THE FOLDER rr\_win CAN BE DELETED ONCE ADEQUATE H5 WAS CREATED. I SHOULD MAKE ANOTHER EMPTY FOLDER WITH THE SAME NAME. aging folder CANNOT BE DELETED

Order:

Addending2rr. Only performed once and saved to a folder that should not be deleted (aging for instance). This results in the full rr time series and their adequate labels.

Rr\_win\_y: divides the rr in (aging for instance) to any segments you’d like and saves in rr\_win. The labels contain: id, age, med, win\_num

Convert2hdf: stores the windows in aging\_and\_ac8.h5 according to instructions below and comments in the code.

For aging HRV use mice analysis (in mhrv) and then hrv\_processing (in C:\Users\smorandv.STAFF\Documents\PhD\aging and meds). The hdf is created there.

Delete rr\_win and create a new empty one

* Create 2 hdf files. One for rr and one for hrv. Each would have two groups: aging and ac8. The hierarchy would be the following:
* Rr.h5:

\aging

\ Nbeats\_number\_input

\ Nbeats\_number\_label

\ac8

\ Nbeats\_number\_input

\ Nbeats\_number\_label

* Hrv.h5:

\aging

\ Win\_len\_number\_phase\_number\_input

\ Win\_len\_number\_phase\_number\_label

\ac8

\ Win\_len\_number\_phase\_number\_input

\ Win\_len\_numer\_phase\_number\_label

For hrv, another mat file containing cells of features names will be save with aging/ac8 and win\_len and phase.

0 – no med (control)

1 – double block

2 – Atropine

3 – Doubatamine

4 - Propanolol

* Copy locs data into the directory (aging) in order to create rr intervals with id, age and med for aging data.
* Run mhrv batch and make sure to have the columns of id, age and med. Do it as a csv or xlsx. **NOTICE: mhrv expects locs so use it as in mice\_analysis in C:\Users\smorandv.STAFF\Documents\PhD\mhrv**