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The Effect of Different Initialization Methods on VAEs for Modeling Cancer using RNA Genome Expressions

TU Delft

1 Background

- Cancer hard to treat, need for personalized treatment plans
- Success with **Variational Auto-Encoders** (VAE)
- VAEs perform dimension reduction to find disentangled representations
- Initialization techniques set the weights of the nodes in the layers
- Initialization methods can **increase performance** of VAEs
- RNA genome expressions from **The Cancer Genome Atlas** (TCGA) [1]
- Samples include different cancer types

2 Research Question

Quantify the impact of different initialization methods.

Compare different VAE models to conclude if some models are **more sensitive** to initialization methods

3 Method

VAE models:
- VAE [2]
- IWEA [3]
- InfoVAE [4]
- LogCoshVAE [5]

Initialization methods:
- Default PyTorch implementation:

$$\mathcal{U}\left(-\sqrt{\frac{1}{fan\_in}}, \sqrt{\frac{1}{fan\_in}}\right)$$

- Normal:

$$\mathcal{N}(0,1)$$

- Uniform:

$$\mathcal{U}(0,1)$$

- Glorot Normal (Xavier normal):

$$\mathcal{N}(0,\sigma^2)$$

$$\sigma = gain \cdot \sqrt{\frac{2}{fan\_in + fan\_out}}$$

- Glorot Uniform (Xavier uniform):

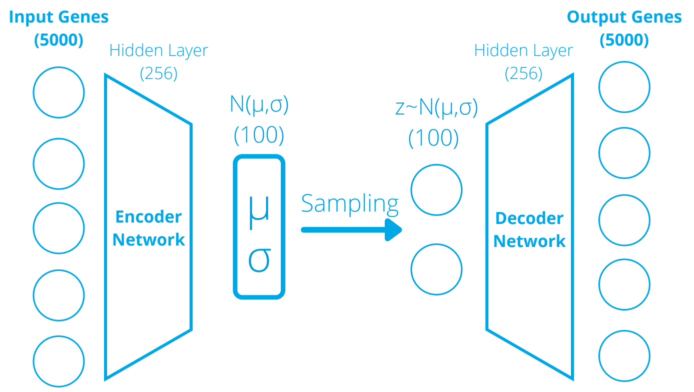
$$\mathcal{U}(-a,a)$$

$$a = gain \cdot \sqrt{\frac{6}{fan\_in + fan\_out}}$$

Empirical analysis on the loss function of the validation set

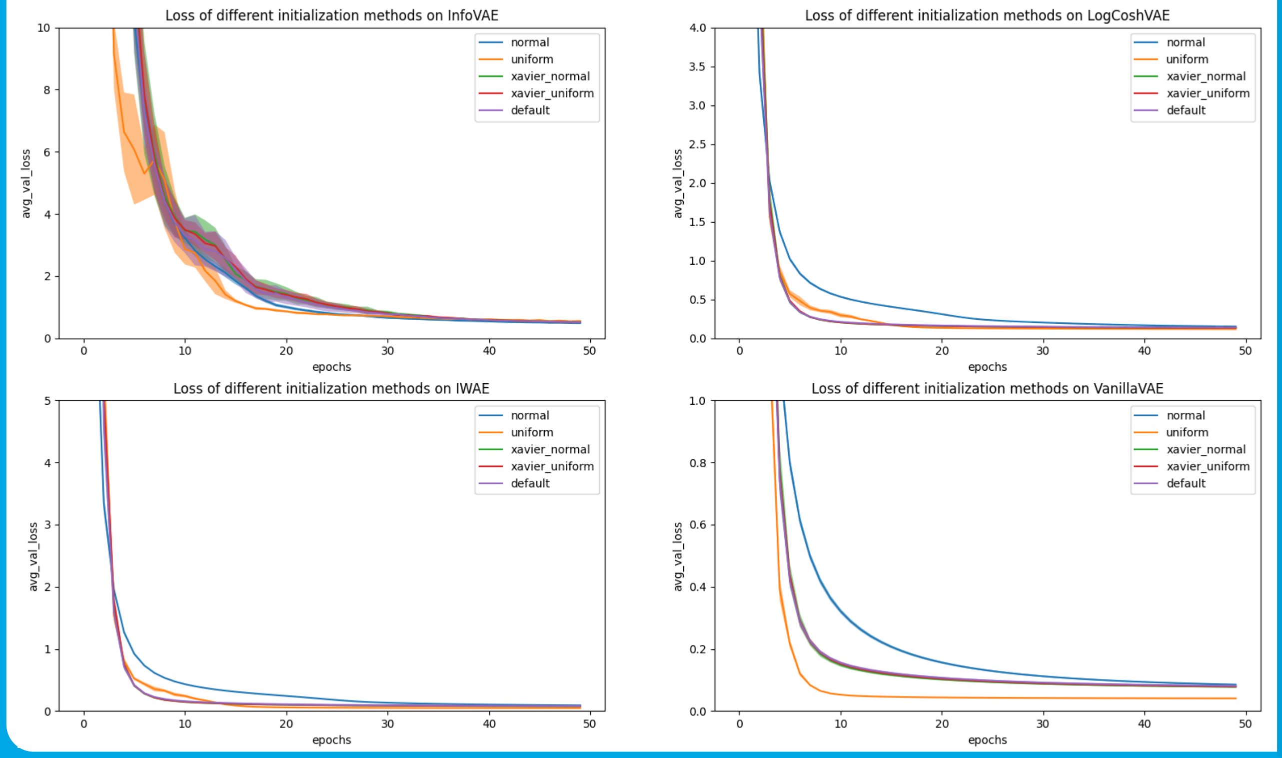
Using a **80% 20%** split for training and validation

Normalize the data and use only the **5000** most variable genes

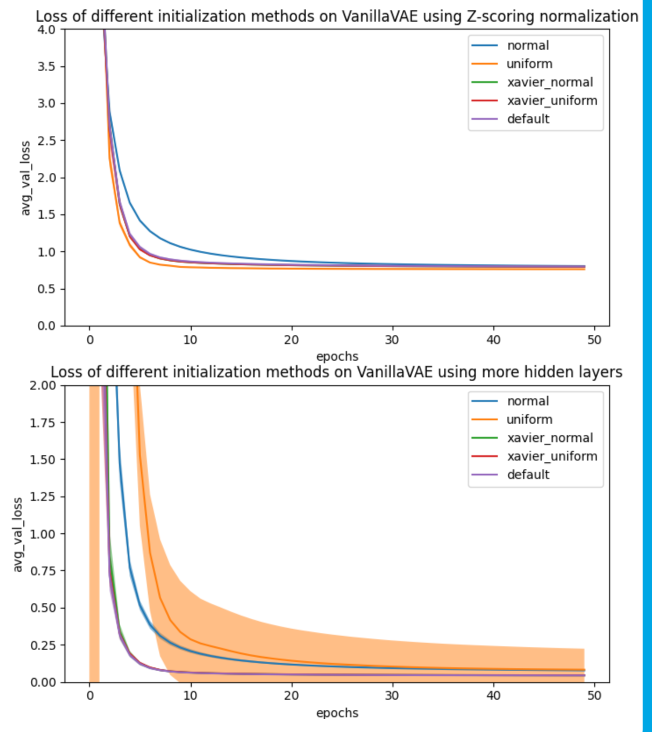


4 Results

All four models using 0-1 normalization



VanillaVAE using z-scoring normalization or more hidden layers



5 Conclusion

Using different normalization techniques does not influence results

VanillaVAE **most sensitive** to initialization methods

When using **one hidden layer**:
- Uniform performs best for VanillaVAE and InfoVAE
- Xavier Normal, Xavier Uniform & Default performs best for IWAE and LogCoshVAE

When using **more hidden layers**:
- Use Xavier Normal, Xavier Uniform & Default

[1] National Cancer Institute", "The Cancer Genome Atlas Program." [Online]. Available: https://www.cancer.gov/about-nci/organization/ccg/research/ structural-genomics/tcga
[2] D. P. Kingma and M. Welling, "Auto-encoding variational bayes," 2014.
[3] Y. Burda, R. Grosse, and R. Salakhutdinov, "Importance weighted autoencoders," 2016.
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[11] P. Chen, G. Chen, and S. Zhang, "Log hyperbolic cosine loss improves variational autoencoder," 2019. [Online]. Available: https://openreview.net/forum?id=rkglvsC9Ym