

S10 Text: Efficiency Analysis.

SCRaPL: A Bayesian hierarchical framework for detecting technical associates in single cell multiomics data.

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As part of the newer Tensorflow implementation we performed efficiency analysis to understand model's scalability. In preliminary implementations we experimented with both Markov Chain Monte Carlo (MCMC) and Variational Inference (VI). Unfortunately VI did not yield accurate results so we abandoned it in favor of MCMC. Hence execution time as a function of scaling is summarized in the figure below.

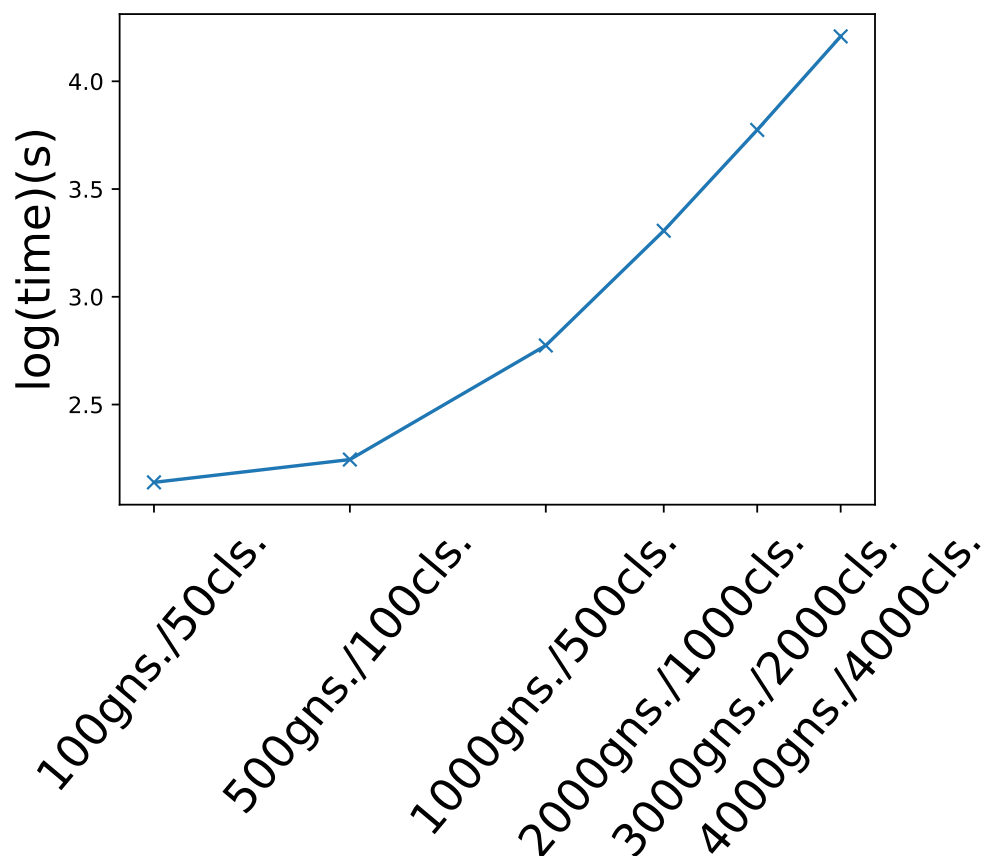


Fig A. Execution times as a function (features/cell numbers).