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Supplemental information

**FastRNA: An efficient solution for PCA
of single-cell RNA-sequencing data based
on a batch-accounting count model**

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Supplementary Figures

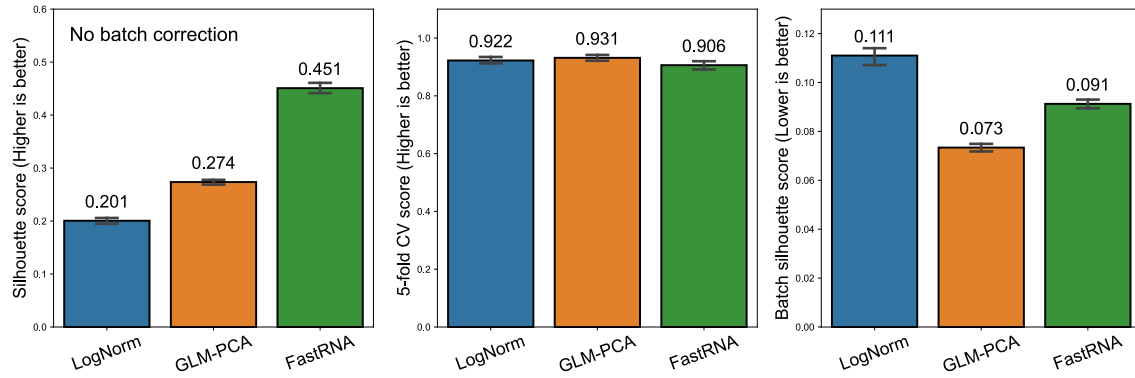


Figure S1: Benchmark of common normalization methods in a PBMC dataset from three 10X experiments. As Figure 3a-3c but log-normalization, GLM-PCA and FastRNA without batch correction.

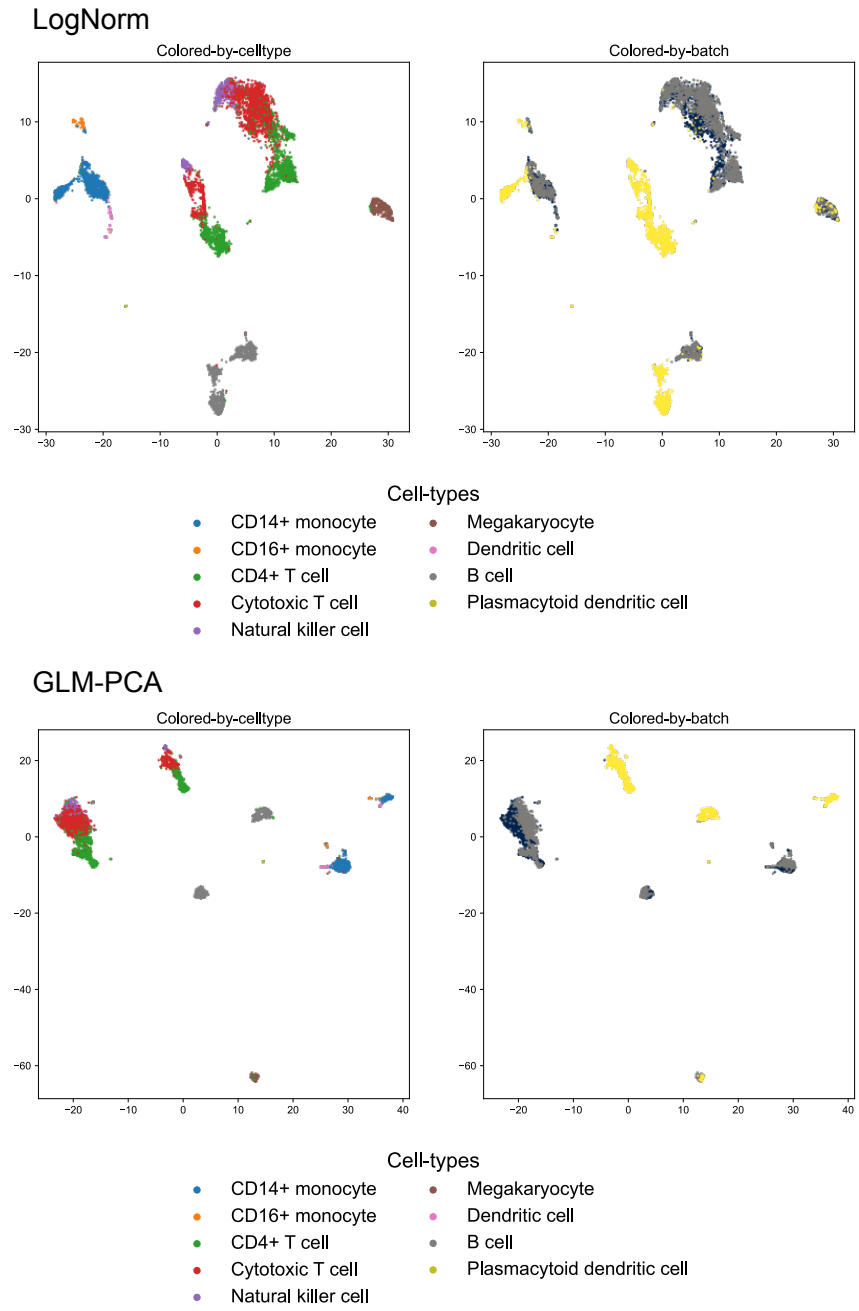


Figure S2: Benchmark of common normalization methods in a PBMC dataset from three 10X experiments. As Figure 3d-3e but log-normalization and GLM-PCA without batch correction.

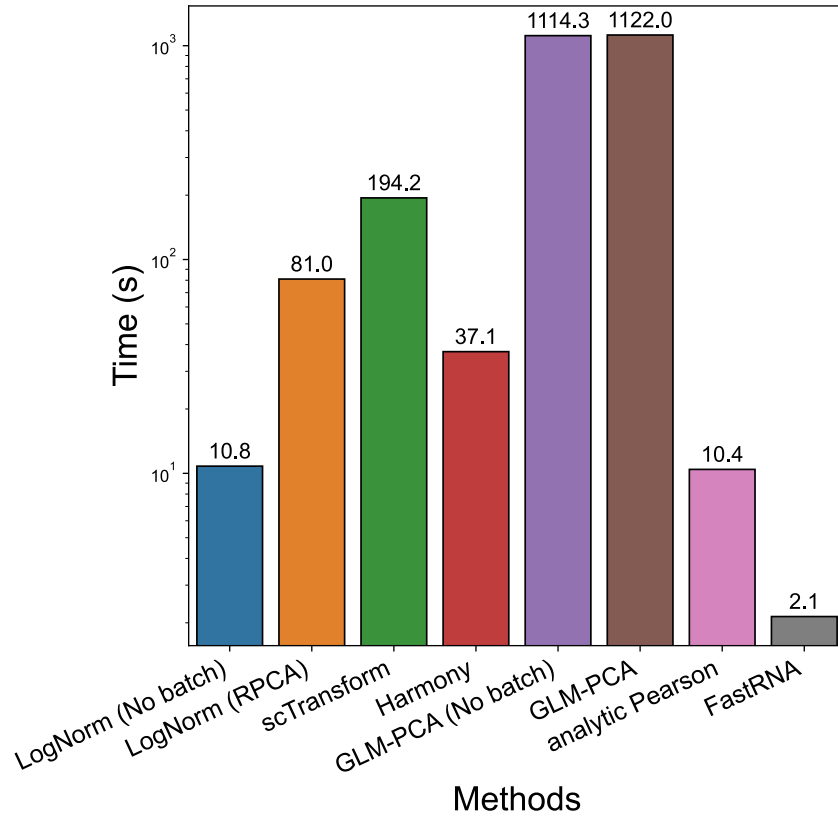


Figure S3: Benchmark of common normalization methods in a PBMC dataset from three 10X experiments. Runtime of eight methods. Total 9806 cells from three batches.