**ALIGNING SIGNALS**

***Finding long hypoxic episodes***

1. Compile a list of patients and the dates on which we have Somnostar data collected.
   1. If we have Somnostar data, we most likely have corresponding NIRS data (i.e., the data of interest)
   2. Compiled list: **somnostar\_times.xlsx**
2. Aggregate all the HDF5 and results.mat files for each patient at each Somnostar data collection period AND where there is at least one hypoxic period >= 60 seconds long.
   1. The **results.mat** files list hypoxic periods. From each of these files, a new **HYPOXIA\_**….**mat** file was created containing variables for
      1. Hypoxia start and stop times
      2. Hypoxia length
      3. Rows containing hypoxias >= 60 seconds
   2. Script for aggregation: **locate\_results.py**
   3. Script for results.mat parsing: **locate\_60s\_hypoxia.m**
   4. List of files with long hypoxias: **files\_with\_hypoxias.mat**
3. Create a new spreadsheet containing all the long hypoxic episodes along with the patient number, patient age, and corresponding file
   1. List: **hypoxias\_by\_pt.xlsx**

***Time syncing Bedmaster/Medicollector, Somnostar signals***

1. Graph Bedmaster/Medicollector respiratory signal for apneic episodes
   1. Script: **read\_resp.m**
2. Graph Somnostar chest impedance signal
   1. Script: **read\_som.m**
3. Start by looking at five-hour differences between both signals
   1. Find a good apneic episode in the BM/MC signal first
   2. Then, look to see if there’s a corresponding apneic episode in the Somnostar signal
   3. Aligning signals is easiest during episodes of periodic breathing
4. Log 20 corresponding time points and average the time difference. This will be the offset of BM/MC from Somnostar (and NIRS)
   1. Zoom into peaks and troughs to get a more precise point selection
   2. List: **alignment\_v2.xlsx**
      1. 2073 : 36 weeks
      2. 2085 : 32 weeks
      3. 2004 : 32 weeks

**COMPILING DATA OF INTEREST**

*NIRS provides the rSO2 data, sampled every four seconds. Bedmaster/Medicollector provides the SpO2 data, sampled every second.*

***Finding SpO2 signals***

1. Convert NIRS data (.nms format) to .csv using SenSmart software
   1. Data can be found in the L:\PreVent\Nonin NIRS and Neurodevelopment\ folder
2. Shift BM/MC to CT time based on determined average offset.
   1. Export rSO2 as **XXXX\_rso2.csv**
   2. Export SpO2 as **XXXX\_spo2.csv**
   3. NIRS is up to 1 minute behind Somnostar, both of which are recorded in CT. This variability will be accounted for with a widened time interval in the final plots, to be discussed

***Configuring rSO2 and SpO2 data to get hypoxic periods of length XX only***

*This is done in* ***configure\_signals.m***

1. Start by looking for hypoxic episodes
   1. (i.e., SpO2 <= 80%) that lasted at least 20 seconds long
   2. Record the
      1. Row number at which this hypoxic period begins (added a 1-second buffer) in the SpO2 dataset
      2. The number of rows (corresponding to seconds in SpO2 data) for this episode
2. Get the corresponding hypoxia interval times in the rSO2 data, accounting for differences in sampling rate
   1. Store all of the relevant rows for the hypoxia intervals for each of the datasets (rather than storing the count; this allows us to quickly index the relevant rows in the matrix)

**VISUALIZING DATA**

***Displaying hypoxic periods with rSO2 and SpO2 data***

*This is done in* ***display\_hypoxia.m***

1. For each hypoxic interval, plot the rSO2 and SpO2 signal on its own subplot
   1. Give both datasets different y-axes to better visualize signals