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scVI

The output of a scRNAseq experiment is a matrix of counts with N rows (the number of cells) and G columns (the number of genes), where each entry x_{ng} is an integer representing how many transcripts of gene g where seen in cell n. scVI is a generative hierarchical Bayesian model for scRNAseq data with conditional distributions parametrized by neural networks for each gene.[1] There are technical variables to account for different batches (s_n) and for library size (l_n, which can be interpreted as cell size or sequencing depth). Thus the number of networks being trained is $2 \cdot G \cdot K$, where K is the total the number of batches (datasets).

Conditional distribution $p\left(x_{ng} \mid z_n, l_n, s_n\right)$ is a zero-inflated negative binomial distribution (ZINB) to model the kinetics of stochastic gene expression with some entries replaced by zeros. It can also be modelled using Negative binomial or Zero-inflated negative binomial using the `gene_likelihood` argument.

The neural networks f_w^g and f_h^g use dropout regularization and batch nomalization to model gene expression while accounting for library sizes and batch effects respectively. Each network typically has 3 fully connected-layers, with 128-256 nodes each. The activation functions are ReLU, exponential, or linear. f_w has a final softmax layer to represent normalized expected frequencies of gene expression as in. Weights for some layers are shared between f_w and f_h.

[1] Lopez et al., "Deep Generative Modeling for Single-Cell Transcriptomics," *Nature Methods* 15, no. 12 (2018): 1053–58.

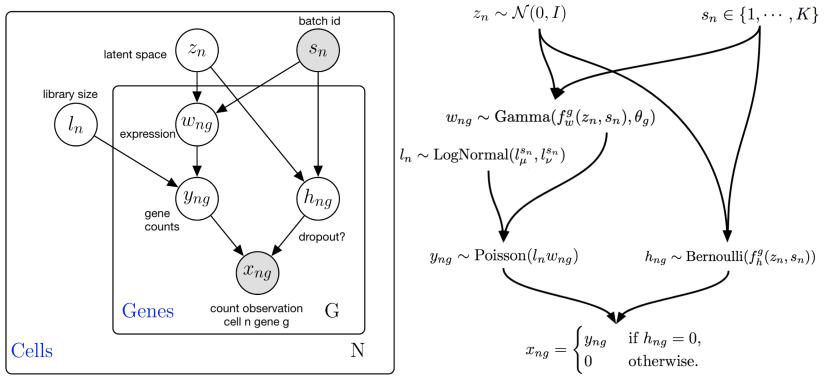

Figure 1: Fancy plot

References

Lopez, Romain, Jeffrey Regier, Michael B Cole, Michael I Jordan, and Nir Yosef. "Deep Generative Modeling for Single-Cell Transcriptomics." *Nature Methods* 15, no. 12 (2018): 1053–58.