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# Bayesian Streaming Sparse Tucker Decomposition (Supplementary material)

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Shikai Fang, Robert M. Kirby, Shandian Zhe

School of Computing, University of Utah  
Salt Lake City, UT 84112

shikai.fang@utah.edu, kirby@cs.utah.edu, zhe@cs.utah.edu

## SUPPLEMENTARY MATERIAL

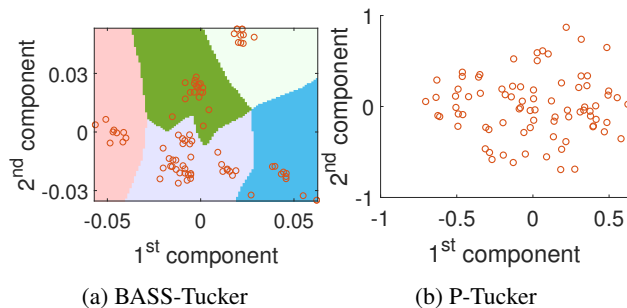


Figure 1: The structures of the estimated core-tensor (folded at the second mode) by BASS-Tucker and P-Tucker.

First, in Fig. 1, we show the first two principal components of the core-tensor folded at the second mode. As we can see, the results of BASS-Tucker exhibit clear grouping structures, implying different patterns of the interactions between non-mode-2 and mode-2 factors. Again, we ran the k-means algorithm and filled the cluster regions with different colors to highlight these patterns. As a comparison, the results of P-Tucker do not reflect meaningful structures, and the interaction strengths are distributed like a symmetric Gaussian. It again demonstrates the potential of BASS-Tucker in discovering interesting and important patterns.

Second, in Fig. 2, we show the running time of BASS-Tucker and POST with different streaming batch sizes. We tested on a Windows desktop with Intel i9-9900K CPU. As we can see, on *Alog* and *ACC* datasets with  $R = 5$ , BASS-Tucker is much faster than POST under all the streaming batch sizes (*i.e.*, Fig. 2 a and b). Note that POST is based on CP, which is much simpler (and less parameterized) than Tucker decomposition. This might be because POST needs to run many iterations to converge in optimizing the mean-field variational posterior (the default setting of the maximum number of iterations is 500). In other cases, the speed of BASS-Tucker is comparable to and even faster than POST with the largest streaming batch size (*i.e.*,  $2^{11} = 2048$ ). To-

gether this shows the advantage of our one-shot incremental update, which does not need to sequentially go through each entry in the batch as in standard ADF, and also does not need to perform iterative optimization as in SVB.

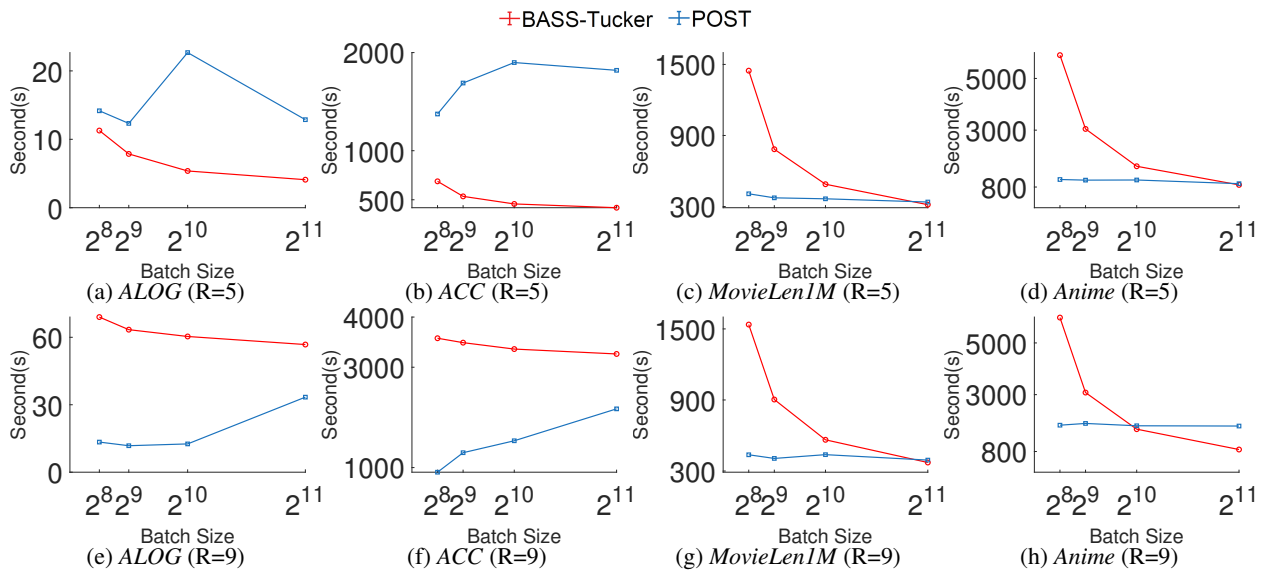


Figure 2: Running time with different sizes of streaming batches.