#### A brief introduction to deep generative models

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February 3, 2022

#### Outline

Generative Models

References

#### The logic of generative modeling

Say we have a set of variables  $x = (x_1, x_2, ..., x_n)$  which might have some statistical dependence

The variable x might be an amino acid sequence, gene expression data, microscopy image, etc.

- ▶ Often we are handed a batch of empirical samples  $\{x_i\}_{i=1}^N$
- ▶ We want to know the generating distribution p(x)

In supervised generative learning, we try to explicitly learn the joint distribution  $p(x) = \prod_{i=1}^{N-1} p(x_i|x_{i+1:N})p(x_N)$ , which is generally more difficult than discriminative learning.

## Perks of generative modeling

- Fitting complete multivariate distributions p(x) goes beyond correlation-based or clustering approaches
- Correlations cannot discover partial correlation in the context of other neighbors
- Fitting p(x) permits sampling based inference

## Why generative modeling is difficult

When describing a distribution over multiple variables, we may not know the proper normalization Z. That is,

$$p(x) = \frac{1}{Z}\tilde{p}(x)$$

This very important situation arises in several contexts:

- 1. In Bayesian inference where  $p(x_1|x_2) = p(x_2|x_1)p(x_1)/p(x_2)$  is intractable due to  $Z = p(x_2) = \int p(x_2|x_1)p(x_1)dx_1$ . This integral can be very difficult or impossible to compute.
- 2. In models from statistical physics, e.g. the Ising model, we only know  $\tilde{p}(x) = e^{-H(x)}$  where H(x) is the Hamiltonian

# Variational autoencoders (VAEs)

#### A variational solution to generative modeling

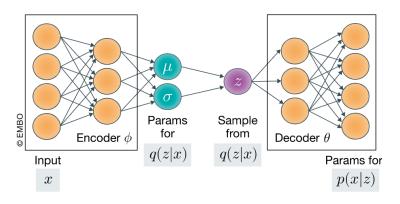


Figure 1: Variational autoencoder architecture Taken from Lopez 2020 in FMBO

#### Bayesian inference

The variable x has a latent representation or code z. We often say that z is the *causal source* of x. Ultimately, we would like to know the distribution  $P_{\Phi}(x)$ 

$$P_{\phi}(\mathsf{x}) = rac{P_{\phi}(\mathsf{x}|\mathsf{z})P_{\phi}(\mathsf{z})}{Q_{\psi}(\mathsf{z}|\mathsf{x})}$$

in order to find the model parameters that maximize the likelihood of the observed data:

$$\Phi^* = \operatorname*{argmin}_{\Phi} - \log P_{\Phi}(x)$$

but we generally do not know  $P_{\psi}(\mathbf{z}|\mathbf{x})$  due to the intractable integral  $Z = \int P_{\phi}(\mathbf{x}|\mathbf{z})P_{\phi}(\mathbf{z})d\mathbf{z}$  (see slide 5)

#### Computing the evidence

We can rewrite the evidence as

$$\begin{aligned} P_{\phi}(\mathsf{x}) &= \int P_{\phi}(\mathsf{z}) P_{\phi}(\mathsf{x}|\mathsf{z}) d\mathsf{z} \\ &= \int P_{\phi}(\mathsf{z}) P_{\phi}(\mathsf{x}|\mathsf{z}) \frac{P_{\phi}(\mathsf{z}|\mathsf{x})}{P_{\phi}(\mathsf{z}|\mathsf{x})} d\mathsf{z} \\ &= \mathbb{E}_{\mathsf{z} \sim P_{\phi}(\mathsf{z}|\mathsf{x})} \frac{P_{\phi}(\mathsf{z}) P_{\phi}(\mathsf{x}|\mathsf{z})}{P_{\phi}(\mathsf{z}|\mathsf{x})} \end{aligned}$$

where  $P_{\phi}(\mathbf{z}|\mathbf{x})$  is our model "encoder"

# The evidence lower bound (ELBO)

$$\begin{split} \log P_{\phi}(\mathbf{x}) &= \log \int_{\mathbf{z}} P(\mathbf{x}, \mathbf{z}) d\mathbf{x} \\ &= \log \int_{\mathbf{z}} P(\mathbf{x}, \mathbf{z}) \frac{Q(\mathbf{z}|\mathbf{x})}{Q(\mathbf{z}|\mathbf{x})} d\mathbf{z} \\ &= \log \mathbb{E}_{\mathbf{z} \sim P_{\phi}(\mathbf{z}|\mathbf{x})} \frac{P(\mathbf{x}|\mathbf{z}) P(\mathbf{z})}{Q(\mathbf{z}|\mathbf{x})} \\ &\geq \mathbb{E}_{\mathbf{z} \sim P_{\phi}(\mathbf{z}|\mathbf{x})} \log \frac{Q(\mathbf{x}|\mathbf{z})}{P(\mathbf{z})} + \log P(\mathbf{x}|\mathbf{z}) \\ - \log P_{\phi}(\mathbf{x}) &\leq \mathbb{E}_{\mathbf{z} \sim P_{\phi}(\mathbf{z}|\mathbf{x})} \log \frac{Q(\mathbf{x}|\mathbf{z})}{P(\mathbf{z})} - \log P(\mathbf{x}|\mathbf{z}) \end{split}$$

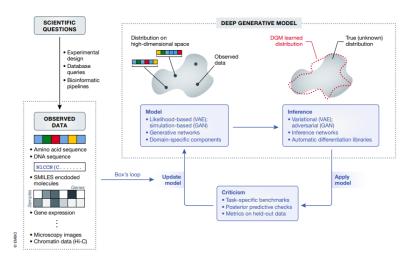
#### The ELBO objective

$$\begin{split} \Phi^* &= \mathcal{L}(\Phi) \\ &= \underset{\Phi}{\operatorname{argmin}} \ \mathbb{E}_{\mathbf{x} \sim \operatorname{Pop}, \ \mathbf{z} \sim P_{\phi}(\mathbf{z}|\mathbf{x})} \log \frac{Q_{\Psi}(\mathbf{z}|\mathbf{x})}{P(\mathbf{z})} - \log P(\mathbf{x}|\mathbf{z}) \end{split}$$

The ELBO can be rewritten in terms of a KL-divergence and population entropy. We often think of  $\Phi$  as "position" and the loss  $\mathcal L$  as an "energy"

#### Stochastic gradient descent

#### Applying deep generative models to biological data



#### A recent VAE for transcriptomics data: scV1

#### Recent improvements of interpretability

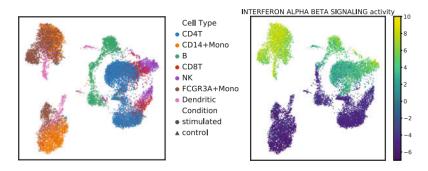


Figure 2: Phenotype segregation using a VAE on single-cell transcriptomics data. Taken from Seninge et al.

## Previous studies lack interpretability

#### Previous studies lack spatial information

## Multiplexed RNA imaging

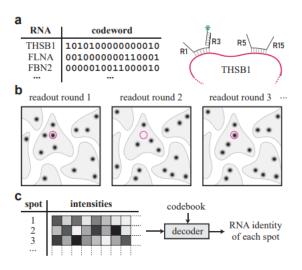


Figure 3:

## Minimum Hamming Distance (MHD) codes

Very basic codes that generate codewords  $x \in \mathcal{C}$  based on Hamming distance:

$$D = \sum_{n=1}^{L} \mathbb{I}(x_n = \hat{x}_n)$$

 $2^L$  possible code words (with  $2^L - 1$  usable ones)

## Binary symmetric channel (BSC)

#### References I