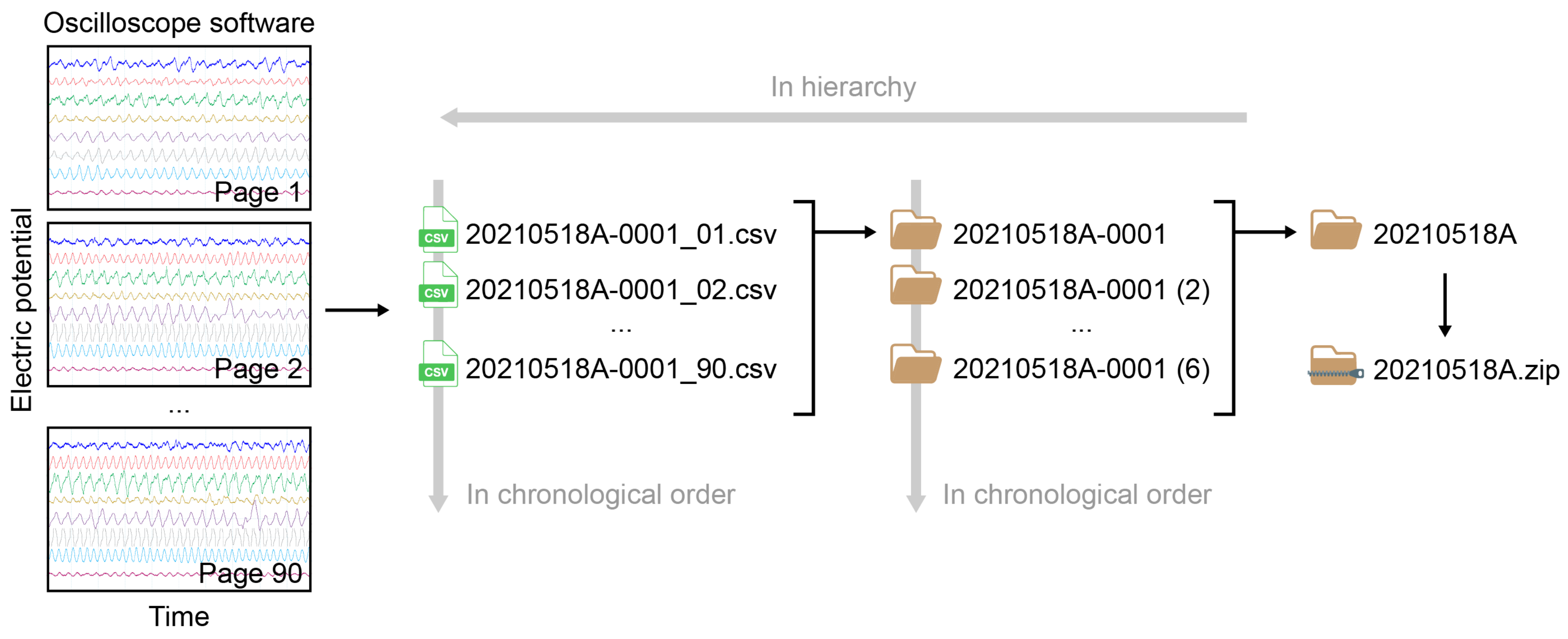


Figure 2 An example data structure of the data files produced by the oscilloscope software Picoscope (v6, Pico Techology, UK). Each 'page' of the software is saved as separate .csv files nested within a folder. After a defined number of pages, the software resets and creates another folder in which 'pages' are again saved as separate .csv files. The files and folders are automatically named in chronological order and are finally nested within a single folder which is compressed to a .zip file for the function `collatedata`. This function reads the data in chronological order and in hierarchy (as indicated by the vertical and horizontal grey arrows respectively) and collates them to give a single data table for subsequent analyses.

Table 1 Variables used in heart rate computation that allow user customization.

Variable	Definition	Default value
`an_in`	As in 'analysis interval': the length of a sequence to be analyzed in parallel (minute).	1
`reduce_res`	The time interval of cardiac data to be analyzed at a reduced resolution (seconds).	0.01
`pop_size`#	As in 'population size*': the number of sub-sequences to analyze within each sequence in the genetic algorithm.	10
`max_gen`#	As in 'maximum generations*': the maximum number of rounds to repeat the selection and mutation procedures in the genetic algorithm.	20
`patience`#	The number of rounds to repeat when there are no further changes in the sub-sequence durations before terminating the genetic algorithm.	2
`acf_thres`	The threshold used in ACF to classify periodic and aperiodic data. Increasing this threshold may increase the power to screen off noises but also lead to greater data loss.	0.5
`lr_thres`	The threshold used in the linear extrapolation of when establishing the tracking index.	0.7

*see **Supplementary S2 of the publication** for the equivalent terms used in the typical genetic algorithm and the present study
#variables that are in potential tradeoff with computation time (i.e. increasing these numbers may facilitate the optimization process of the genetic algorithm but increase the computation time)

Table 2 The relationship between time lag, the corresponding heart rate and resolution (as implied by the difference in heart rate by a time lag difference of 1) when analyzing cardiac data with the time interval = 0.01s. The resolution increases with time lag and the relationship is not linear (see also **Figure 3**): for the same time lag difference of 1, the difference in heart rate computed is large at small time lags, whereas the difference is small at large time lags. As a result, in this package all data are first analyzed at a reduced time interval to minimize computation time and are only re-analyzed at the finest time interval when the corresponding percentage difference is ≥ 2% (i.e. for results with time lag ≤ 49 in this example).

Time lag	Period (s / beat)	Heart rate (bpm)	Difference in heart rate between time lag *t* and *t+1* (bpm)	% difference
0	NA	NA	NA	NA
1	0.01	6000	3000	50.0
2	0.02	3000	1000	33.3
3	0.03	2000	500	25.0
4	0.04	1500	300	20.0
5	0.05	1200	200	16.7
6	0.06	1000	143	14.3
7	0.07	857	107	12.5
8	0.08	750	83	11.1
9	0.09	667	67	10.0
10	0.10	600	55	9.1
…				
46	0.46	130.4	2.8	2.13
47	0.47	127.7	2.7	2.08
48	0.48	125.0	2.6	2.04
49	**0.49**	**122.4**	**2.4**	**2.00**
50	0.50	120.0	2.4	1.96
51	0.51	117.6	2.3	1.92
52	0.52	115.4	2.2	1.89

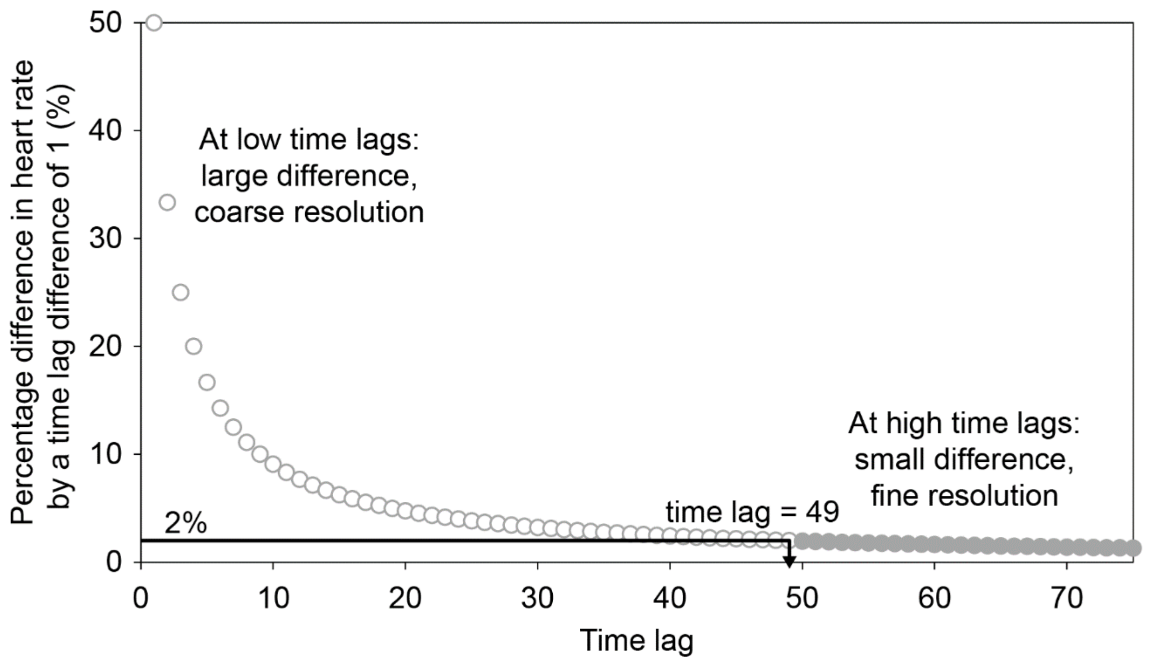


Figure 3 The relationship between the percentage difference in heart rate computed across a time lag difference of 1 with time lag. All data are first analyzed at the reduced resolution to minimize computation time (as indicated by the closed dots) and are only re-analyzed at the finest time interval when the percentage difference is ≥ 2% (when time lag ≤ 49; as indicated by the open dots).

Table 3 The output from function `computeHR` per channel consisting of four items, with `finalsubseq` and `candidateHR` indicating the results from the genetic algorithm, and `results_ACF` and `results_TI` indicating the final heart rates after evaluating the candidate heart rates, checking for resolution and weighting for durations.

Variable	Content
`finalsubseq`	A list of positions and durations of the final periodic sub-sequences
`candidateHR`	A list of candidate heart rates extracted from ACF for each sub-sequence
`results_ACF`	Results obtained from evaluating the candidate heart rates of each sub-sequence based on autocorrelation values (i.e. following the "ACF + GA" approach as described in the main manuscript). Consisted of three items: 1) `subseqHR`: a list of sub-sequences and the corresponding heart rates and durations; 2) `weightedHR`: a list of final heart rates per sequence after weighting; and 3) `plot`: a plot of final heart rates against time
`results_TI`	Results obtained from evaluating the candidate heart rates of each sub-sequence using a tracking index (i.e. following the "ACF + GA + TI" approach as described in the main manuscript). Consisted of three items: 1) `subseqHR`: a list of sub-sequences and the corresponding heart rates and durations; 2) `weightedHR`: a list of final heart rates per sequence after weighting; and 3) `plot`: a plot of final heart rates against time