

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

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]
- IWAE [3]
- InfoVAE [4]
- LogCoshVAE [5]

Initialization methods:

- Default PyTorch implementation:

$$U(-\sqrt{\frac{1}{fan_in}}, \sqrt{\frac{1}{fan_in}})$$

- 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):

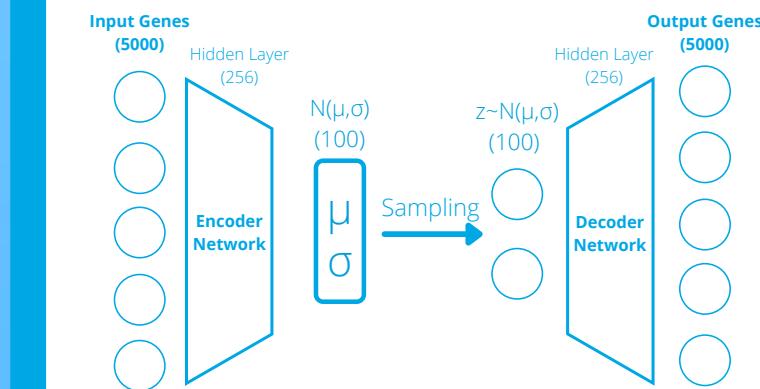
$$\mathcal{U}(-a, a)$$

$$a = gain \cdot \sqrt{\frac{6}{fan_in + fan_out}}$$

Empirical analysis on the loss function of the validation set

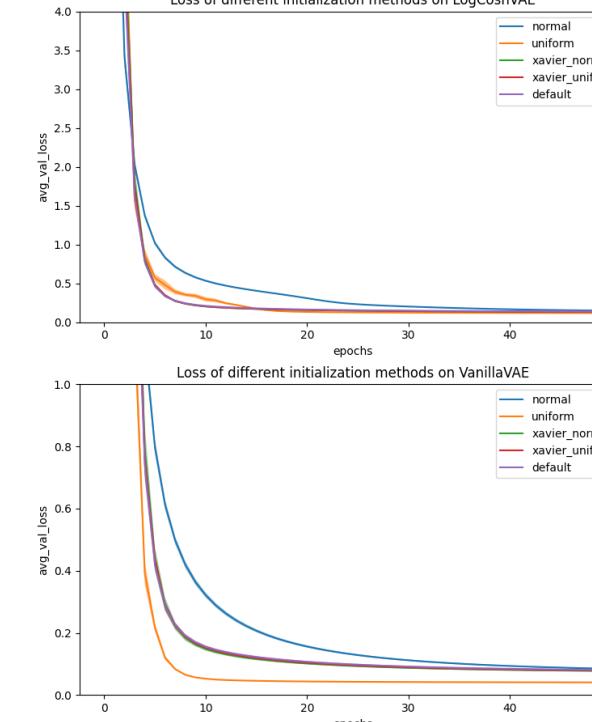
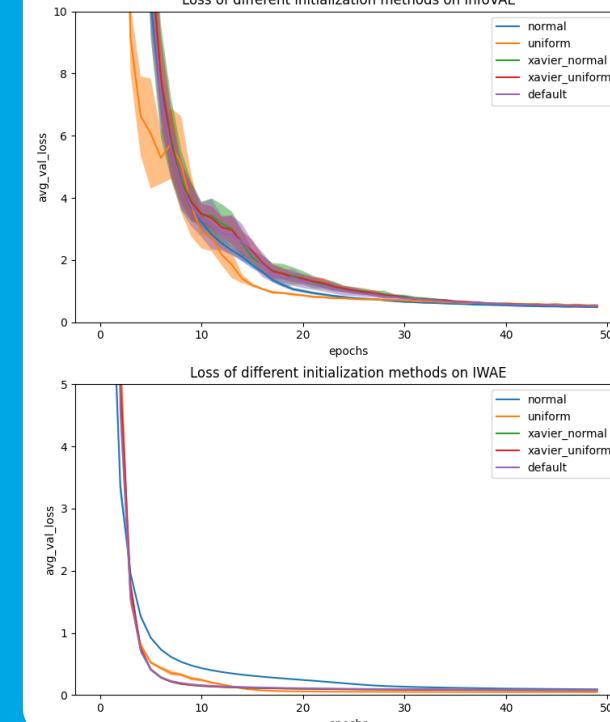
Using a **80% 20%** split for training and validation

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

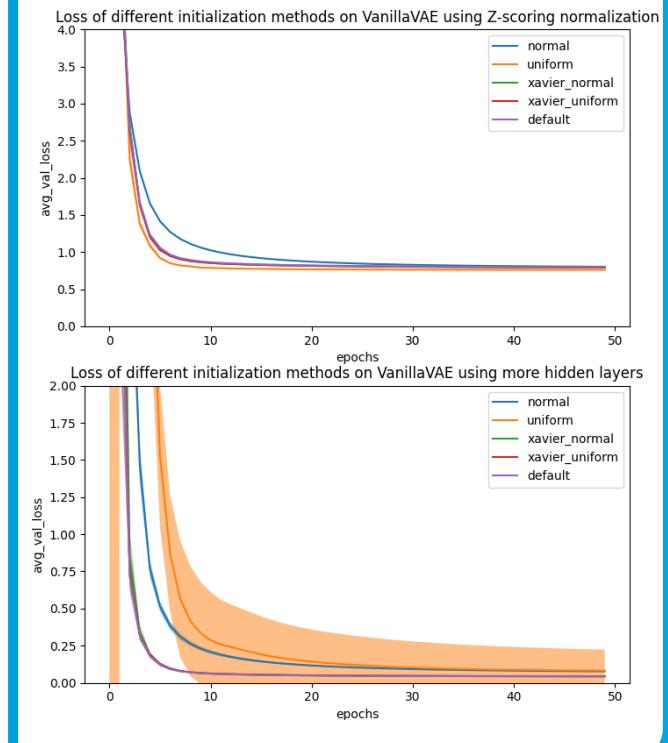


4 Results

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