

# Lecture 20 — Hidden markov models; intro to GANs.

Alex Schwing and Matus Telgarsky

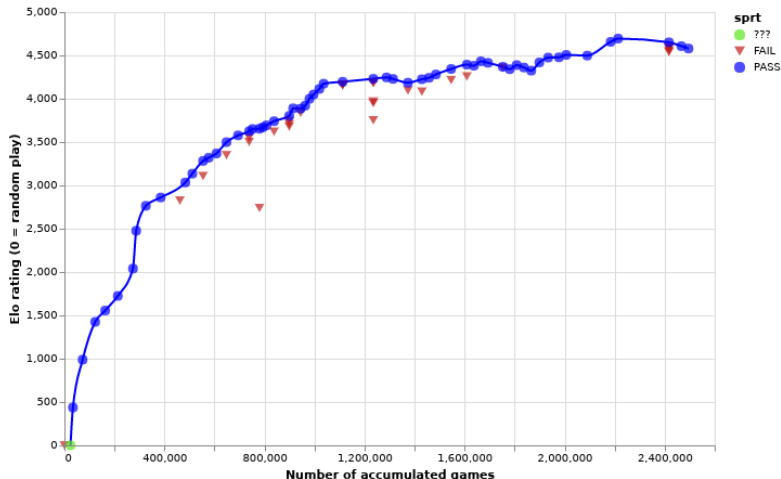
April 5, 2018

# Announcements.

- ▶ Midterms available in **TA** office hours.
  - ▶ 8 more days for regrade requests.
- ▶ Homework 12 pushed back 1 week.
- ▶ Ongoing questions:
  - ▶ Midterm solutions available ...?
  - ▶ Videos ...?

# A fun project.

Iczero — open source, distributed AlphaGo Zero for chess.



## Active Users

223 users in the last day have played 214791 games

# Where is E-M still used?

This was asked last time.

- ▶ The shortest answer: many applied fields still use E-M, Gaussian mixtures, HMMs (e.g., speech, bioinformatics), however slowly it seems everything is transitioning to deep learning!

Therefore the natural question still becomes: **why learn this stuff?**

- ▶ To be able to discuss current ML, compare ML methods.
- ▶ To be able to reason about ML methods in different ways.
- ▶ Always useful to learn more tools.
- ▶ Cynical view: worst case, analogous to learning basic algorithms for coding interviews. . .

# Regarding bioinformatics.



## Volume 34, Issue 5

01 March 2018

ISSN 1367-4803  
EISSN 1460-2059

► DISCOVERY NOTE

► ORIGINAL PAPERS

► APPLICATIONS NOTES

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## ORIGINAL PAPERS

### GENOME ANALYSIS

#### ARCS: scaffolding genome drafts with linked reads

Sarah Yeo; Lauren Coombe; René L Warren; Justin Chu; Inanc Birol

*Bioinformatics*, Volume 34, Issue 5, 1 March 2018, Pages 725–731,  
<https://doi.org/10.1093/bioinformatics/btx675>

[Abstract ▼](#)   [View article](#)   [Supplementary data](#)

#### Chromatin accessibility prediction via a hybrid deep convolutional neural network

Qiao Liu; Fei Xia; Qijin Yin; Rui Jiang

*Bioinformatics*, Volume 34, Issue 5, 1 March 2018, Pages 732–738,  
<https://doi.org/10.1093/bioinformatics/btx679>

[Abstract ▼](#)   [View article](#)   [Supplementary data](#)

DL

### SEQUENCE ANALYSIS

#### Bartender: a fast and accurate clustering algorithm to count barcode reads

Lu Zhao; Zhimin Liu; Sasha F Levy; Song Wu

*Bioinformatics*, Volume 34, Issue 5, 1 March 2018, Pages 739–747,  
<https://doi.org/10.1093/bioinformatics/btx655>

[Abstract ▼](#)   [View article](#)   [Supplementary data](#)

ML

#### Evaluation of tools for long read RNA-seq splice-aware alignment

Krešimir Križanović; Amina Echchiki; Julien Roux; Mile Šikić

*Bioinformatics*, Volume 34, Issue 5, 1 March 2018, Pages 748–754,  
<https://doi.org/10.1093/bioinformatics/btx668>

# Regarding bioinformatics.



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- DISCOVERY NOTE
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## DEEPre: sequence-based enzyme EC number prediction by deep learning

Yu Li; Sheng Wang; Ramzan Umarov; Bingqing Xie; Ming Fan ...

*Bioinformatics*, Volume 34, Issue 5, 1 March 2018, Pages 760–769,  
<https://doi.org/10.1093/bioinformatics/btx680>

[Abstract](#) ▼ [View article](#) [Supplementary data](#)

DL

## STRUCTURAL BIOINFORMATICS

## Machine learning accelerates MD-based binding pose prediction between ligands and proteins

Kei Terayama; Hiroaki Iwata; Mitsugu Araki; Yasushi Okuno; Koji Tsuda

*Bioinformatics*, Volume 34, Issue 5, 1 March 2018, Pages 770–778,  
<https://doi.org/10.1093/bioinformatics/btx638>

[Abstract](#) ▼ [View article](#) [Supplementary data](#)

ML  
MBI

## Predicting protein–DNA binding free energy change upon missense mutations using modified MM/PBSA approach: SAMPDI webserver

Yunhui Peng; Lexuan Sun; Zhe Jia; Lin Li; Emil Alexov

*Bioinformatics*, Volume 34, Issue 5, 1 March 2018, Pages 779–786,  
<https://doi.org/10.1093/bioinformatics/btx698>

[Abstract](#) ▼ [View article](#) [Supplementary data](#)

## GENETICS AND POPULATION ANALYSIS

## QuASAR-MPRA: accurate allele-specific analysis for massively parallel reporter assays

Cynthia A Kalita; Gregory A Moyerbrailean; Christopher Brown; Xiaoquan Wen; Francesca Luca ...

(etc.)

Schedule for today.

## Schedule for today.

- ▶ Graphical models; Hidden Markov Models intro.
- ▶ More E-M: learning Hidden Markov Models.
- ▶ Kernel density estimates (“Parzen windows”).
- ▶ GAN intro: distributions and neural networks.
- ▶ GAN intro: sampling with neural networks.



Graphical models; Hidden Markov Models intro.

## Graphical models; Hidden Markov Models intro.

Recall the sampling story for GMMs:

$$\begin{aligned} Y &\sim \text{Discrete}(\pi_1, \dots, \pi_k) && \text{choose cluster;} \\ X|Y=j &\sim \mathcal{N}(\mu_j, \Sigma_k) && \text{choose point.} \end{aligned}$$

$Y$  is **latent/hidden/unobserved**,  $X$  is **observed**.

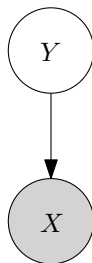
## Graphical models; Hidden Markov Models intro.

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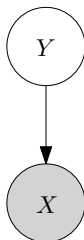
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**Graphical Model:**



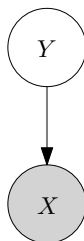
## Graphical model for GMMs.



**Basic rules** (there are more complicated variants):

- ▶ Nodes denote random variables.
- ▶ Edges denote conditional dependence.
- ▶ Shaded nodes are observed; unshaded are unobserved.

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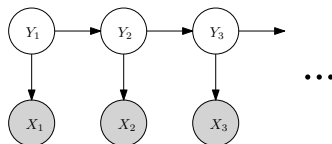
- ▶ Nodes denote random variables.
- ▶ Edges denote conditional dependence.
- ▶ Shaded nodes are observed; unshaded are unobserved.

Gaussian likelihood according to the graphical model:

$$\begin{aligned} p(X_1, \dots, X_n) &= \sum_{j_1 \in [k], \dots, j_n \in [k]} p(X_1, \dots, X_n, Y_1 = j_1, \dots, Y_n = j_n) \\ &= \sum_{j_1 \in [k], \dots, j_n \in [k]} \prod_{i=1}^n p(Y_i = j_i) p(X_i | Y_i = j_i). \end{aligned}$$

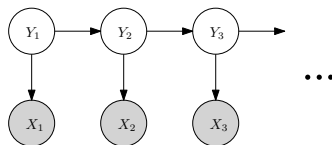
# Hidden Markov Models: basics.

- ▶ As with GMM:
  - ▶ **Observed** random variables ( $X_1, \dots, X_n$ ).
  - ▶ **Latent variables** ( $Y_1, \dots, Y_n$ ).
  - ▶ Conditional independence of observations given latent variables:  
e.g.,  $p(X_i | X_1, \dots, X_{i-1}, X_{i+1}, \dots, X_t, Y_1, \dots, Y_t) = p(X_i | Y_i)$ .
- ▶ **Unlike GMMs:** ( $Y_1, \dots, Y_t$ ) have dependencies!
  - ▶ **Markov assumption:**  $Y_{i+1}$  depends *only* on  $Y_i$ .
- ▶ Graphical model:



# Hidden Markov Models: likelihood.

- Graphical model.



- Likelihood.

$$\begin{aligned} & p(X_1, \dots, X_n, Y_1, \dots, Y_n) \\ &= p(Y_1)p(X_1, \dots, X_n, Y_2, \dots, Y_n | Y_1) \\ &= p(Y_1)p(X_1 | Y_1)p(X_2, \dots, X_n, Y_2, \dots, Y_n | Y_1) \\ &= p(Y_1)p(X_1 | Y_1)p(X_2 | Y_2)p(Y_2 | Y_1)p(X_3, \dots, X_n, Y_2, \dots, Y_n | Y_2, Y_1) \\ &= p(Y_1)p(X_1 | Y_1)p(X_2 | Y_2)p(Y_2 | Y_1)p(X_3, \dots, X_n, Y_2, \dots, Y_n | Y_2) \\ &= p(Y_1) \left( \prod_{i=1}^n p(X_i | Y_i) \right) \left( \prod_{i=2}^n p(Y_i | Y_{i-1}) \right). \end{aligned}$$

## Hidden Markov Models: parameters.

- ▶ Still have parameters for  $p(X_i | Y_i = j)$ .  
E.g., if this is Gaussian, have parameters  $(\mu_j, \Sigma_j)$ .
- ▶ Still have parameters  $(\pi_1, \dots, \pi_k)$  for  $Y_1$ .
- ▶ For  $(Y_2, \dots, Y_k)$  have **transition probabilities**  
 $p(Y_{i+1} = j' | Y_i = j)$ .

These are assumed **homogeneous/time-invariant**: e.g.,

$$p(Y_{i+1} = j' | Y_i = j) = p(Y_{i+2} = j' | Y_{i+1} = j).$$

Write these as a matrix  $A \in [0, 1]^{k \times k}$ :

$$p(Y_{i+1} = l | Y_i = k) = A_{jl}.$$

- ▶ Depiction: like GMM, but have time series over hidden states!



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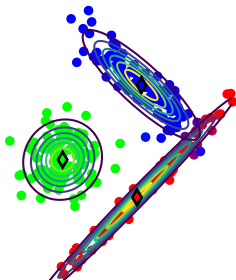
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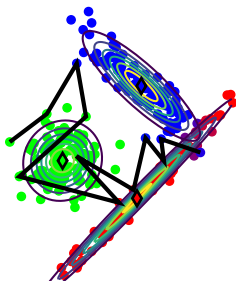
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# Hidden Markov Models: applications.

- ▶ Speech modeling; e.g., phonemes ( $/A/$ ,  $/a/$ ,  $/b/$ , ...).
  - ▶ Multivariate Gaussian is over amplitude or frequency window.
  - ▶ Transition matrix  $A$  allows self-loops!  
Very useful: imagine saying a word slowly.
- ▶ Sequence alignment in biology.
- ▶ See Murphy Chapter 17 for more applications.  
(Many are being replaced with DNNs, RNNs, ...!)

## Other applications of graphical models.

- ▶ Popular in sciences, for interpretability, and easy inclusion of domain knowledge?
- ▶ Example: phylogenetic trees (“Mr. Bayes”).

More E-M: learning Hidden Markov Models.

## More E-M: learning Hidden Markov Models.

Another interpretation of E-M

(useful for HMMs, and appears on homework?):

E-M maximizes the **expected complete log-likelihood**

$$\mathbb{E}_{\theta} [\ln p_{\theta}(X_1, \dots, X_n, Y_1, \dots, Y_n) | x_1, \dots, x_n] ,$$

where “ $\mathbb{E}_{\theta}$ ” means the distribution uses the learned parameters  $\theta$ ,  
and “ $|x_1, \dots, x_n$ ” means we condition on the observed data.

## More E-M: learning Hidden Markov Models.

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and “ $|x_1, \dots, x_n$ ” means we condition on the observed data.

For GMMs, this becomes

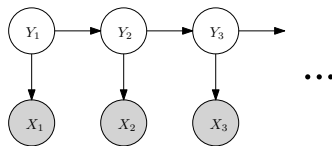
$$\begin{aligned} &= \mathbb{E}_{\theta} \left[ \sum_{i=1}^n \ln p_{\theta}(X_i = x_i, Y_i) \right] \\ &= \frac{1}{k} \sum_{i=1}^n \sum_{j=1}^k p_{\theta}(Y_i = j | X_i = x_i) \ln p_{\theta}(X_i = x_i, Y_i = j), \end{aligned}$$

which matches what we optimized before; specifically,

$$p_{\theta}(Y = j | X = x) = \frac{\pi_j p_{\theta}(X = x | Y = j)}{\sum_{l=1}^k \pi_l p_{\theta}(X = x | Y = l)}.$$

# Expected complete log-likelihood for HMMs.

Graphical model:



Expected complete log-likelihood:

$$\begin{aligned} & \mathbb{E}_{\theta} \left[ \ln p_{\theta}(X_1, \dots, X_n, Y_1, \dots, Y_n) | x_1, \dots, x_n \right] \\ &= \mathbb{E}_{\theta} \left[ \ln \left( p_{\theta}(Y_1) \left( \prod_{i=1}^n p_{\theta}(X_i | Y_i) \right) \left( \prod_{i=2}^n p_{\theta}(Y_i | Y_{i-1}) \right) \right) \right] \\ &= \sum_{j=1}^k p_{\theta}(Y_1 | x_1, \dots, x_k) \ln \pi_j + \sum_{i=1}^n \sum_{j=1}^k p_{\theta}(Y_i = j | x_1, \dots, x_n) \ln p_{\theta}(X_i | Y_i) \\ &\quad + \sum_{i \geq 2} \sum_{j, j'=1}^k p_{\theta}(Y_i = j, Y_{i-1} = j' | x_1, \dots, x_n) \ln p_{\theta}(Y_i = j | Y_{i-1} = j') \end{aligned}$$



## Expected complete log-likelihood for HMMs.

Expected complete log-likelihood:

$$\begin{aligned} & \sum_{j=1}^k p_{\theta}(Y_1|x_1, \dots, x_k) \ln \pi_j + \sum_{i=1}^n \sum_{j=1}^k p_{\theta}(Y_i = j|x_1, \dots, x_n) \ln p_{\theta}(X_i|Y_i = j) \\ & + \sum_{i \geq 2} \sum_{j, j'=1}^k p_{\theta}(Y_i = j, Y_{i-1} = j'|x_1, \dots, x_n) \ln p_{\theta}(Y_i = j|Y_{i-1} = j'). \end{aligned}$$

- ▶ M step for observable  $p_{\theta}(X_i|Y_i)$  similar to mixture case; replace old  $\sum_i A'_{ij}$  with new  $\sum_i p_{\theta}(Y_i|x_1, \dots, x_n)$ .
- ▶ M step for  $\pi$  and  $A_{jj'} = p_{\theta}(Y_i = j|Y_{i-1} = j')$  also easy.
- ▶ Real annoyance is computing the conditional probabilities (E step)!

## E-step for HMMs.

- ▶ Need to compute  $p_{\theta}(Y_1|x_1, \dots, x_k)$ ,  $p_{\theta}(Y_i = j|x_1, \dots, x_n)$ ,  $p_{\theta}(Y_i = j, Y_{i-1} = j'|x_1, \dots, x_n) \ln p_{\theta}(Y_i = j|Y_{i-1} = j')$ .
- ▶ Boils down to a bunch of games with conditioning.  
Kindof cool but I decided to skip.  
See Murphy book (Chapter 17) for details.

## Summary of HMMs.

- ▶ Graphical models give a succinct way to specify conditional dependencies of random variables.
- ▶ Expected complete log likelihood is another way to reason about E-M.
- ▶ HMMs allow dependence amongst latent variables.

Kernel density estimates (“Parzen windows”).

Let's cover one more standard distribution modeling tool.

## Kernel density estimates (“Parzen windows”).

Let's cover one more standard distribution modeling tool.

- ▶ Let random draw  $(x_i)_{i=1}^n$  from some density be given.
- ▶ Define  $\hat{p}(x) := \frac{1}{n} \sum_{i=1}^n k\left(\frac{x-x_i}{h}\right)$ ,  
where  $k$  is a **kernel function** (not the SVM one!),  
 $h$  is the “bandwidth”; for example:
  - ▶ Gaussian:  $\propto \exp(-\|x\|^2/2)$ ;
  - ▶ Epanechnikov  $\propto \max\{0, 1 - \|x\|^2\}$ .

## Kernel density estimates: illustration.

Taken from Larry Wasserman's "All of nonparametric statistics":

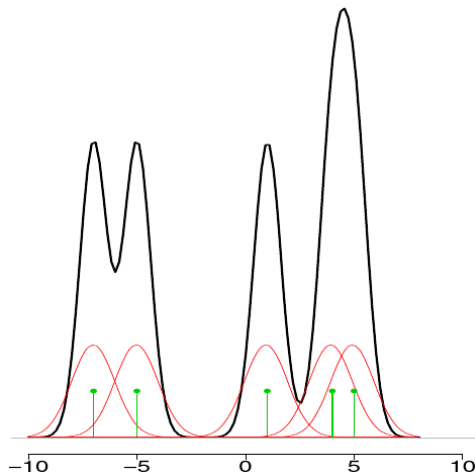


FIGURE 6.4. A kernel density estimator  $\hat{f}_n$ . At each point  $x$ ,  $\hat{f}_n(x)$  is the average of the kernels centered over the data points  $X_i$ . The data points are indicated by short vertical bars. The kernels are not drawn to scale.

## Kernel density estimates (KDE) vs GMM.

- ▶ KDE fits (basically) any density as  $n \rightarrow \infty$  (and variance (“bandwidth”) on kernel is tuned).
- ▶ GMM fits any density as  $k \rightarrow \infty$  (and variance is tuned).
- ▶ GMM can succinctly fit some densities for which KDE needs many samples.
- ▶ KDE is computationally trivial; GMM a mess.

Distributions and neural networks.



# Distributions and neural networks.

Let's survey our approaches to density estimation.

- ▶ Graphical models:  
can be interpretable,  
can encode domain knowledge.
- ▶ Kernel density estimation:  
easy to implement, converges to the right thing,  
suffers a curse of dimension.
- ▶ **Training:** easy for KDE, messy for graphical models.  
**Interpretability:** fine for both.  
**Sampling:** easy for both.  
**Probability measurements:** easy for KDE, sometimes easy  
for graphical model.

# Distributions and neural networks.

- ▶ Neural networks are good at **function approximation**.
- ▶ We can use a neural network to approximate a density, **or** we can use it for efficient sampling.
- ▶ It seems we can't get both?  
(I guess this is true?)

# Modeling densities with neural networks.

- ▶ Suppose  $(x_i)_{i=1}^n$  drawn from density  $p$ .
- ▶ Suppose we train a network  $f$  to approximate this density (e.g., asking it to approximate the KDE); two issues:
  - ▶ How to sample?  
Answer: nasty MCMC methods, for instance Langevin.
  - ▶ How to guarantee  $\int f = 1$ ?  
Answer: nasty MCMC again.  
Good luck getting good convergence rates.

## Sampling with neural networks: pushforward maps.

Let's discuss **generator networks**;  
neural networks used for sampling.

# Sampling with neural networks: pushforward maps.

Let's discuss **generator networks**;  
neural networks used for sampling.

Basic story:

- ▶ Sample  $x$  from some efficiently sample-able distribution (uniform, Gaussian).
- ▶ Output  $g(x)$ , where  $g$  is a neural network.

Basic properties:

- ▶ Clear running time (compare to MCMC!).
- ▶ Usual neural network issues (unclear what it's actually doing, unclear how to train).

# Pushforward maps?

Recall the definition of a random variable.

- ▶ A random variable is a *function* from a sample space to  $\mathbb{R}$ .  
E.g., let  $X$  denote the sum of two dice. Then  
 $\Pr[X = 3] = (1 + 1)/36$ . In general, measure probabilities with inversion:  $\Pr[X = 3] = \Pr[X^{-1}(3)] = \Pr[\{(1, 2), (2, 1)\}]$ .

A convenient notation is a **pushforward**.

- ▶ Let  $\mu$  denote a single distribution (e.g., one dice).
- ▶ Let  $f$  be a function over the sample space.
- ▶ Let  $f\#\mu$  be the distribution that samples  $x \sim \mu$  and outputs  $f(x)$ ; equivalently, the probability of a set  $S$  is  $\Pr_\mu[f^{-1}(S)]$ .

## Distances over probability spaces?

So we have a way to write down and discuss generator networks:

- ▶  $f\#\mu$ , where  $f$  is a neural network,  $\mu$  is efficiently sampled.

# Distances over probability spaces?

So we have a way to write down and discuss generator networks:

- ▶  $f\#\mu$ , where  $f$  is a neural network,  $\mu$  is efficiently sampled.

We want  $f\#\mu$  to be *close* to some target density  $p$ .

How to formalize “close”?

- ▶ Standard notion for probability measures: total variation:

$$\frac{1}{2} \int |p(x) - g(x)| dx.$$

(Picture drawn in class.)

- ▶ Problem: very unforgiving for even small errors!



## Wasserstein distance.

Easy version of it (suffices for our present purposes): we look at all mappings of one distribution to another. Sometimes this is called “earth mover’s distance”.

$$W_1(f\#\mu, \nu) \\ = \inf \left\{ \int \|f(x) - T(f(x))\| dx \quad : \quad T : \mathbb{R}^d \rightarrow \mathbb{R}^d, T\#(f\#\mu) = \nu \right\}.$$

(Pictures drawn in class.)

## Summary.

## Summary.

- ▶ Graphical models and their diagrams.
- ▶ HMMs and dependencies amongst latent variables.
- ▶ KDE / Parzen windows, comparison to GMMs.
- ▶ Densities with neural nets? No thanks.
- ▶ Sampling with neural nets? Yes please.