

ADNI Progress report

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Part I

Using HMMs to predict disease progression

Training set: randomly picked 1000 patients.
Testing set: Remaining 398 patients.

1 Sanity Check

As a sanity check, the HMM was trained with the number of states $k = 3$.

Following are the temporal parameters, as learned by the HMM and contrasted with the ground truth.

$$\begin{aligned} gt.pi &= [0.3062 \quad 0.4667 \quad 0.2272] \\ model.pi &= [0.3352 \quad 0.1826 \quad 0.4822] \\ gt.A &= \begin{bmatrix} 0.9359 & 0.0569 & 0.0071 \\ 0.0260 & 0.8516 & 0.1224 \\ 0 & 0.0084 & 0.9916 \end{bmatrix} \\ model.A &= \begin{bmatrix} 0.9721 & 0.0258 & 0.0022 \\ 0.0040 & 0.9923 & 0.0037 \\ 0.0090 & 0.0146 & 0.9764 \end{bmatrix} \end{aligned}$$

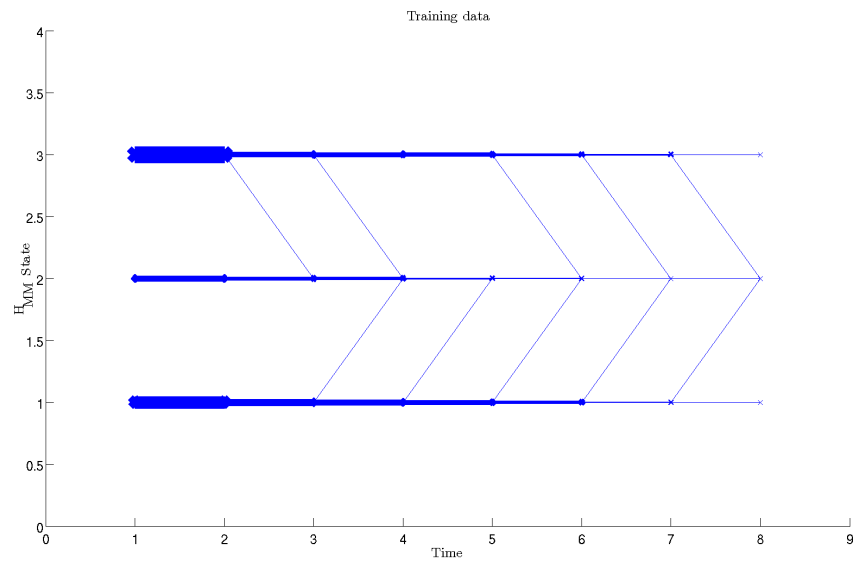


Figure 1: Viterbi trellis for training set

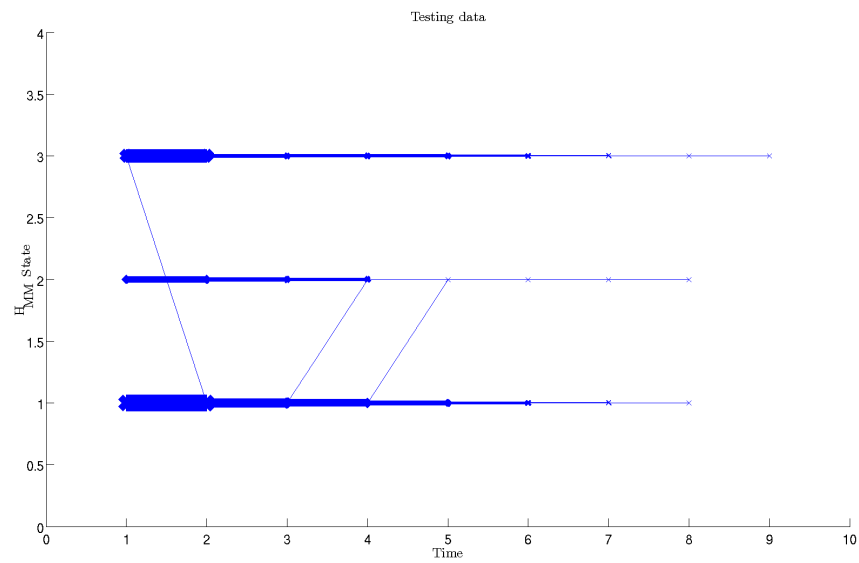


Figure 2: Viterbi trellis for testing set

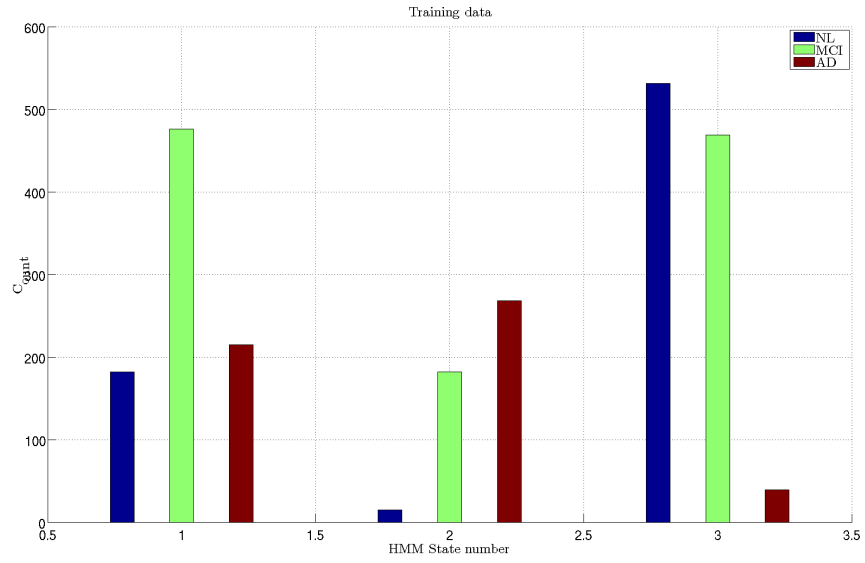


Figure 3: Distribution of states for training set

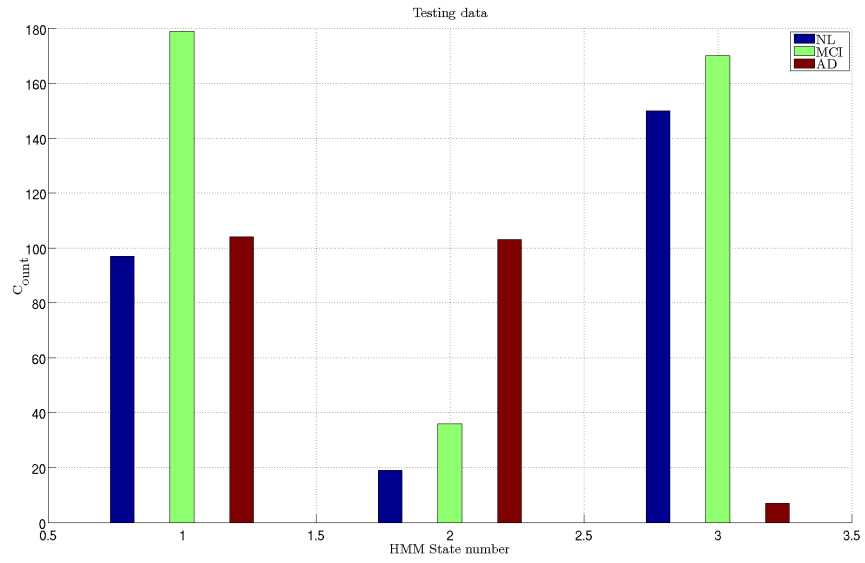


Figure 4: Distribution of states for testing set

1.1 Analysing the transitions

The following is a matrix that visualizes where MCI→AD transitions in the labelled data end up in the HMM state space. That is, for every MCI→AD transition in the real world, we look at the corresponding transition in the HMM state space. The rows represent the source HMM state, whereas the columns are the destination HMM state. This data is aggregated over time, so there is no temporal aspect.

For the training set, the conversion matrix is:

$$\begin{bmatrix} 37 & 2 & 0 \\ 0 & 36 & 0 \\ 0 & 2 & 16 \end{bmatrix}$$

For the testing set, the conversion matrix is:

$$\begin{bmatrix} 13 & 0 & 0 \\ 0 & 6 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

That is, MCI→AD transitions in the real world are reflected as stationary transitions in the HMM state space.

2 HMM with larger state space

$$\begin{aligned} model.pi &= [0.2103 \quad 0.2825 \quad 0.1518 \quad 0.1325 \quad 0.2229] \\ model.A &= \begin{bmatrix} 0.9424 & 0.0043 & 0.0426 & 0.0061 & 0.0046 \\ 0.0224 & 0.9445 & 0.0055 & 0.0099 & 0.0177 \\ 0.0040 & 0.0036 & 0.9842 & 0.0046 & 0.0037 \\ 0.0066 & 0.0062 & 0.0073 & 0.9720 & 0.0079 \\ 0.0046 & 0.0045 & 0.0114 & 0.0063 & 0.9733 \end{bmatrix} \end{aligned}$$

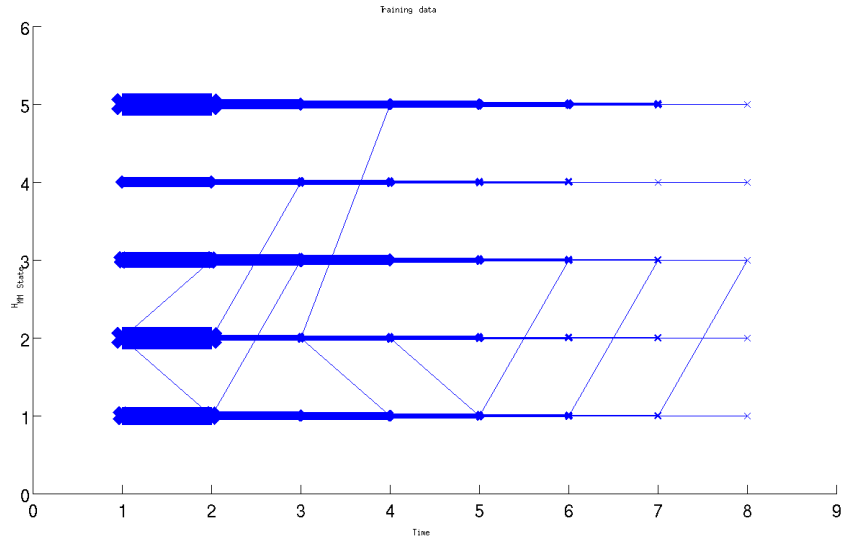


Figure 5: Viterbi trellis for training set

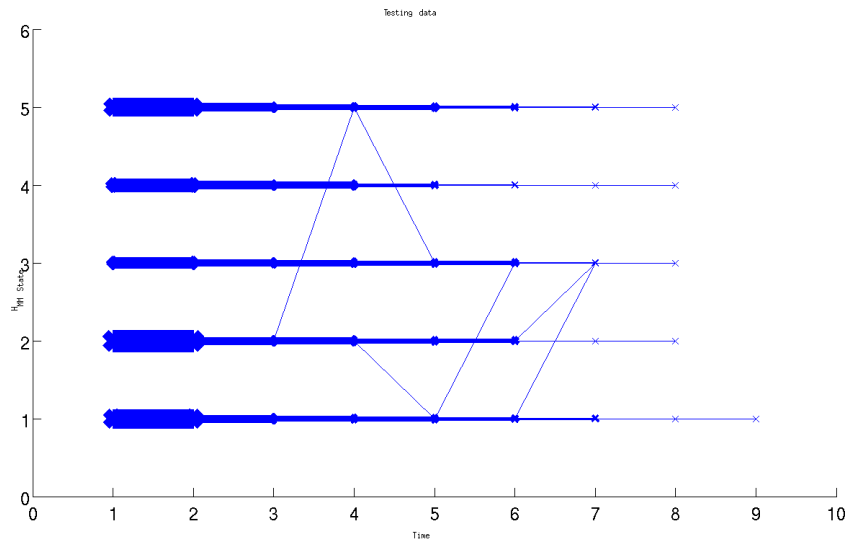


Figure 6: Viterbi trellis for testing set

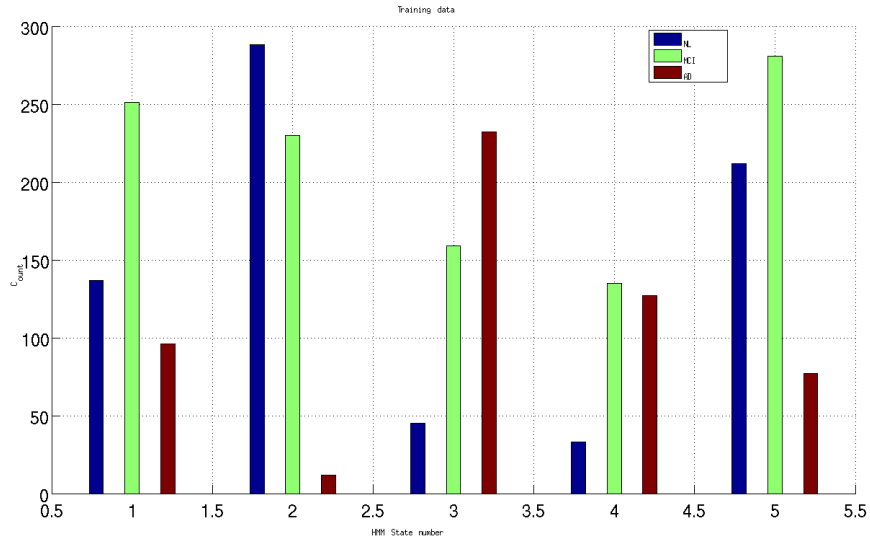


Figure 7: Distribution of states for training set

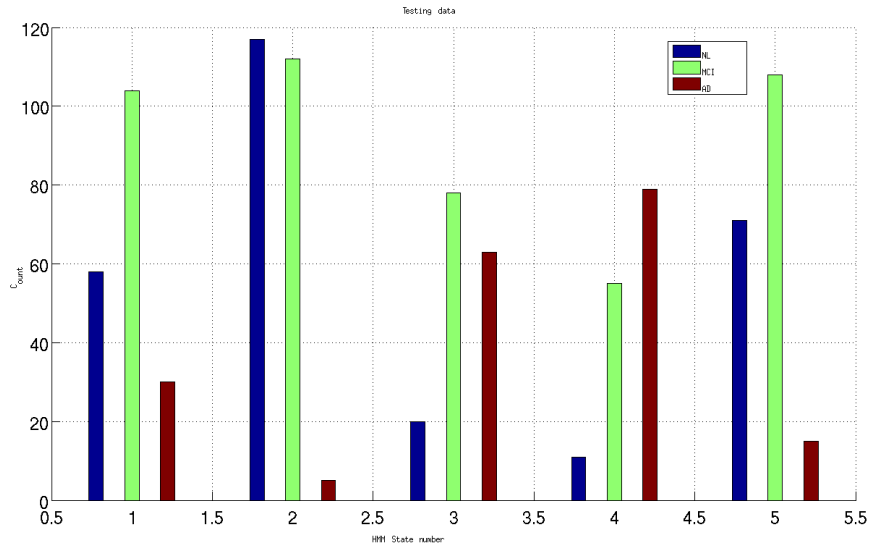


Figure 8: Distribution of states for testing set