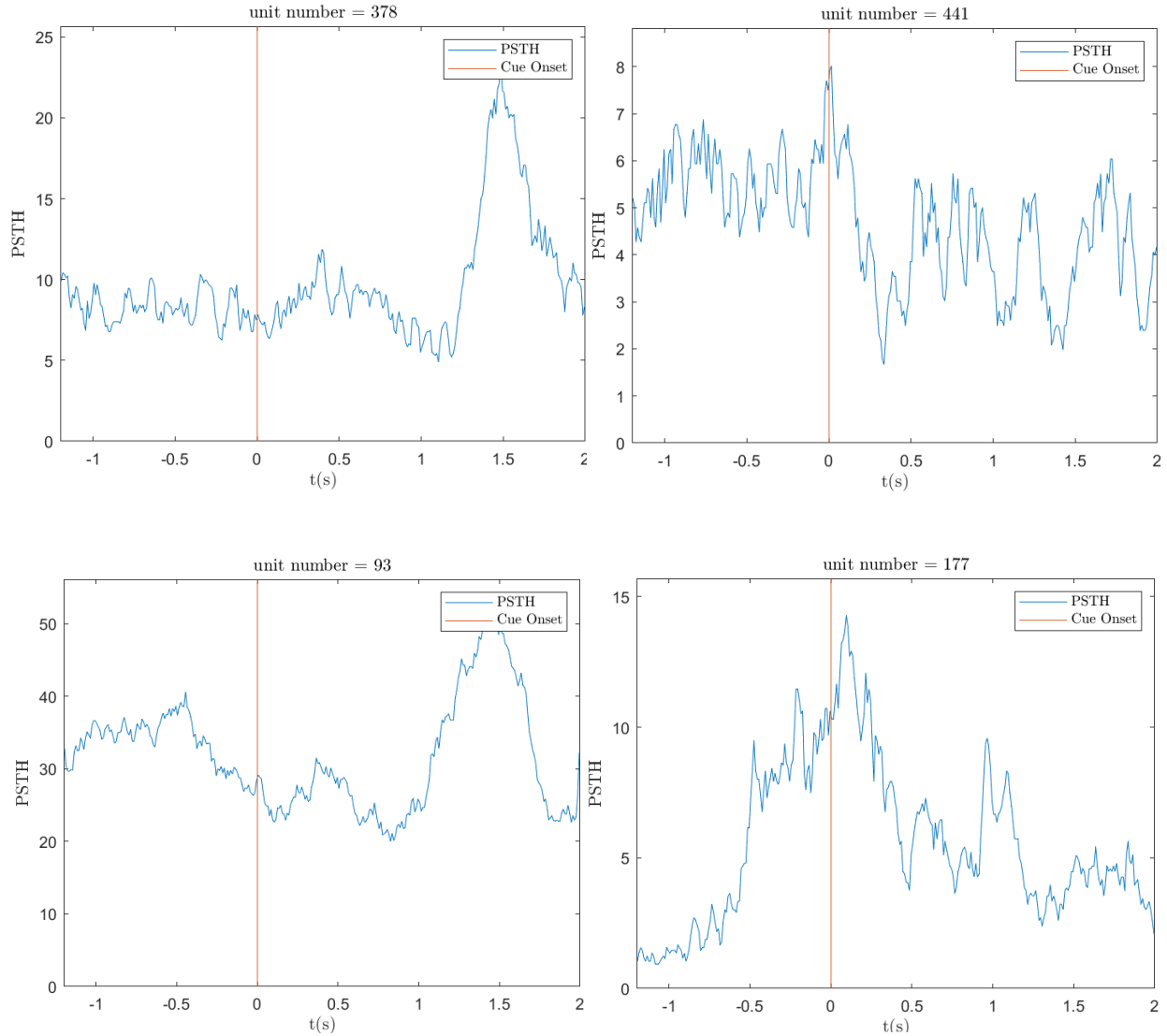# In The Name of God

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Advanced Neuroscience HW1

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# Step 1:

At first, the PSTH, using a 1ms window size, is calculated for each unit, without considering different conditions. In fact, different conditions are averaged. Here are the results for 4 randomly selected units:

As we see, PSTH plot shows that a unit is overall related to this task's processes or not. We can see as an example that unit number 93 and 378 have an increase in their firing rates after "Cue Onset" comes.

Then, we tried to show the PSTH of the units in different conditions through subplots, and here are the results for the previous 4 randomly selected units:
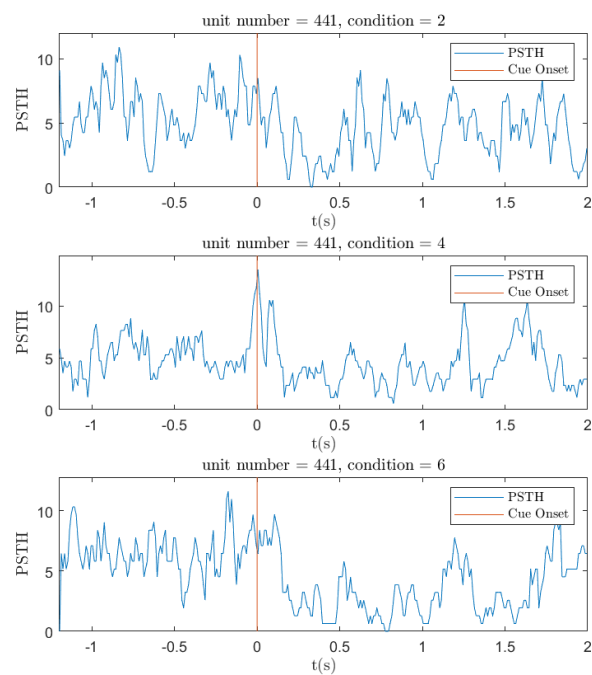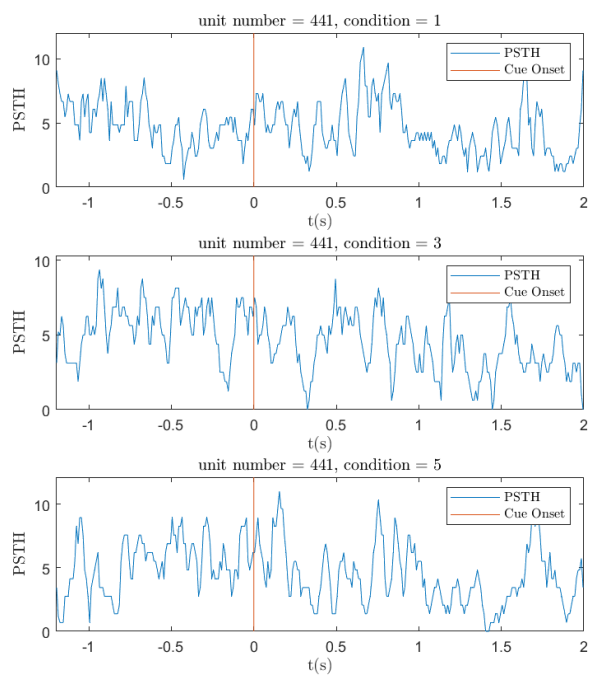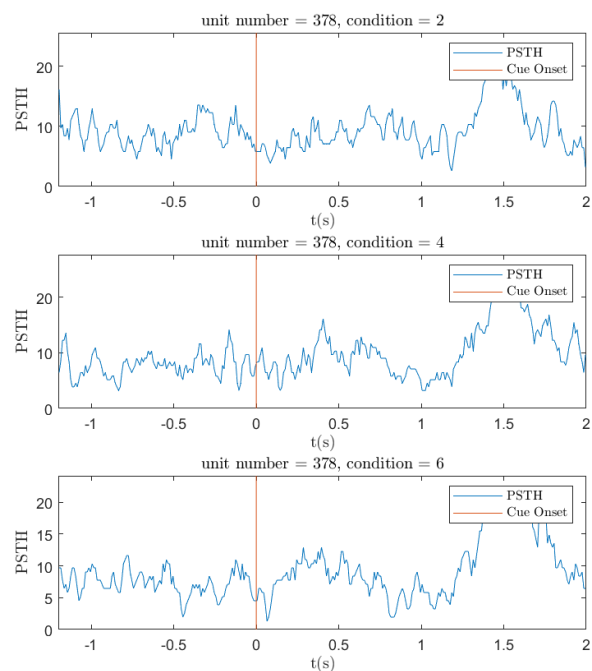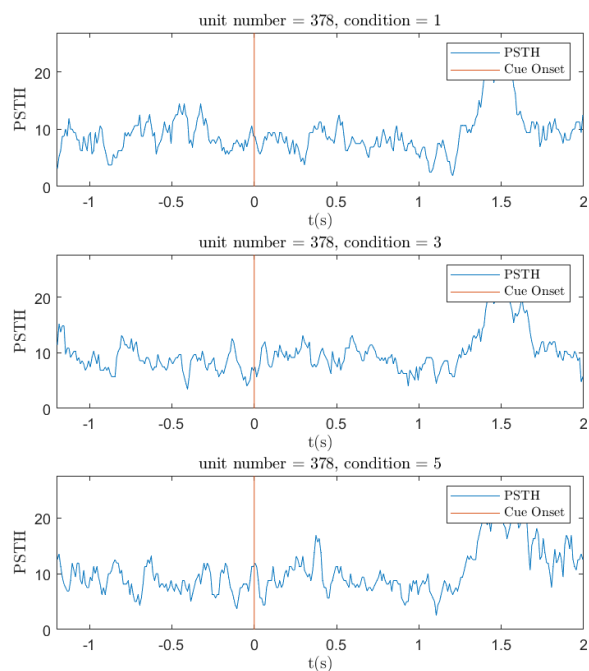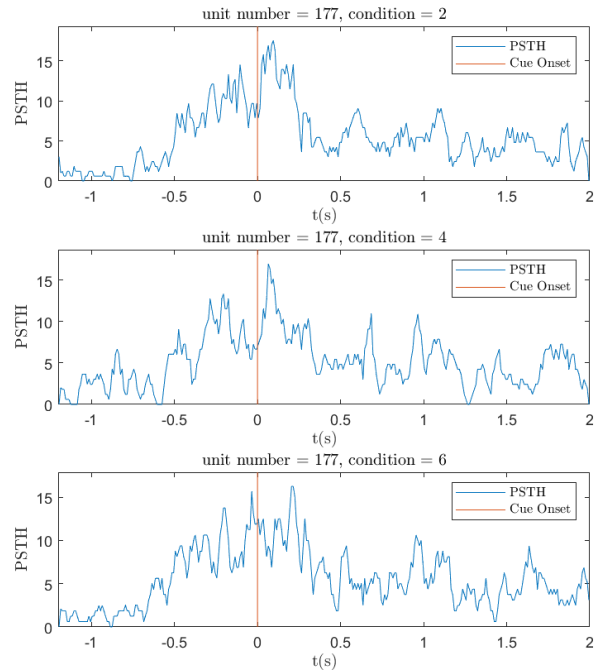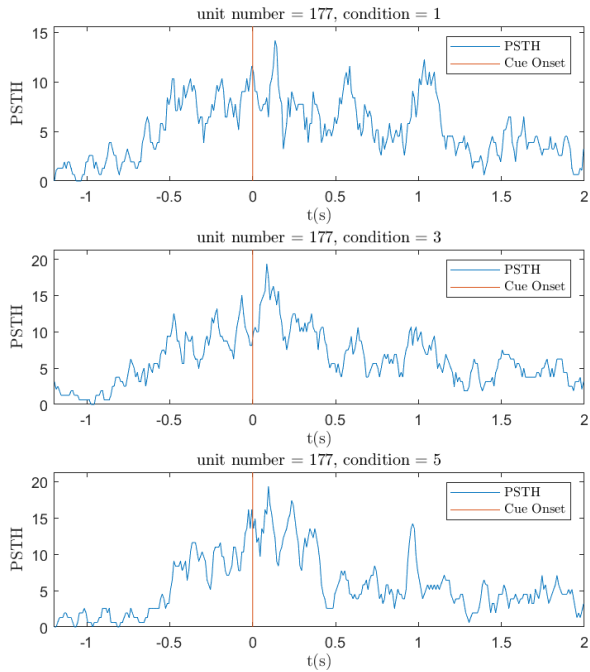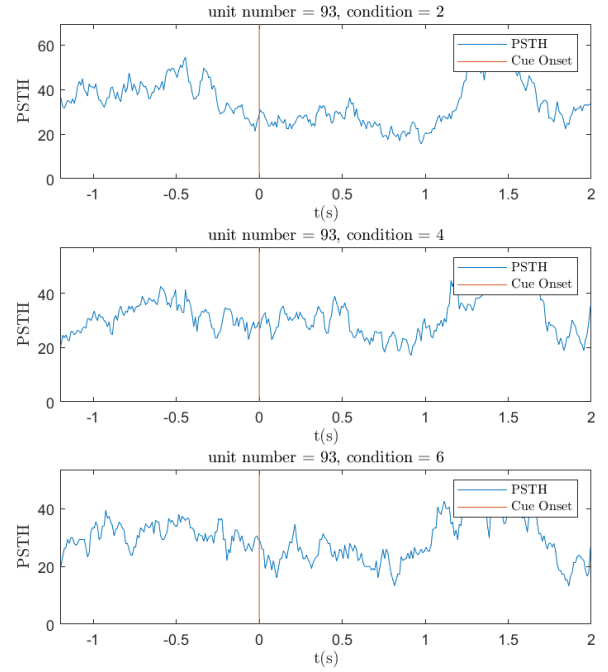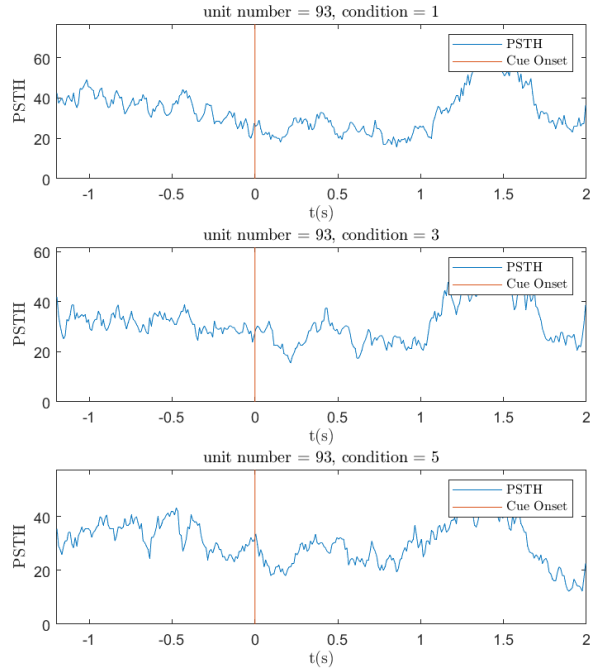
As we see, PSTH plot shows that a unit is related to a condition's processing or not. We can see as an example that unit number 93 and 378 have an increase in their firing rates after "Cue Onset" comes in different conditions.

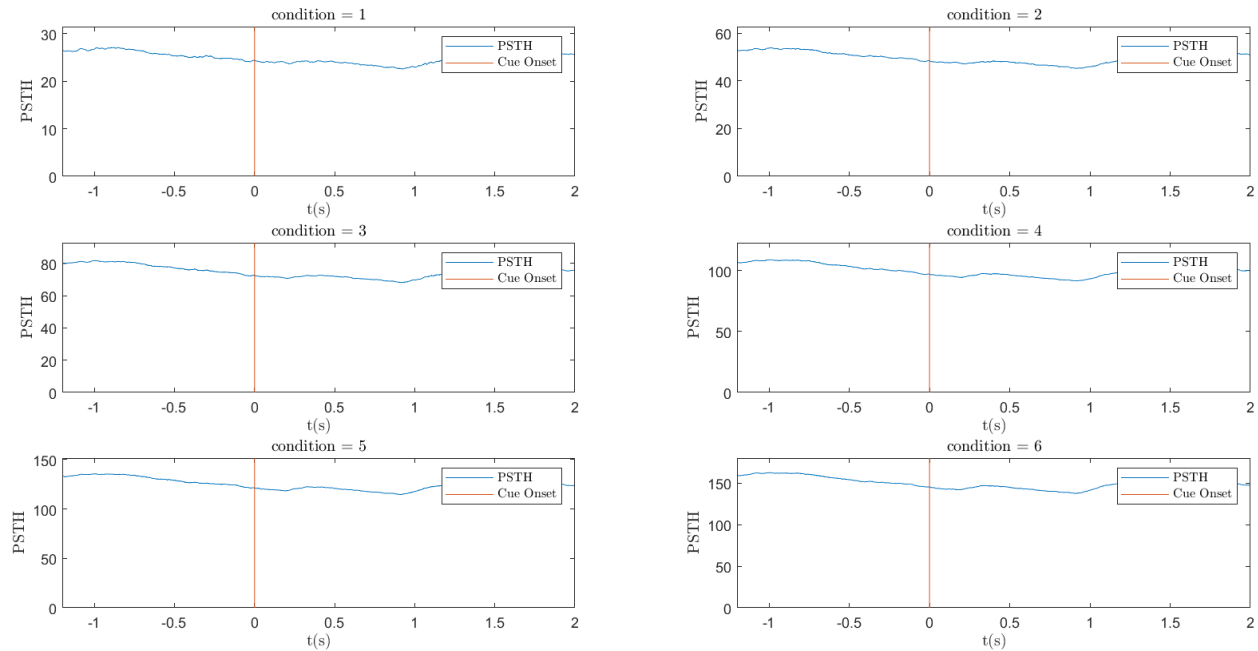And at last, we tried to calculate the average PSTH of different units for each condition, and now we get:

It can be seen that this will damage the encoding information. The cause is that we are actually taking average on both the units which are sensitive to this task and the units which are not. So, we loss the information of PSTH signals.

Step 2:

In this part we use Matlab's fitglm() function to fit a GLM on our data. Our data is different units' PSTH for different trials. In this way we can have a P-value score for each unit, when fitting to different conditions for the two parameters, location and reward value. The plot below shows the P-value for each unit, when fitting to location and reward value with different colors.
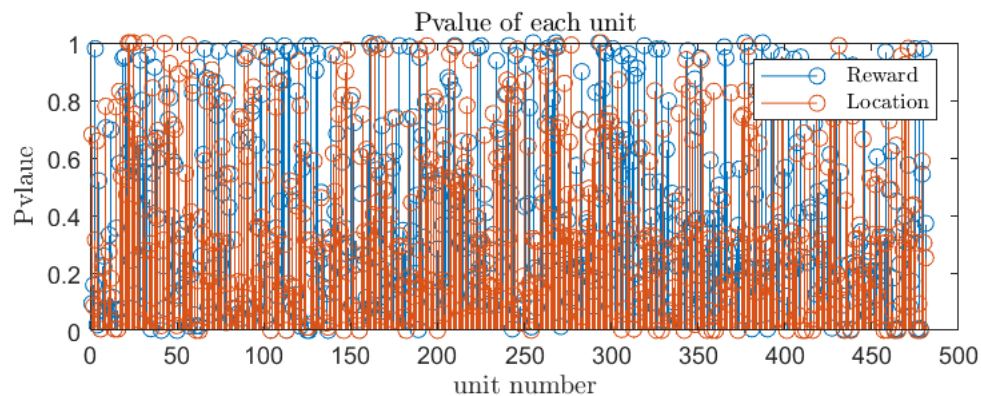
Now, we try to determine which units are encoding the location and reward value information. So, we omit the units with a P-value higher than 0.05 for both location and reward value and now we have:
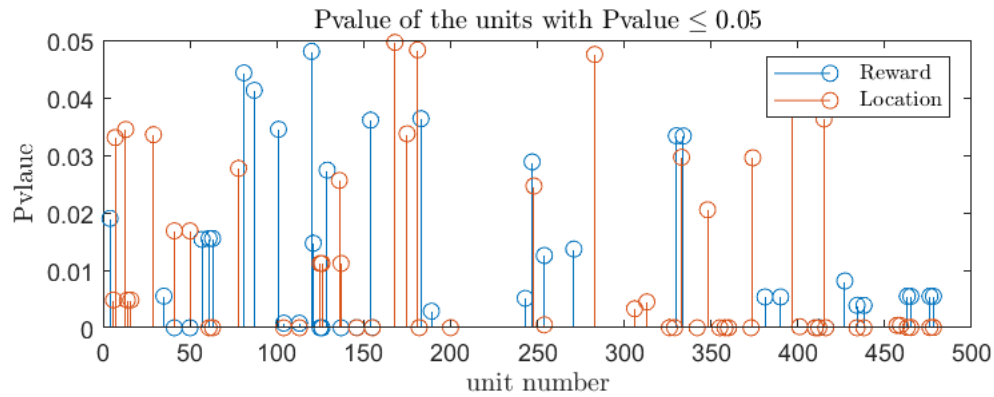
The plot above indicates which units are location encoders and which units are reward value encoders.

Step 3:

In this part, we use PCA for dimension reduction. We saw in the first part that we have as many dimensions as observations which is equal to the number of units; However, not all units have meaningful information in their PSTH, as we saw in the first part. Therefore, we here use dimension reduction to detect the three most meaningful information. Here is the resulted trajectory caused by plotting population activity in three dimensions:
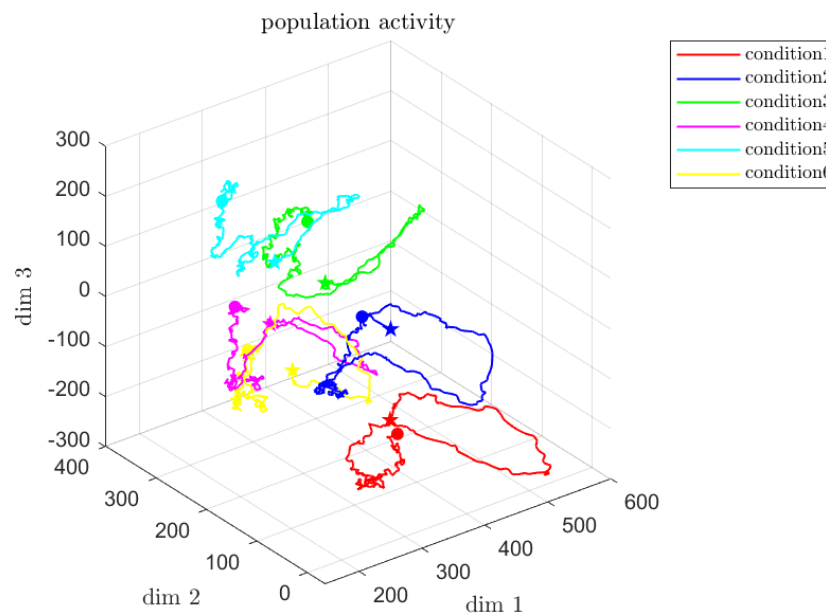
This figure shows us that different conditions' trajectories are almost separable from each other and that each one has certain information for encoding the condition. Moreover, the plot almost shows that the fifth and third condition's trajectories have the same behavior which leads to encoding the location "-1" and this is almost the same for the first and second condition's trajectories which leads to encoding the reward value "3" and for the fourth and sixth, which leads to encoding the location "1" according to the table below.

	Reward value	*Location*
Condtion1	*3*	*-1*
Condtion2	*3*	*1*
Condtion3	*6*	*-1*
Condtion4	*6*	*1*
Condtion5	*9*	*-1*
Condtion6	*9*	*1*

Step 4:

In this step, the previous data is shuffled using the CFR method mentioned in the class. The data is shuffled through time, conditions and units for 100 times and this is the resulted population activity plot, using the same method to the previous part for dimension reduction:
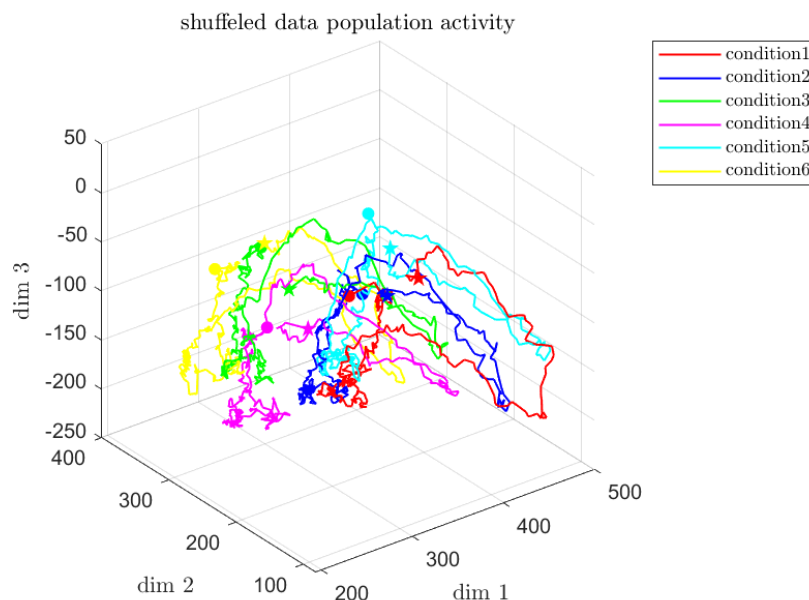
We know that each trajectory indeed shows 3 units PSTH in a certain condition, which is derived by taking an average on different trials. When we compare the population activity before shuffling with the one after shuffling, we can see that after shuffling the encoding rules are almost destroyed. Moreover, we see that different conditions' trajectories got closer together. This was predictable because when we merge the population activities information, no information will remain so when we take an average on trials, the result should be approximately the same for different conditions, with no more meaningful dependencies as populations activities information. Therefore, we can say that there is actually some information in the population activity.