Deep Generative Models

AIGenomics101 Week 4



Part 2 Feb 14, 2020

Many of slides borrowed from from: Fei-Fei Li & Serena Yeung, Stanford

Course

Julie Hussin & Ahmad Pesaranghader

Overview

- Unsupervised Learning
- Generative Models
 - Variational Autoencoders (VAE)
 - Generative Adversarial Networks (GAN)

Generative Adversarial Nets in Genomics

a)

Generating and designing DNA with deep generative models

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Abstract

We propose generative neural network methods to generate DNA sequences and tune them to have desired properties. We present three approaches: creating synthetic DNA sequences using a generative adversarial network (GAN); a DNAbased variant of the activation maximization ("deep dream") design method; and a joint procedure which combines these two approaches together. We show that these tools capture important structures of the data and, when applied to designing probes for protein binding microarrays (PBMs), allow us to generate new sequences whose properties are estimated to be superior to those found in the training data. We believe that these results open the door for applying deep generative models to advance genomics research.

1 Introduction

A major trend in deep learning is the development of new generative methods, with the goal of creating synthetic data with desired structures and properties. This trend includes generative models such as generative adversarial networks (GANs) [1], variational autoencoders (VAEs) [2], and deep autoregressive models [3, 4], as well as generative design procedures like activation maximization (popularly known as "deep dream") [5–7] and style transfer [8]. These powerful generative tools bring many new opportunities. When data is costly, we can use a generative method to inexpensively simulate data. We can also use generative tools to explore the space of possible data configurations, tuning the generated data to have specific target properties, or to invent novel, unseen configurations



b) TGAGAGTGATGTATT<mark>CGAATTGA</mark>TGCCTCACCTCTGCTTGCAGACTGTCA GGAATGAACTGGGGGAGACAGGCCCAGA<mark>GGAATTGA</mark>GAAAGTAATGAGCAC GCCCTG<mark>CGTTTTAA</mark>GAAATACTGTTGCATCAGGGCAAATGTAAGATTTTG TTTTGTTTGAGATCTGTGGGGGTATGCT<mark>GGAATTAA</mark>AGTCTGGACTACCAC CTGATACTGAATGCAGATTTGAAGAACAAAG<mark>CGTATTAA</mark>AACACATGCTT GATCCCCAAGTGT<u>GGAATTGA</u>GAAGGAAGCTGGAGAATCCCCAAACTCTG CAGCCACATCAGCTTACCTAA<mark>GGAAGTGA</mark>TGTGTTTTAAAAACCAGCTTTG TAGAATTTTTCTT<u>GGTATTAA</u>TGATGATCTAGGCTTACACAGGGACATCA GACATTGCTTAGTCTGAGGGGATACAGTGGGGGAGTG<mark>GGTATTAA</mark>AATCTCC ACATGCCTGAGACATTCCTGCTCTTGAATCTGA<mark>GCAATTAT</mark>GCTTAATCC

Figure 7: Motif-matching experiment: a) Sequence logo for the PWM detected by the predictor. Letter heights reflect their relative frequency at each position. Sequences which have a strong match with this motif will score highly. b) Sample sequences tuned to have a high predictor score. The boxes indicate strong motif matches for each sequence.

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Supervised Learning

Data: (x, y) x is data, y is label

Goal: Learn a *function* to map x -> y

Examples: Classification, regression, object detection, semantic segmentation, image captioning, etc.

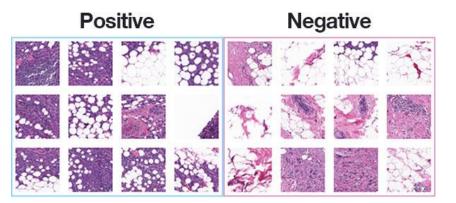
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Supervised Learning

Data: (x, y) x is data, y is label

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Examples: Classification, regression, object detection, semantic segmentation, image captioning, etc. The breast cancer histology image dataset



Classification

This image is CC0 public domain

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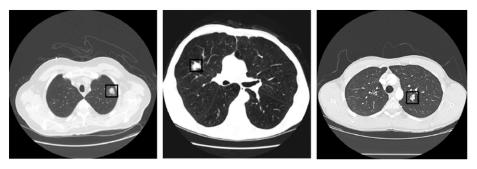
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Supervised Learning

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Examples: Classification, regression, object detection, semantic segmentation, image captioning, etc. Lung nodule detection with several levels of malignancy (LIDC dataset)



Object Detection

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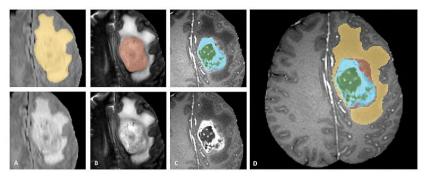
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Supervised Learning

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Examples: Classification, regression, object detection, semantic segmentation, image captioning, etc. BraTs-Segmentation-Challenge (Brain MRI)



Semantic Segmentation

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Supervised Learning

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Examples: Classification, regression, object detection, semantic segmentation, image captioning, etc.

Findings: The cardiac silhouette is enlarged and has a globular appearance. Mild bibasilar include pericardial effusion or dilated cardiomyopathy.

Medical Report Captioning

dependent atelectasis. No pneumothorax or large pleural effusion. No acute bone abnormality. Impression: Cardiomegaly with globular appearance of the cardiac silhouette Considerations would

Image captioning

Caption generated using neuraltalk2 Image is CC0 Public domain

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Unsupervised Learning

Data: x Just data, no labels!

Goal: Learn some underlying hidden *structure* of the data

Examples: Clustering, dimensionality reduction, feature learning, density estimation, etc.

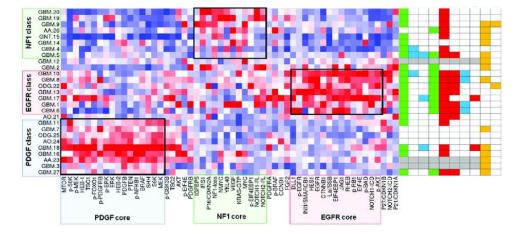
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Unsupervised Learning

Data: x Just data, no labels!

Goal: Learn some underlying hidden *structure* of the data

Examples: Clustering, dimensionality reduction, feature learning, density estimation, etc. K-means clustering of gliomas by signature-defining proteins



K-means or t-SNE clustering

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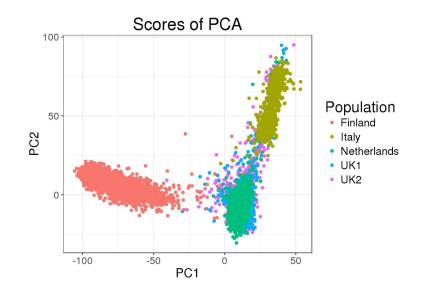
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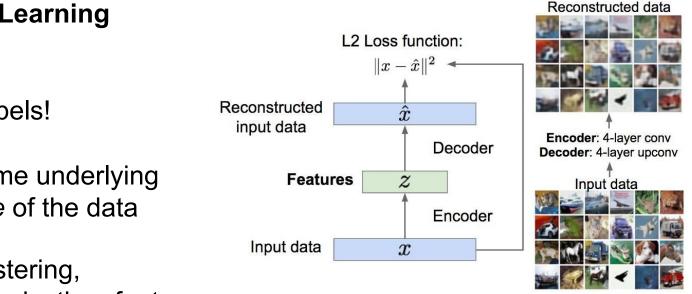
Examples: Clustering, dimensionality reduction, feature learning, density estimation, etc.



Principal Component Analysis (Dimensionality reduction)

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Autoencoders (Feature learning/representation)

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Unsupervised Learning

Data: x Just data, no labels!

Goal: Learn some underlying hidden *structure* of the data

Examples: Clustering, dimensionality reduction, feature learning, density estimation, etc.

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Unsupervised Learning

Data: x Just data, no labels!

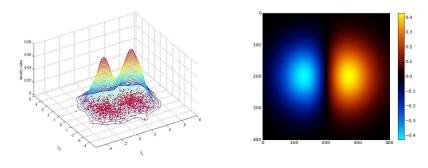
Goal: Learn some underlying hidden *structure* of the data

Examples: Clustering, dimensionality reduction, feature learning, density estimation, etc.



Figure copyright Ian Goodfellow, 2016. Reproduced with permission.

1-d density estimation



2-d density estimation

2-d density images left and right are CC0 public domain

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Supervised Learning

Data: (x, y) x is data, y is label

Goal: Learn a *function* to map x -> y

Examples: Classification, regression, object detection, semantic segmentation, image captioning, etc.

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Generative Models

Given training data, generate new samples from same distribution





Training data ~ $p_{data}(x)$ Generated samples ~ $p_{model}(x)$ Want to learn $p_{model}(x)$ similar to $p_{data}(x)$

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Generative Models

Given training data, generate new samples from same distribution





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Training data ~
$$p_{data}(x)$$
 Generated samples ~ $p_{model}(x)$
Want to learn $p_{model}(x)$ similar to $p_{data}(x)$

Addresses density estimation, a core problem in unsupervised learning **Several flavors:**

- Explicit density estimation: explicitly define and solve for p_{model}(x)
- Implicit density estimation: learn model that can sample from p_{model}(x) w/o explicitly defining it

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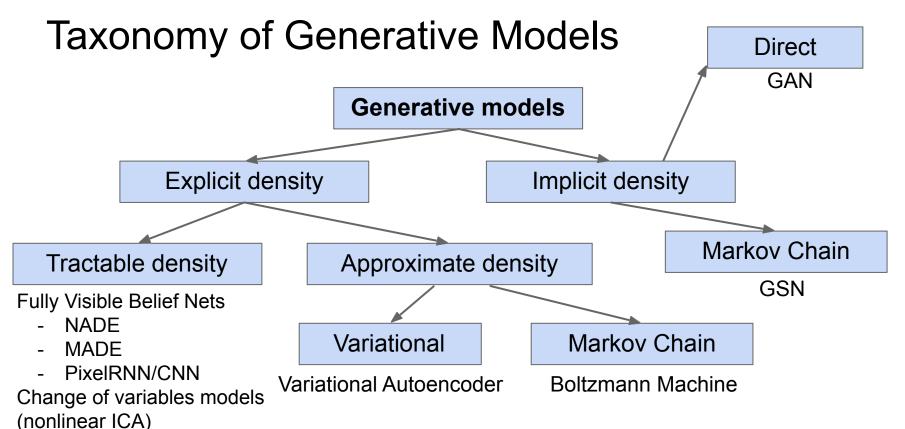


Figure copyright and adapted from Ian Goodfellow, Tutorial on Generative Adversarial Networks, 2017.

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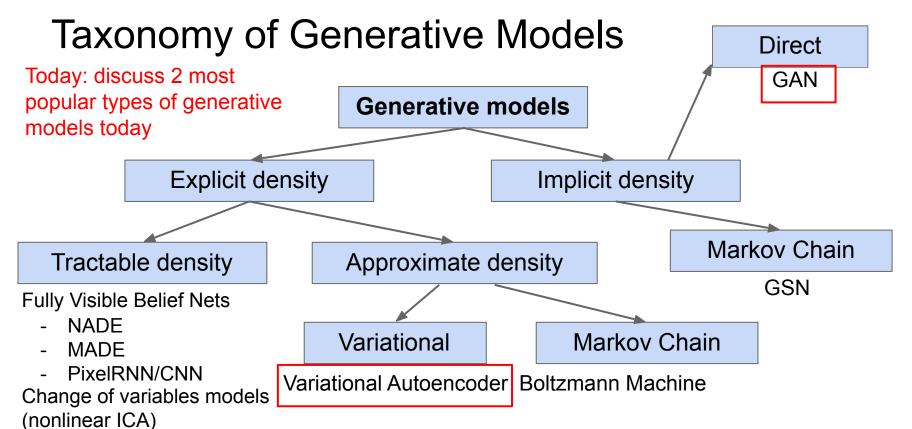


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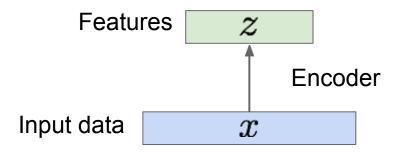
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Variational Autoencoders (VAE)

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Some background first:

Utoencoders hsupervised approach for learning a lower-dimensional feature representation from unlabeled training data

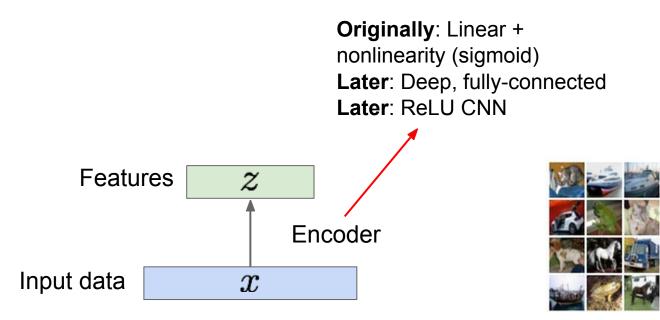




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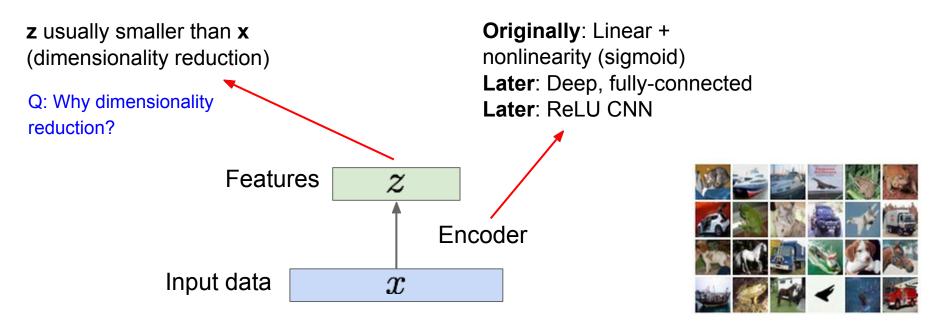
Some background first: Autoencoders Unsupervised approach for learning a lower-dimensional feature representation

from unlabeled training data



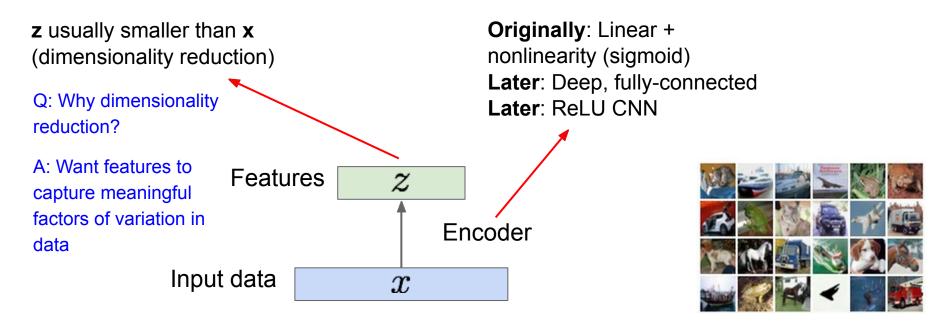


Some background first: Autoencoders Unsupervised approach for learning a lower-dimensional feature representation from unlabeled training data

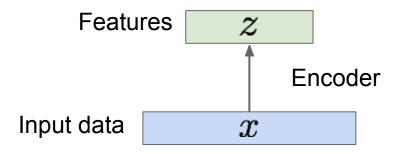


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Some background first: Autoencoders Unsupervised approach for learning a lower-dimensional feature representation from unlabeled training data



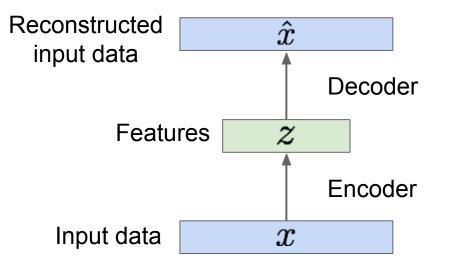
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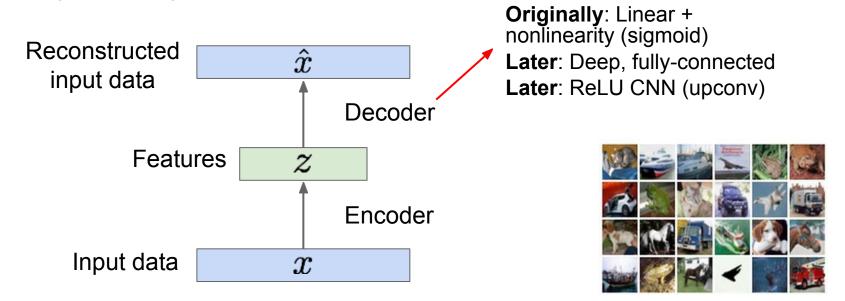
Train such that features can be used to reconstruct original data "Autoencoding" - encoding itself





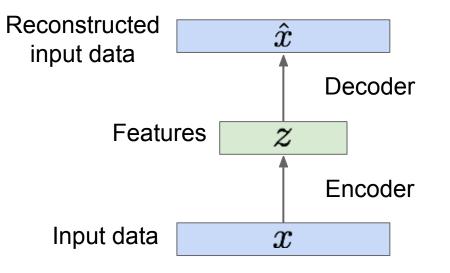
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Train such that features can be used to reconstruct original data "Autoencoding" - encoding itself



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Train such that features can be used to reconstruct original data "Autoencoding" - encoding itself



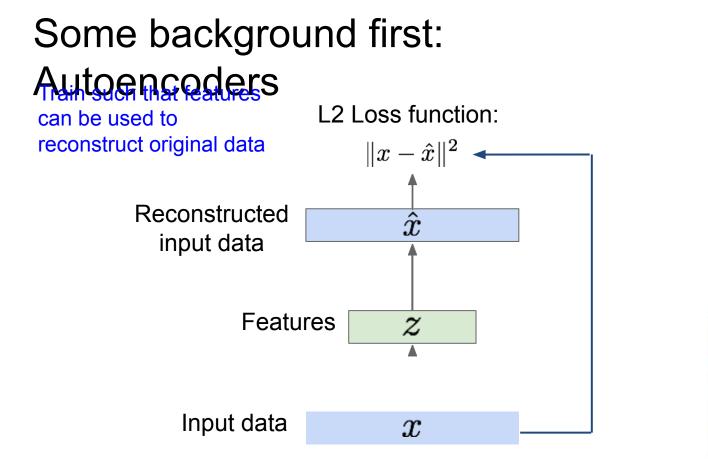
Reconstructed data



Encoder: 4-layer conv Decoder: 4-layer upconv



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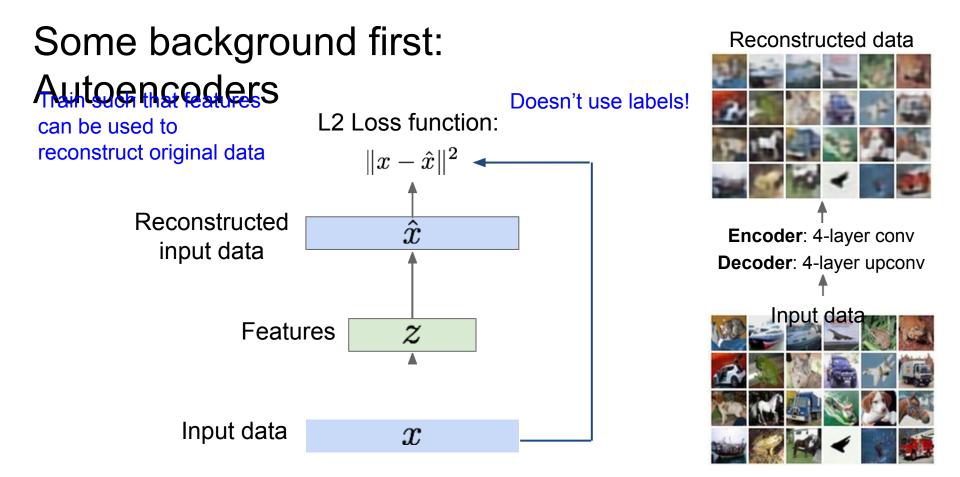
Reconstructed data



Encoder: 4-layer conv Decoder: 4-layer upconv

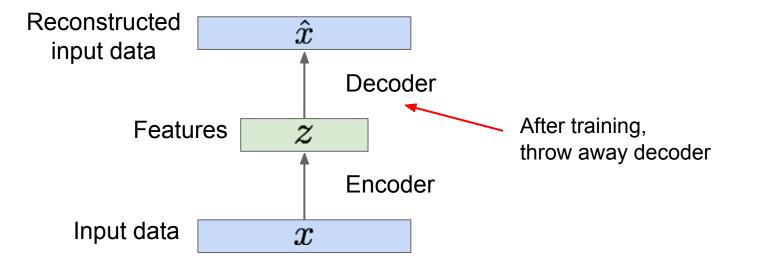


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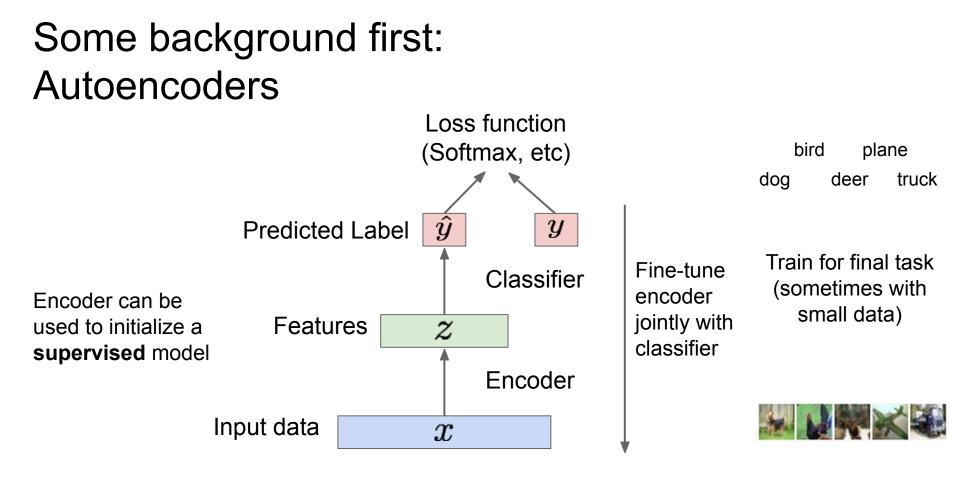


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Some background first: Autoencoders

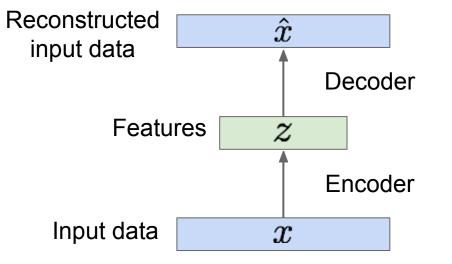


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Some background first: Autoencoders



Autoencoders can reconstruct data, and can learn features to initialize a supervised model

Features capture factors of variation in training data. Can we generate new images from an autoencoder?

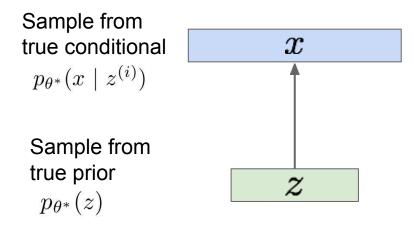
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Probabilistic spin on autoencoders - will let us sample from the model to generate data!

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Probabilistic spin on autoencoders - will let us sample from the model to generate data!

Assume training data $\{x^{(i)}\}_{i=1}^N$ is generated from underlying unobserved (latent) representation ${\bf z}$

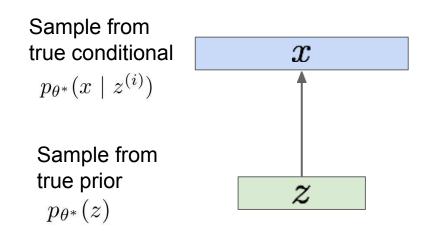


Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Probabilistic spin on autoencoders - will let us sample from the model to generate data!

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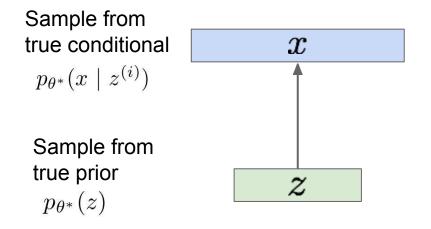


Intuition (remember from autoencoders!):x is an image, z is latent factors used to generate x: attributes, orientation, etc.

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

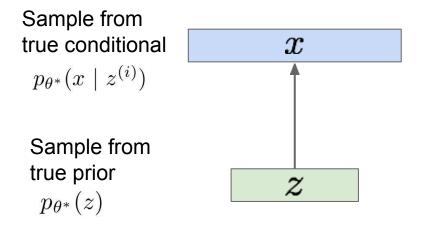
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We want to estimate the true parameters θ^* of this generative model.



Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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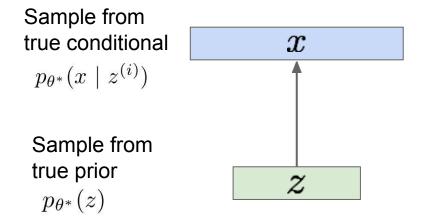


We want to estimate the true parameters θ^* of this generative model.

How should we represent this model?

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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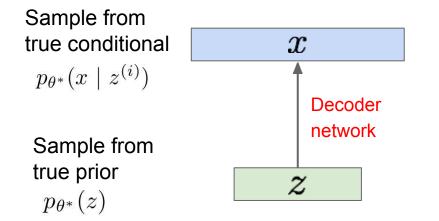
We want to estimate the true parameters θ^* of this generative model.

How should we represent this model?

Choose prior p(z) to be simple, e.g. Gaussian. Reasonable for latent attributes, e.g. pose, how much smile.

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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We want to estimate the true parameters θ^* of this generative model.

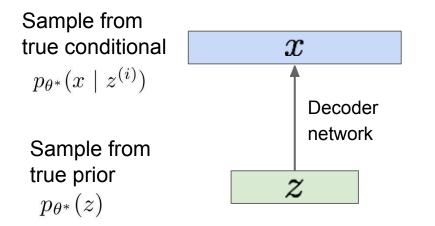
How should we represent this model?

Choose prior p(z) to be simple, e.g. Gaussian.

Conditional p(x|z) is complex (generates image) => represent with neural network

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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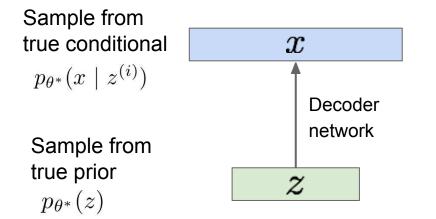


We want to estimate the true parameters θ^* of this generative model.

How to train the model?

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We want to estimate the true parameters θ^* of this generative model.

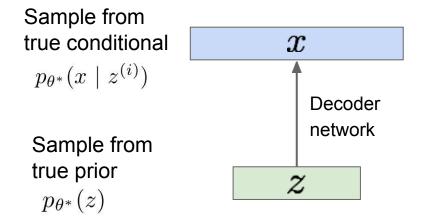
How to train the model?

Learn model parameters to maximize likelihood of training data

$$p_{\theta}(x) = \int p_{\theta}(z) p_{\theta}(x|z) dz$$

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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We want to estimate the true parameters θ^* of this generative model.

How to train the model?

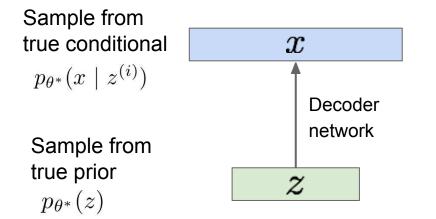
Learn model parameters to maximize likelihood of training data

$$p_{\theta}(x) = \int p_{\theta}(z) p_{\theta}(x|z) dz$$

Now with latent z

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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We want to estimate the true parameters θ^* of this generative model.

How to train the model?

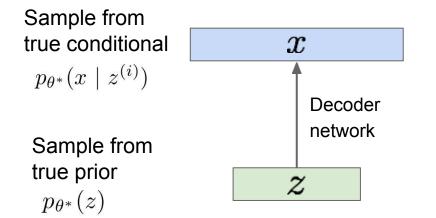
Learn model parameters to maximize likelihood of training data

$$p_{\theta}(x) = \int p_{\theta}(z) p_{\theta}(x|z) dz$$

Q: What is the problem with this?

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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We want to estimate the true parameters θ^* of this generative model.

How to train the model?

Learn model parameters to maximize likelihood of training data

 $p_{\theta}(x) = \int p_{\theta}(z) p_{\theta}(x|z) dz$ Q: What is the problem with this?

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Data likelihood: $p_{\theta}(x) = \int p_{\theta}(z) p_{\theta}(x|z) dz$

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Data likelihood:
$$p_{\theta}(x) = \int p_{\theta}(z) p_{\theta}(x|z) dz$$

Simple Gaussian prior

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Data likelihood: $p_{\theta}(x) = \int p_{\theta}(z)p_{\theta}(x|z)dz$

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Data likelihood:
$$p_{\theta}(x) = \int p_{\theta}(z) p_{\theta}(x|z) dz$$

Intractible to compute $p(x|z)$ for every z!

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Variational Autoencoders: Intractability :($p_{\theta}(x) = \int p_{\theta}(z)p_{\theta}(x|z)dz$

Posterior density also intractable: $p_{\theta}(z|x) = p_{\theta}(x|z)p_{\theta}(z)/p_{\theta}(x)$

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Variational Autoencoders: Intractability :(Data likelihood: $p_{\theta}(x) = \int p_{\theta}(z)p_{\theta}(x|z)dz$ Posterior density also intractable: $p_{\theta}(z|x) = p_{\theta}(x|z)p_{\theta}(z)/p_{\theta}(x)$ Intractable data likelihood

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Variational Autoencoders: Intractability :(Data likelihood: $p_{\theta}(x) = \int p_{\theta}(z)p_{\theta}(x|z)dz$ Posterior density also intractable: $p_{\theta}(z|x) = p_{\theta}(x|z)p_{\theta}(z)/p_{\theta}(x)$

Solution: In addition to decoder network modeling $p_{\theta}(x|z)$, define additional encoder network $q_{\phi}(z|x)$ that approximates $p_{\theta}(z|x)$

Will see that this allows us to derive a lower bound on the data likelihood that is tractable, which we can optimize

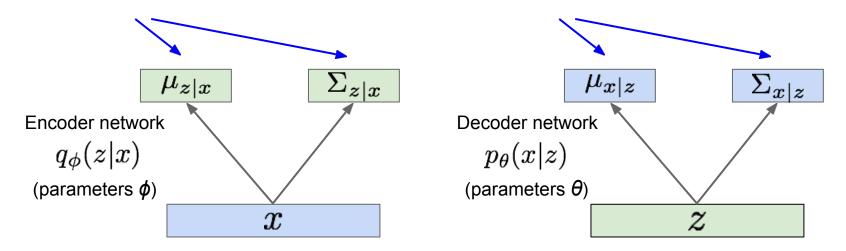
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Since we're modeling probabilistic generation of data, encoder and decoder networks are probabilistic

Mean and (diagonal) covariance of **z** | **x**

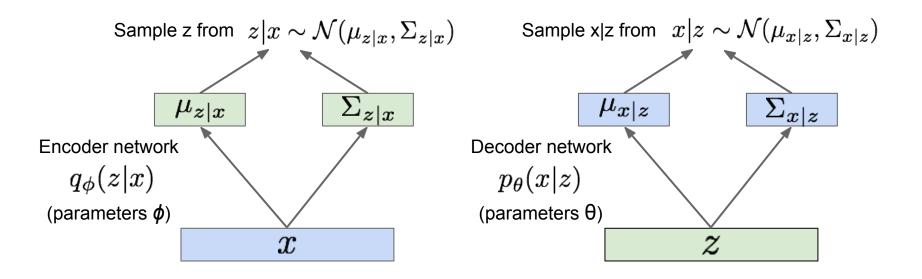
Mean and (diagonal) covariance of x | z



Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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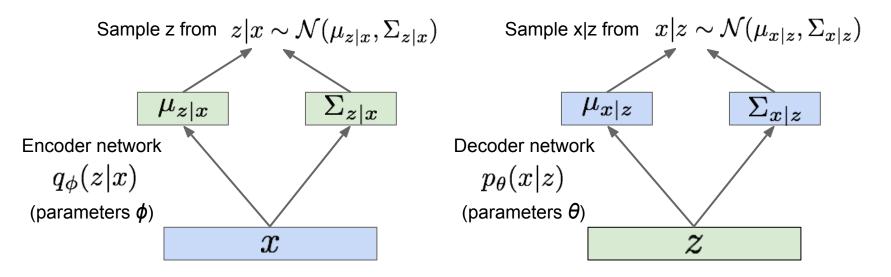
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Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Since we're modeling probabilistic generation of data, encoder and decoder networks are probabilistic



Encoder and decoder networks also called

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"recognition"/"inference" and "generation" networks

Now equipped with our encoder and decoder networks, let's work out the (log) data likelihood:

 $\log p_{\theta}(x^{(i)}) = \mathbf{E}_{z \sim q_{\phi}(z|x^{(i)})} \left[\log p_{\theta}(x^{(i)}) \right] \quad (p_{\theta}(x^{(i)}) \text{ Does not depend on } z)$

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Now equipped with our encoder and decoder networks, let's work out the (log) data likelihood:

 $\log p_{\theta}(x^{(i)}) = \mathbf{E}_{z \sim q_{\phi}(z|x^{(i)})} \left[\log p_{\theta}(x^{(i)}) \right] \quad (p_{\theta}(x^{(i)}) \text{ Does not depend on } z)$ Taking expectation wrt. z
(using encoder network) will
come in handy later

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$$\log p_{\theta}(x^{(i)}) = \mathbf{E}_{z \sim q_{\phi}(z|x^{(i)})} \left[\log p_{\theta}(x^{(i)}) \right] \quad (p_{\theta}(x^{(i)}) \text{ Does not depend on } z)$$
$$= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \right] \quad (\text{Bayes' Rule})$$

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$$\log p_{\theta}(x^{(i)}) = \mathbf{E}_{z \sim q_{\phi}(z|x^{(i)})} \left[\log p_{\theta}(x^{(i)}) \right] \quad (p_{\theta}(x^{(i)}) \text{ Does not depend on } z)$$
$$= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \right] \quad (\text{Bayes' Rule})$$
$$= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \frac{q_{\phi}(z \mid x^{(i)})}{q_{\phi}(z \mid x^{(i)})} \right] \quad (\text{Multiply by constant})$$

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Now equipped with our encoder and decoder networks, let's work out the (log) data likelihood:

$$\begin{split} \log p_{\theta}(x^{(i)}) &= \mathbf{E}_{z \sim q_{\phi}(z|x^{(i)})} \left[\log p_{\theta}(x^{(i)}) \right] & (p_{\theta}(x^{(i)}) \text{ Does not depend on } z) \\ &= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \right] & (\text{Bayes' Rule}) \\ &= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \frac{q_{\phi}(z \mid x^{(i)})}{q_{\phi}(z \mid x^{(i)})} \right] & (\text{Multiply by constant}) \\ &= \mathbf{E}_{z} \left[\log p_{\theta}(x^{(i)} \mid z) \right] - \mathbf{E}_{z} \left[\log \frac{q_{\phi}(z \mid x^{(i)})}{p_{\theta}(z)} \right] + \mathbf{E}_{z} \left[\log \frac{q_{\phi}(z \mid x^{(i)})}{p_{\theta}(z \mid x^{(i)})} \right] & (\text{Logarithms}) \end{split}$$

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$$\begin{split} \log p_{\theta}(x^{(i)}) &= \mathbf{E}_{z \sim q_{\phi}(z|x^{(i)})} \left[\log p_{\theta}(x^{(i)}) \right] \quad (p_{\theta}(x^{(i)}) \text{ Does not depend on } z) \\ &= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \right] \quad (\text{Bayes' Rule}) \\ &= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \frac{q_{\phi}(z \mid x^{(i)})}{q_{\phi}(z \mid x^{(i)})} \right] \quad (\text{Multiply by constant}) \\ &= \mathbf{E}_{z} \left[\log p_{\theta}(x^{(i)} \mid z) \right] - \mathbf{E}_{z} \left[\log \frac{q_{\phi}(z \mid x^{(i)})}{p_{\theta}(z)} \right] + \mathbf{E}_{z} \left[\log \frac{q_{\phi}(z \mid x^{(i)})}{p_{\theta}(z \mid x^{(i)})} \right] \quad (\text{Logarithms}) \\ &= \mathbf{E}_{z} \left[\log p_{\theta}(x^{(i)} \mid z) \right] - D_{KL}(q_{\phi}(z \mid x^{(i)}) || p_{\theta}(z)) + D_{KL}(q_{\phi}(z \mid x^{(i)}) || p_{\theta}(z \mid x^{(i)})) \end{split}$$

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Now equipped with our encoder and decoder networks, let's work out the (log) data likelihood:

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Now equipped with our encoder and decoder networks, let's work out the (log) data likelihood:

$$\log p_{\theta}(x^{(i)}) = \mathbf{E}_{z \sim q_{\phi}(z|x^{(i)})} \left[\log p_{\theta}(x^{(i)})\right] \quad (p_{\theta}(x^{(i)}) \text{ Does not depend on } z)$$

$$= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})}\right] \quad (\text{Bayes' Rule})$$

$$= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \frac{q_{\phi}(z \mid x^{(i)})}{q_{\phi}(z \mid x^{(i)})}\right] \quad (\text{Multiply by constant})$$

$$= \mathbf{E}_{z} \left[\log p_{\theta}(x^{(i)} \mid z)\right] - \mathbf{E}_{z} \left[\log \frac{q_{\phi}(z \mid x^{(i)})}{p_{\theta}(z)}\right] + \mathbf{E}_{z} \left[\log \frac{q_{\phi}(z \mid x^{(i)})}{p_{\theta}(z \mid x^{(i)})}\right] \quad (\text{Logarithms})$$

$$= \mathbf{E}_{z} \left[\log p_{\theta}(x^{(i)} \mid z)\right] - D_{KL}(q_{\phi}(z \mid x^{(i)}) \mid p_{\theta}(z)) + D_{KL}(q_{\phi}(z \mid x^{(i)}) \mid p_{\theta}(z \mid x^{(i)}))$$

$$\uparrow$$
This KL term (between Gaussians for encoder and z prior) has nice closed-form solution!
$$= \mathbf{E}_{z} \left[\operatorname{ust} we \text{ know KL divergence always} >= 0.$$

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Now equipped with our encoder and decoder networks, let's work out the (log) data likelihood:

$$\begin{split} \log p_{\theta}(x^{(i)}) &= \mathbf{E}_{z \sim q_{\phi}(z|x^{(i)})} \left[\log p_{\theta}(x^{(i)}) \right] \quad (p_{\theta}(x^{(i)}) \text{ Does not depend on } z) \\ &= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \right] \quad (\text{Bayes' Rule}) \\ &= \mathbf{E}_{z} \left[\log \frac{p_{\theta}(x^{(i)} \mid z)p_{\theta}(z)}{p_{\theta}(z \mid x^{(i)})} \frac{q_{\phi}(z \mid x^{(i)})}{q_{\phi}(z \mid x^{(i)})} \right] \quad (\text{Multiply by constant}) \\ &= \mathbf{E}_{z} \left[\log p_{\theta}(x^{(i)} \mid z) \right] - \mathbf{E}_{z} \left[\log \frac{q_{\phi}(z \mid x^{(i)})}{p_{\theta}(z)} \right] + \mathbf{E}_{z} \left[\log \frac{q_{\phi}(z \mid x^{(i)})}{p_{\theta}(z \mid x^{(i)})} \right] \quad (\text{Logarithms}) \\ &= \underbrace{\mathbf{E}_{z} \left[\log p_{\theta}(x^{(i)} \mid z) \right] - D_{KL}(q_{\phi}(z \mid x^{(i)}) \mid p_{\theta}(z))}_{\mathcal{L}(x^{(i)}, \theta, \phi)} + \underbrace{D_{KL}(q_{\phi}(z \mid x^{(i)}) \mid p_{\theta}(z \mid x^{(i)}))}_{\geq 0} \end{split}$$

Tractable lower bound which we can take gradient of and optimize! ($p_{\theta}(x|z)$ differentiable, KL term differentiable)

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Now equipped with our encoder and decoder networks, let's work out the (log) data likelihood:

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Now equipped with our encoder and decoder networks, let's work out the (log) data likelihood:

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Putting it all together: maximizing the likelihood lower bound

$$\underbrace{\mathbf{E}_{z}\left[\log p_{\theta}(x^{(i)} \mid z)\right] - D_{KL}(q_{\phi}(z \mid x^{(i)}) \mid\mid p_{\theta}(z))}_{\mathcal{L}(x^{(i)}, \theta, \phi)}$$

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Putting it all together: maximizing the likelihood lower bound

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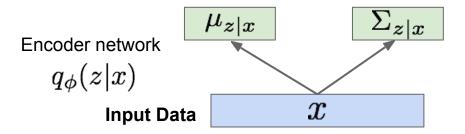
Let's look at computing the bound (forward pass) for a given minibatch of input data

> Input Data *x* Part 2 Feb 14, 2020

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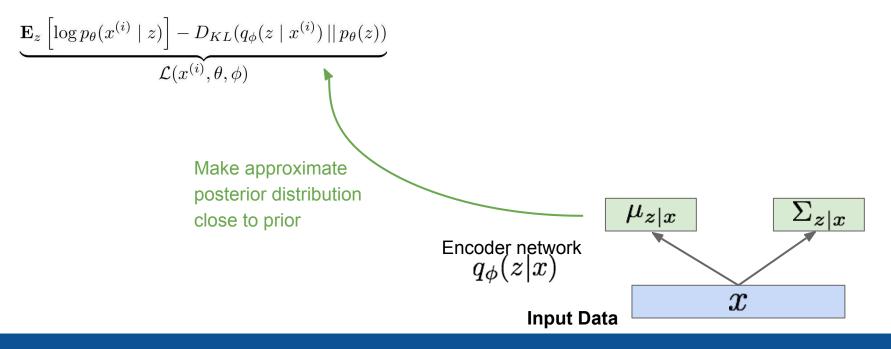
Putting it all together: maximizing the likelihood lower bound

$$\underbrace{\mathbf{E}_{z}\left[\log p_{\theta}(x^{(i)} \mid z)\right] - D_{KL}(q_{\phi}(z \mid x^{(i)}) \mid\mid p_{\theta}(z))}_{\mathcal{L}(x^{(i)}, \theta, \phi)}$$



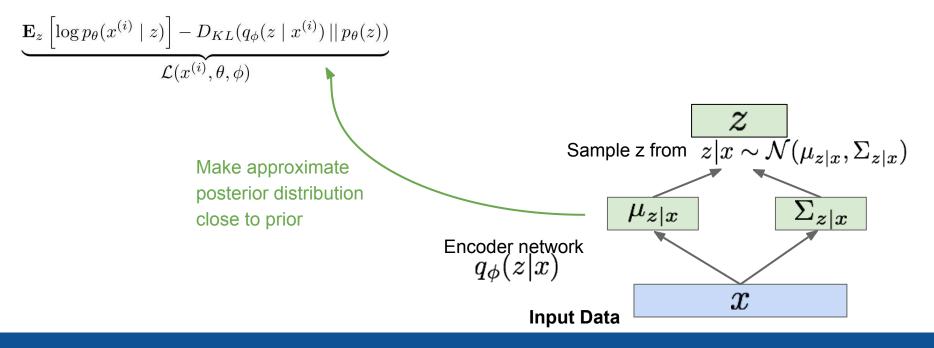
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Putting it all together: maximizing the likelihood lower bound



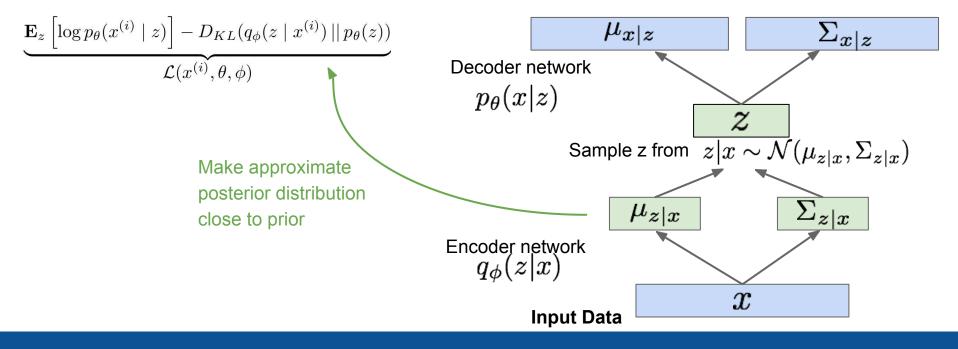
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Putting it all together: maximizing the likelihood lower bound

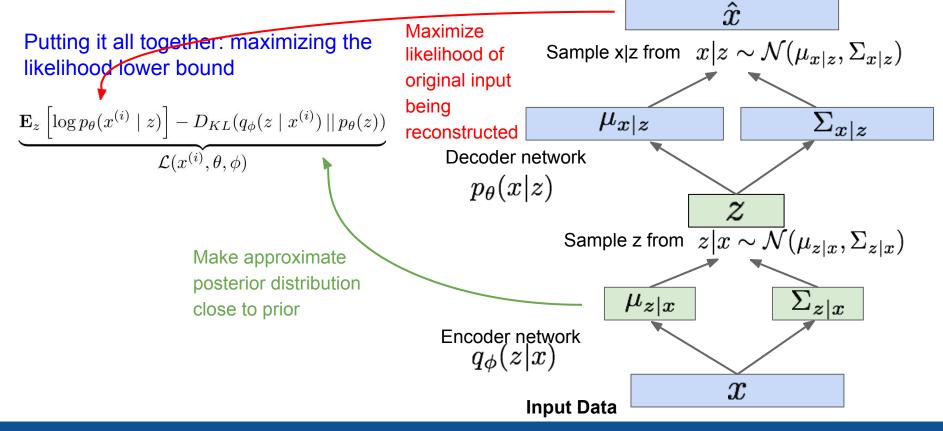


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Putting it all together: maximizing the likelihood lower bound

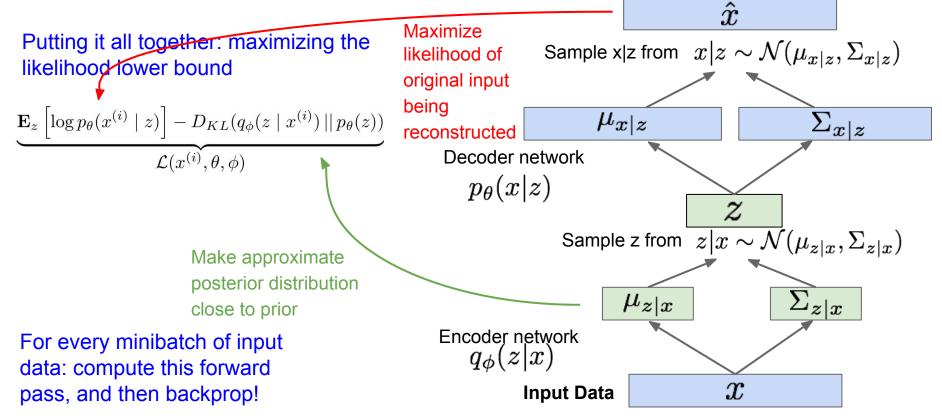


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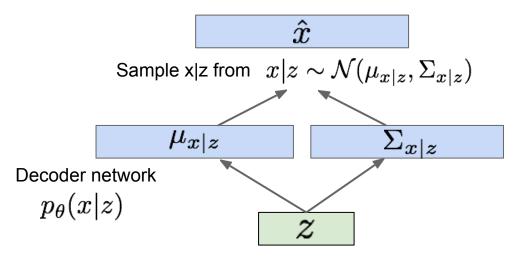
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Variational Autoencoders



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Use decoder network. Now sample z from prior!

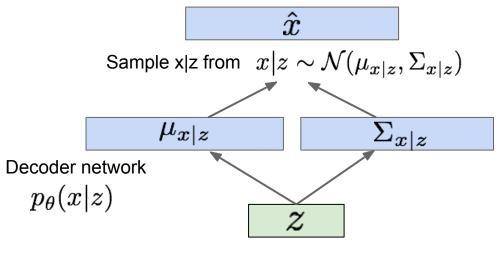


Sample z from $\, z \sim \mathcal{N}(0, I) \,$

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Use decoder network. Now sample z from prior!



Sample z from $\, z \sim \mathcal{N}(0, I) \,$

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Use decoder network. Now sample z from prior! Data manifold for 2-d z

Sample z from $\, z \sim \mathcal{N}(0, I) \,$

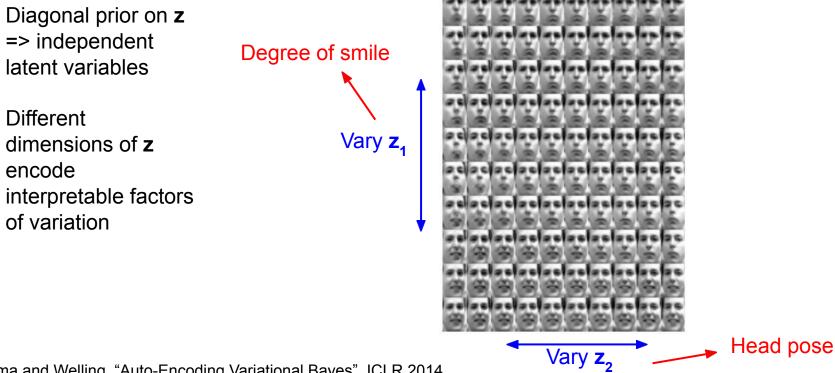
Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

666666666666666666 00000000 0 Vary z,

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Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Diagonal prior on z => independent Degree of smile latent variables Different Vary z, dimensions of z claciaciaciaciacia encode interpretable factors ela ela ela ela ela ela ela of variation elaclaciaciaciaci Also good feature representation that can be computed using $q_{\phi}(z|x)!$ Head pose Vary z,

Kingma and Welling, "Auto-Encoding Variational Bayes", ICLR 2014

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Labeled Faces in the Wild

32x32 CIFAR-10

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Variational Autoencoders in Genomics

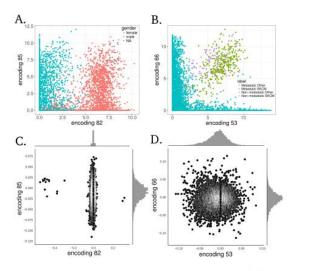


Fig. 3. Specific examples of Tybalt features capturing biological signals. (A) Encoding 82 stratified patient sex. (B) Together, encodings 53 and 66 separated melanoma tumors. Distributions of gene coefficients contributing to each plot above for (C) patient sex and (D) melanoma. The gene coefficients consist of the Tybalt learned weights for each feature encoding.

not Biocomputing 2018 Down 13/20. Re-use and distribut 70.27.238.24 A Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders

Gregory P. Way Genomics and Computational Biology Graduate Program, University of Pennsylvania, Philadelphia, PA 19104, USA E-mail: greguay@mail.med.upenn.edu

Casey S. Greene* Department of Systems Pharmacology and Translational Therapeutics University of Pennsylvania, Philadelphia, PA 19104, USA E-mail: csgreene@mail.med.upenn.edu

The Cancer Genome Atlas (TCGA) has profiled over 10,000 tumors across 33 different cancer-types for many genomic features, including gene expression levels. Gene expression measurements capture substantial information about the state of each tumor. Certain classes of deep neural network models are capable of learning a meaningful latent space. Such a latent space could be used to explore and generate hypothetical gene expression profiles under various types of molecular and genetic perturbation. For example, one might wish to use such a model to predict a tumor's response to specific therapies or to characterize complex gene expression activations existing in differential proportions in different tumors. Variational autoencoders (VAEs) are a deep neural network approach capable of generating meaningful latent spaces for image and text data. In this work, we sought to determine the extent to which a VAE can be trained to model cancer gene expression, and whether or not such a VAE would capture biologically-relevant features. In the following report, we introduce a VAE trained on TCGA pan-cancer RNA-seq data, identify specific patterns in the VAE encoded features, and discuss potential merits of the approach. We name our method "Tybalt" after an instigative, cat-like character who sets a cascading chain of events in motion in Shakespeare's "Romeo and Juliet". From a systems biology perspective, Tybalt could one day aid in cancer stratification or predict specific activated expression patterns that would result from genetic changes or treatment effects.

 $\mathit{Keywords}$: Deep Learning; Gene Expression; Variational Autoencoder, The Cancer Genome Atlas

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Variational Autoencoders in Genomics

They present a two-step VAE-based models for drug response prediction, which first predicts the post- from the pre-treatment state in an unsupervised manner, then extends it to the final semi-supervised prediction. The model is based on data from Genomics of Drug Sensitivity in Cancer (GDSC; Yang et al., 2013) and Cancer Cell Line Encyclopedia (CCLE; Barretina et al., 2012).

1706.08203v2 [stat.ML] 6 Jul 2017

Dr.VAE: Drug Response Variational Autoencoder

Abstract

We present two deep generative models based on Variational Autoencoders to improve the accuracy of drug response prediction. Our models, Perturbation Variational Autoencoder and its semi-supervised extension, Drug Response Variational Autoencoder (Dr.VAE), learn latent representation of the underlying gene states before and after drug application that depend on: (i) drug-induced biological change of each gene and (ii) overall treatment response outcome. Our VAE-based models outperform the current published benchmarks in the field by anywhere from 3 to 11% AUROC and 2 to 30% AUPR. In addition, we found that better reconstruction accuracy does not necessarily lead to improvement in classification accuracy and that jointly trained models perform better than models that minimize reconstruction error independently.

1 Introduction

Despite tremendous advances in the pharmaceutical industry, many patients worldwide do not respond to the first medication they are prescribed. Personalized medicine, an approach that uses patients' own genomic data, promises to tailor the treatment program to increase

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Variational Autoencoders

Probabilistic spin to traditional autoencoders => allows generating data Defines an intractable density => derive and optimize a (variational) lower bound

Pros:

- Principled approach to generative models
- Allows inference of q(z|x), can be useful feature representation for other tasks

Cons:

- Maximizes lower bound of likelihood
- Samples blurrier and lower quality compared to state-of-the-art (GANs)

Active areas of research:

- More flexible approximations, e.g. richer approximate posterior instead of diagonal Gaussian

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- Incorporating structure in latent variables

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Generative Adversarial Networks (GAN)

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Generative Adversarial Networks (GAN)

GANs don't work with any explicit density function! What they care the most, is the samples which are close to real data (ie. learn to generate from training distribution through 2-player game)

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Generative Adversarial Networks

lan Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Problem: Want to sample from complex, high-dimensional training distribution. No direct way to do this!

Solution: Sample from a simple distribution, e.g. random noise. Learn transformation to training distribution.

Q: What can we use to represent this complex transformation?

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Generative Adversarial Networks

lan Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

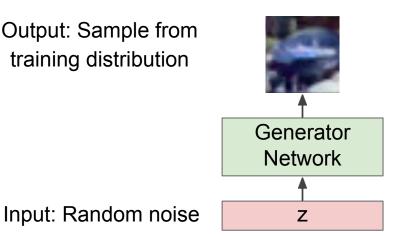
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Problem: Want to sample from complex, high-dimensional training distribution. No direct way to do this!

Solution: Sample from a simple distribution, e.g. random noise. Learn transformation to training distribution.

Q: What can we use to represent this complex transformation?

A: A neural network!



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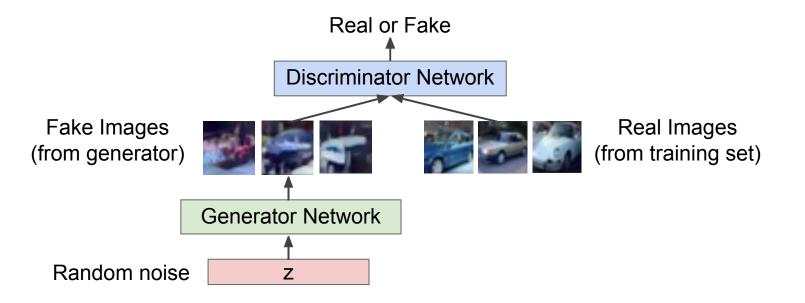
Ian Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Generator network: try to fool the discriminator by generating real-looking images (or DNAs, etc) **Discriminator network**: try to distinguish between real and fake images (or DNAs, etc)

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lan Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Generator network: try to fool the discriminator by generating real-looking images **Discriminator network**: try to distinguish between real and fake images



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Ian Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Generator network: try to fool the discriminator by generating real-looking images **Discriminator network**: try to distinguish between real and fake images

Train jointly in minimax game

Minimax objective function:

$$\min_{\theta_g} \max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$

Ian Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

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Generator network: try to fool the discriminator by generating real-looking images **Discriminator network**: try to distinguish between real and fake images

Train jointly in minimax game

Discriminator outputs likelihood in (0,1) of real image

Minimax objective function:

$$\min_{\theta_g} \max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$
Discriminator output for for real data x generated fake data G(z)

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lan Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Generator network: try to fool the discriminator by generating real-looking images **Discriminator network**: try to distinguish between real and fake images

Train jointly in **minimax game**

Discriminator outputs likelihood in (0,1) of real image

Minimax objective function:

$$\min_{\theta_g} \max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$
Discriminator output for for real data x generated fake data G(z)

- Discriminator (θ_d) wants to **maximize objective** such that D(x) is close to 1 (real) and D(G(z)) is close to 0 (fake)
- Generator (θ_g) wants to **minimize objective** such that D(G(z)) is close to 1 (discriminator is fooled into thinking generated G(z) is real)

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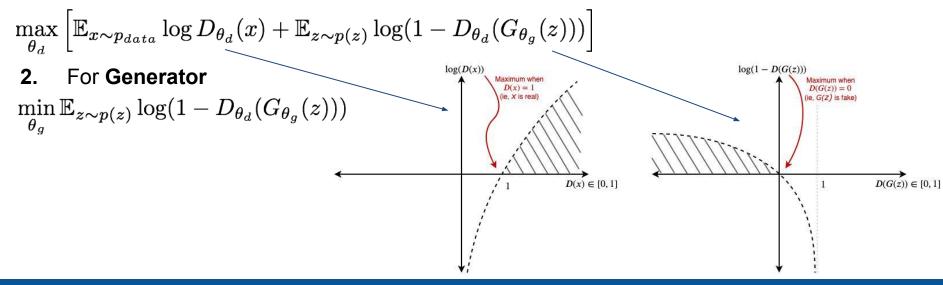
lan Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Minimax objective function:

$$\min_{\theta_g} \max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$

Alternate between:

1. For Discriminator



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$\min_{\theta_g} \max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$

Alternate between:

1. For **Discriminator**

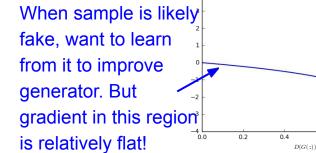
Minimax objective function:

$$\max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$

2. For Generator

$$\min_{\theta_g} \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z)))$$

In practice, optimizing this generator objective does not work well!



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lan Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Gradient signal

where sample is

already good

0.6

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dominated by region

 $\log(1 - D(G(z)))$

0.8

1.0

Training GANs: Two-player game

Ian Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Minimax objective function:

$$\min_{\theta_g} \max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$

Alternate between:

1. For Discriminator

$$\max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$

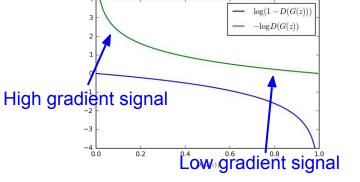
2. For Generator

different objective

$$\max_{\theta_g} \mathbb{E}_{z \sim p(z)} \log(D_{\theta_d}(G_{\theta_g}(z)))$$

Instead of minimizing likelihood of discriminator being correct, now maximize likelihood of discriminator being wrong. Same objective of fooling discriminator, but now higher gradient signal for bad samples => works much better! Standard in practice.

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Ian Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Minimax objective function:

$$\min_{\theta_g} \max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$

Alternate between:

1. For Discriminator

$$\max_{\theta_d} \left[\mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$

2. For Generator

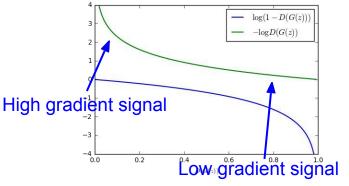
different objective

$$\max_{\theta_g} \mathbb{E}_{z \sim p(z)} \log(D_{\theta_d}(G_{\theta_g}(z)))$$

Instead of minimizing likelihood of discriminator being correct, now maximize likelihood of discriminator being wrong. Same objective of fooling discriminator, but now higher gradient signal for bad samples => works much better! Standard in practice.

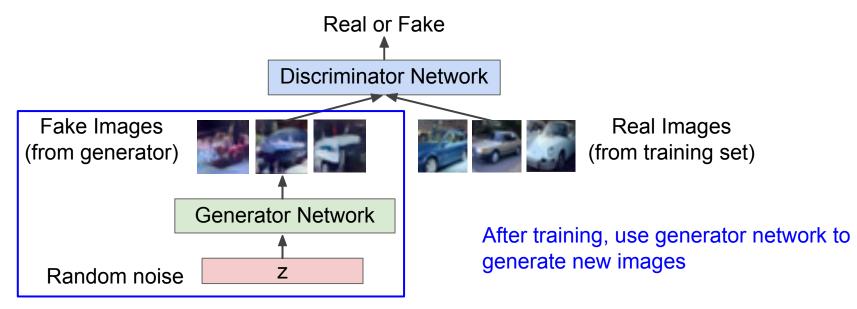
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Aside: Jointly training two networks is challenging, can be unstable. Choosing objectives with better loss landscapes helps training, is an active area of research.



lan Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

Generator network: try to fool the discriminator by generating real-looking images **Discriminator network**: try to distinguish between real and fake images



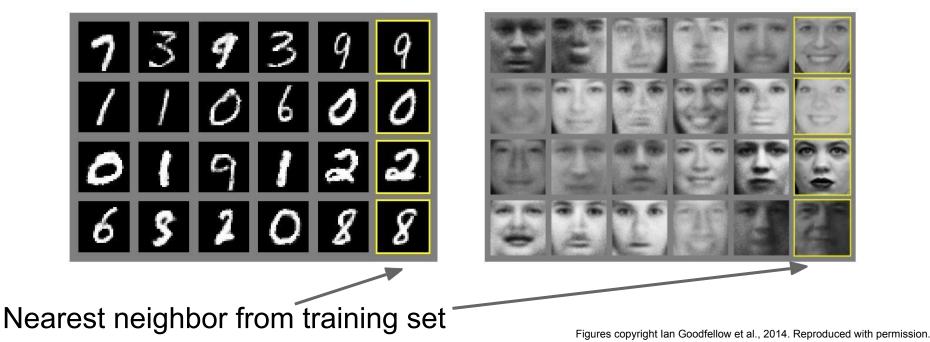
Fake and real images copyright Emily Denton et al. 2015. Reproduced with permission.

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Ian Goodfellow et al., "Generative Adversarial Nets", NIPS 2014

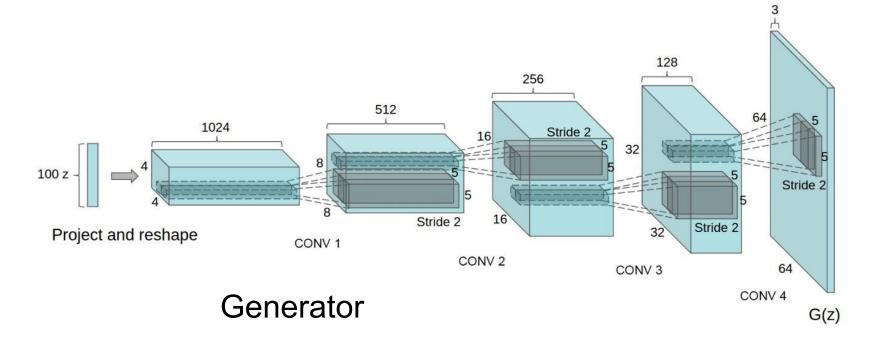
Generative Adversarial Nets

Generated samples



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Generative Adversarial Nets: Convolutional Architectures



Radford et al, "Unsupervised Representation Learning with Deep Convolutional Generative Adversarial Networks", ICLR 2016

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Generative Adversarial Nets: Convolutional Architectures

Samples from the model look amazing!



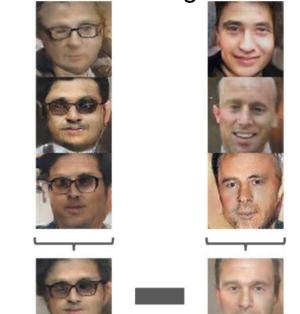
Radford et al,

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Generative Adversarial Nets: Interpretable Vector Math

Glasses man

No glasses manNo glasses woman





Radford et al,

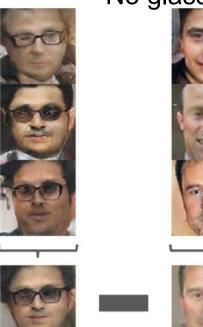
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Generative Adversarial Nets: Interpretable Vector Math

Glasses man

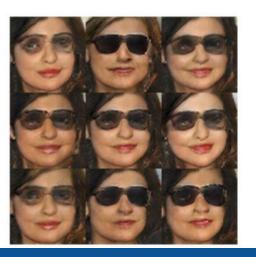
No glasses manNo glasses woman

Radford et al, ICLR 2016





Woman with glasses



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Better training and generation





(a) Church outdoor.



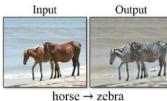


(c) Kitchen. (d) Conference room. LSGAN. Mao et al. 2017.



BEGAN. Bertholet et al. 2017.

Source->Target domain transfer



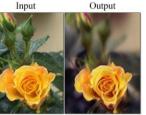


 $zebra \rightarrow horse$





CycleGAN. Zhu et al. 2017.





→ summer Yosemite



Text -> Image Synthesis

this small bird has a pink breast and crown, and black almost all black with a red primaries and secondaries.

this magnificent fellow is crest, and white cheek patch.





Reed et al. 2017.

Many GAN applications





Pix2pix. Isola 2017. Many examples at https://phillipi.github.io/pix2pix/

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Generative Adversarial Nets in Genomics

a)

Generating and designing DNA with deep generative models

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Abstract

We propose generative neural network methods to generate DNA sequences and tune them to have desired properties. We present three approaches: creating synthetic DNA sequences using a generative adversarial network (GAN); a DNAbased variant of the activation maximization ("deep dream") design method; and a joint procedure which combines these two approaches together. We show that these tools capture important structures of the data and, when applied to designing probes for protein binding microarrays (PBMs), allow us to generate new sequences whose properties are estimated to be superior to those found in the training data. We believe that these results open the door for applying deep generative models to advance genomics research.

1 Introduction

A major trend in deep learning is the development of new generative methods, with the goal of creating synthetic data with desired structures and properties. This trend includes generative models such as generative adversarial networks (GANs) [1], variational autoencoders (VAEs) [2], and deep autoregressive models [3, 4], as well as generative design procedures like activation maximization (popularly known as "deep dream") [5–7] and style transfer [8]. These powerful generative tools bring many new opportunities. When data is costly, we can use a generative method to inexpensively simulate data. We can also use generative tools to explore the space of possible data configurations, tuning the generated data to have specific target properties, or to invent novel, unseen configurations



b) TGAGAGTGATGTATT<mark>CGAATTGA</mark>TGCCTCACCTCTGCTTGCAGACTGTCA **GGAATGAA**CTGGGGAGACAGGCCCAGA<mark>GGAATTGA</mark>GAAAGTAATGAGCAC GCCCTG<mark>CGTTTTAA</mark>GAAATACTGTTGCATCAGGGCAAATGTAAGATTTTG TTTTGTTTGAGATCTGTGGGGGTATGCT<mark>GGAATTAA</mark>AGTCTGGACTACCAC CTGATACTGAATGCAGATTTGAAGAACAAAG<mark>CGTATTAA</mark>AACACATGCTT GATCCCCAAGTGT<mark>GGAATTGA</mark>GAAGGAAGCTGGAGAATCCCCAAACTCTG CAGCCACATCAGCTTACCTAA<mark>GGAAGTGA</mark>TGTGTTTTAAAACCAGCTTTG TAGAATTTTTCTT<u>GGTATTAA</u>TGATGATCTAGGCTTACACAGGGACATCA GACATTGCTTAGTCTGAGGGGATACAGTGGGGGAGTG<mark>GGTATTAA</mark>AATCTCC ACATGCCTGAGACATTCCTGCTCTTGAATCTGA<mark>GGAATTAT</mark>GCTTAATCC

Figure 7: Motif-matching experiment: a) Sequence logo for the PWM detected by the predictor. Letter heights reflect their relative frequency at each position. Sequences which have a strong match with this motif will score highly. b) Sample sequences tuned to have a high predictor score. The boxes indicate strong motif matches for each sequence.

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Generative Adversarial Nets in Genomics

Bioinformatics, 34, 2018, i603–i611 doi: 10.1093/bioinformatics/bty563 ECCB 2018

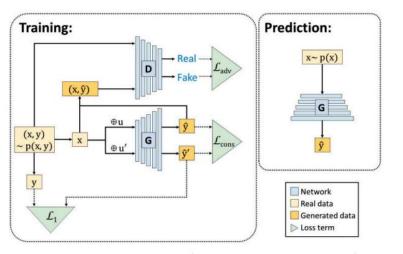


Fig. 1. Illustration of GGAN architecture and its loss functions. We use $(\mathbf{x}, \mathbf{y}) \in \mathbb{R}^{l+t}$ to denote a gene expression profile, where $\mathbf{x} \in \mathbb{R}^l$ corresponds to the landmark genes and $\mathbf{y} \in \mathbb{R}^l$ represents the target genes. Our goal is to learn a generator function G which takes \mathbf{x} as the input and output $\hat{\mathbf{y}}$ as the prediction of the target genes construct an appropriate prediction function G, we consider three loss terms in our model: \mathcal{L}_{cons} , \mathcal{L}_{adv} and \mathcal{L}_1 . \mathcal{L}_{cons} measures the consist- ency of the prediction from G when the input \mathbf{x} is perturbed by random noise \mathbf{u} and \mathbf{u}' . \mathcal{L}_1 measures the difference between the prediction vector $\hat{\mathbf{y}}$ and the ground truth \mathbf{y} . For the term \mathcal{L}_{adv} , we construct a discriminator D which takes both (\mathbf{x}, \mathbf{y}) and $(\mathbf{x}, \hat{\mathbf{y}})$ as the input. The discriminator D tries to distinguish the real' sample (\mathbf{x}, \mathbf{y}) from the 'fake' sample $(\mathbf{x}, \hat{\mathbf{y}})$ while the G tries to predict the realistic $\hat{\mathbf{y}}$ vector to fool the discriminator. \mathcal{L}_{adv} measures the adversarial loss in the game between the generator G and discriminator D

Conditional generative adversarial network for gene expression inference

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[†]The authors wish it to be known that, in their opinion, the first two authors should be regarded as Joint First Authors.

Abstract

Motivation: The rapid progress of gene expression profiling has facilitated the prosperity of recent biological studies in various fields, where gene expression data characterizes various cell conditions and regulatory mechanisms under different experimental circumstances. Despite the widespread application of gene expression profiling and advances in high-throughput technologies, profiling in genome-wide level is still expensive and difficult. Previous studies found that high correlation exists in the expression pattern of different genes, such that a small subset of genes can be informative to approximately describe the entire transcriptome. In the Library of Integrated Network-based Cell-Signature program, a set of ~1000 landmark genes have been identified that contain ~80% information of the whole genome and can be used to predict the expression of landmark genes and then infer the expression of other target genes via linear models. However, linear models do not have the capacity to capture the non-linear associations in gene regulatory networks.

Results: As a flexible model with high representative power, deep learning models provide an alternate to interpret the complex relation among genes. In this paper, we propose a deep learning architecture for the inference of target gene expression profiles. We construct a novel conditional generative adversarial network by incorporating both the adversarial and ℓ_1 -norm loss terms in our model. Unlike the smooth and blurry predictions resulted by mean squared error objective, the coupled adversarial and ℓ_1 -norm loss function leads to more accurate and sharp predictions. We validate our method under two different settings and find consistent and significant improvements over all the comparing methods.

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"The GAN Zoo"

- GAN Generative Adversarial Networks
- 3D-GAN Learning a Probabilistic Latent Space of Object Shapes via 3D Generative-Adversarial Modeling
- acGAN Face Aging With Conditional Generative Adversarial Networks
- AC-GAN Conditional Image Synthesis With Auxiliary Classifier GANs
- AdaGAN AdaGAN: Boosting Generative Models
- AEGAN Learning Inverse Mapping by Autoencoder based Generative Adversarial Nets
- AffGAN Amortised MAP Inference for Image Super-resolution
- AL-CGAN Learning to Generate Images of Outdoor Scenes from Attributes and Semantic Layouts
- ALI Adversarially Learned Inference
- AM-GAN Generative Adversarial Nets with Labeled Data by Activation Maximization
- AnoGAN Unsupervised Anomaly Detection with Generative Adversarial Networks to Guide Marker Discovery
- ArtGAN ArtGAN: Artwork Synthesis with Conditional Categorial GANs
- b-GAN b-GAN: Unified Framework of Generative Adversarial Networks
- Bayesian GAN Deep and Hierarchical Implicit Models
- BEGAN BEGAN: Boundary Equilibrium Generative Adversarial Networks
- BiGAN Adversarial Feature Learning
- BS-GAN Boundary-Seeking Generative Adversarial Networks
- CGAN Conditional Generative Adversarial Nets
- CaloGAN CaloGAN: Simulating 3D High Energy Particle Showers in Multi-Layer Electromagnetic Calorimeters
 with Generative Adversarial Networks
- CCGAN Semi-Supervised Learning with Context-Conditional Generative Adversarial Networks
- CatGAN Unsupervised and Semi-supervised Learning with Categorical Generative Adversarial Networks
- CoGAN Coupled Generative Adversarial Networks

- Context-RNN-GAN Contextual RNN-GANs for Abstract Reasoning Diagram Generation
- · C-RNN-GAN C-RNN-GAN: Continuous recurrent neural networks with adversarial training
- CS-GAN Improving Neural Machine Translation with Conditional Sequence Generative Adversarial Nets
- CVAE-GAN CVAE-GAN: Fine-Grained Image Generation through Asymmetric Training
- CycleGAN Unpaired Image-to-Image Translation using Cycle-Consistent Adversarial Networks
- DTN Unsupervised Cross-Domain Image Generation
- DCGAN Unsupervised Representation Learning with Deep Convolutional Generative Adversarial Networks
- DiscoGAN Learning to Discover Cross-Domain Relations with Generative Adversarial Networks
- DR-GAN Disentangled Representation Learning GAN for Pose-Invariant Face Recognition
- DualGAN DualGAN: Unsupervised Dual Learning for Image-to-Image Translation
- EBGAN Energy-based Generative Adversarial Network
- f-GAN f-GAN: Training Generative Neural Samplers using Variational Divergence Minimization
- FF-GAN Towards Large-Pose Face Frontalization in the Wild
- GAWWN Learning What and Where to Draw
- GeneGAN GeneGAN: Learning Object Transfiguration and Attribute Subspace from Unpaired Data
- Geometric GAN Geometric GAN
- GoGAN Gang of GANs: Generative Adversarial Networks with Maximum Margin Ranking
- GP-GAN GP-GAN: Towards Realistic High-Resolution Image Blending
- IAN Neural Photo Editing with Introspective Adversarial Networks
- iGAN Generative Visual Manipulation on the Natural Image Manifold
- IcGAN Invertible Conditional GANs for image editing
- ID-CGAN Image De-raining Using a Conditional Generative Adversarial Network
- Improved GAN Improved Techniques for Training GANs
- InfoGAN InfoGAN: Interpretable Representation Learning by Information Maximizing Generative Adversarial Nets
- LAGAN Learning Particle Physics by Example: Location-Aware Generative Adversarial Networks for Physics
 Synthesis
- LAPGAN Deep Generative Image Models using a Laplacian Pyramid of Adversarial Networks

https://github.com/hindupuravinash/the-gan-zoo

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Now, it's time to practice...

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