

Deep generative models for biologists

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Outline

Deep Generative Models

Probabilistic Graphical Models

References

Discriminative and generative models

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

The variable x might be an amino acid sequence, DNA sequence, microscopy image, etc.

In supervised **discriminative** learning, we may use observations of x to try and learn distributions such as $p(x_2|x_1)$ (i.e., inference)

In supervised **generative** learning, we try to explicitly learn the joint distribution $p(x) = p(x_1|x_2, \dots, x_n)p(x_2|x_3, \dots, x_n), \dots, p(x_n)$, which is generally more difficult.

The basic sampling problem

Suppose we are given a joint distribution

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

where $p(x)$ is easy to compute but Z is (too) hard to compute.

This **very important** situation arises in several contexts:

1. In **Bayesian models** where $p(x_1, x_2) := p(x_1|x_2)p(x_2)$ is easy to compute but $Z = \int p(x_1|x_2)p(x_2)dx_2$ 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 - the Ising model is an example of a **Markov network** or an **undirected graphical model**.

Approximating the joint distribution

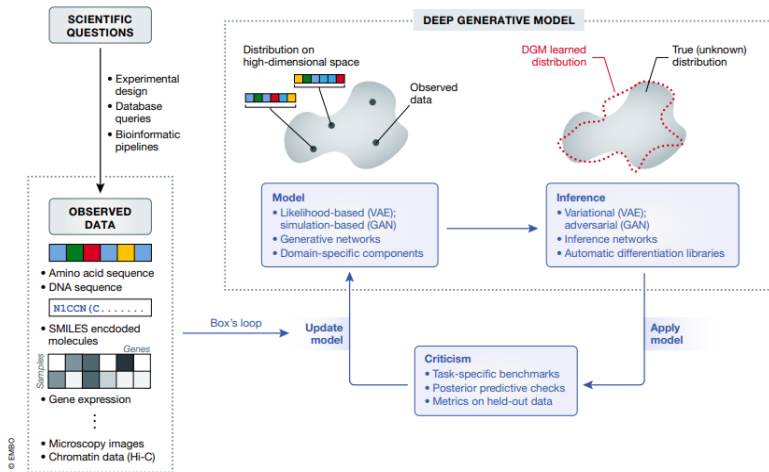
We would like to approximate $p(x)$

Variational methods are generally useful for Bayesian inference like $p(x_1|x_2)$ but can also be used to evaluate $p(x)$ by autoencoding x (called a variational autoencoder)

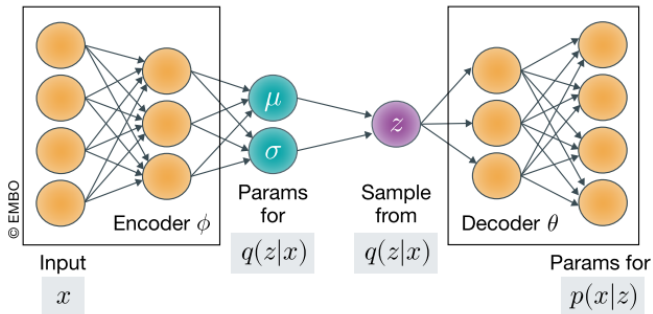
Generative adversarial networks (GANs) model $p(x)$ directly

In special scenarios, we may know $\tilde{p}(x)$ and we can use **Monte-Carlo Markov Chain (MCMC)** methods

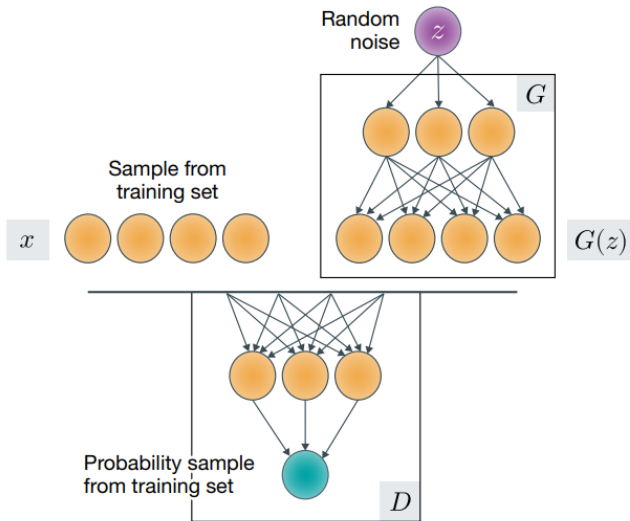
Applying deep generative models to biological data



Generative models: variational autoencoder



Generative models: adversarial networks



Cool biological applications of VAEs and GANs

Sequencing, Imaging, Other stuff

Monte-Carlo Markov Chain (MCMC)

- ▶ MCMC algorithms were originally developed in the 1940's by physicists at Los Alamos
- ▶ They were interested in modeling the probabilistic behavior of collections of atomic particles
- ▶ Simulation was difficult – the normalization constant Z was not known
- ▶ The term “Monte-Carlo” was coined at Los Alamos.
- ▶ Ulam and Metropolis overcame this problem by constructing a Markov chain for which the desired distribution was the stationary distribution
- ▶ Introduced to statistics and generalized with the Metropolis-Hastings algorithm (1970) and the Gibbs sampler of Geman and Geman (1984).

Monte-Carlo Markov Chain (MCMC)

MCMC is used when we know the functional form of $p(x)$ up to the normalization constant e.g., Ising model

MCMC methods do not model $p(x)$ directly but allow us to draw samples $x \sim p(x)$

Gibbs sampling

- ▶ Suppose $p(x)$ is a p.d.f. or p.m.f. that is difficult to sample from directly.
- ▶ Suppose, though, that we *can* easily sample from the conditional distributions e.g., $p(x_1|x_2, \dots, x_n)$.
- ▶ The Gibbs sampler proceeds as follows:
 1. set x to some initial starting values
 2. then sample $x_1|x_2, \dots, x_n$, then sample $x_2|x_1, \dots, x_n$, and so on.

Gibbs sampling

0. Set (x_0, y_0) to some starting value.
1. Sample $x_1 \sim p(x|y_0)$, that is, from the conditional distribution $X \mid Y = y_0$.
Current state: (x_1, y_0)
Sample $y_1 \sim p(y|x_1)$, that is, from the conditional distribution $Y \mid X = x_1$.
Current state: (x_1, y_1)
2. Sample $x_2 \sim p(x|y_1)$, that is, from the conditional distribution $X \mid Y = y_1$.
Current state: (x_2, y_1)
Sample $y_2 \sim p(y|x_2)$, that is, from the conditional distribution $Y \mid X = x_2$.
Current state: (x_2, y_2)
- \vdots

Repeat iterations 1 and 2, M times.

Markov blankets

When one wants to infer a random variable with a set of variables, usually a subset is enough.

The useful information is called a **Markov blanket**

Probabilistic graphical models

Using Gibbs sampling with graphical models

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