

# GMMVAE model for scRNAseq

Classification, synthetic data generation and treatment effect prediction

Yiftach Kolb and Martin Vingron

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Berlin

November 17, 2022

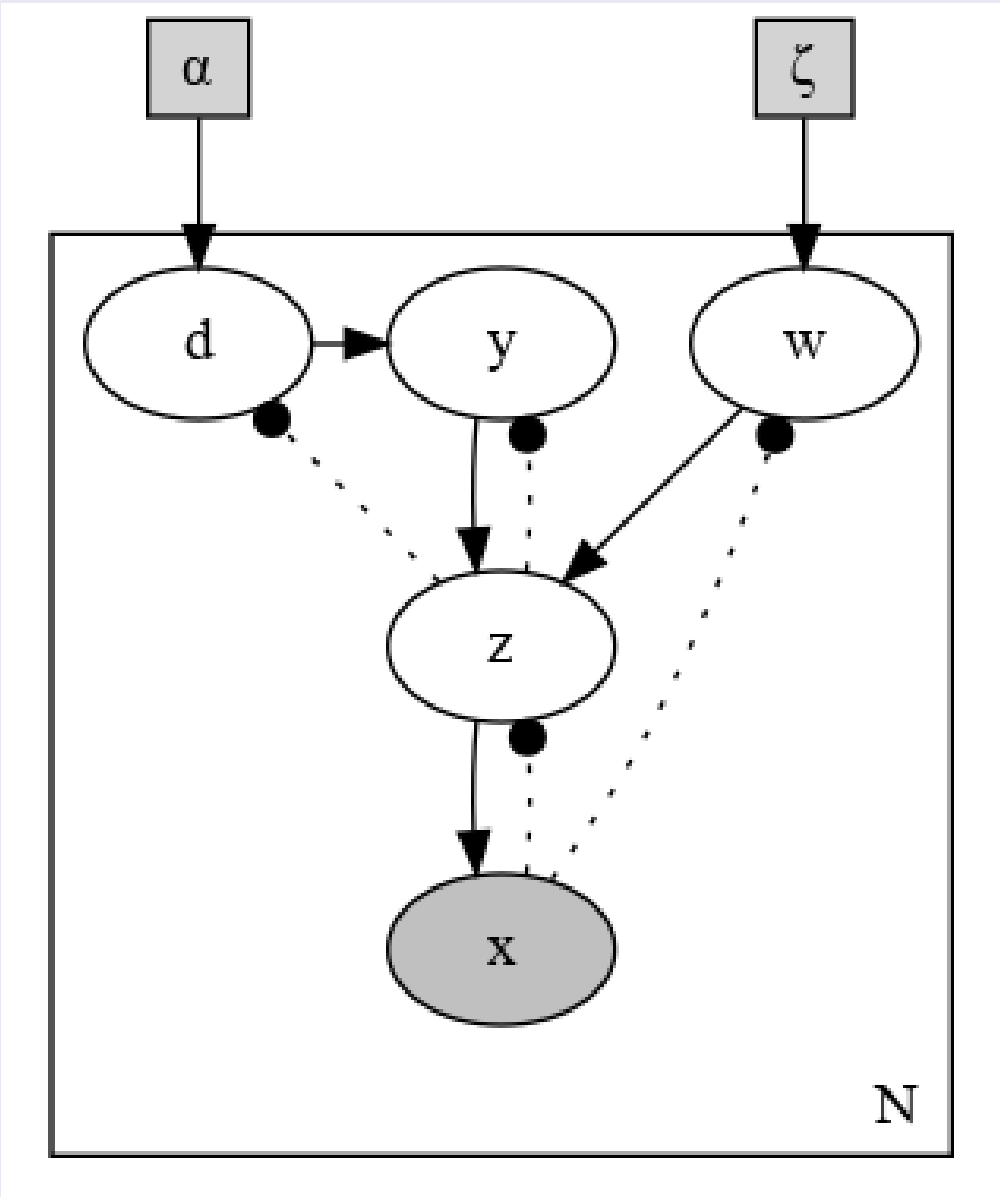
## Abstract

The Gaussian Mixture VAE Model has been demonstrated to be a rather powerful model for unsupervised and (semi)supervised learning tasks on image sets [1]. We use a slightly modified and theoretically improved GMMVAE model and tested it on

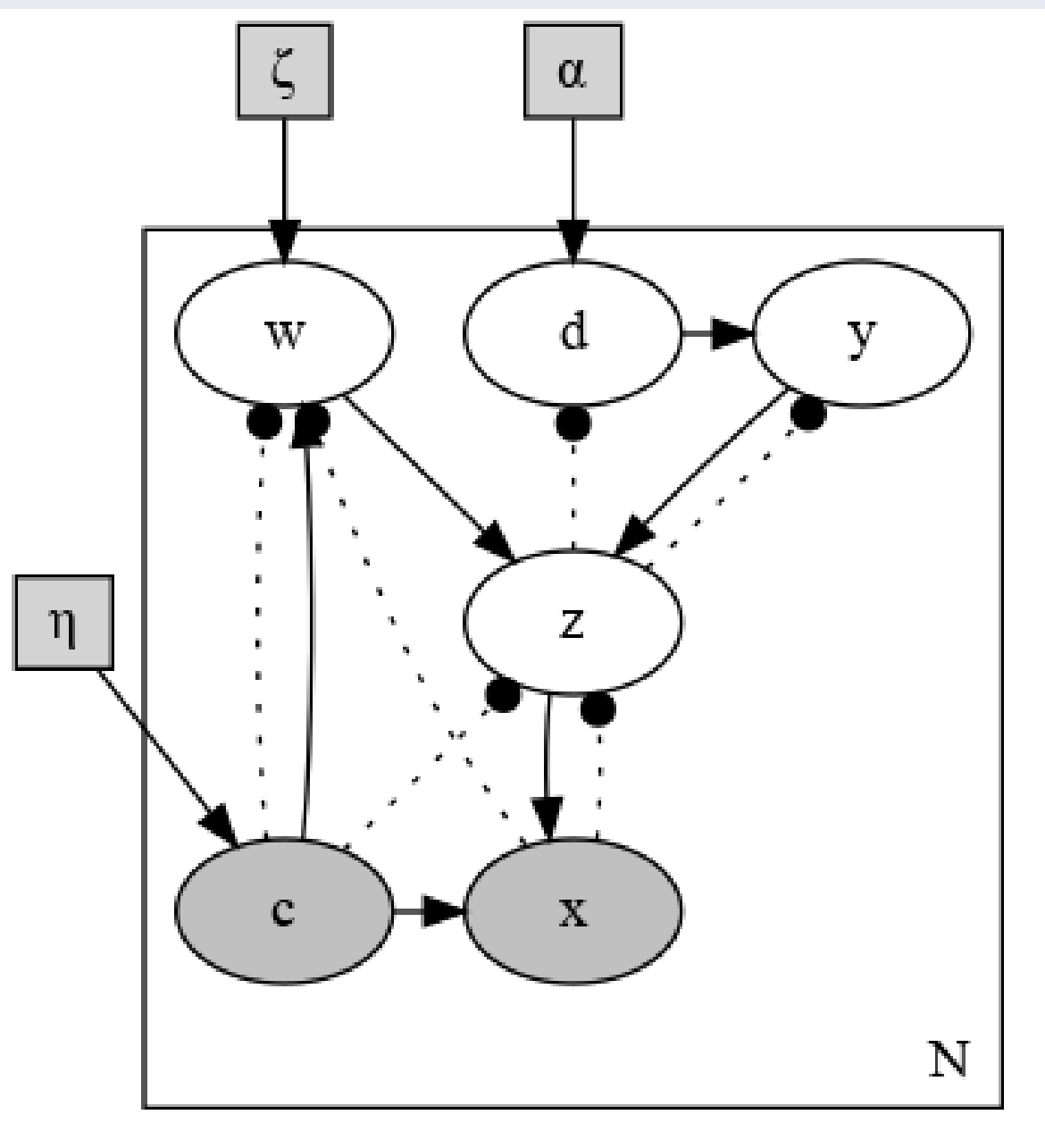
scRNAseq data. We also tested a conditional version of our GMMVAE for the purpose of predicting treatment effect on control cells of specific cell type. Our results suggests that the GMMVAE in (semi)supervised learning

is able to learn to both accurately classify and to generate the data. synthetic data generation is one possible application. As for prediction of treatment effect—our cGMMVAE have similar results to one method we compared [3].

## GMMVAE models



(a) GMMVAE



(b) cGMMVAE

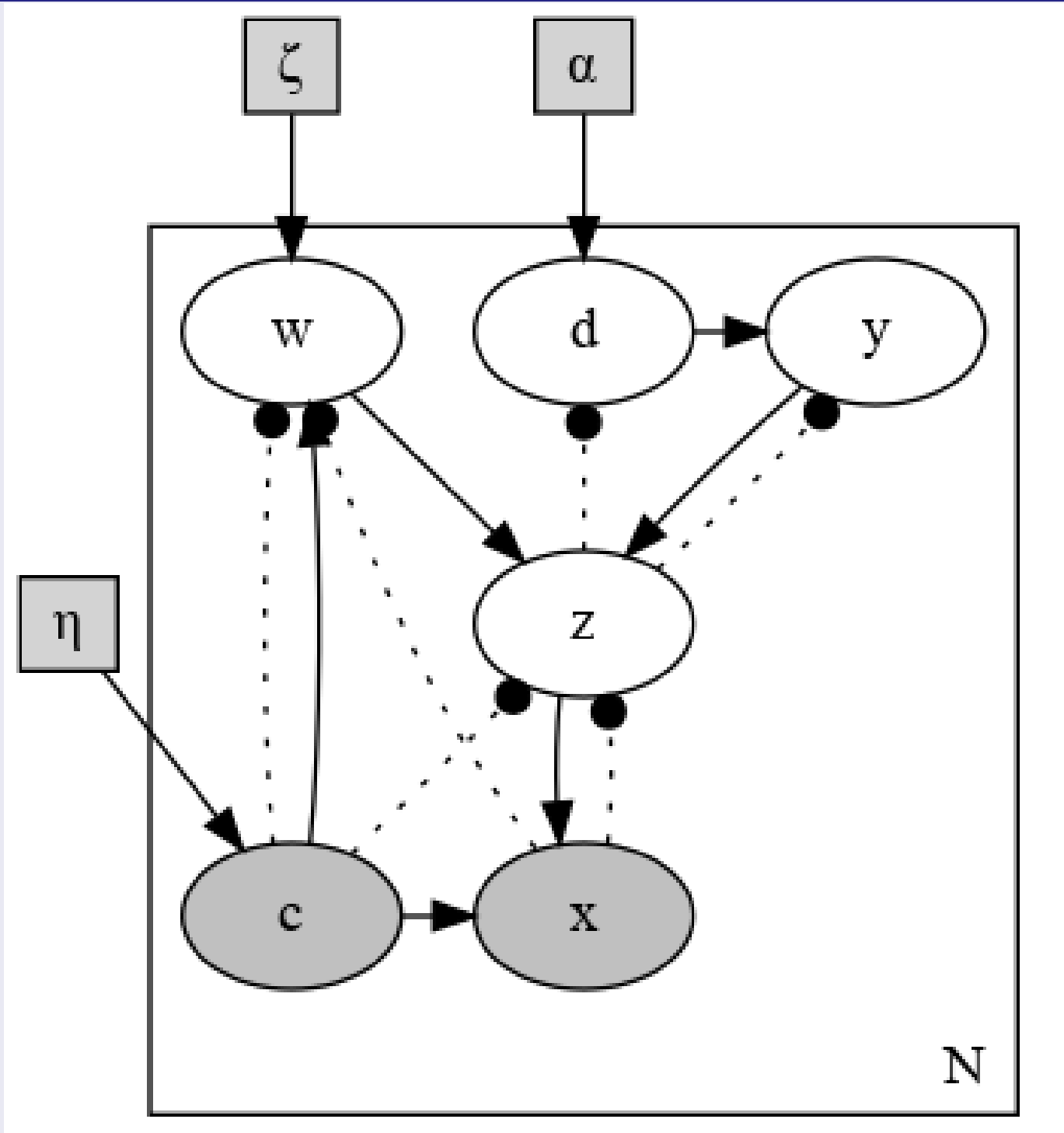
## Reference

- [1] Nat Dilokthanakul et al. “Deep unsupervised clustering with gaussian mixture variational autoencoders”. In: *arXiv preprint arXiv:1611.02648* (2016).
- [2] Xifeng Guo et al. “Improved deep embedded clustering with local structure preservation.”. In: *Ijcai*. 2017, pp. 1753–1759.
- [3] Mohammad Lotfollahi, F Alexander Wolf, and Fabian J Theis. “Generative modeling and latent space arithmetics predict single-cell perturbation response across cell types, studies and species”. In: *bioRxiv* (2018), p. 478503.
- [4] Nikolai Russkikh et al. “Style transfer with variational autoencoders is a promising approach to RNA-Seq data harmonization and analysis”. In: *Bioinformatics* 36.20 (2020), pp. 5076–5085.

## Abstract

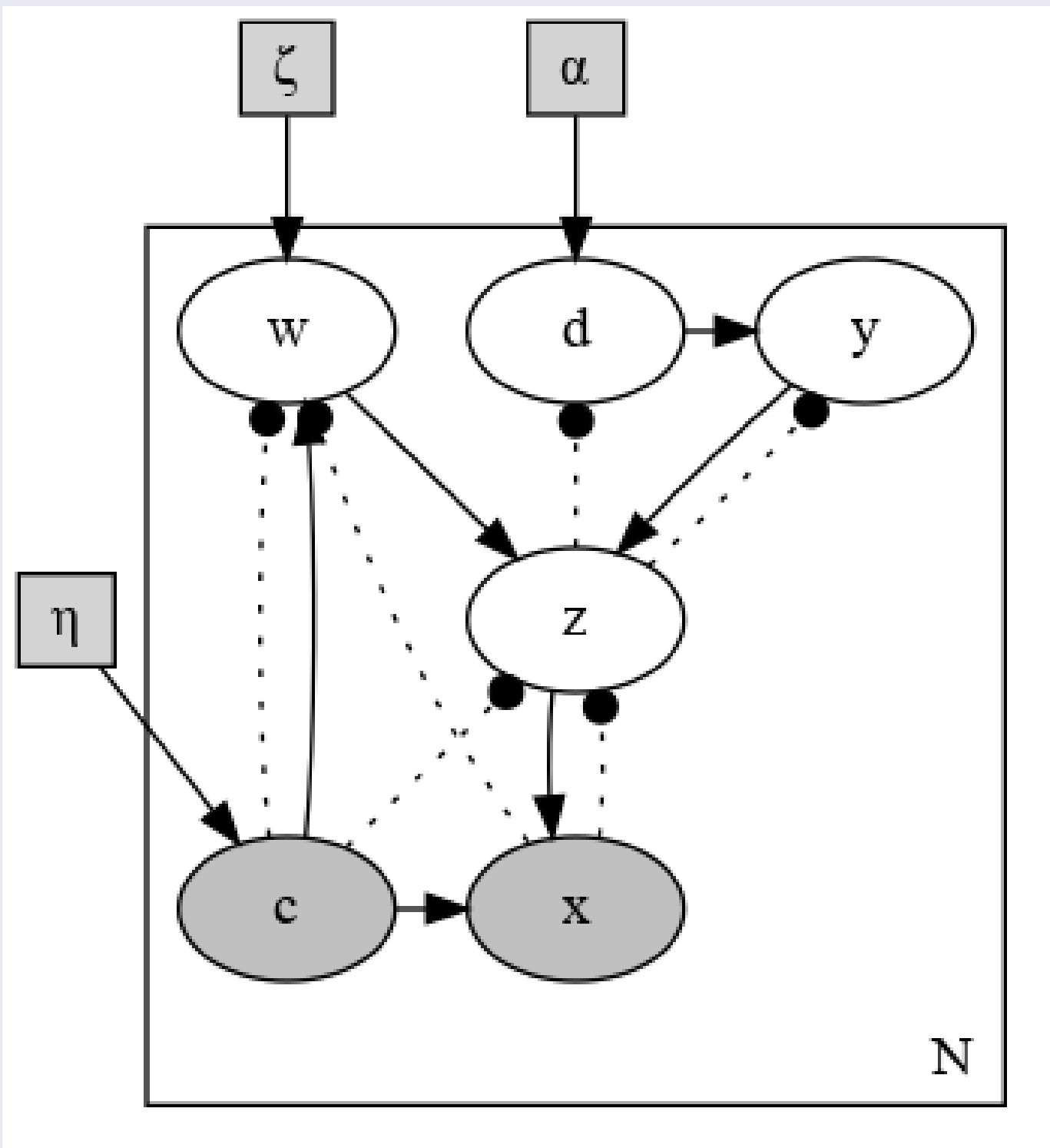
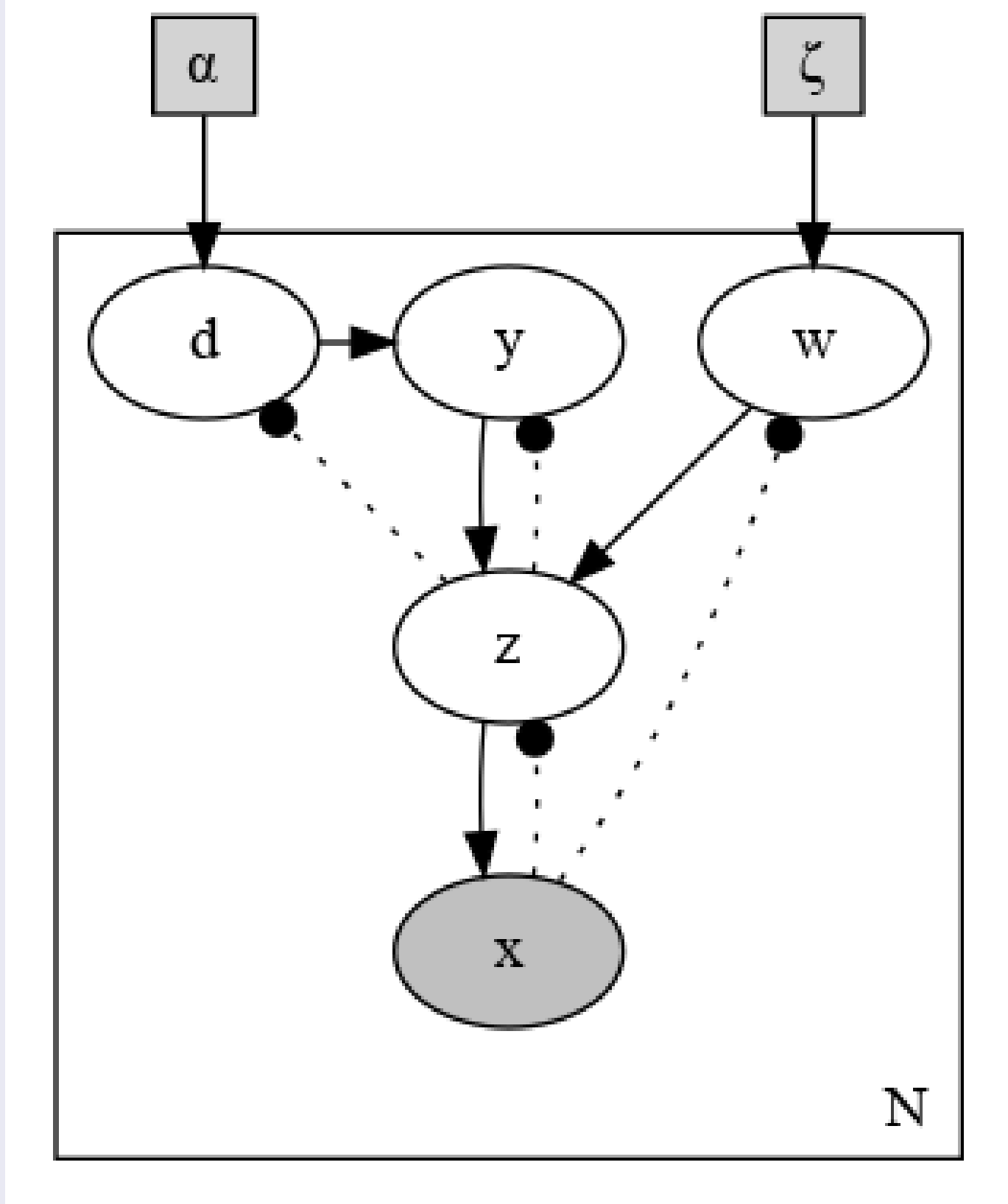
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The Gaussian Mixture VAE Model has been demonstrated to be a rather powerful model for unsupervised and (semi)supervised learning tasks on image sets [1]. We use a slightly modified and theoretically improved GMMVAE model and tested it on scRNAseq data. We also tested a conditional version of our GMMVAE for the purpose of predicting treatment effect on control cells of specific cell type.



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