# Analysis Plan

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## About

This analysis plan pertains to the fMRI-BOLD data from a movie viewing task for the HMM Video studies. At the time of writing the analysis plan, data acquisition was completed but no statistical analyses were conducted. See GitHub link for timestamps on analysis pipeline (<https://github.com/jxli25/Video_HMM>). Analyses will only take place once this analysis plan has been uploaded, and time stamped on the Open Science Framework. If the researchers decide to conduct additional analysis, this will be stated in any publication (“post-hoc analyses”).

## Data Collection

The experiment involved showing participants a 4 minute video stimulus. Approximately 40 of these participants had a diagnosed psychotic illness, and 40 were controls. fMRI-BOLD scans were conducted on participants during movie viewing.

## Pre-processing

### Cleaning

Scans were normalised to the the MNI152NLin6Asym standard space. Head-motion related movement artefacts were removed. A band-pass filter was applied (high pass = 0.01Hz, low pass = 0.15Hz) to filter out large scale frequency drifts and physiological noise. Spatial smoothing was not applied.

### Parcellation

fMRI-BOLD sequences were standardised and parcellated according to the Yeo-17-thick atlas.

## HMM Model

### Training

We will train an HMM Model on our data after subtracting a hold-out dataset of 10 control group and 10 experimental group participants. The settings as per Table 1 will be used for this model.

Table 1HMM Model input settings for object Options on MATLAB using the HMM-MAR package

|  |  |
| --- | --- |
| Options. \_\_\_\_\_\_\_ | Setting |
| K | Can specify upper range, and model will fit with least number with no empty states. |
| covtype | full |
| DirichletDiag | Use holdout dataset to estimate parameters |
| cyc | 300 |
| initrep | 10 |
| initcyc | 10 |

### Outputs & Analysis

The outputs of interest for this analysis are described in Table 2.

Table 2 Outputs of interest for analysis from HMM Model and analysis to be performed

|  |  |
| --- | --- |
| Output | Analysis |
| Hidden States (HS; analysis exclusively based on Meer, 2020) | Hidden State Decoding: Choose 16 general terms of the Neurosynth database. Forward associate each Hidden State to the topic maps of these 16 general terms. Correlate the spatial distribution of each brain state to the topic maps. (<https://github.com/neurosynth/neurosynth>).  Averaging State Paths: Use a sliding window of 3 (9 for Meer for a 20 min movie clip, our clip is 4 min, 9/5 approx to 2 however 327 scans is divisible by 3) consecutive BOLD volumes for each segment and identify the most frequently expressed state, as well as the number of participants that expressed each Hidden State at least once.  ~~Consistency: For each sliding window segment, calculate the consistency of expression for each Hidden State (take the most frequently expressed HS, calculate how many participants expressed this state out of whole experimental/control group for a %). For each state and each participant, construct a binary vector of 0 (brain state not expressed) and 1(brain state expressed) for each time point. To compare between experimental and control group, calculate the Jaccard Overlap index between the binary vectors for each brain state and average them.~~ |
| Transition Probability | Use Network-Based Statistics Toolbox to visualise the network of state transitions that are significantly more expressed for experiment vs control groups. Use t test to test for significant differences between each transition probability (# HNs x # HNs matrix) |
| Fractional Occupancy (FO) | Obtain an average of FO for experimental and control group. Need to clarify dim = 2 before further planning, probably a paired t test for each 327 time point between experimental vs control groups? |
| Viterbi Path | Paired t test for each 327 time point between experimental vs control groups |
| Switching Rates | Perform t test for each HS |
| Heart Rate | Calculate mean and variance for each 327 time point then conduct paired t test for mean and variance.  Calculate average HR for each HN in EG vs CG and do t test to test for significant difference |

## Hypotheses

* 1. The time spent in defined brain states is significantly shorter for participants with psychotic illness compared to healthy controls.
  2. The time spent in brain states with high emotional valence is higher for health controls compared to participants with psychotic illness.
  3. Hidden States expressed by experimental group is less consistent than Hidden State expressed by control group
  4. Switching rate is significantly higher for experimental group due to more ambiguity of activation of ROIs
  5. Significant difference between mean and variance of heart rate