Learning disentangled representations with VAE

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1.Background

Variational autoencoders (VAE) is a class of deep learning models that can find a low dimensional representation from high dimensional data.

The goal is to disentangle biological processes into a single latent dimension.

Data is from braincells from a mouse hippocampus. The data consists of gene expressions.

3.Experimental method

VAE models that will be tested:
- Vanilla VAE
- Beta-VAE
- BetaTC-VAE
- DIP-VAE

Train the models and try to find a correlation with a latent dimension and one of the biological processes. The pearson correlation coefficient will be used for calculating the correlations.

2.Research question

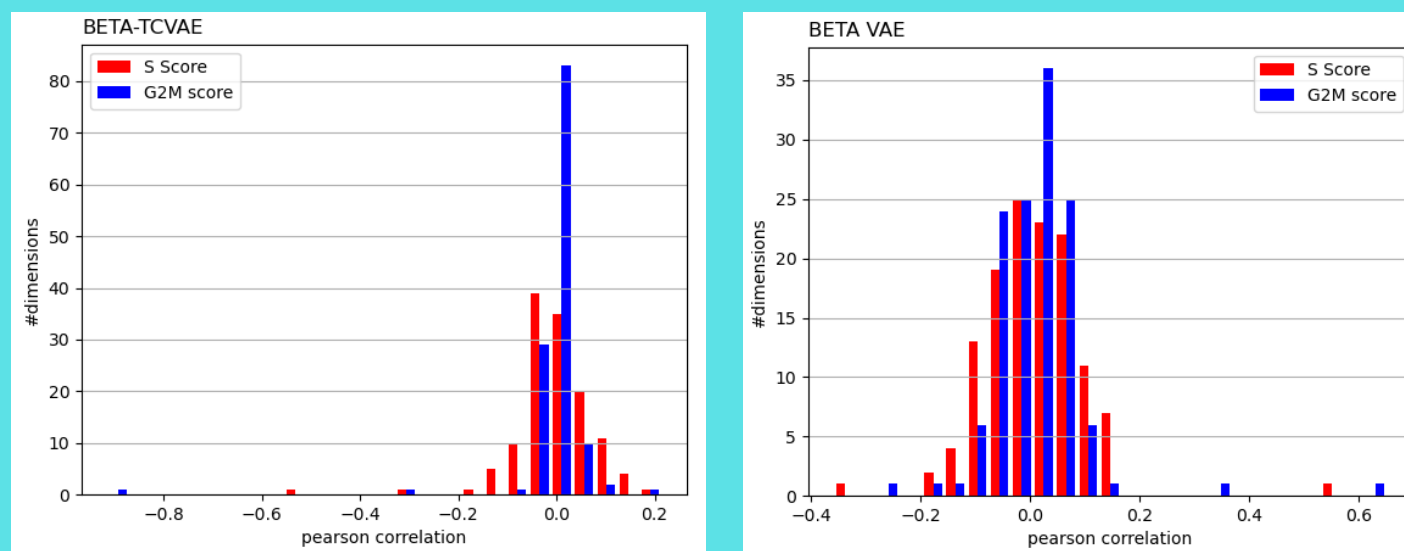**How good are different VAEs at learning disentangled representations?**

Figure 1: Histograms showing how many dimensions correlated for a certain amount with the cell cycle scores.

Model	S-Score	G2M-Score	Latent time
VAE	-0.2620	0.3037	-0.0297
BetaVAE	0.5332	0.6518	0.0345
DIP-VAE	0.2403	0.3121	0.0152
BetaTCVAE	-0.5405	-0.9157	-0.0277

Table1: The best correlations found with each single one of the biological processes by each model.

4.Results

In general the models had a more difficult time encoding the latent time into a single latent dimensions than they had with encoding the cell cycle scores.

However, it's quite clear that VAE and DIP-VAE perform by far the worst when just looking at the cell cycle score. What's interesting is that when looking at the latent time, DIP-VAE still performs the worst but VAE now performs on par with the other models.

5.Conclusion

Both BetaVAE and BetaTCVAE performed better than VAE and DIP-VAE by quite a big margin. This can clearly be seen when looking at table 1. The correlations found by these two models are always higher than those found by VAE and DIP-VAE. Besides this they often encoded this high correlation into a single dimension.

Neither VAE or DIP-VAE performed great, never finding very high correlations. However often DIP-VAE performed even worse than VAE.