Slide 1:

Hidden Markov Models are an efficient way to characterize resting-state fMRI. Most existing work focuses only on the unsupervised learning aspect of the model. In this presentation, we introduce a new algorithm that combines Hidden Markov Models with supervised learning, making it more accurate for classification-based problems.

Slide 2:

We declare that there is no conflict of interest. The data used is publicly accessible, with patients' information properly protected. This work is supported by the NIH.

Slide 3:

Here we summarize different models used to characterize brain connectivity. After dimensionality reduction, we obtain low-dimensional time series corresponding to different anatomical regions. Starting from static analysis of resting-state data, recent work increasingly focuses on the dynamic features of resting-state fMRI. Commonly used methods include the sliding window approach and Hidden Markov Models. Due to the lack of ground truth, both methods fall under unsupervised learning. The connectivity derived from each model can also be used for classification, usually involving a two-step process: first evaluating connectivity, then training a classifier. Our model presents a new way to perform both connectivity evaluation and classification in a single step using a Hidden Markov Model.

Slide 4:

We use the ADNI dataset with amyloid-positive subjects. The study group includes three classes across different disease stages, with roughly 100 subjects per class. We apply group Independent Component Analysis to decompose the original time series into a lower-dimensional representation. Based on anatomical findings, we divide them into 9 groups corresponding to different brain regions. The final dimensionality of the time series we use is shown on the right.

Slide 5:

We assume that the ICA components from each subject follow a Hidden Markov Model. The model contains several hidden states (chosen to be 3 in this study), uses transition probabilities to characterize state transitions, and assumes Gaussian distributions for the emission probabilities to link hidden states with observations. These components involve a few unknown parameters, which are determined using the Expectation-Maximization algorithm. We define the joint probability of the system, which characterizes the total probability of observing a sequence given all parameters. One way to apply Hidden Markov Models to multiple classes is to build separate models for each class and use their joint probabilities to evaluate new samples. However, this approach is still considered unsupervised since it does not incorporate inter-class information. Practically, we find that this often results in poor classification accuracy.

Slide 6:

To implement supervised learning, we define probabilities using the joint probabilities from Hidden Markov Models. Mathematically, this means evaluating the time series across different

models and selecting the one with the highest likelihood, followed by applying a discriminative loss function. Mathematically, this model is equivalent to the Hidden Conditional Random Fields framework previously used in machine learning studies. Practically, we divide the data into training, validation, and testing sets with a ratio of 7:2:1. Starting from the unsupervised results, we use gradient descent to minimize the cross-entropy loss on the training dataset and monitor validation accuracy until it reaches a minimum.

Slide 7:

Here we show the classification accuracy results for our dataset. As the dataset is relatively small, we average results over 100 cross-fold validations. In general, two-class classification yields higher accuracy than three-class, with the largest accuracy observed between normal and AD groups. Additionally, our new supervised method outperforms the unsupervised approach, yielding better classification accuracy. In terms of connectivity, we arrange the connectivity states from homogeneous (matrices with fewer off-diagonal values) to inhomogeneous states. We find that, for MCI and AD, transitions from inhomogeneous to homogeneous states increase, consistent with previous studies.

Slide 8:

Finally, we compare our new model with previously published models. Compared to the sliding window approach, Hidden Markov Models are more suitable for fast state transitions. Compared to previous unsupervised approaches, our new model shows improved classification performance. Another advantage is that our approach does not require an additional classifier, which simplifies the process, as the joint probability already characterizes the likelihood of a sequence belonging to a given model.

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