Reviewer’s report

Title: Scalable non-negative matrix tri-factorization

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Reviewer: Rui Kuang

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The paper presents a block-wise approach to perform parallel matrix tri-factorization by GPU. The algorithm partitions the data matrix into disjoint submatrices that can be used separately in parallel computation by several steps in each update iteration. The implementation is publicly available through GitHub, and the experiments shown the GPU acceleration is 100-times faster than a single CPU.

1. It is important work to improve the scalability of matrix tri-factorization for biological data analysis. As big data research, it is insufficient to test datasets in the size of only 100s of megabytes. There are larger high-dimensional datasets such as data of a million CNV features and SNPs for thousands of samples by Affymetrix SNP array 6.0 or larger integrated GEO datasets (e.g. search NCBI GEO with "20000:100000[Number of Samples]"). It will be more interesting to report the memory consumption and running time on one of these larger datasets.

2. To show the potential as a useful research tool or software, it will be helpful to include a case study on a particular tri-factorization problem on a large-scale biological dataset with more interpretations of the results such as bi-clustering of a million CNV features and a thousand samples. In particular, does the "S" matrix reveal interesting relations between feature modules and sample clusters compared with NMF?

3. The block-wise version of the matrix tri-factorization algorithm is iteratively solved by multiplicative update rules, adapted from the original matrix tri-factorization algorithm. A brief mathematical proof is needed to show the output of the parallel algorithm is equivalent to the original algorithm.

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