Weekly Goals

- [x] Work on sectioning WT, drug data by time
- [x] Section WT, drug data by number of spikes
- [x] Read through some of the literature (Kass, Heil) and create note of references
- [x] Write 1-2 pages describing work done so far. What are main ideas and problems? What questions are we trying to answer?

- [x] Run data fitting for all WT data
- [x] For data fitting with p<.05, try different initial guesses (trial and error) to see if you can fit data properly
- [x] Make slides for WT 1-26
- [x] Attempt data fitting for drug treated and mutant data
- [x] Manual override for mutant/drug data
- [ ] Hockey stick data sets -- do google search for distributions with fast decays and heavy tails
- [ ] Read Tom's Thesis
- [ ] Pre/post drug data borrow parameters
- [ ] Refine data fitting where possible
- [ ] Think through p value
- [ ] Run analyses for door model (SRC, spike rate, rec/quant map, hyperexp mod)
- [ ] Change as you vary parameters? prel_max small? tclose/tpoen shorter, longer?

Monday, June 20th

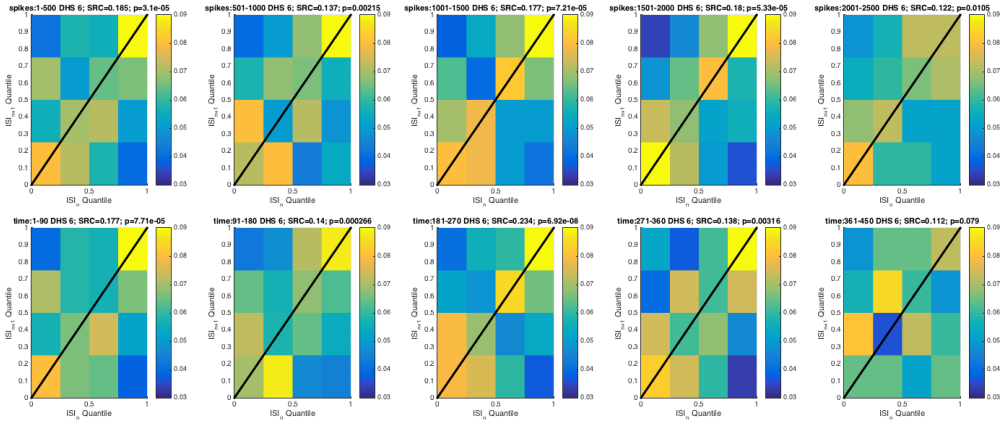
- Created boxplots between pre and post drug for DHS, DKAH, and ZD

Sectioning Off Quantile Color Maps

- colormapByNum and colormapByTime
    - Two new methods which create a figure with several subplots
        - Width of figure set at 24 inches
        - Height set at 24/counter, where counter is the number of subplots
        - Should yield roughly square colormaps
    - Subplots can contain recmaps sectioned by either number of spikes or time
    - Working on ways to find a good # of spikes, or time interval to divide by
        - Automatically sections into 4 or 5 bins.
        - Use num=50*ceil(N(ii)/5/50) to round to nearest 50's for num spikes
        - Use timeint=30*ceil(max(tspike)/5/30) to round to nearest 30s for time interval
            - POSSIBLE ACTION: add if statement to remove section if fewer

than 100 spikes

- Also try using above methods on WT data



Problems with looking at quantile maps over time

- How do we calculate deviation?
  - Current deviation calculates the "distance" from a uniform distribution, but does not tell us where the bright spots are
  - Need to characterize whether deviation stays the same = pattern stays the same over time
  - POSSIBLE ACTION: Try plotting all 16 qi_j's over time?

Subplot

- Subplot() function still giving me some trouble with using my own methods
- Try to call subplots with different sizes (Can set axes points) when there's extra time

Tuesday, June 21st

Looking at literature for information on dealing with serial correlation, see ‘Relevant Literature'

Relevant Literature

Compiling summary of the work done so far, see attached doc ‘Week 3 - Progress Report'

Wednesday, June 22nd

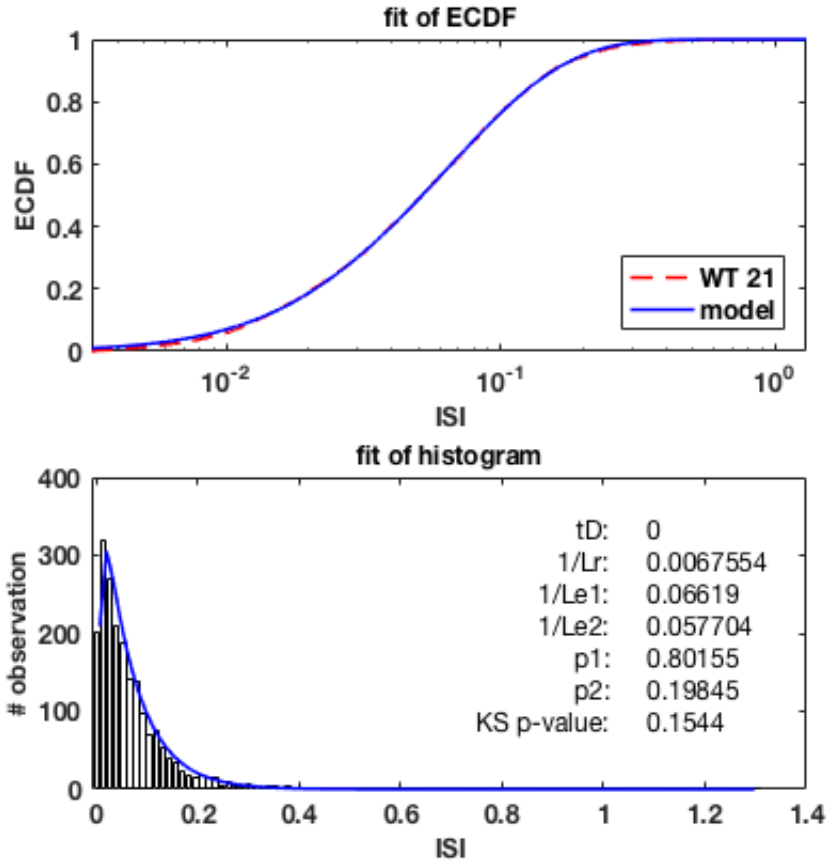
Meeting with Prof. Tania

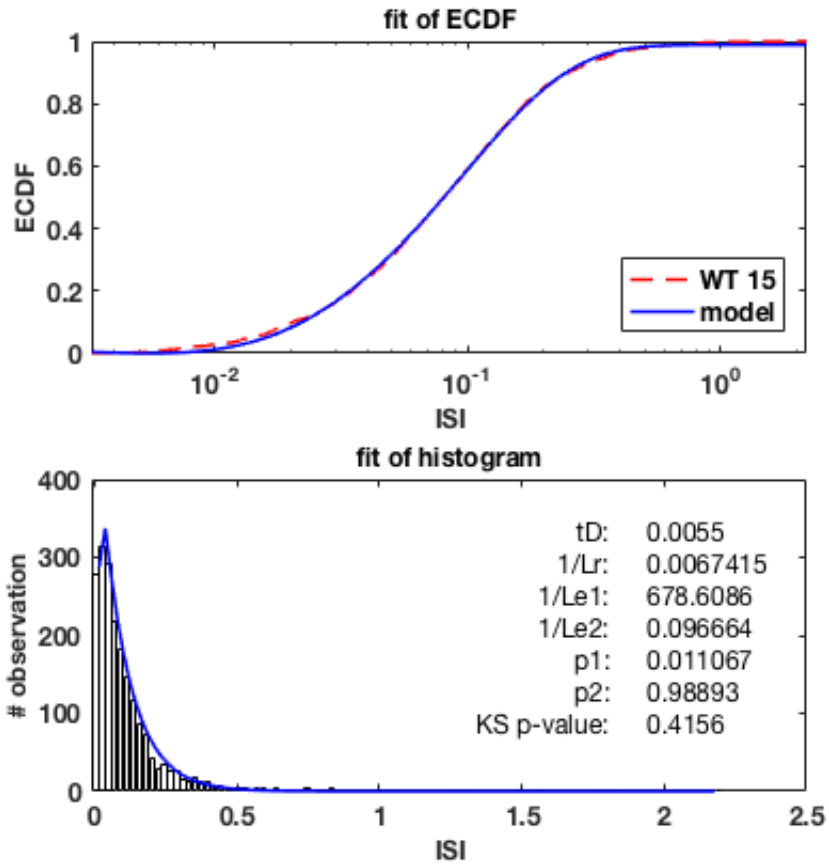
- Walk through data fitting, calculating KS statistics
- KS p-values
  - Measuring KS_observed with a distribution of KS statistics generated using our parameter values
  - If the p-value is high, then there are a large number of KS statistics generated that are more extreme than our value, so the model is a good fit.
  - If the p-value is low, then our observed value of KS is extreme

    - H0: our distribution of ISI's fits the distribution created by the model
    - Ha: our distribution of ISI's does not fit the distribution created by the model
- Output parameter values into an excel file, create slides for each figure

Thursday, June 23rd
Edited code for KS_Test_hyperex_excitation_ALL.m

- Outputs parameter values into the figure automatically,
- Move legend to SouthEast corner to avoid clash with the model
- Fix error for WT i=7 where 'xcenter' is the wrong size for plotting hist_model*N(ii) by using xcenter(1:100)
- Output stored in .csv file
    - According to internet search, some Macs are not compatible with xlswrite()
- Manual fitting
    - Some datasets require tD larger than minimum ISI for strong model fits (p-values ~.45)
    - Some datasets, like WT 10/21 seem to benefit from no minimum recovery period, a tD value of 0
    - Some datasets, like 5/8/15 seem to benefit from long recovery periods, longer than minimum ISI's


fit of ECDF
ECDF
ISI
WT 21
model
fit of histogram
observation
ISI
tD: 0
1/Lr: 0.0067554
1/Le1: 0.06619
1/Le2: 0.057704
p1: 0.80155
p2: 0.19845
KS p-value: 0.1544



WT Parameter Fitting powerpoint

- Contains slides for WT data 1-26
- Contains notes for models with issues

DHS, DKAH, ZD Parameter Fitting powerpoint

- Slides contain figures and tables but no notes yet
- No manual fitting yet
- pre/post side by side

RB CDH Parameter Fitting powerpoint

- Slides contain figures and tables but no notes yet
- Started manual fitting, notes.

Parameter Fitting by Type.xlsx

- Mark when probabilities p1 and p2 are too extreme (<.025)
- Mark when Le1 and Le2 are too similar
- Mark when p-value is too low, (<.05)
- What should we do when p1 and p2 are too extreme? Eg, when a single exponential fits better?
- Manually changing tD values also improve p-values for models that already had high p-values… Can we optimize t also?

Distributions with Fast Decay, Heavy Tails.. Things to look into?

- Lognormal
- Kurtosis Risk

Friday, June 24th
Meeting with Prof. Tania, under Week 3 Scans

- Take post drug values with high p-value, use them as our initial guess for par0
- Refine data fitting process
- Also, think about p-value
    - Is it measuring what we want it to measure?
    - Is the code correct?
    - Are we doing the right goodness of fit test? (KS test)?
    - Explore door model
    - Read through papers

Using post drug values with high p-value

- Doesn't improve p-values for pre, or vice versa
- In some cases, actually decreases p-value
- Some datasets still can't be fit by the hyperexponential model

Simple Door Model

- Create new excel sheet spont_DOOR
- topen, tclose, prel_max
- 1: .3, 20, .7
- 2: .3, 10, .7
- 3: .7 20 .7
- 4: .3 20 .3
- Run analyses next week