**Same-Day First-Pass Data Analysis**

**A. Data collection, storage and pre-processing.**

Collect data using -3SD threshold on all channels.

Save in a format such that threshold-crossing events = spikes. All threshold-crossing events on a given channel (corresponding to a single electrode) belong to one "neuron." There is no spike-sorting at this stage. Also save - for long-term analysis - the continuous voltages.

Convert to a three-dimensional matrix organized according to electrode (dimension = number of electrodes), condition (dimension = number of conditions) and time in 10 ms bins from -150 ms to +650 ms relative to stimulus onset (dimension = 80).

**B. General plan**

Input manually at first-pass run-time

1. Pathname of data file

2. Number of groups (G).

3. Condition numbers in each group.

4. Target for each group 1 to G.

5. Number of constellations (C).

6. Group numbers in each constellation 1 to C.

7. Number of comparisons (K).

8. Constellations in each comparison 1 to K.

"Group": There could be one group for each condition. However, we might operate on a number of groups less than the number of conditions. For example, if we cared about the effect of image identity and not location, we might combine conditions in which the same image was presented at different locations into a single group. In general, in the analyses we're contemplating, "group" and "image" will mean the same thing.

"Target": Targets come into play for trajectory analysis. In trajectory analysis, we analyze how closely the pattern of population activity in each early bin corresponds to the late "target" pattern for the group in question. The target typically is defined as the pattern of population activity late in the trial for the same group. In this case, we enter "target" as the number of the group itself. However, to compute the trajectory for an image degraded by manipulating contrast or noise (one group), we might want to treat as "target" the pattern of late population activity elicited by the undegraded image (another group). In this case, we enter as "target" as the number of the undegraded group.

"Constellation": This is a set of groups for which we intend to analyze population discriminability and trajectory. For example, if four good images (associated with large reward) and four bad images (associated with small reward) had been presented, and if we wanted to compute discriminability and trajectory independently for good and bad images, then we would set up the four good conditions as one constellation and the four bad images as another constellation. Note that a single group might in principle participate in more than one constellation.

"Comparison": When we compare constellations with regard to how well the component groups are discriminated (inter-group distance) or how rapidly the representations develop (trajectory), we generally are interested in the differences between certain subsets of constellations. For example, we might want to compare familiar and novel constellations at low contrast and, independently, compare them a high contrast. Defining comparisons allows outputting a separate trajectory plot for each such case. Each comparison is a subset of constellations to be compared. In the event that we wanted the first comparison to be between constellations 3 and 4, we would enter the values 3 and 4 under comparison 1.

Output to printable display

1. All of the information entered as input.

2. The numbers of the electrodes classified as responsive.

For raw and normalized data separately:

3. A bar display showing mean response strength with one bar for each group.

4. A bar display showing mean response strength with one bar for each constellation.

5. For each constellation, a bar display showing the inter-group distance for each pair.

6. For each bar display above the corresponding numeric values.

7. For each comparison, superimposed linear plots representing mean discrimination index versus time for each constellation.

**C. Steps of analysis**

Electrode winnowing. The aim of this step is to identify electrodes at which there is a visual response. Stipulate the conditions on which the responsivity test should be based. For each electrode, across all trials conforming to the stipulated set of conditions, compute the mean and standard deviation of firing rate in two window: -150 to +50 ms and +50 to 350 ms relative to image onset. Carry out a two-tailed paired t-test. Any electrode at which the difference is significant (p ≤ 0.05) and positive (post > pre) is classified as a "responsive electrode".

Carry out subsequent steps of analysis solely on responsive electrodes.

Compute a raw PSTH for each condition at each responsive electrode. This is the average firing rate as a function of time, across all trials for that condition, in 10 ms bins extending from -150 ms to +650 ms relative to image onset. Each PSTH consists of firing rates in 80 bins.

Compute a normalized PSTH for each condition at each responsive electrode. This is the raw PSTH divided by the mean firing rate across all bins in all conditions at that electrode.

Carry out subsequent steps of analysis separately for raw and normalized PSTHs.

Create a PSTH for each group at each responsive electrode. If the group contains multiple conditions, this means averaging PSTHs across the conditions. If the group contains a single condition, this means simply assigning to the group the PSTH for that condition. The PSTH contains 80 bins.

Compute a target vector for each group. This is the vector of mean firing rates at all responsive electrodes with the firing rates in fixed order by electrode number. Typically, we base this vector on mean firing rate in a window from 150 to 350 ms post-stimulus-onset. The vector has dimensionality equal to the number of responsive electrodes.

MEASURE 1. Response strength. For each group, compute the average, across all responsive electrodes, of firing rate 50-650 ms following stimulus onset. This is based on the respective PSTHs.

MEASURE 2. Mean inter-group distance within each constellation. The aim of this step is to determine how far apart in activation space the groups in a constellation are. For each pair of groups, compute the Euclidean distance in population space between those groups. This is based on the groups' population vectors. For image Alpha, population vector Va = [ A1, A2, A3, ... An] where An is the response to Alpha at responsive electrode n. For image Beta, Vb = [ B1, B2, B3, ... Bn]. Euclidean distance is computed as {(A1-B1)^2 + (A2-B2)^2 + (A3-B3)^2}^ 0.5. And so on. Compute the average across all group-pairs of this distance.

MEASURE 3. Trajectory within each constellation. The aim of this step is to characterize how population activity evolves over time to signal that the trial belongs to one group in a constellation and not to the other groups in that constellation. The analysis is based on the PSTHs for the groups in the constellation and on the target vectors for those groups.

Step 1. Compute vector M. This is the vector average of the target vectors of the groups in the constellation. It has dimensionality equal to the number of responsive electrodes.

Step 2. Normalize the target vector of each group to M. This means Tn' = Tn - M where Tn is the target vector of group n. Tn and M have dimensionality equal to the number of responsive electrodes.

Step 3. For each group in the constellation, create, from the initial 80-bin PSTH, a smoothed 75-bin PSTH by the following process. The value in bin N of the smoothed histogram is set to the average of the five values in bins N-4 through N in the initial histogram.

Step 4. For each group in the constellation, for each time bin in the smoothed PSTH, normalize the vector of firing rates to M. This means B'(t) = B(t) - M where B(t) and M are vectors with dimensionality equal to the number of responsive electrodes.

Step 5. For each group in the constellation, for each time bin in the normalized smoothed PSTH, compute the correlation coefficient between B'(t), the normalized bin vector for that group, and T', the normalized target vector for that group. The correlation coefficient is the cosine of the angle between the bin vector and the target vector. For each group in the constellation, this will yield a 75-bin cosine PSTH.

Step 6. Compute the average cosine PSTH across all groups in the constellation. The cosine PSTH represents the time-course of the developing population signal indicating which of the groups in the constellation was presented. We expect this to hover around zero before onset of the response and to climb into the positive range as the response progresses.