THE UNIVERSITY OF CHICAGO | DEPARTMENT OF STATISTICS

Master's Thesis Presentation

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"GLIMES-Based Differential Expression with Comparative Low-Dimensional Representations in Paired scRNA-seq of BBIBP-CorV Vaccination"

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Abstract

We analyze paired scRNA-seq data from a BBIBP-CorV vaccination setting to characterize early transcriptional changes between Day0 (baseline) and Day7 (follow-up) in a donor-aware framework. Focusing on TS-only CD4^{+} T cells, we perform gene-wise differential expression using GLIMES Poisson GLMM with Benjamini--Hochberg (BH) FDR control. After a 5\% detection filter, 5{,}120 genes are tested and 2{,}037 are significant at $p<0.05$; however, most significant genes exhibit modest effect sizes, with many discoveries concentrated near $|\log_2\mathrm{FC}|<0.3$. To improve interpretability, we report post hoc prioritized gene sets that incorporate effect size and expression support, yielding a compact shortlist (57 recommended; 7 strict). As a complementary view of prevalence/zero-expression changes, the GLIMES Binomial GLMM identifies 1{,}910 genes at $p<0.05$, largely overlapping with the Poisson results and showing strong directional concordance. For visualization, we compare ordinary PCA, NB-GLM-PCA, and Flag-PCA (with UMAP as a nonlinear display layer). Embedding separation is heterogeneous across donors; GLM-PCA often produces clearer directional separation than PCA, while Flag-PCA is less consistently beneficial and substantially more expensive under our residual-based Stiefel-manifold implementation. Future work will examine variance/dispersion and higher-order distributional shape (skewness and excess kurtosis).
