BRS-R v1.0

**Batch process baroreflex sensitivity analysis using the sequence method**

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The BRS-R program is designed to utilize beat-by-beat physiological data using R-R interval (RRI) and systolic blood pressure (SBP). The program requires the download of R 4.2.2 (link) and RStudio (link)

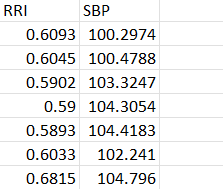
# File Preparation:

Because the program processes files as a batch, many files can be completed at once, if files are prepared correctly.

The program will accept only **.csv** files

These files should be named with participant and condition ID – the filename determines the output folder name after BRS processing

Below is an example of a properly prepared file.



Files must have only 2 columns, RRI in seconds, and SBP in mmHg. **COLUMNS MUST BE LABELLED RRI AND SBP**. Naming is important as the program requires the columns to be exact matches – check for spaces at the end of column names.

RRI and SBP data can be pulled using beat by beat identification in labchart and copied from the datapad. Approximately 5 minutes of data or more is recommended for adequate sequence count.

# Folder Preparation:

Begin setting up for analysis by creating a folder where you want to store the completed BRS analysis. This can be on CPPH or on your desktop.

Drop the BRS-R v1.0 R file into the empty folder. Your folder should now look like this:

A screenshot of a computer

Description automatically generated

Open the R script by double clicking on the file. RStudio will open and the script will be in the script console in the top right quadrant (see below).

A screenshot of a computer program

Description automatically generated

Now that RStudio is open, highlight all of the code in the script (right click in the script and select all) and click Run (highlighted above via the red circle). The console in the bottom left will begin running the script. Let the program run until it is completed – The console message will say “BRS Analyzed” when complete.

The program will install any required dependencies and create your base file structure inside your original working folder. The working folder will now look like this.

A screenshot of a computer

Description automatically generated

Your folder is now ready for batch processing your BRS files. Place all prepared csv files into the data\_csv folder.

# Running the program:

After placing all files you would like processed into data\_csv, the data\_csv will look like this, except with the csv files you prepared.

A screenshot of a computer

Description automatically generated

The program can now be run again as described in the previous section. The console in the bottom left will begin running the script. Let the program run until it is completed. It will take longer this time but be patient – The console message will say “BRS Analyzed” when complete.

# Output Files:

Once the processing is complete, your working folder will have a new “**export**” folder. The results from the program are stored here.

A screenshot of a computer

Description automatically generated

Each file from the data\_csv folder will now have its own export folder.

Exported files include:

* BRS results.csv
  + This file contains the summary info that has been filtered. Mean slope, Slope SD, and sequence count for lag 0,1,2 will be in this file. Outlier sequence slopes that do not meet criteria (R2<0.85, or mean slope >1.5 IQR) have been removed from these values.
* lag0\_slope
  + List of the sequences identified using lag 0 with their slopes and r2 values
* lag0\_data
  + All of the beats identified as part of a sequence using lag 0
* lag1\_slope
* lag1\_data
* lag2\_slope
* lag2\_data

In addition to these files, there will be a “plots” folder in the export for each file.

These plots are visualizations of every identified sequence, and are not necessary for data extraction, but can be helpful if troubleshooting a particular file. The plots are associated with the slopes in the unfiltered lagX\_slope.csv files, with figures going left to right in increasing order.