CSEP 527 Spring 2016

4. Maximum Likelihood Estimation and the E-M Algorithm

#### Outline

HW#2 Discussion MLE: Maximum Likelihood Estimators EM: the Expectation Maximization Algorithm

Next: Motif description & discovery

### HW # 2 Discussion

	Species	Name	Description	Access -ion	score to #l
I	Homo sapiens (Human)	MYODI_HUMAN	Myoblast determination protein I	P15172	1709
2	Homo sapiens (Human)	TALI_HUMAN	T-cell acute lymphocytic leukemia protein I (TAL-I)		143
3	<u>Mus musculus (Mouse)</u>	MYOD1_MOUSE	Myoblast determination protein I	P10085	1494
4	<u>Gallus gallus (Chicken)</u>	MYODI_CHICK	Myoblast determination protein I homolog (MYOD1 homolog)	P16075	1020
5	Xenopus laevis (African clawed frog)	MYODA_XENLA	Myoblast determination protein I homolog A (Myogenic factor I)	P13904	978
6	<u>Danio rerio (Zebrafish)</u>	MYODI_DANRE	Myoblast determination protein I homolog (Myogenic factor I)		893
7	<u>Branchiostoma belcheri (Amphioxus)</u>	Q8IU24_BRABE	MyoD-related	Q8IU24	428
8	<u>Drosophila melanogaster (Fruit fly)</u>	MYOD_DROME	Myogenic-determination protein (Protein nautilus) (dMyd)		368
9	<u>Caenorhabditis elegans</u>	LIN32_CAEEL	Protein lin-32 (Abnormal cell lineage protein 32)		118
10	Homo sapiens (Human)	SYFM_HUMAN	Phenylalanyl-tRNA synthetase, mitochondrial	O95363	56













### Learning From Data: MLE

#### Maximum Likelihood Estimators

### Parameter Estimation

**Given:** independent samples  $x_1, x_2, ..., x_n$  from a parametric distribution  $f(x|\theta)$ 

**Goal:** estimate  $\theta$ .

**E.g.:** Given sample HHTTTTTHTHTHTTHH of (possibly biased) coin flips, estimate

 $\theta$  = probability of Heads

 $f(x|\theta)$  is the Bernoulli probability mass function with parameter  $\theta$ 

### Likelihood

$$\begin{split} \mathsf{P}(\mathsf{x} \mid \theta): \ \mathsf{Probability} \ \mathsf{of} \ \mathsf{event} \ \mathsf{x} \ \mathsf{given} \ \mathit{model} \ \theta \\ \mathsf{Viewed} \ \mathsf{as} \ \mathsf{a} \ \mathsf{function} \ \mathsf{of} \ \mathsf{x} \ (\mathsf{fixed} \ \theta), \ \mathsf{it's} \ \mathsf{a} \ \mathit{probability} \\ \mathsf{E.g.}, \ \Sigma_{\mathsf{x}} \ \mathsf{P}(\mathsf{x} \mid \theta) = \mathsf{I} \end{split}$$

Viewed as a function of  $\theta$  (fixed x), it's called likelihood

E.g.,  $\Sigma_{\theta} P(x \mid \theta)$  can be anything; *relative* values of interest. E.g., if  $\theta$  = prob of heads in a sequence of coin flips then P(HHTHH | .6) > P(HHTHH | .5),

I.e., event HHTHH is more likely when  $\theta$  = .6 than  $\theta$  = .5

And what θ make HHTHH most likely?

### Likelihood Function



## Maximum Likelihood Parameter Estimation

One (of many) approaches to param. est. Likelihood of (indp) observations  $x_1, x_2, ..., x_n$ 

$$L(x_1, x_2, \dots, x_n \mid \theta) = \prod_{i=1}^n f(x_i \mid \theta)$$

As a function of  $\theta$ , what  $\theta$  maximizes the likelihood of the data actually observed Typical approach:  $\frac{\partial}{\partial \theta} L(\vec{x} \mid \theta) = 0$  or  $\frac{\partial}{\partial \theta} \log L(\vec{x} \mid \theta) = 0$ 

# Example I

n independent coin flips,  $x_1, x_2, ..., x_n$ ;  $n_0$  tails,  $n_1$  heads,  $n_0 + n_1 = n$ ;  $\theta = \text{probability of heads}$   $L(x_1, x_2, ..., x_n \mid \theta) = (1 - \theta)^{n_0} \theta^{n_1}$   $\log L(x_1, x_2, ..., x_n \mid \theta) = n_0 \log(1 - \theta) + n_1 \log \theta$   $\frac{\partial}{\partial \theta} \log L(x_1, x_2, ..., x_n \mid \theta) = \frac{-n_0}{1 - \theta} + \frac{n_1}{\theta}$ Setting to zero and solving: Observed fraction of successes in sample is

$$\hat{\theta} = \frac{n_1}{n}$$

Observed fraction of successes in *sample* is MLE of success probability in *population* 

(Also verify it's max, not min, & not better on boundary)

### Parameter Estimation

**Given:** indp samples  $x_1, x_2, ..., x_n$  from a parametric distribution  $f(x|\theta)$ , estimate:  $\theta$ .



# Ex2: I got data; a little birdie tells me it's normal, and promises $\sigma^2 = I$



#### Which is more likely: (a) this?

 $\mu$  unknown,  $\sigma^2 = 1$ 



#### Which is more likely: (b) or this?

 $\mu$  unknown,  $\sigma^2 = 1$ 



#### Which is more likely: (c) or this?

 $\mu$  unknown,  $\sigma^2 = 1$ 



#### Which is more likely: (c) or this?

 $\mu$  unknown,  $\sigma^2 = 1$ 

Looks good by eye, but how do I optimize my estimate of  $\mu$  ?



**Ex. 2:** 
$$x_i \sim N(\mu, \sigma^2), \ \sigma^2 = 1, \ \mu$$
 unknown  

$$L(x_1, x_2, \dots, x_n | \theta) = \prod_{i=1}^n \frac{1}{\sqrt{2\pi}} e^{-(x_i - \theta)^2/2}$$

$$\ln L(x_1, x_2, \dots, x_n | \theta) = \sum_{i=1}^n -\frac{1}{2} \ln(2\pi) - \frac{(x_i - \theta)^2}{2}$$

$$\frac{d}{d\theta} \ln L(x_1, x_2, \dots, x_n | \theta) = \sum_{i=1}^n (x_i - \theta)$$
And verify it's max,  
not min & not better  
on boundary  

$$= \left(\sum_{i=1}^n x_i\right) - n\theta = 0$$

$$\widehat{\theta} = \left(\sum_{i=1}^n x_i\right) / n = \overline{x}$$
Sample mean is MLE of

Sample mean is MLE of population mean

#### Hmm ..., density ≠ probability

So why is "likelihood" function equal to product of *densities*?? (Prob of seeing any specific x<sub>i</sub> is 0, right?)

a) for maximizing likelihood, we really only care about *relative* likelihoods, and density captures that

b) has desired property that likelihood increases with better fit to the model

and/or

c) if density at x is f(x), for any small  $\delta > 0$ , the probability of a sample within  $\pm \delta/2$  of x is  $\approx \delta f(x)$ , but  $\delta$  is *constant* wrt  $\theta$ , so it just drops out of  $d/d\theta \log L(...) = 0$ .  $u \pm 1$ 

# Ex3: I got data; a little birdie tells me it's normal (but does *not* tell me $\mu$ , $\sigma^2$ )



#### Which is more likely: (a) this?

 $\mu, \sigma^2$  both unknown



#### Which is more likely: (b) or this?

 $\mu, \sigma^2$  both unknown



#### Which is more likely: (c) or this?

 $\mu, \sigma^2$  both unknown



#### Which is more likely: (d) or this?

 $\mu,\sigma^2$  both unknown



#### Which is more likely: (d) or this?

 $\mu, \sigma^2$  both unknown

Looks good by eye, but how do I optimize my estimates of  $\mu \& \sigma^2$ ?



**Ex 3:** 
$$x_i \sim N(\mu, \sigma^2), \ \mu, \sigma^2$$
 both unknown

$$\ln L(x_1, x_2, \dots, x_n | \theta_1, \theta_2) = \sum_{i=1}^n -\frac{1}{2} \ln(2\pi\theta_2) - \frac{(x_i - \theta_1)^2}{2\theta_2}$$

$$\frac{\partial}{\partial \theta_1} \ln L(x_1, x_2, \dots, x_n | \theta_1, \theta_2) = \sum_{i=1}^n \frac{(x_i - \theta_1)}{\theta_2} = 0$$
Likelihood
$$\widehat{\theta_1} = \left(\sum_{i=1}^n x_i\right)/n = \overline{x}$$

 $\theta_2$ 

# Sample mean is MLE of population mean, again

In general, a problem like this results in 2 equations in 2 unknowns. Easy in this case, since  $\theta_2$  drops out of the  $\partial/\partial \theta_1 = 0$  equation 29

# Ex. 3, (cont.)

$$\ln L(x_1, x_2, \dots, x_n | \theta_1, \theta_2) = \sum_{i=1}^n -\frac{1}{2} \ln(2\pi\theta_2) - \frac{(x_i - \theta_1)^2}{2\theta_2}$$
$$\frac{\partial}{\partial \theta_2} \ln L(x_1, x_2, \dots, x_n | \theta_1, \theta_2) = \sum_{i=1}^n -\frac{1}{2} \frac{2\pi}{2\pi\theta_2} + \frac{(x_i - \theta_1)^2}{2\theta_2^2} = 0$$
$$\widehat{\theta_2} = \left(\sum_{i=1}^n (x_i - \widehat{\theta_1})^2\right) / n = \overline{s}^2$$

Sample variance is MLE of population variance

Ex. 3, (cont.)

Bias? if Y is sample mean

$$Y = (\Sigma_{1 \le i \le n} X_i)/n$$

then

 $E[Y] = (\sum_{1 \le i \le n} E[X_i])/n = n \ \mu/n = \mu$ so the MLE is an *unbiased* estimator of population mean

Similarly,  $(\Sigma_{1 \le i \le n} (X_i - \mu)^2)/n$  is an unbiased estimator of  $\sigma^2$ . Unfortunately, if  $\mu$  is unknown, estimated from the same data, as above,  $\hat{\theta}_2 = \sum_{1 \le i \le n} \frac{(x_i - \hat{\theta}_1)^2}{n}$  is a consistent, but biased estimate of population variance. (An example of overfitting.) Unbiased estimate is:

$$\hat{\theta}_2' = \sum_{1 \le i \le n} \frac{(x_i - \hat{\theta}_1)^2}{n - 1}$$

I.e.,  $\lim_{n\to\infty} = correct$ 

Moral: MLE is a great idea, but not a magic bullet

# More on Bias of $\hat{\theta}_2$

Biased? Yes. Why? As an extreme, think about n = I. Then  $\hat{\theta}_2 = 0$ ; probably an underestimate!

Also, consider n = 2. Then  $\hat{\theta}_1$  is exactly between the two sample points, the position that exactly minimizes the expression for  $\theta_2$ . Any other choices for  $\theta_1$ ,  $\theta_2$ make the likelihood of the observed data slightly *lower*. But it's actually pretty unlikely (probability 0, in fact) that two sample points would be chosen exactly equidistant from, and on opposite sides of the mean, so the MLE  $\hat{\theta}_2$  systematically underestimates  $\theta_2$ .

(But not by much, & bias shrinks with sample size.)

# Summary

MLE is one way to estimate parameters from data

You choose the *form* of the model (normal, binomial, ...)

Math chooses the value(s) of parameter(s)

Defining the "Likelihood Function" (based on the form of the model) is often the critical step; the math/algorithms to optimize it are generic

Often simply  $(d/d\theta)(\log \text{Likelihood}) = 0$ 

Has the intuitively appealing property that the parameters maximize the *likelihood* of the observed data; basically just assumes your sample is "representative"

Of course, unusual samples will give bad estimates (estimate normal human heights from a sample of NBA stars?) but that is an unlikely event

Often, but not always, MLE has other desirable properties like being *unbiased*, or at least *consistent* 

### Conditional Probability & Bayes Rule

Conditional probability of E given F: probability that E occurs given

that F has occurred.

"Conditioning on F"

Written as P(E|F)

Means "P(E has happened, given F observed)"





$$P(E \mid F) = \frac{P(EF)}{P(F)}$$

where 
$$P(F) > 0$$

#### E and F are events in the sample space S $E = EF \cup EF^{c}$



 $EF \cap EF^c = \emptyset$ 

 $\Rightarrow$  P(E) = P(EF) + P(EF<sup>c</sup>)

Most common form:

$$P(F \mid E) = \frac{P(E \mid F)P(F)}{P(E)}$$

Expanded form (using law of total probability):

$$P(F \mid E) = \frac{P(E \mid F)P(F)}{P(E \mid F)P(F) + P(E \mid F^c)P(F^c)}$$
Proof:

$$P(F \mid E) = \frac{P(EF)}{P(E)} = \frac{P(E \mid F)P(F)}{P(E)}$$

# EM

#### The Expectation-Maximization Algorithm (for aTwo-Component Gaussian Mixture)

### A Hat Trick

Two slips of paper in a hat:

Pink:  $\mu = 3$ , and

Blue:  $\mu = 7$ .

You draw one, then (without revealing color or  $\mu$ ) reveal a single sample X ~ Normal(mean  $\mu$ ,  $\sigma^2 = 1$ ).

You happen to draw X = 6.001.

Dr. Mean says "your slip = 7." What is P(correct)?

What if X had been 4.9?

#### **A Hat Trick**



### Another Hat Trick

Two secret numbers,  $\mu_{\text{pink}}$  and  $\mu_{\text{blue}}$ 

On pink slips, many samples of Normal( $\mu_{pink}, \sigma^2 = 1$ ),

Ditto on blue slips, from Normal( $\mu_{blue}, \sigma^2 = 1$ ).

Based on 16 of each, how would you "guess" the secrets (where "success" means your guess is within ±0.5 of each secret)?

Roughly how likely is it that you will succeed?

#### Another Hat Trick (cont.)

Pink/blue = red herrings; separate & independent Given X<sub>1</sub>, ..., X<sub>16</sub> ~ N( $\mu$ ,  $\sigma^2$ ),  $\sigma^2 = 1$ Calculate Y =  $(X_1 + ... + X_{16})/16 \sim N(?, ?)$  $E[Y] = \mu$  $Var(Y) = \frac{16\sigma^2}{16^2} = \frac{\sigma^2}{16} = \frac{1}{16}$ I.e., X<sub>i</sub>'s are all ~ N( $\mu$ , I); Y is ~ N( $\mu$ , I/16) and since  $0.5 = 2 \operatorname{sqrt}(1/16)$ , we have: "Y within ±.5 of  $\mu$ " = "Y within ±2  $\sigma$  of  $\mu$ "  $\approx$  95% prob

#### Note I: Y is a point estimate for $\mu$ ; Y ± 2 $\sigma$ is a 95% confidence interval for $\mu$ (More on this topic later)



#### Hat Trick 2 (cont.)

Note 2:

What would you do if some of the slips you pulled had coffee spilled on them, obscuring color?

If they were half way between means of the others? If they were on opposite sides of the means of the others



# Previously: How to estimate $\mu$ given data





(A modeling decision, not a math problem..., but if the later, what math?)

## A Living Histogram



male and female genetics students, University of Connecticut in 1996 <u>http://mindprod.com/jgloss/histogram.html</u>

#### **Another Real Example:**

CpG content of human gene promoters



"A genome-wide analysis of CpG dinucleotides in the human genome distinguishes two distinct classes of promoters" Saxonov, Berg, and Brutlag, PNAS 2006;103:1412-1417

Gaussian Mixture Models / Model-based Clustering







### A What-If Puzzle



Messy: no closed form solution known for finding  $\theta$  maximizing L

But what if we knew the  $z_{ij} = \begin{cases} 1 & \text{if } x_i \text{ drawn from } f_j \\ 0 & \text{otherwise} \end{cases}$ 

# EM as Egg vs Chicken

*IF* parameters  $\theta$  known, could estimate  $z_{ij}$ E.g.,  $|\mathbf{x}_i - \mu_1|/\sigma_1 \gg |\mathbf{x}_i - \mu_2|/\sigma_2 \Rightarrow P[z_{i1}=1] \ll P[z_{i2}=1]$  $\mathcal{H}$  IF  $z_{ij}$  known, could estimate parameters  $\theta$ E.g., only points in cluster 2 influence  $\mu_2$ ,  $\sigma_2$ But we know neither; (optimistically) iterate: Hach / E-step: calculate expected  $z_{ij}$ , given parameters M-step: calculate "MLE" of parameters, given  $E(z_{ij})$ Overall, a clever "hill-climbing" strategy

#### Simple Version: clarity concepts "Classification EM"

50

homework

If  $E[z_{ij}] < .5$ , pretend  $z_{ij} = 0$ ;  $E[z_{ij}] > .5$ , pretend it's I I.e., *classify* points as component 1 or 2 Now recale  $\theta$ , assuming that partition (standard MLE) Then recale  $E[z_{ij}]$ , assuming that  $\theta$ Then re-recale  $\theta$ , assuming new E[ $z_{ii}$ ], etc., etc.

"Full EM" is slightly more involved, (to account for uncertainty in classification) but this is the crux.

Another contrast: HMM parameter estimation via "Viterbi" vs "Baum-Welch" training. In both, "hidden data" is "which state was it in at each step?" Viterbi is like E-step in classification EM: it makes a single state prediction. B-W is full EM: it captures the uncertainty in state prediction, too. For either, M-step maximizes HMM emission/ 54 transition probabilities, assuming those fixed states (Viterbi) / uncertain states (B-W).

"K-means clustering," essentially

### Full EM

 $x_i$ 's are known;  $\theta$  unknown. Goal is to find MLE  $\theta$  of:

 $L(x_1,\ldots,x_n \mid heta)$  (hidden data likelihood)

Would be easy if  $z_{ij}$ 's were known, i.e., consider:

 $L(x_1,\ldots,x_n,z_{11},z_{12},\ldots,z_{n2}\mid heta)$  (complete data likelihood) But  $z_{ij}$ 's aren't known.

Instead, maximize *expected* likelihood of visible data

$$E(L(x_1,...,x_n,z_{11},z_{12},...,z_{n2} \mid \theta)),$$

where expectation is over distribution of hidden data  $(z_{ij}$ 's)





Assume  $\theta$  known & fixed  $E = 0 \cdot P(0) + 1 \cdot P(1)$ A (B): the event that  $x_i$  was drawn from  $f_1$  (f<sub>2</sub>) D: the observed datum  $x_i$ Expected value of  $z_{i1}$  is P(A|D) $\underline{P(D|A)}P(A)$  $E[z_{il}] = P(A|D)$ Repeat for P(D) = P(D|A)P(A) + P(D|B)P(B)each Xi  $= f_1(x_i|\theta_1) \tau_1 + f_2(x_i|\theta_2) \tau_2$ 

Note: denominator = sum of numerators - i.e. that which normalizes sum to 1 (typical Bayes)

#### A Hat Trick



## Complete Data Likelihood

Recall:

$$z_{1j} = \begin{cases} 1 & \text{if } x_1 \text{ drawn from } f_j \\ 0 & \text{otherwise} \end{cases}$$

so, correspondingly,

Formulas with "if's" are messy; can we blend more smoothly? Yes, many possibilities. Idea 1:

$$L(x_1, z_{1j} \mid \theta) = z_{11} \cdot \tau_1 f_1(x_1 \mid \theta) + z_{12} \cdot \tau_2 f_2(x_1 \mid \theta)$$

Idea 2 (Better):

 $L(x_1, z_{1j} \mid \theta) = (\tau_1 f_1(x_1 \mid \theta))^{z_{11}} \cdot (\tau_2 f_2(x_1 \mid \theta))^{z_{12}}$ 

M-step:



#### Find $\theta$ maximizing E(log(Likelihood))

(For simplicity, assume  $\sigma_1 = \sigma_2 = \sigma; \tau_1 = \tau_2 = \tau = 0.5$ )

W

$$\begin{split} L(\vec{x}, \vec{z} \mid \theta) &= \prod_{i=1}^{n} \underbrace{\frac{\tau}{\sqrt{2\pi\sigma^2}} \exp\left(-\sum_{j=1}^{2} z_{ij} \frac{(x_i - \mu_j)^2}{(2\sigma^2)}\right)}_{(2\sigma^2)} \\ E[\log L(\vec{x}, \vec{z} \mid \theta)] &= E\left[\sum_{i=1}^{n} \left(\log \tau - \frac{1}{2}\log(2\pi\sigma^2) - \sum_{j=1}^{2} z_{ij} \frac{(x_i - \mu_j)^2}{2\sigma^2}\right)\right]_{(x_i = 1)} \\ \swarrow \\ \text{wrt dist of } z_{ij} \\ &= \sum_{i=1}^{n} \left(\log \tau - \frac{1}{2}\log(2\pi\sigma^2) - \sum_{j=1}^{2} E[z_{ij}] \frac{(x_i - \mu_j)^2}{2\sigma^2}\right) \end{split}$$

Find  $\theta$  maximizing this as before, using  $E[z_{ij}]$  found in E-step. Result:  $\mu_j = \sum_{i=1}^n E[z_{ij}]x_i / \sum_{i=1}^n E[z_{ij}] |$  (intuit: avg, weighted by subpop prob)

#### Hat Trick 2 (cont.)

Note 2: red/blue separation is just like the M-step of EM if values of the hidden variables (z<sub>ij</sub>) were known.

What if they're not? E.g., what would you do if some of the slips you pulled had coffee spilled on them, obscuring color?

If they were half way between means of the others? If they were on opposite sides of the means of the others



Х

#### M-step:calculating mu's

$$\mu_j = \sum_{i=1}^n E[z_{ij}] x_i / \sum_{i=1}^n E[z_{ij}]$$

In words:  $\mu_j$  is the average of the observed  $x_i$ 's, weighted by the probability that  $x_i$  was sampled from component j.

								row sum	avg
E's	$E[z_{i1}]$	0.99	0.98	0.7	0.2	0.03	0.01	2.91	
old	$E[z_{i2}]$	0.01	0.02	0.3	0.8	0.97	0.99	3.09	
	Xi	9	10	11	19	20	21	90	15
	$E[z_{i1}]x_i$	8.9	9.8	7.7	3.8	0.6	0.2	31.0	10.66
	$E[z_{i1}]x_i$	0.1	0.2	3.3	15.2	19.4	20.8	59.0	19.09

new µ's

### 2 Component Mixture

#### $\sigma_1 = \sigma_2 = 1; \ \tau = 0.5$

		mu1	-20.00		-6.00		-5.00		-4.99
		mu2	6.00		0.00		3.75		3.75
x1	-6	z11		5.11E-12		1.00E+00		1.00E+00	
x2	-5	z21		2.61E-23		1.00E+00		1.00E+00	
х3	-4	z31		1.33E-34		9.98E-01		1.00E+00	
x4	0	z41		9.09E-80		1.52E-08		4.11E-03	
x5	4	z51		6.19E-125		5.75E-19		2.64E-18	
x6	5	z61		3.16E-136		1.43E-21		4.20E-22	
x7	6	z71		1.62E-147		3.53E-24		6.69E-26	

#### Essentially converged in 2 iterations

(Excel spreadsheet on course web)

# EM Summary

Fundamentally a maximum likelihood parameter estimation problem; broader than just Gaussian

Useful if 0/1 hidden data, and if analysis would be more tractable if hidden data z were known

Iterate:

E-step: estimate E(z) for each z, given  $\theta$ M-step: estimate  $\theta$  maximizing E[log likelihood] given E[z] [where "E[logL]" is wrt random z ~ E[z] = p(z=1)]

### EM Issues

Under mild assumptions (DEKM sect 11.6), EM is guaranteed to increase likelihood with every E-M iteration, hence will converge. But it may converge to a *local*, not global, max. (Recall the 4-bump surface...) Issue is intrinsic (probably), since EM is often applied to NP-hard problems (including clustering, above and motif-discovery, soon) Nevertheless, widely used, often effective

# Applications

Clustering is a remarkably successful exploratory data analysis tool

Web-search, information retrieval, gene-expression, ...

Model-based approach above is one of the leading ways to do it

Gaussian mixture models widely used

With many components, empirically match arbitrary distribution Often well-justified, due to "hidden parameters" driving the visible data

EM is extremely widely used for "hidden-data" problems Hidden Markov Models – speech recognition, DNA analysis, ...

#### A "Machine Learning" Example Handwritten Digit Recognition

Given:  $10^4$  unlabeled, scanned images of handwritten digits, say 25 x 25 pixels,

Goal: automatically classify new examples Possible Method:



Each image is a point in  $\mathbb{R}^{625}$ ; the "ideal" 7, say, is one such point; model other 7's as a Gaussian cloud around it

Do EM, as above, but 10 components in 625 dimensions instead of 2 components in 1 dimension

"Recognize" a new digit by best fit to those 10 models, i.e., basically max E-step probability

# Relative entropy

# Relative Entropy

- AKA Kullback-Liebler Distance/Divergence, AKA Information Content
- Given distributions P, Q

$$H(P||Q) = \sum_{x \in \Omega} P(x) \log \frac{P(x)}{Q(x)}$$

#### Notes:

Let 
$$P(x)\log \frac{P(x)}{Q(x)} = 0$$
 if  $P(x) = 0$  [since  $\lim_{y \to 0} y \log y = 0$ ]

Undefined if 0 = Q(x) < P(x)

68

**Relative Entropy**  
$$H(P||Q) = \sum_{x \in \Omega} P(x) \log \frac{P(x)}{Q(x)}$$

- Intuition: A quantitative measure of how much P "diverges" from Q. (Think "distance," but note it's not symmetric.)
  - If  $P \approx Q$  everywhere, then  $log(P/Q) \approx 0$ , so  $H(P||Q) \approx 0$
  - But as they differ more, sum is pulled above 0 (next 2 slides)
- What it means quantitatively: Suppose you sample x, but aren't sure whether you're sampling from P (call it the "null model") or from Q (the "alternate model"). Then log(P(x)/Q(x)) is the log likelihood ratio of the two models given that datum. H(P||Q) is the expected per sample contribution to the log likelihood ratio for discriminating between those two models.
- Exercise: if H(P||Q) = 0.1, say. Assuming Q is the correct model, how many samples would you need to confidently (say, with 1000:1 odds) reject P?



### **Theorem:** $H(P||Q) \ge 0$

 $H(P||Q) = \sum_{x} P(x) \log \frac{P(x)}{Q(x)}$   $\geq \sum_{x} P(x) \left(1 - \frac{Q(x)}{P(x)}\right)$   $= \sum_{x} (P(x) - Q(x))$   $= \sum_{x} P(x) - \sum_{x} Q(x)$  = 1 - 1= 0 Idea: if  $P \neq Q$ , then  $P(x)>Q(x) \Rightarrow \log(P(x)/Q(x))>0$ and  $P(y) \leq Q(y) \Rightarrow \log(P(y)/Q(y)) \leq 0$ Q: Can this pull H(P||Q) < 0? A: No, as theorem shows. Intuitive reason: sum is weighted by P(x), which is bigger at the positive log ratios vs the negative ones.

Furthermore: H(P||Q) = 0 if and only if P = QBottom line: "bigger" means "more different"