Spikedata\_problem.mat

Data: 17 neurons, 43 left trials, 43 right trials.

Variables:

Average Firing rates over entire trial

leftfr: 43X17 (trials X Nneurons)

rightfr: 43X17 (trials X Nneurons)

Firing rate in 100ms bins from -200 ms to 800 ms, with stimulus onset at 0.

Lefttrials: 17X1 cell array. Each cell corresponds to one neuron is a 43X10 matrix, representing the binned spike count (binsize = 100ms) of that neuron in each of 43 trials

Righttrials: Same for right trials.

Problem:  
1) For the leftfr and rightfr matrices, can use dimensionality reduction (PCA) to visualize population activity in 2-dim (2 PCs) or 3-dim space (3PCs)? How much variance is explained by the first 3 PCs? Can you see separation between left and right trials?

2) Can you do the same as above, but compute PCs for each time bin, and plot the average (average across trials) time evolution/ average trajectory of the population activity in 2-dim (2 PCs) or 3-dim space (3 PCs)? Can you see the separation of the trajectories for left vs. right trials?

3) Using either the entire firing rate, or the binned firing rate, can you use glm with cross-validation to quantify whether you can predict left or right trials using the population activity?

Can you instead use Bayesian decoding or SVM methods for a similar prediction?