MEA Acute pre-processing notes

# Things would be good to discuss with lab

* I get the experiment.date and the run\_type determination from the time in the Neural stats compiler header. However, Seline told me this clock is not always right.
  + Is the date generally reliable?
  + Would you update the clock mid-run? (i.e., can I trust the run\_type determination based on this?)

# Checklist for lab folks to do before send off data

* Make sure that the culture dates in folder names are present and correct (I know sometimes you may plan to do a culture on one day, then it gets pushed back. So please make sure that the culture dates are correct).
  + I will pull the culture dates from 8-digit numbers in the folder names
  + If there is variability in the cultures for files within a given group, communicate that.
* Make sure that raw LDH files contains the word “LDH” in file name

# Approach for this document/the run\_me

* I’m thinking more text to explain the “Why” is better than fool proof code. Because the code is going to have to change.

# Abbreviations

* NSC = Neural Statistics Compiler
* CTB = Cell Titer Blue. Same assay as Alamar Blue
* AB = Alamar Blue. Same assay as Cell Titer Blue

# Things I might need to debug

* I’m currently pulling all meta data from only the CTB and LDH columns. If I ever discover in the lab notebook that the dosing arrangement is different in the CTB/LDH from the MEA plate… would need to create some script to read from the sheet by plate
  + I imagine this could happen if there was a mix up when transferring the contents from the MEA plate to the LDH/CTB plates

# Tips

* If having errors in extractAllData, or actually in fileToLongdat, can wrap line 31 to create “Add.dat” in a tryCatch, with pulling up browser on error, so that you can determine which file is giving an issue
* Whenever you encounter an error, debug() and debugonce() are your friend!!

# Well quality

* Note experiment.date vs culture.date in the well quality tables… not sure how to standardize, but for now, do what is best.

# Level 1

* Analysis duration
  + This should be 2400 seconds (or 40 minutes). If the recording duration is significantly different than 2400 seconds, then you may want to assess whether this recording is still usable.
    - The definition of “significantly different than 2400 seconds” is up for interpretation. Previously, I have used a coarse filter of 500 seconds above or below 2400 to flag recordings.
    - Note that some endpoints are summed across the recording (e.g. number of spikes, number of bursts), so these endpoints are definitely affected by the analysis\_duration.
* Analysis start
  + I think this corresponds to the start time of the data relative for the beginning of the .RAW recording that is used to calculate the endpoint values with the NSC.
  + This field is taken from the neural statistics compiler header. If the analysis start is significantly different than 0, check if there were any abnormalities in the amount of rest time before the recording started (there should be 20 minutes usually). If so, flag the recording for follow-up analysis to determine if the data is still usable.

# Level 4

* Check if all compounds dissolved in DMSO, or is variable (if variable, will want to create a column that documents… but it’s kind of optional?)
  + Also may need to determine how to normalize, if can collapse controls…
* Determine dose units for all compounds (uM or ug/mL, or other?). Ultimately, need to convert all to uM