Probabilistic Count Matrix Factorization for Single Cell Expression Data Analysis
Ghislain Durif, Laurent Modolo, Jeff Mold, Sophie Lambert-Lacroix, Franck Picard

To cite this version:

HAL Id: hal-01962030
https://hal.archives-ouvertes.fr/hal-01962030
Submitted on 20 Dec 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
Probabilistic Count Matrix Factorization for Single Cell Expression Data Analysis

G. Durif\textsuperscript{1,2}, L. Modolo\textsuperscript{1,3,4}, J. E. Mold\textsuperscript{4}, S. Lambert-Lacroix\textsuperscript{5} and F. Picard\textsuperscript{1}

\textsuperscript{1} LBBE, UMR CNRS 5558, Université Lyon 1, F-69622 Villeurbanne, France
\textsuperscript{2} Univ. Grenoble Alpes, Inria, CNRS, Grenoble INP, LJK, F-38000 Grenoble, France
\textsuperscript{3} LBMC UMR 5239 CNRS/ENS Lyon, F-69007 Lyon, France
\textsuperscript{4} Department of Cell and Molecular Biology, Karolinska Institutet, Stockholm, Sweden
\textsuperscript{5} UMR 5525 Université Grenoble Alpes/CNRS/TIMC-IMAG, F-38041 Grenoble, France

The combination of massive parallel sequencing with high-throughput cell biology technologies has given rise to single-cell Genomics. Similar to the paradigm shift of the 90s characterized by the first molecular profiles of tissues, it is now possible to characterize molecular heterogeneities at the cellular level (Saliba et al., 2014). The statistical characterization of heterogeneities in single-cell expression data thus requires an appropriate model, since the transcripts abundance is quantified for each cell using read counts. Hence, standard methods based on Gaussian assumptions are likely to fail to catch the biological variability of lowly expressed genes, and Poisson or Negative Binomial distributions constitute an appropriate framework (Chen et al., 2016). Moreover, dropouts, either technical (due to sampling difficulties) or biological (no expression or stochastic transcriptional activity), constitute another major source of variability in scRNA-seq (single-cell RNA-seq) data, which has motivated the development of the so-called Zero-Inflated models (Kharchenko et al., 2014). A standard and popular way of quantifying and visualizing the variability within a dataset is dimension reduction, principal component analysis (PCA) being the most widely used technique in practice. Model-based PCA (Collins et al., 2001) offers the unique advantage to be adapted to the data distribution and to be based on an appropriate metric, the Bregman divergence. It consists in specifying the distribution of the data through a statistical model. A probabilistic zero-inflated version of the Gaussian PCA was proposed by Pierson & Yau (2015) in the context of single cell data analysis (the ZIFA method). However, scRNA-seq data may be better analyzed by methods dedicated to count data such as the Non-negative Matrix Factorization (Lee & Seung, 1999, NMF) or the Gamma-Poisson factor model (Cemgil, 2009). However, none of the currently available dimension reduction methods fully model single-cell expression data, characterized by overdispersed zero inflated counts (Zappia et al., 2017). Our method is based on a probabilistic count matrix factorization (pCMF). We propose a dimension reduction method that is dedicated to over-dispersed counts with dropouts, in high dimension. Our factor model takes advantage of the Poisson Gamma representation to model counts from scRNA-seq data (Zappia et al., 2017). In particular, we use Gamma priors on the distribution of principal components. We model...
dropouts with a Zero-Inflated Poisson distribution, and we introduce sparsity in
the model thanks to a spike-and-slab approach (Malsiner-Walli & Wagner, 2011)
that is based on a two component sparsity-inducing prior on loadings (Titsias &
Lázaro-Gredilla, 2011). The model is inferred using a variational EM algorithm
that scales favorably to data dimension, as compared with Markov Chain Monte
Carlo (MCMC) methods (Blei et al., 2017). Then we propose a new criterion to
assess the quality of fit of the model to the data, as a percentage of explained
deviance, because the standard variance reduction that is used in PCA needs
to be adapted to the new framework dedicated to counts. We show that pCMF
better catches the variability of simulated data and experimental scRNA-seq
datasets. Finally, pCMF is available in the form of a R package available at
https://gitlab.inria.fr/gdurif/pCMF.

References

Computational Intelligence and Neuroscience, 2009.
gene expression from single-cell RNA-seq profiling. BMC Genomics, 17(Suppl 7).
components analysis to the exponential family. In Advances in Neural Information
Processing Systems, (pp. 617–624).
for multi-task and multiple kernel learning. In Advances in Neural Information
Processing Systems, (pp. 2339–2347).
sequencing data. Genome Biology, 18, 174.