10707 Deep Learning: Spring 2021

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Lecture 8:

Intro to unsupervised learning

Recap: unsupervised learning

Unsupervised learning

"Pure" Reinforcement Learning (cherry)

- The machine predicts a scalar reward given once in a while.
- A few bits for some samples

Supervised Learning (icing)

- The machine predicts a category or a few numbers for each input
- Predicting human-supplied data
- 10→10,000 bits per sample

Unsupervised/Predictive Learning (cake)

- The machine predicts any part of its input for any observed part.
- Predicts future frames in videos
- Millions of bits per sample
 - (Yes, I know, this picture is slightly offensive to RL folks. But I'll make it up)



Unsupervised learning

Learning from data without labels.

What can we hope to do:

Task A: Fit a parametrized **structure** (e.g. clustering, low-dimensional subspace, manifold) to data to reveal something meaningful about data. (**Structure learning**)

Task B: Learn a (parametrized) **distribution** *close* to data generating distribution. (**Distribution learning**)

Task C: Learn a (parametrized) distribution that implicitly reveals an "embedding"/"representation" of data for downstream tasks. (Representation/feature learning)

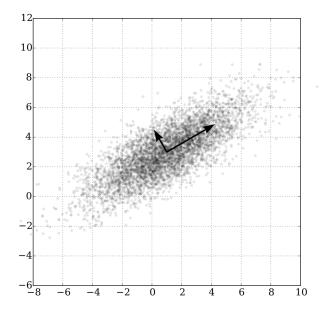
Entangled! The "structure" and "distribution" often reveals an embedding.

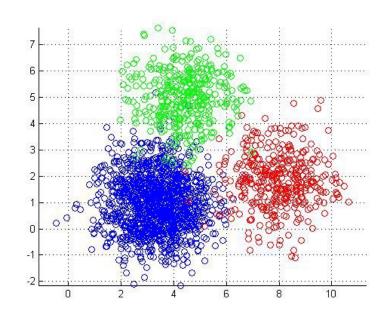
Structure learning

Fit a parametrized **structure** (e.g. clustering, low-dimensional subspace) to data to reveal something meaningful about data.

PCA(principal component analysis), direction of highest variance

Clustering

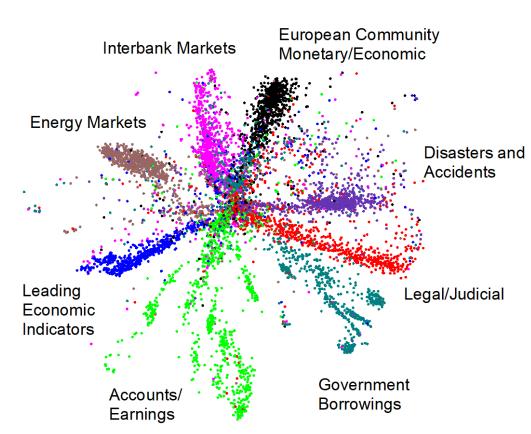




Structure learning

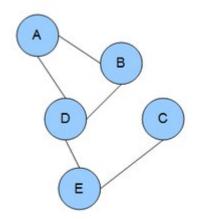


804,414 newswire stories



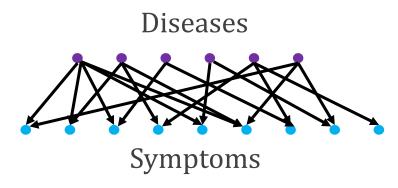
Some typical choices of parametrized distributions:

Classical choices: fully-observed graphical models (undirected and directed), latent-variable graphical models (mixture models, sparse coding, topic models).



Markov Random Fields:

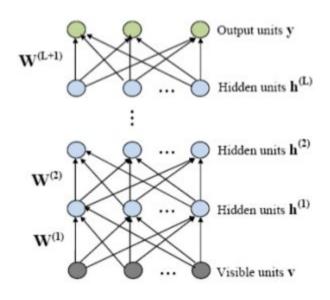
sparse independence structure: "A is independent of other vars, given B, D"



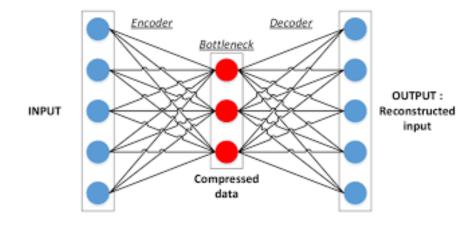
Latent variable models: data is "simple" conditioned on some unobserved (latent) variables

Some typical choices of parametrized distributions:

Semi-modern choices: deep Boltzmann machines, deep belief networks, (variational) auto-encoders, energy models.



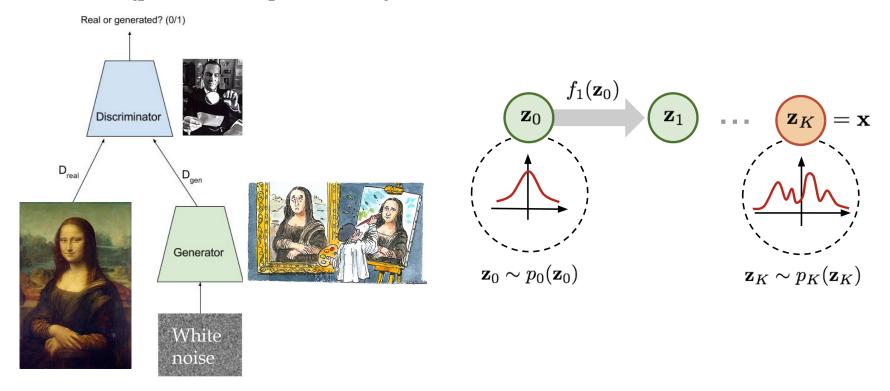
Deep Boltzmann machines, belief networks: graphical model analogues of deep neural networks.



(Variational) autoencoders: model data by enforcing a latent space "bottleneck:

Some typical choices of parametrized distributions:

Modern choices: generative adversarial networks, autoregressive models (pixelRNN, pixelCNN), flow models, etc.





Training
Data(CelebA)

Model Samples (Karras et.al., 2018)

4 years of progression on Faces







Brundage et al., 2017



Which face is real. com



BigGAN, Brock et al '18

Conditional generative model P(zebra images | horse images)



Style Transfer



Input Image



Monet



Van Gogh

Zhou el al., Cycle GAN 2017

Source actor



Real-time reenactment

Target actor

Representation learning and selfsupervised learning

Given unlabeled data, design supervised tasks that induce a good representation for downstream tasks.

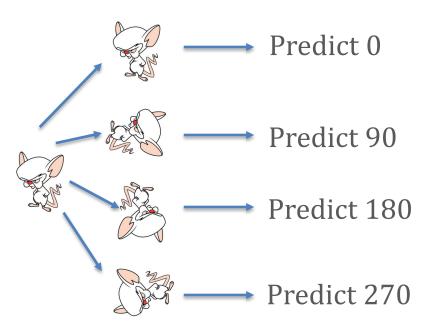
No good mathematical formalization, but the intuition is to "force" the predictor used in the task to learn something "semantically meaningful" about the data.

Examples in NLP: predict next word, given previous 5 words; predict middle word, given surrounding 5 words; etc.

Representation learning and selfsupervised learning

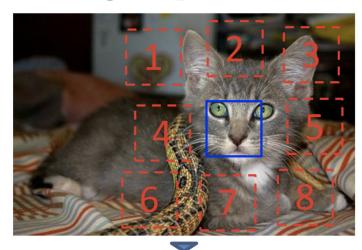
Examples in vision: a lot, and quite different in nature.

Rotation prediction



Predict one of four angles an image is rotated by

Jigsaw puzzles



Predict position of second piece wrt to first

Relationships between the tasks

Structure learning and feature learning often blend

E.g. low dimensional features in PCA or cluster a point belongs to in clustering can be viewed as features.

Structure learning/feature learning is in general weaker than distribution learning:

E.g. methods like PCA/clustering can't be used to generate new samples.

Feature, not a bug: it has been argued that self-supervised learning works because the task we are solving is easier (both computationally and statistically)

Relationships between the tasks

Distribution learning often implies representation learning:

Many distributions we fit are **latent-variable** models (i.e. model the joint distribution between some latent variables \mathbf{h} and the observed data \mathbf{x})

$$P_{\theta}(x,h) = P_{\theta}(h)P_{\theta}(x|h)$$

The latent variables are often viewed as a "representation".

The **posterior** distribution $P_{\theta}(h|x)$ captures a distribution over representations, given some values of the observed data.

However, a-priori, distribution $P_{\theta}(h|x)$ is a-priori not an easy distribution to **approximate/sample** from!

$$P_{\theta}(h|x) = \frac{P_{\theta}(x|h)p(h)}{\int_{h'} p(h')p(x|h')} Hard high-dimensional sum/integral$$

Common ways to get a handle of $P_{\theta}(h|x)$: variational methods and MCMC methods.

Question: how accurately do we need to approximate $P_{\theta}(h|x)$ if we want a good representation?

(Arora-Risteski blogpost: http://www.offconvex.org/2017/06/26/unsupervised1/)

Answer: Let $Q_{\theta}(h|x)$ be an approximation of $P_{\theta}(h|x)$ s.t.

$$KL(Q_{\theta}(h|x) \mid P_{\theta}(h|x)) \le \epsilon$$

(KL is a natural metric, as a lot of the variational methods operate in this metric. Stay tuned!)

(Recall the definition of KL divergence: $KL(q || p) = \mathbb{E}_q \log \left(\frac{q}{p}\right)$)

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Suppose the way we will use the representation h is to solve **classification tasks.** Namely, let's say the labels for task are:

$$(x_t, c(h_t))$$
, where $(h_t, x_t) \sim P_{\theta}(h, x)$ and $c(h_t) \in \{\pm 1\}$

In other words, the labels are a function of the **latent** variables, and the observables are the data.

Let $Q_{\theta}(h|x)$ be an approximation of $P_{\theta}(h|x)$ s.t.

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Suppose the way we will use the representation h is to solve classification tasks. Namely, let's say the binary classification task is:

$$(x_t, c(h_t))$$
, where $(h_t, x_t) \sim P_{\theta}(h, x)$ and $c(h_t) = \{\pm 1\}$

The natural way to measure the distance with an eye towards classification tasks is total variation distance:

$$\left[TV(Q_{\theta}(\cdot \mid x) \mid \mid P_{\theta}(\cdot \mid x)) = \sup_{\Omega} \left| \Pr_{h \sim Q_{\theta}(\cdot \mid x)} [\Omega] - \Pr_{h \sim P_{\theta}(\cdot \mid x)} [\Omega] \right|$$

Why is this useful? Take $\Omega = \{ \text{"C(h)} \text{ is the correct label"} \}$

 $\Pr_{h \sim Q_{\theta}(\cdot|x)}[\Omega]$ is the probability of having the correct answer using $Q_{\theta}(\cdot|x)$

 $\begin{vmatrix} \Pr_{h \sim Q_{\theta}(\cdot|x)}[\Omega] - \Pr_{h \sim P_{\theta}(\cdot|x)}[\Omega] \end{vmatrix}$ is the *difference in probability* of having the correct answer between $Q_{\theta}(\cdot|x)$!

Let $Q_{\theta}(h|x)$ be an approximation of $P_{\theta}(h|x)$ s.t.

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Hence, $TV(Q_{\theta}(\cdot | x) | P_{\theta}(\cdot | x)) \le \epsilon'$ implies that the difference in performance b/w using $P_{\theta}(\cdot | x)$ and $Q_{\theta}(\cdot | x)$ is at most ϵ' (on the input sample x)

Hence, $\mathbb{E}_x[TV(Q_\theta(\cdot|x)||P_\theta(\cdot|x))] \le \epsilon'$ implies that the difference in performance on the classification task is at most ϵ' .

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To conclude, by Pinsker's inequality, we have

$$TV(Q_{\theta}(\cdot \mid x) \mid \mid P_{\theta}(\cdot \mid x)) \leq \sqrt{\frac{1}{2}KL(Q_{\theta}(\cdot \mid x) \mid \mid P_{\theta}(\cdot \mid x))} \leq \sqrt{\frac{1}{2}\epsilon}$$

So, if we want a good performance on classification task, we need an extremely close approximation to the posterior!

The classic unsupervised structure learning-methods

Figure 1: Population structure within Europe.

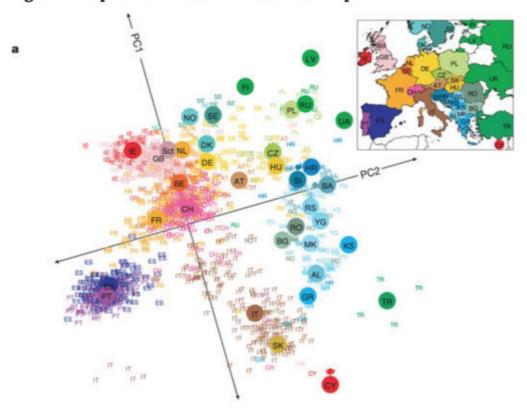


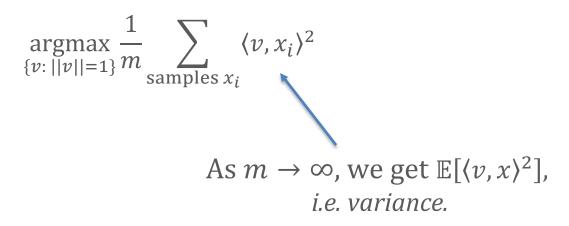
Figure 6: Plot from [1], depicting genomes for 1387 Europeans projected onto top 2 principal components. Colors/labels of datapoints correspond to geographic location of the individuals. Map of Europe (with same coloring) included in upper right for reference.

Novembre et al '08

Goal: find a k-dimensional (linear) subspace explaining most of the variance in the data.

Assume the data is centered, that is $\mathbb{E}[x] = 0$

Warmup: let k=1.



Goal: find a k-dimensional (linear) subspace explaining most of the variance in the data.

$$\underset{\{v_1, v_2, \dots, v_k\}}{\operatorname{argmax}} \frac{1}{m} \sum_{\text{samples } x_i} \left(\text{length of } \mathbf{x_i} \text{ on } \operatorname{span}(v_1, v_2, \dots, v_k) \right)^2$$

$$= \underset{\text{orthonormal } \{v_1, v_2, \dots, v_k\}}{\operatorname{argmax}} \frac{1}{m} \sum_{\text{samples } x_i} \sum_{j=1}^{k} \langle x_i, v_j \rangle^2$$

As
$$m \to \infty$$
, we get $\mathbb{E}[\sum_{j} \langle v_j, x \rangle^2]$

How to do this efficiently?

$$\underset{\text{orthonormal }\{v_1, v_2, \dots, v_k\}}{\operatorname{argmax}} \frac{1}{m} \sum_{\text{samples } x_i} \sum_{j=1}^k \langle x_i, v_j \rangle^2$$

A convenient rewrite:

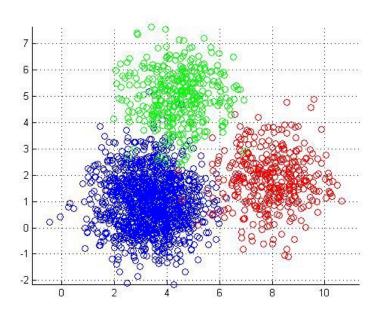
$$\underset{\text{orthonormal }\{v_1, v_2, \dots, v_k\}}{\operatorname{argmax}} \sum_{j=1}^k v_j^T \left(\frac{1}{m} \sum_{\text{samples } x_i} \left(x_i x_i^T\right)\right) v_j$$

$$\coloneqq D, \text{ (covariance matrix)}$$

How to do this efficiently? - Singular Value Decomposition!!

Argmax are the **top k eigenvectors** of D

The classics: clustering



Goal: group the data into clusters of nearby points.

What's needed for clustering?

- Proximity measure, either
 - similarity measure $s(x_i, x_k)$: large if x_i, x_k are similar
 - dissimilarity(or distance) measure $d(x_i, x_k)$: small if x_i, x_k are similar



large **s**, small **d**

2. Criterion function to evaluate a clustering





Algorithm to compute clustering

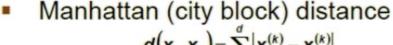
The classics: clustering

Popular distance metrics:

Euclidean distance

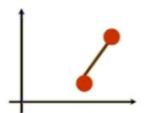
$$d(x_i, x_j) = \sqrt{\sum_{k=1}^{d} (x_i^{(k)} - x_j^{(k)})^2}$$

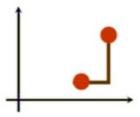
translation invariant



$$d(x_i,x_j) = \sum_{k=1}^d |x_i^{(k)} - x_j^{(k)}|$$

 approximation to Euclidean distance, cheaper to compute





They are special cases of Minkowski distance:

$$d_p(\mathbf{x}_i, \mathbf{x}_j) = \left(\sum_{k=1}^m \left| x_{ik} - x_{jk} \right|^p \right)^{\frac{1}{p}}$$

(p is a positive integer)

The classics: clustering

Criterion functions:

Intra-cluster cohesion

 Cohesion measures how near the data points in a cluster are to the cluster "center".

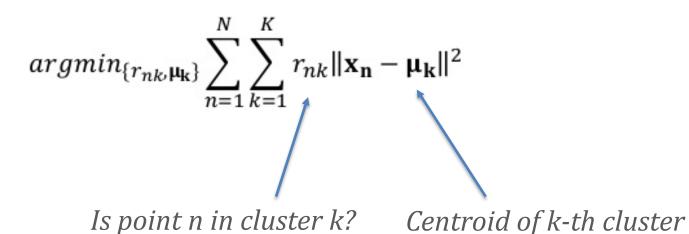
Inter-cluster separation

 Separation means that different cluster centroids should be far away from one another.

In most applications, expert judgments are still the key.

K-means clustering

If the distance metric is the Euclidean distance, and the measure of cohesion is the average distance from the centroid: we get the **k-means objective.**



K-means clustering

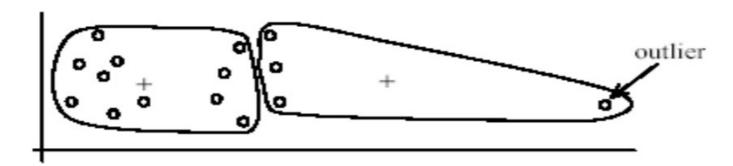
A natural iterative algorithm, which as we will see later is a variant of the **EM** (expectation-maximization) algorithm:

```
Input: Data set X = \{x^{(1)}, x^{(2)}, \dots, x^{(m)} | x^{(i)} \in \mathbb{R}^n \}
    Output: Cluster centroids \mu_{i=1,\dots,k} \in \mathbb{R}^n; Cluster assignments c \in \mathbb{Z}
 1 Initialize k cluster centroids \mu_1, \dots, \mu_k \in \mathbb{R}^n randomly from X;
 2 repeat
        for i = 1, \dots, m \text{ do } / / \text{ Update cluster assignments}
           set c^{(i)} = arg \min_{i} ||x^{(i)} - \mu_{j}||^{2};
        end
       for j=1,\cdots,k do // Update cluster centroids
        set \mu_j = \frac{\sum_{i=1}^m 1\{c^{(i)}=j\}x^{(i)}}{\sum_{i=1}^m 1\{c^{(i)}=j\}};
        end
 9 until Convergence;
10 return \mu and c;
```

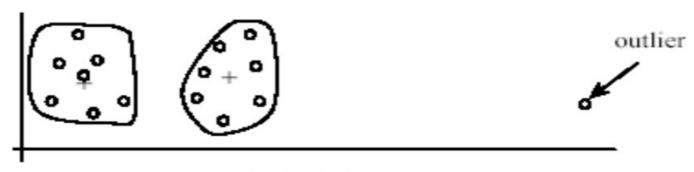
Algorithm 1: Algorithm of batch-version for K-means

Some weaknesses

Very sensitive to outliers:



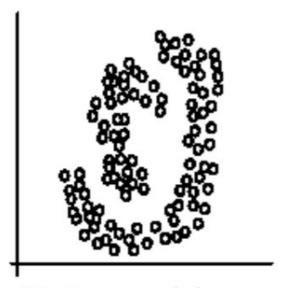
(A): Undesirable clusters



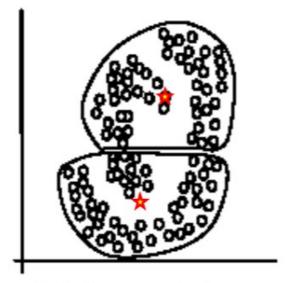
(B): Ideal clusters

Some weaknesses

Not suitable for non-spherical clusters:

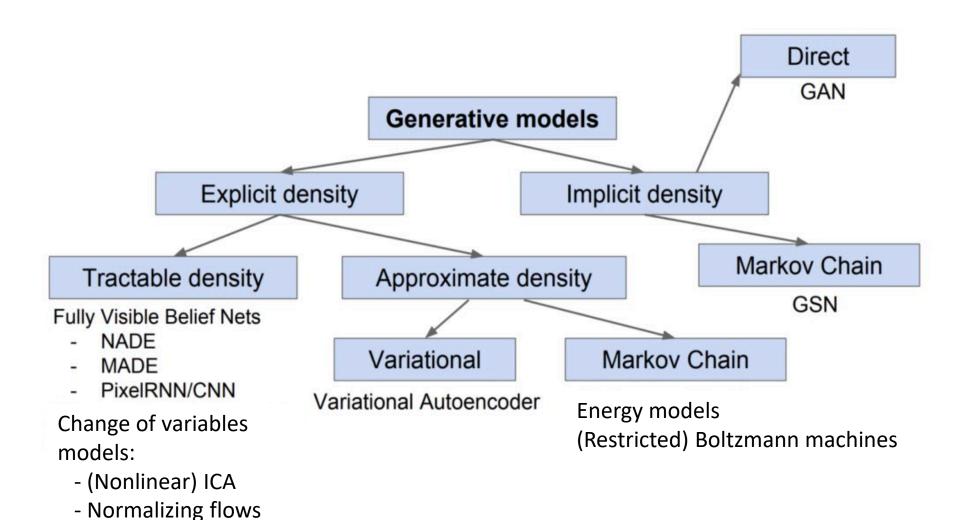


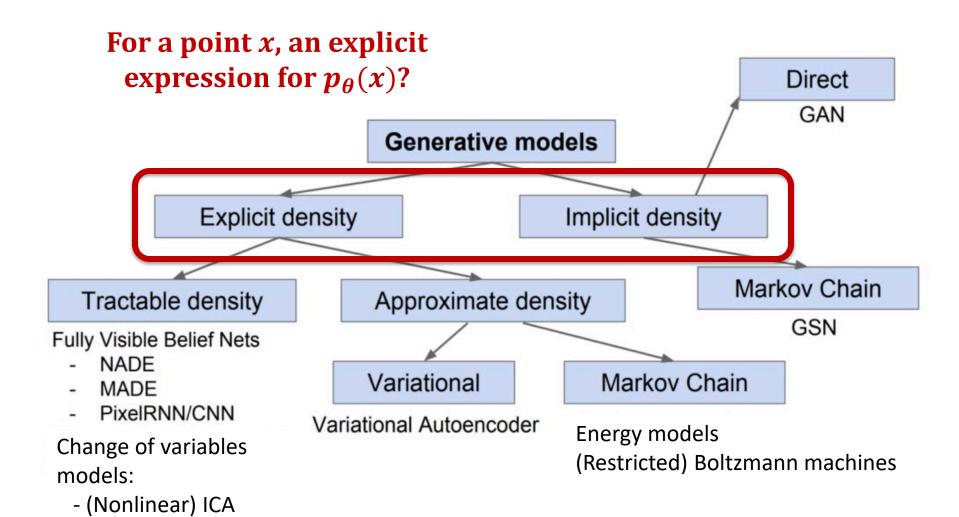
(A): Two natural clusters



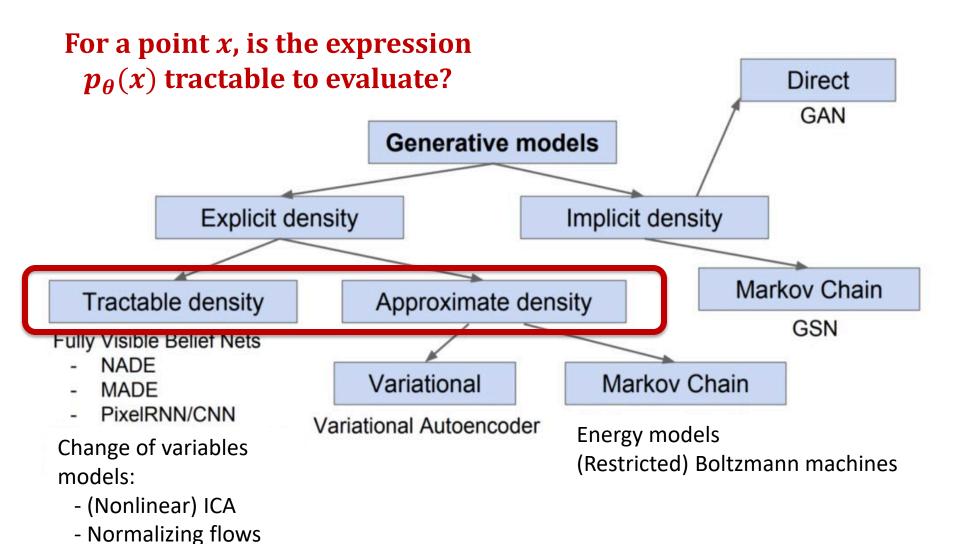
(B): k-means clusters

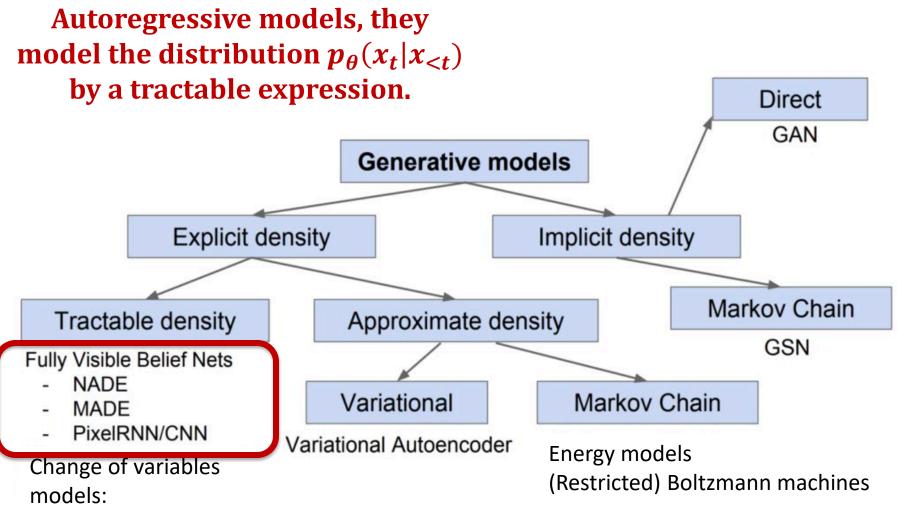
Taxonomy of generative models





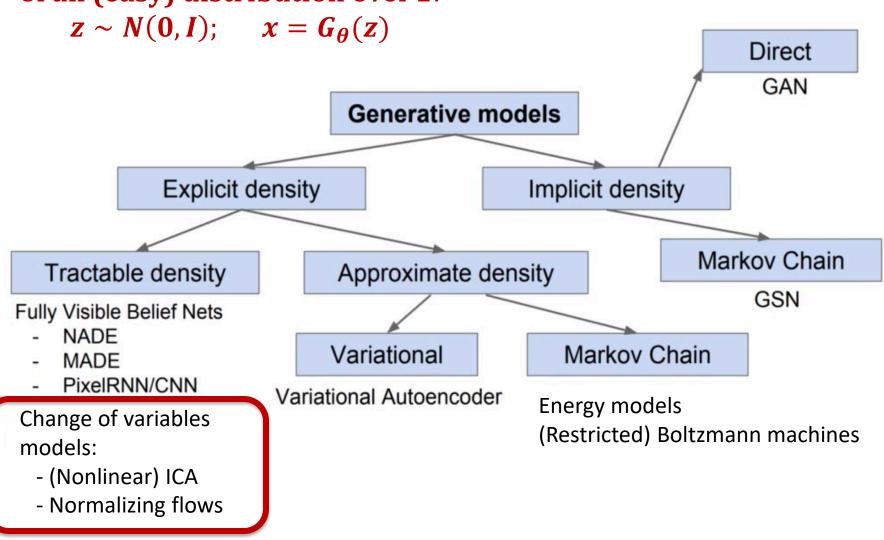
- Normalizing flows



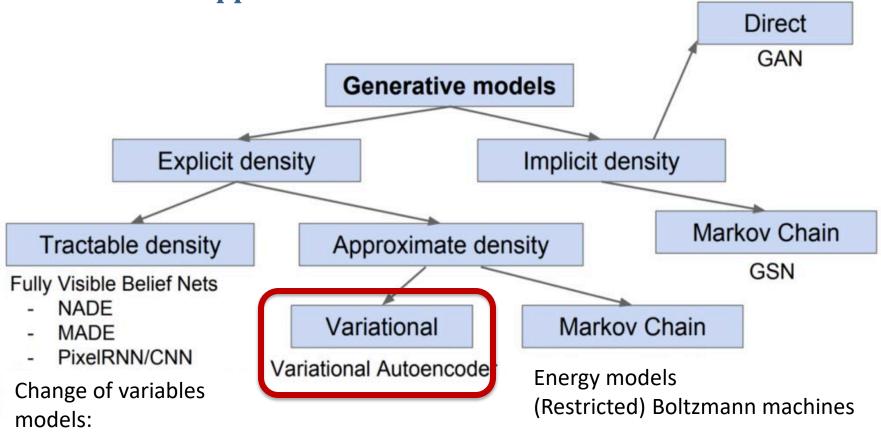


- (Nonlinear) ICA
- Normalizing flows

They model the distribution for x as an invertible transformation of an (easy) distribution over z:



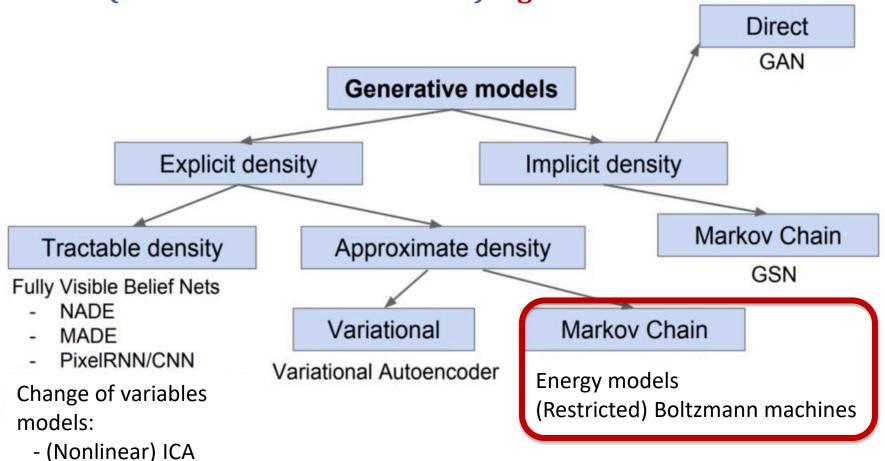
The distribution $p_{\theta}(x)$ does not have a tractable form, but we can write down a variational approximation thereof.



- (Nonlinear) ICA
- Normalizing flows

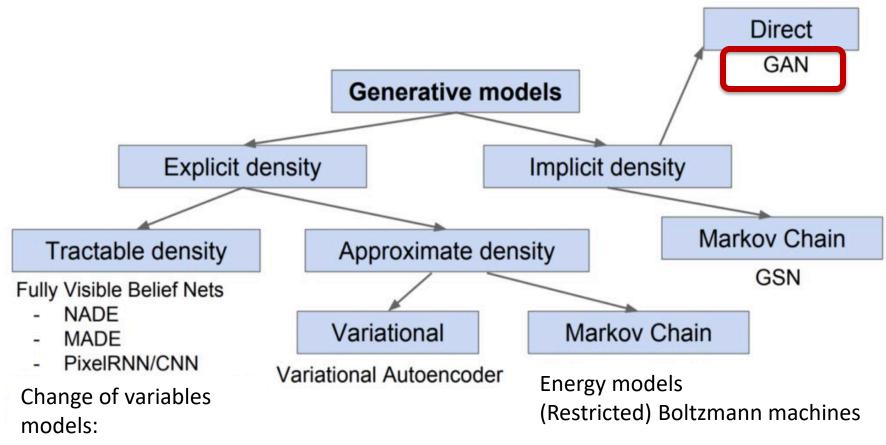
The distribution $p_{\theta}(x)$ does not have a tractable form, but we can approximate it by running a MCMC (Markov Chain Monte Carlo) algorithm.

- Normalizing flows



The distribution $p_{\theta}(x)$ does not have an explicit form, but we can draw samples from it. e.g.

$$z \sim N(0, I); \quad x = G_{\theta}(z)$$



- (Nonlinear) ICA
- Normalizing flows

Likelihood-based: maximize the likelihood of the data under the model (possibly with variational or MCMC approximations)

$$\max_{\theta} \sum_{\text{samples } x_i} \log p_{\theta}(x_i)$$

In the limit of infinite number of samples:

$$\max_{\theta} \mathbb{E}_{x \sim p} \log p_{\theta}(x) = -(\mathbb{E}_{x \sim p} \log \frac{1}{p_{\theta}(x)} + \mathbb{E}_{x \sim p} \log p(x) - \mathbb{E}_{x \sim p} \log p(x))$$

$$= -(KL(p||p_{\theta}) + H(p))$$

Hence, we are minimizing KL divergence (H(p)) is a constant).

Likelihood-based: maximize the likelihood of the data under the model (possibly with variational or MCMC approximations)

Pros

Easy training: can just maximize via gradient descent.

Evaluation: evaluating the fit of the model can be done by evaluating the likelihood (on test data)

Cons

Larger models needed:

likelihood objective is hard, to fit well need very big model

Likelihood encourages averaging:

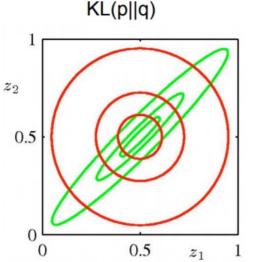
produced samples tend to be blurrier, as likelihood encourages "coverage" of training data.

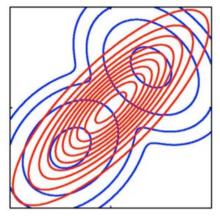
$$\mathrm{KL}(p||q) = -\int p(\mathbf{Z}) \ln \frac{q(\mathbf{Z})}{p(\mathbf{Z})} d\mathbf{Z}.$$

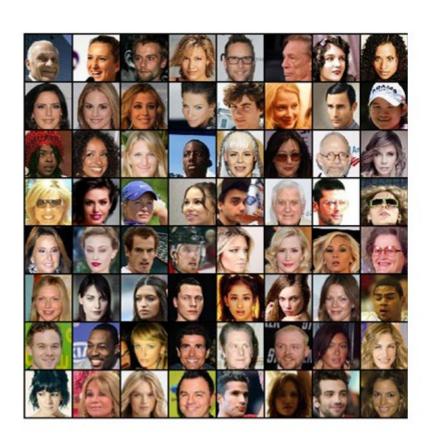
There is a large positive contribution to the KL divergence from regions of Z space in which:

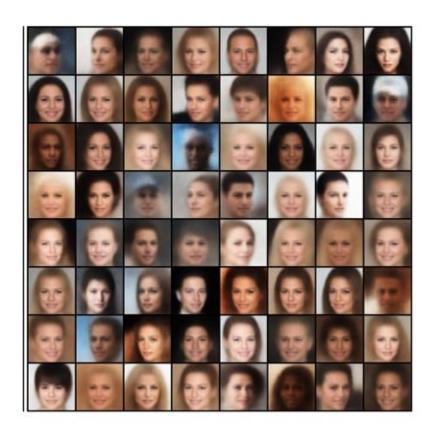
- -q(Z) is near zero,
- unless p(Z) is also close to zero.

Minimizing KL(p||q) leads to distributions q(Z) that are nonzero in regions where p(Z) is nonzero.



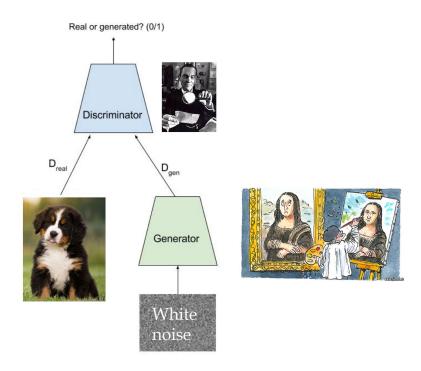






Faces generated using a trained VAE

Likelihood-free: use a surrogate loss – e.g. in GANs, train a discriminator to tell real and generated samples apart;



Likelihood-free: use a surrogate loss – e.g. in GANs, train a discriminator to tell real and generated samples apart;

Pros

Better objective, smaller models needed: objective itself (i.e. discriminator) is "learned" – can result in visually better images w/ smaller models.

Cons

Unstable training: typically minmax (saddle point) problems.

Evaluation: no way to evaluate likelihood, so no way to evaluate quality of fit.