



Figure 5: (a) MoCap feature matrices associated with BP-AR-HMM (top-left) and HDP-AR-HMM (top-right) estimated sequences over iterations 15,000 to 20,000, and MAP assignment of the GMM (bottom-left) and HMM (bottom-right) using first-difference observations and 12 clusters/states. (b) Hamming distance versus number of GMM clusters / HMM states on raw observations (blue/green) and first-difference observations (red/cyan), with the BP- and HDP- AR-HMM segmentations (black) and true feature count (magenta) shown for comparison. Results are for the most-likely of 10 EM initializations using Murphy’s HMM Matlab toolbox [16].

As an illustrative example, we examined a set of six CMU MoCap exercise routines [23], three from Subject 13 and three from Subject 14. Each of these routines used some combination of the following motion categories: running in place, jumping jacks, arm circles, side twists, knee raises, squats, punching, up and down, two variants of toe touches, arch over, and a reach out stretch.

From the set of 62 position and joint angles, we selected 12 measurements deemed most informative for the gross motor behaviors we wish to capture: one body torso position, two waist angles, one neck angle, one set of right and left (R/L) shoulder angles, the R/L elbow angles, one set of R/L hip angles, and one set of R/L ankle angles. The MoCap data are recorded at 120 fps, and we block-average the data using non-overlapping windows of 12 frames. Using these measurements, the prior distributions were set exactly as in the synthetic data experiments except the scale matrix, S_0 , of the MNIW prior which was set to 5 times the empirical covariance of the first difference observations. This allows more variability in the observed behaviors. We ran 25 chains of the sampler for 20,000 iterations and then examined the chain whose segmentation minimized the expected Hamming distance to the set of segmentations from all chains over iterations 15,000 to 20,000. Future work includes developing split-merge proposals to further improve mixing rates in high dimensions.

The resulting MCMC sample is displayed in Fig. 4 and in the supplemental video available online. Although some behaviors are merged or split, the overall performance shows a clear ability to find common motions. The split behaviors shown in green and yellow can be attributed to the two subjects performing the same motion in a distinct manner (e.g., knee raises in combination with upper body motion or not, running with hands in or out of sync with knees, etc.). We compare our performance both to the HDP-AR-HMM and to the Gaussian mixture model (GMM) method of Barbič et al. [1] using EM initialized with k-means. Barbič et al. [1] also present an approach based on probabilistic PCA, but this method focuses primarily on change-point detection rather than behavior clustering. As further comparisons, we look at a GMM on first difference observations, and an HMM on both data sets. The results of Fig. 5(b) demonstrate that the BP-AR-HMM provides more accurate frame labels than any of these alternative approaches over a wide range of mixture model settings. In Fig. 5(a), we additionally see that the BP-AR-HMM provides a superior ability to discover the shared feature structure.

7 Discussion

Utilizing the beta process, we developed a coherent Bayesian nonparametric framework for discovering dynamical features common to multiple time series. This formulation allows for object-specific variability in how the dynamical behaviors are used. We additionally developed a novel exact sampling algorithm for non-conjugate beta process models. The utility of our BP-AR-HMM was demonstrated both on synthetic data, and on a set of MoCap sequences where we showed performance exceeding that of alternative methods. Although we focused on switching VAR processes, our approach could be equally well applied to a wide range of other switching dynamical systems.

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