

Lecture 23

Expectation Maximization

Previously

- latent variables
- mixture models
- supervised learning, MCMC
- unsupervised learning, MCMC

- semi-supervised learning, MCMC
- clustering problems with sampling
- fix my marginalizing over discrete variables
- log-sum-exp trick

Latent variables

- instead of bayesian vs frequentist, think hidden vs not hidden
- key concept: full data likelihood vs partial data likelihood
- probabilistic model is a *joint distribution* $p(\mathbf{x}, \mathbf{z})$
- observed variables \mathbf{x} corresponding to data, and latent variables \mathbf{z}

Generative model

$$p(x, z) = p(x|z)p(z)$$

From edwardlib: $p(\mathbf{x} \mid \mathbf{z})$

describes how any data \mathbf{x} depend on the latent variables \mathbf{z} .

- **The likelihood posits a data generating process**, where the data \mathbf{x} are assumed drawn from the likelihood conditioned on a particular hidden pattern described by \mathbf{z} .
- The *prior* $p(\mathbf{z})$ is a probability distribution that describes the latent variables present in the data. **The prior posits a generating process of the hidden structure.**

Any bayesian parameters can be considered as \mathbf{z} .

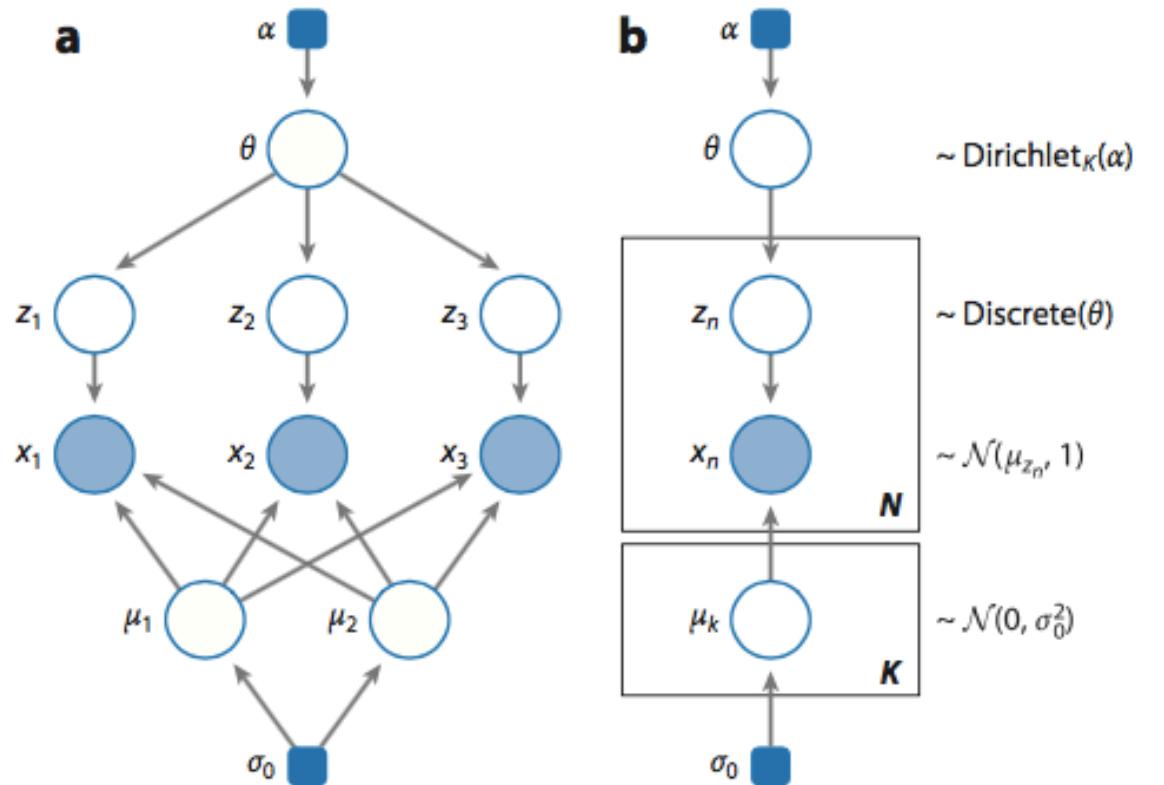


Figure 3

(a) A graphical model for a mixture of two Gaussians. There are three data points. The shaded nodes are observed variables, the unshaded nodes are hidden variables, and the blue square boxes are fixed hyperparameters (such as the Dirichlet parameters). (b) A graphical model for a mixture of K Gaussians with N data points.

More generally posit hidden structure →

A distribution $p(x|\{\theta_k\})$ is a mixture of K component distributions p_1, p_2, \dots, p_K if:

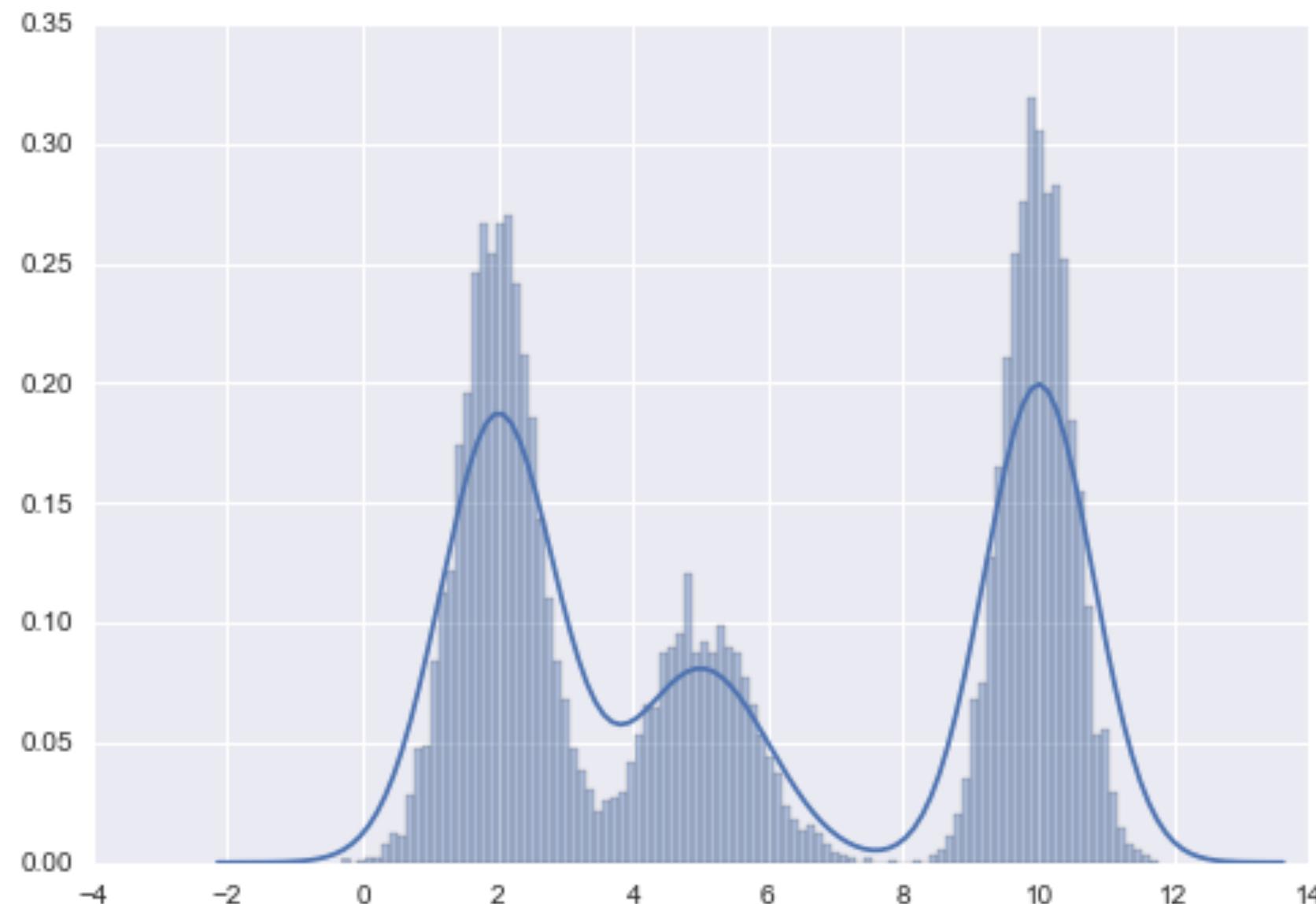
$$p(x|\{\theta_k\}) = \sum_k \lambda_k p_k(x|\theta_k)$$

with the λ_k being mixing weights, $\lambda_k > 0$,

$$\sum_k \lambda_k = 1.$$

Example: Zero Inflated Poisson

Gaussian Mixture Model



$$p(x|\{\theta_k\}) = \sum_k \lambda_k N(x|\mu_k, \Sigma_k)$$

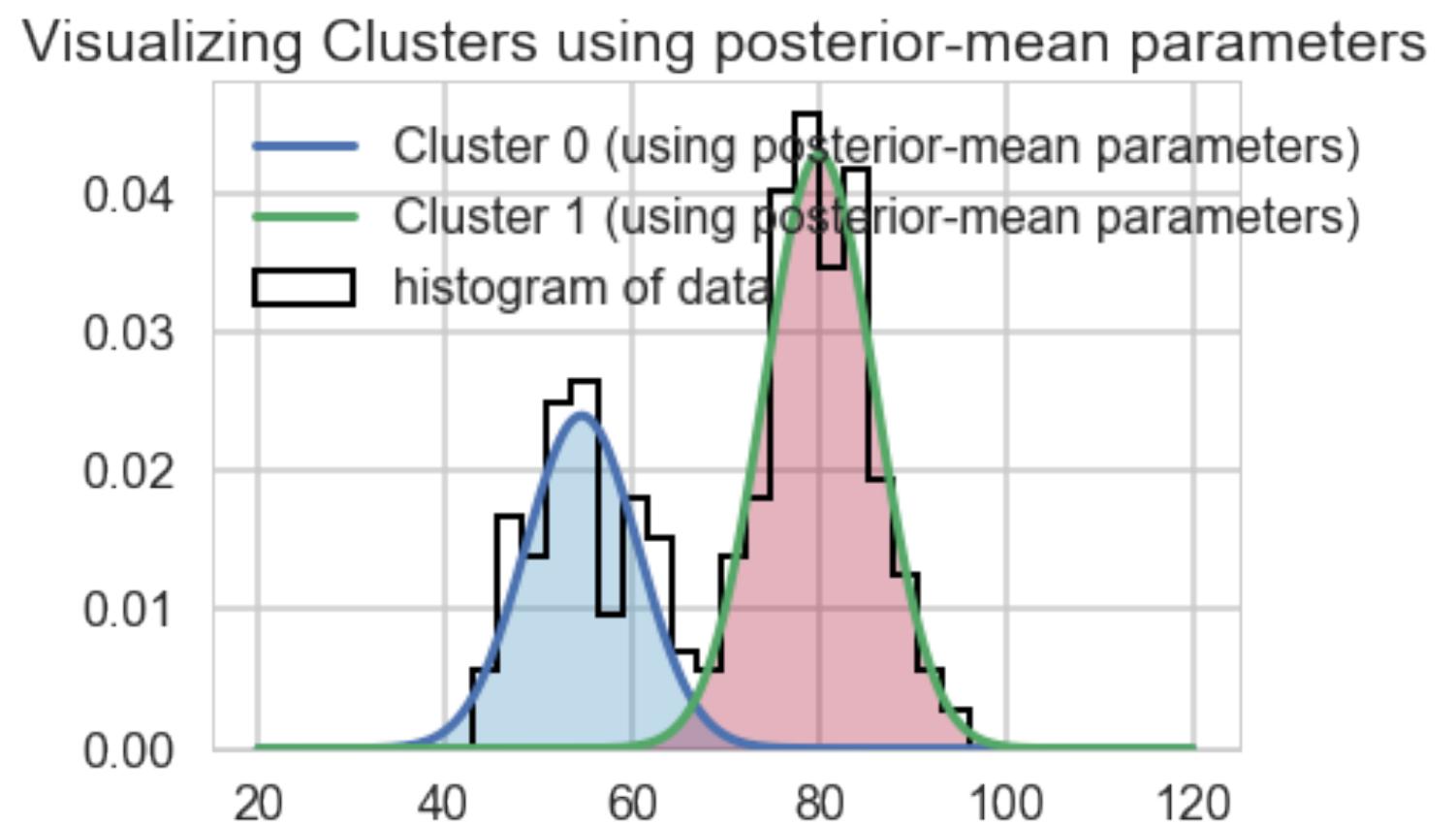
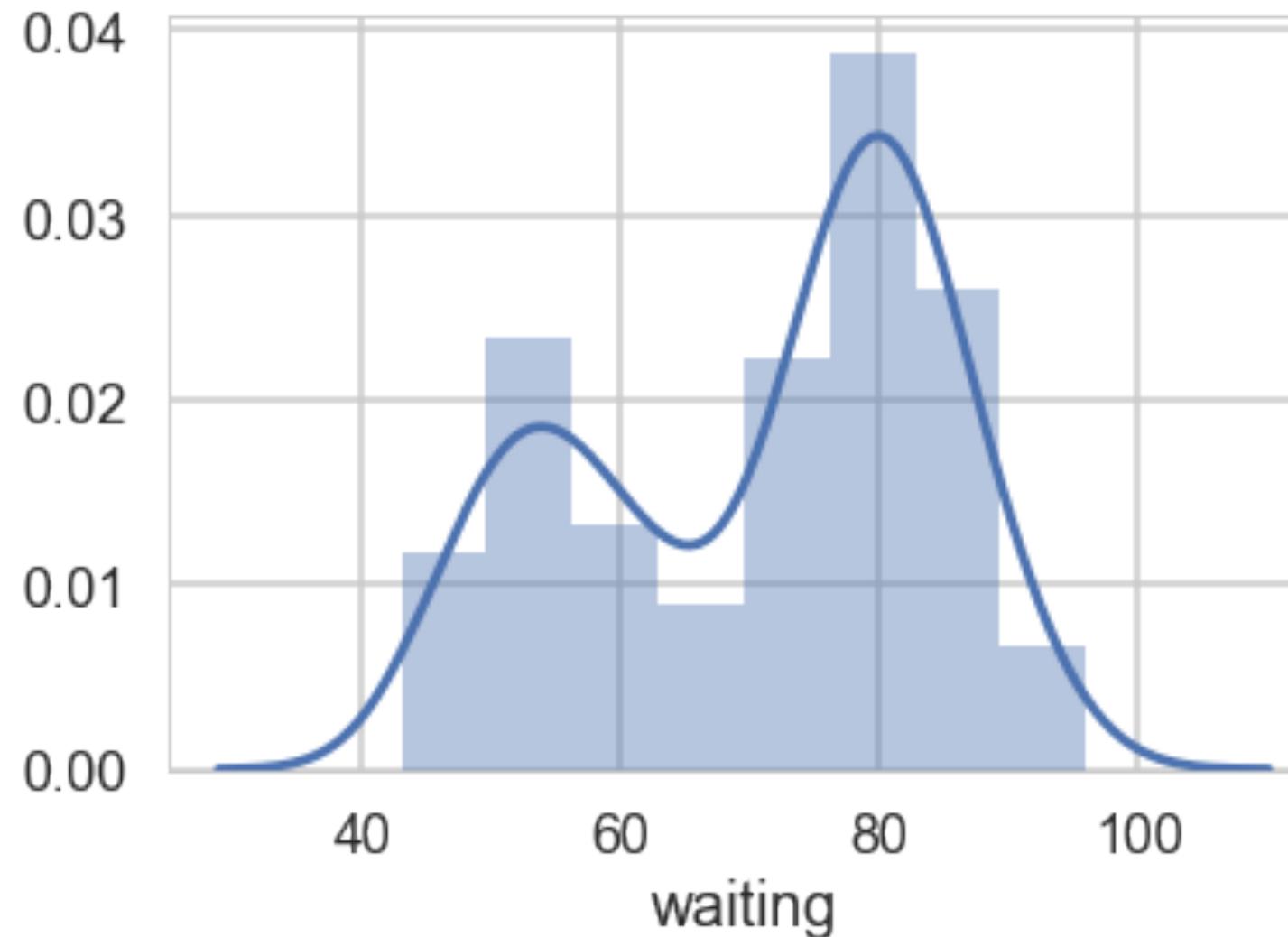
Generative:

```
mu_true = np.array([2, 5, 10])
sigma_true = np.array([0.6, 0.8, 0.5])
lambda_true = np.array([.4, .2, .4])
n = 10000

# Simulate from each distribution according to mixing proportion psi
z = multinomial.rvs(1, lambda_true, size=n) #categorical
x=np.array([np.random.normal(mu_true[i.astype('bool')][0],\
    sigma_true[i.astype('bool')][0]) for i in z])

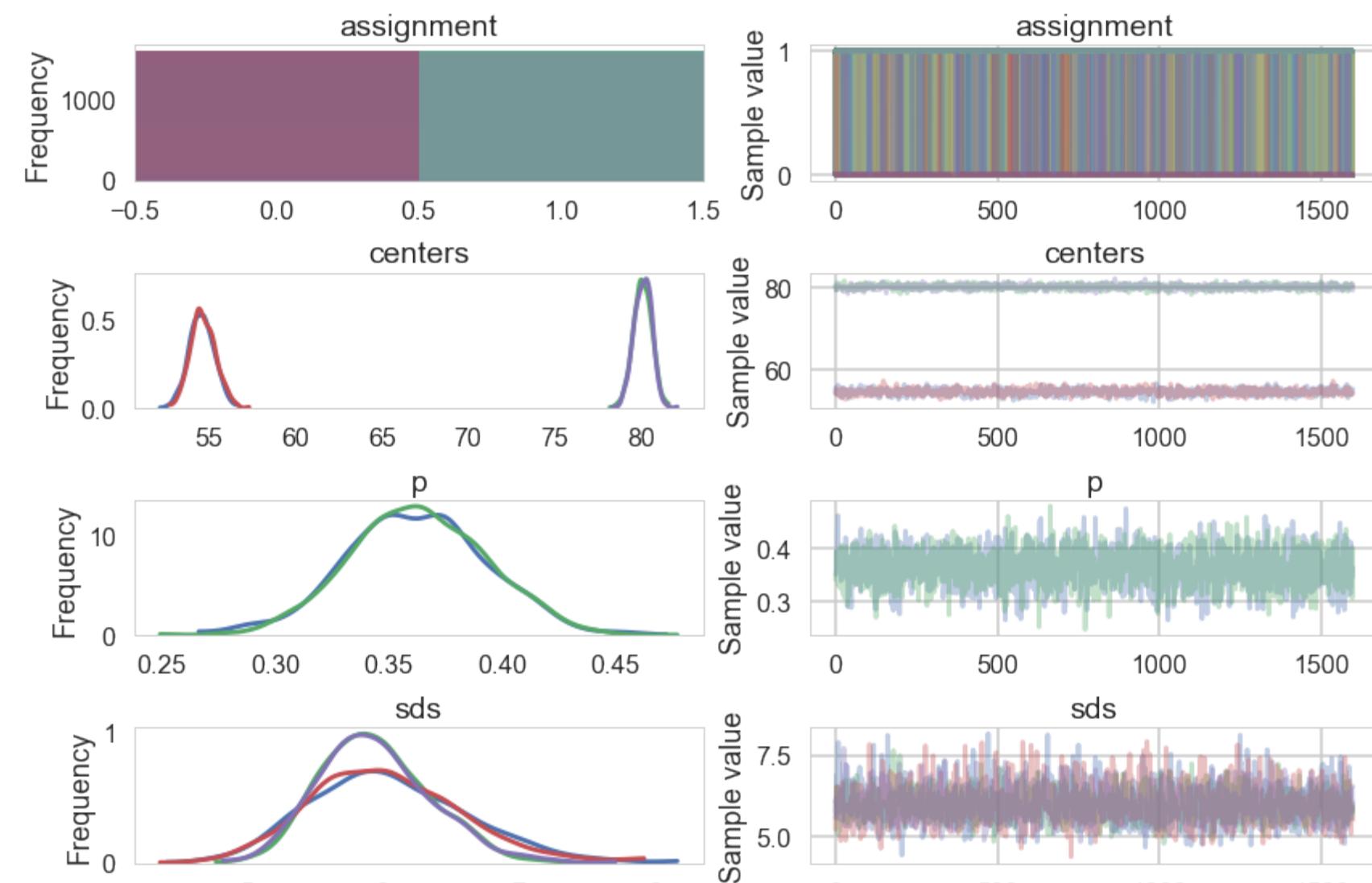
multinomial.rvs(1,[0.6,0.1, 0.3], size=10)
array([[1, 0, 0],[0, 0, 1],...[1, 0, 0],[1, 0, 0]])
```

Old faithful Geyser



Sampling mixture models: 2 Gaussians

```
with pm.Model() as ofmodel:  
    p1 = pm.Uniform('p', 0, 1)  
    p2 = 1 - p1  
    p = tt.stack([p1, p2])  
    assignment = pm.Categorical("assignment", p,  
                                 shape=ofdata.shape[0])  
    sds = pm.Uniform("sds", 0, 40, shape=2)  
    centers = pm.Normal("centers",  
                         mu=np.array([50, 80]),  
                         sd=np.array([20, 20]),  
                         shape=2)  
  
    observations = pm.Normal("obs",  
                             mu=centers[assignment],  
                             sd=sds[assignment],  
                             observed=ofdata.waiting)
```



Supervised vs Unsupervised Learning

In **Supervised Learning**, Latent Variables \mathbf{z} are observed.

In other words, we can write the full-data likelihood $p(\mathbf{x}, \mathbf{z})$

In **Unsupervised Learning**, Latent Variables \mathbf{z} are hidden.

We can only write the observed data likelihood:

$$p(\mathbf{x}) = \sum_z p(\mathbf{x}, \mathbf{z}) = \sum_z p(\mathbf{z})p(\mathbf{x}|\mathbf{z})$$

GMM supervised formulation

$$Z \sim \text{Bernoulli}(\lambda)$$

$$X|z=0 \sim \mathcal{N}(\mu_0, \Sigma_0), X|z=1 \sim \mathcal{N}(\mu_1, \Sigma_1)$$

Full-data loglike:
$$l(x, z|\lambda, \mu_0, \mu_1, \Sigma) = -\sum_{i=1}^m \log((2\pi)^{n/2} |\Sigma|^{1/2})$$
$$-\frac{1}{2} \sum_{i=1}^m \sum_{i=1}^m (x - \mu_{z_i})^T \Sigma^{-1} (x - \mu_{z_i}) + \sum_{i=1}^m [z_i \log \lambda + (1 - z_i) \log(1 - \lambda)]$$

```

with pm.Model() as classmodel1:
    p1 = pm.Uniform('p', 0, 1)
    p2 = 1 - p1
    p = tt.stack([p1, p2])
    #Notice the "observed" below
    assignment_tr = pm.Categorical("assignment_tr", p,
                                    observed=ztr)
    sds = pm.Uniform("sds", 0, 100, shape=2)
    centers = pm.Normal("centers",
                         mu=np.array([130, 170]),
                         sd=np.array([20, 20]),
                         shape=2)
    p_min_potential = pm.Potential('lam_min_potential', tt.switch(tt.min(p) < .1, -np.inf, 0))
    order_centers_potential = pm.Potential('order_centers_potential',
                                           tt.switch(centers[1]-centers[0] < 0, -np.inf, 0))

    # and to combine it with the observations:
    observations = pm.Normal("obs", mu=centers[assignment_tr], sd=sds[assignment_tr], observed=xtr)

```

Solution to MLE

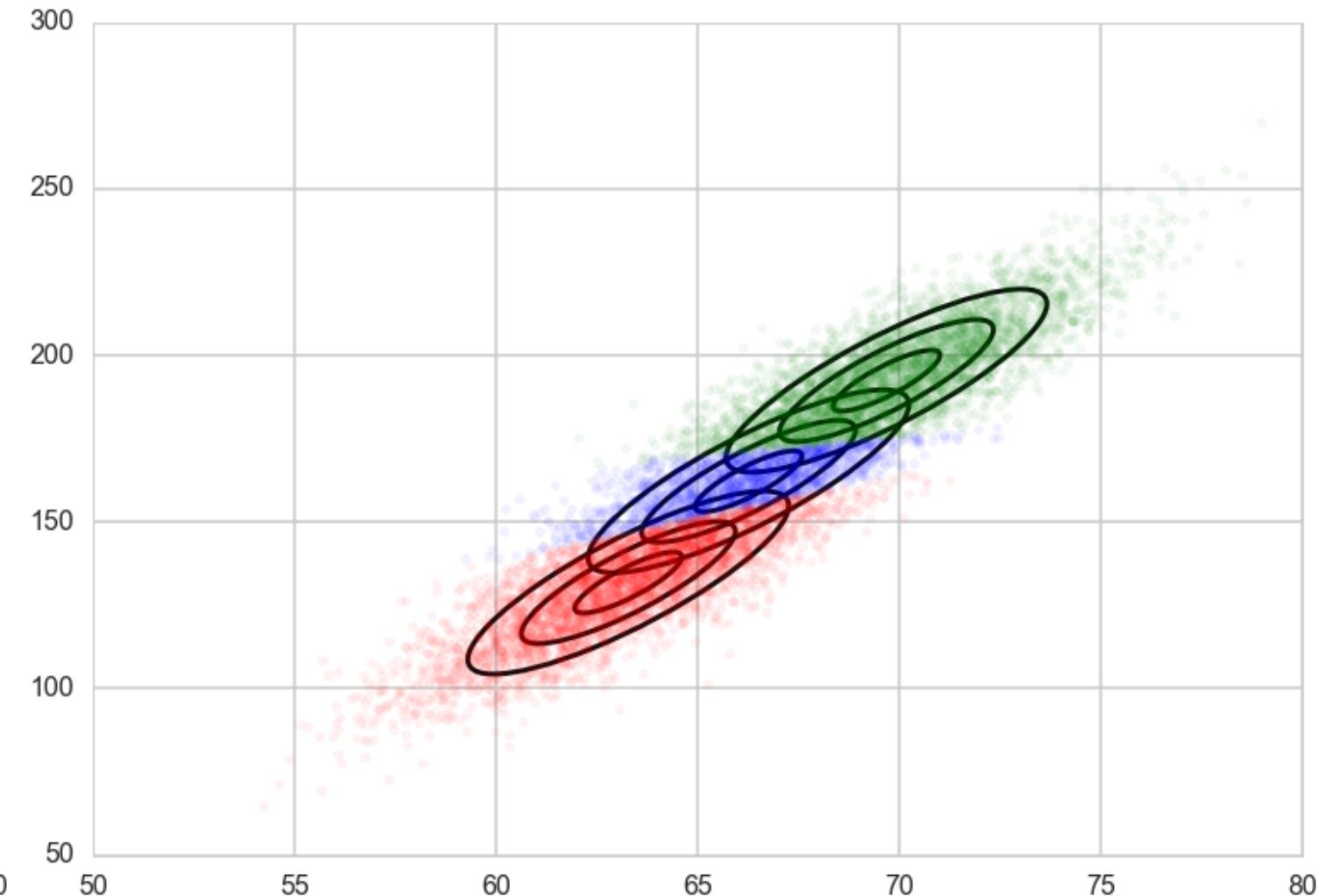
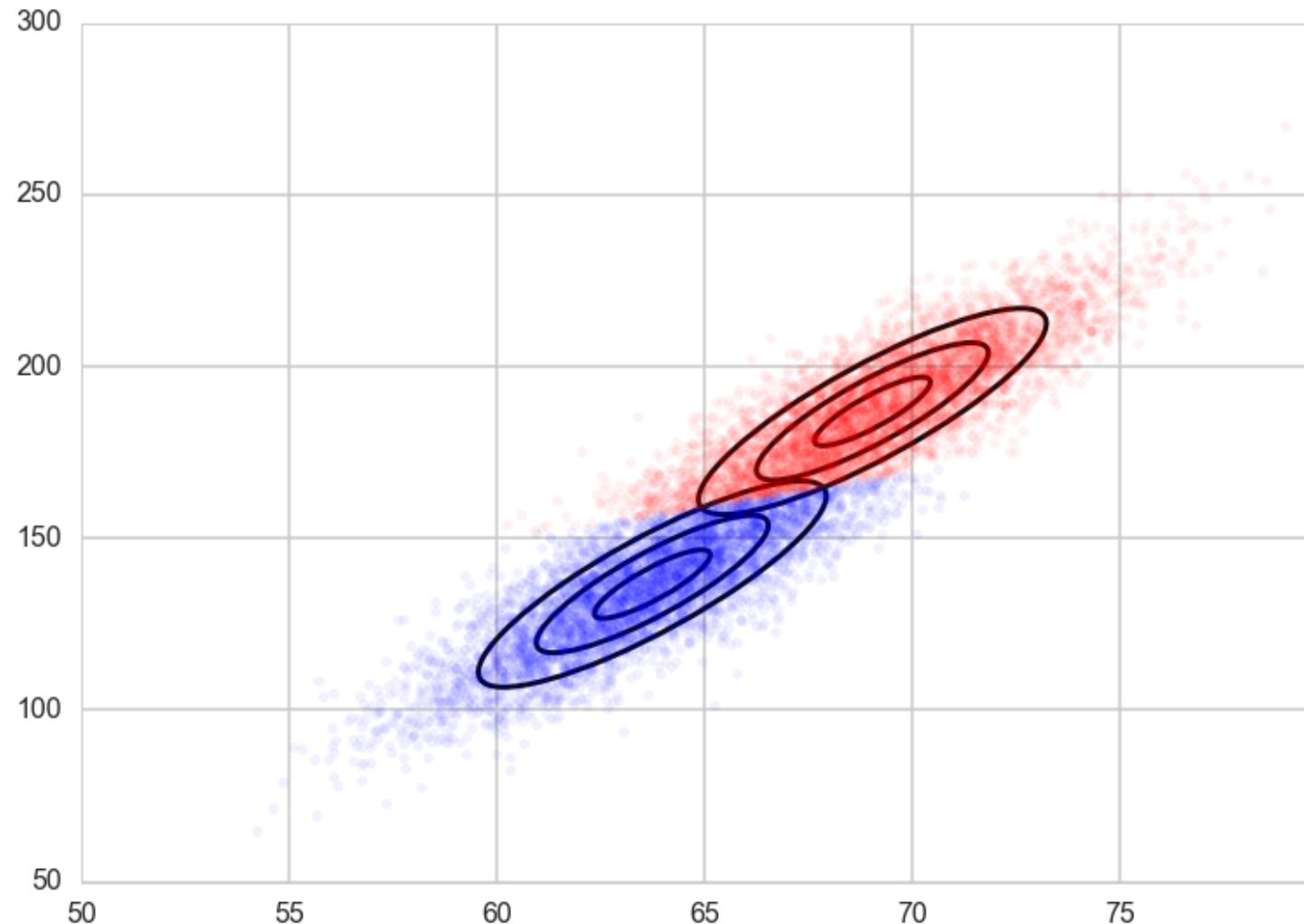
$$\lambda = \frac{1}{m} \sum_{i=1}^m \delta_{z_i,1}$$

$$\mu_0 = \frac{\sum_{i=1}^m \delta_{z_i,0} x_i}{\sum_{i=1}^m \delta_{z_i,0}}$$

$$\mu_1 = \frac{\sum_{i=1}^m \delta_{z_i,1} x_i}{\sum_{i=1}^m \delta_{z_i,1}}$$

$$\Sigma = \frac{1}{m} \sum_{i=1}^m (x_i - \mu_{z_i})(x_i - \mu_{z_i})^T$$

Unsupervised Learning. How many z?



Concrete Formulation of unsupervised learning

Estimate Parameters by \mathbf{x} -MLE:

$$\begin{aligned} l(x|\lambda, \mu, \Sigma) &= \sum_{i=1}^m \log p(x_i|\lambda, \mu, \Sigma) \\ &= \sum_{i=1}^m \log \sum_z p(x_i|z_i, \mu, \Sigma) p(z_i|\lambda) \end{aligned}$$

Not Solvable analytically! EM and Variational. Or do MCMC.

```

with pm.Model() as classmodel1:
    p1 = pm.Uniform('p', 0, 1)
    p2 = 1 - p1
    p = tt.stack([p1, p2])
    #Notice NO "observed" below
    assignment_tr = pm.Categorical("assignment_tr", p)
    sds = pm.Uniform("sds", 0, 100, shape=2)
    centers = pm.Normal("centers",
                         mu=np.array([130, 170]),
                         sd=np.array([20, 20]),
                         shape=2)
    p_min_potential = pm.Potential('lam_min_potential', tt.switch(tt.min(p) < .1, -np.inf, 0))
    order_centers_potential = pm.Potential('order_centers_potential',
                                           tt.switch(centers[1]-centers[0] < 0, -np.inf, 0))

    # and to combine it with the observations:
    observations = pm.Normal("obs", mu=centers[assignment_tr], sd=sds[assignment_tr], observed=xtr)

```

Semi-supervised learning

We have some labels, but typically very few labels: not enough to form a good training set. Likelihood a combination.

$$\begin{aligned} l(\{x_i\}, \{x_j\}, \{z_i\} | \theta, \lambda) &= \sum_i \log p(x_i, z_i | \lambda, \theta) + \sum_j \log p(x_j | \lambda, \theta) \\ &= \sum_i \log p(z_i | \lambda) p(x_i | z_i, \theta) + \sum_j \log \sum_z p(z_j | \lambda) p(x_j | z_j, \theta) \end{aligned}$$

Here i ranges over the data points where we have labels, and j over the data points where we dont.

```

with pm.Model() as classmodel2:
    p1 = pm.Uniform('p', 0, 1)
    p2 = 1 - p1
    p = tt.stack([p1, p2])
    assignment_tr = pm.Categorical("assignment_tr", p,
                                    observed=ztr)
    # we do not know the test assignments
    assignment_te = pm.Categorical("assignment_te", p,
                                    shape=xte.shape[0])
    sds = pm.Uniform("sds", 0, 100, shape=2)
    centers = pm.Normal("centers",
                         mu=np.array([130, 170]),
                         sd=np.array([20, 20]),
                         shape=2)
    p_min_potential = pm.Potential('lam_min_potential', tt.switch(tt.min(p) < .1, -np.inf, 0))
    order_centers_potential = pm.Potential('order_centers_potential',
                                           tt.switch(centers[1]-centers[0] < 0, -np.inf, 0))

    # and to combine it with the observations:
    observations_tr = pm.Normal("obs_tr", mu=centers[assignment_tr], sd=sds[assignment_tr], observed=xtr)
    observations_te = pm.Normal("obs_te", mu=centers[assignment_te], sd=sds[assignment_te], observed=xte)

```

EXPECTATION MAXIMIZATION

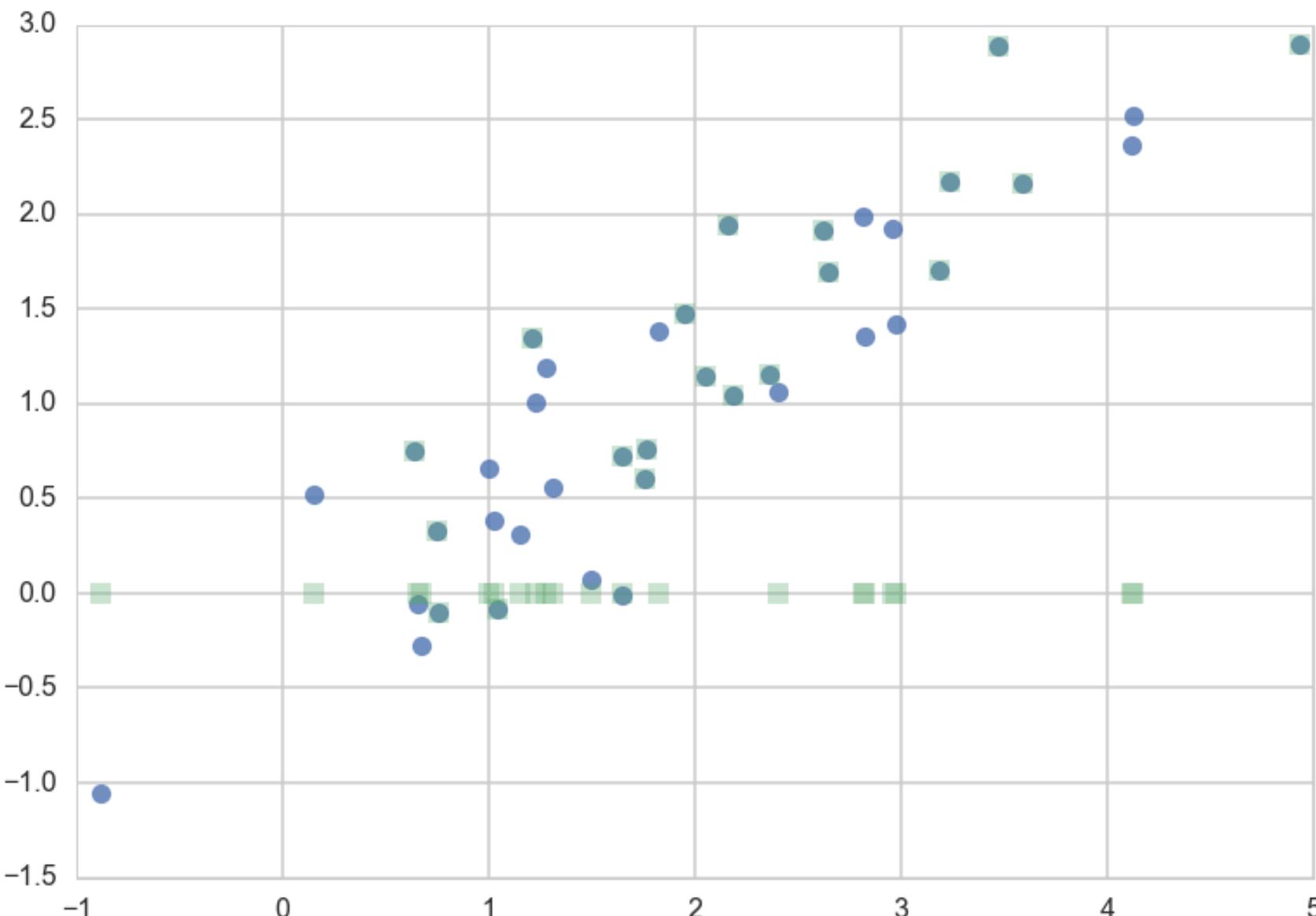
calculate MLE estimates for the incomplete data problem by using the complete-data likelihood. To create complete data, augment the observed data with manufactured data

Toy Example: 2D Gaussian

$$\begin{pmatrix} x_{1i} \\ x_{2i} \end{pmatrix} \stackrel{\text{ind}}{\sim} \mathcal{N}_2 \left(\begin{pmatrix} \mu_1 \\ \mu_2 \end{pmatrix}, \begin{pmatrix} \sigma_1^2 & \sigma_1\sigma_2\rho \\ \sigma_1\sigma_2\rho & \sigma_2^2 \end{pmatrix} \right)$$

```
sig1=1  
sig2=0.75  
mu1=1.85  
mu2=1  
rho=0.82  
means=np.array([mu1, mu2])  
cov = np.array([  
    [sig1**2, sig1*sig2*rho],  
    [sig2*sig1*rho, sig2**2]  
])
```

Lose z = 20 y-values. Set to 0.



MLE for full data problem

$$\hat{\mu}_1 = \sum_1^{40} x_{1i}/40, \quad \hat{\mu}_2 = \sum_1^{40} x_{2i}/40,$$

$$\hat{\sigma}_1 = \left[\sum_1^{40} (x_{1i} - \hat{\mu}_1)^2 / 40 \right]^{1/2}, \quad \hat{\sigma}_2 = \left[\sum_1^{40} (x_{2i} - \hat{\mu}_2)^2 / 40 \right]^{1/2},$$

$$\hat{\rho} = \left[\sum_1^{40} (x_{1i} - \hat{\mu}_1)(x_{2i} - \hat{\mu}_2) / 40 \right] / (\hat{\sigma}_1 \hat{\sigma}_2),$$

```
mu1 = lambda s: np.mean(s[:,0])
mu2 = lambda s: np.mean(s[:,1])
s1 = lambda s: np.std(s[:,0])
s2 = lambda s: np.std(s[:,1])
rho = lambda s: np.mean((s[:,0] - mu1(s))*(s[:,1] - mu2(s)))/(s1(s)*s2(s))
```

But we dont have full data.

Use Censored data with initial imputation

M-step: Maximizing full-data MLE

```
mu1s.append(mu1(samples_censored))
mu2s.append(mu2(samples_censored))
s1s.append(s1(samples_censored))
s2s.append(s2(samples_censored))
rhos.append(rho(samples_censored))
```

M-step done. Use these parameters let us calculate new y-values.

Replace the old-missing-y values (0s) with the means of these fixing the parameters of the multi-variate normal and the non-missing data.

E-step

Use expectation from hidden-data posterior distrib: $E_{p(z|\theta,x)}[z]$

This **posterior** distribution (in the sense of bayes theorem, not bayesian analysis) for the multi-variate gaussian is a gaussian..see [wikipedia](#) for the formulae

$$\bar{y}(t+1) - \hat{\mu}_2(t) = \hat{\rho}(t) \frac{\hat{\sigma}_2(t)}{\hat{\sigma}_1(t)} (\bar{x} - \hat{\mu}_1(t))$$

Iterate

```
def ynew(x, mu1, mu2, s1, s2, rho):
    return mu2 + rho*(s2/s1)*(x - mu1)

newys=ynew(samples_censored[20:,0], mu1s[0], mu2s[0], s1s[0], s2s[0], rhos[0])

for step in range(1,20):
    samples_censored[20:,1] = newys
    #M-step
    mu1s.append(mu1(samples_censored))
    mu2s.append(mu2(samples_censored))
    s1s.append(s1(samples_censored))
    s2s.append(s2(samples_censored))
    rhos.append(rho(samples_censored))
    #E-step
    newys=ynew(samples_censored[20:,0], mu1s[step], mu2s[step], s1s[step], s2s[step], rhos[step])
```

Voila. We converge to stable values of our parameters. Initials:

$\text{sig1}=1$

$\text{sig2}=0.75$

$\text{mu1}=1.85$

$\text{mu2}=1$

$\text{rho}=0.82$

But they may not be the ones we seeded the samples with. The EM algorithm is only good upto finding local minima, and a finite sample size also means that the minimum found can be slightly different.

	mu1	mu2	rho	s1	s2
0	1.966883	0.662900	0.522613	1.185731	0.889247
1	1.966883	0.949428	0.850340	1.185731	0.782217
2	1.966883	1.073320	0.926036	1.185731	0.811543
3	1.966883	1.126917	0.941491	1.185731	0.837711
4	1.966883	1.150122	0.945313	1.185731	0.851228
5	1.966883	1.160180	0.946476	1.185731	0.857421
6	1.966883	1.164547	0.946888	1.185731	0.860139
7	1.966883	1.166447	0.947048	1.185731	0.861307
8	1.966883	1.167277	0.947113	1.185731	0.861801
9	1.966883	1.167641	0.947139	1.185731	0.862008
10	1.966883	1.167802	0.947150	1.185731	0.862092
11	1.966883	1.167874	0.947154	1.185731	0.862125
12	1.966883	1.167907	0.947156	1.185731	0.862137
13	1.966883	1.167922	0.947156	1.185731	0.862141
14	1.966883	1.167929	0.947157	1.185731	0.862142
15	1.966883	1.167933	0.947157	1.185731	0.862142
16	1.966883	1.167934	0.947156	1.185731	0.862142
17	1.966883	1.167935	0.947156	1.185731	0.862141
18	1.966883	1.167936	0.947156	1.185731	0.862141
19	1.966883	1.167936	0.947156	1.185731	0.862141

The EM algorithm

- iterative method for maximizing difficult likelihood (or posterior) problems, first introduced by Dempster, Laird, and Rubin in 1977
- Sorta like, just assign points to clusters to start with and iterate.
- Then, at each iteration, replace the augmented data by its conditional expectation given current observed data and parameter estimates. (E-step)
- Maximize the full-data likelihood (M-step).

Why does it work?

$$p(x|\theta) = \sum_z p(x, z|\theta)$$

where the x and z range over the multiple points in your data set.

Then x-data log-likelihood $\ell(x|\theta) = \log p(x|\theta) = \log \sum_z p(x, z|\theta).$

Hard to maximize for us.

Assume z has some normalized distribution:

$$z \sim q(z).$$

We wish to compute conditional expectations of the type:

$$E_{p(z|x,\theta)}[z]$$

but we dont know this "posterior" (henceforth p).

Lets say we somehow know q .

Consider KL loss function

$$\text{KL}(q||p) = D_{KL}(q, p) = E_q[\log \frac{q}{p}] = -E_q[\log \frac{p}{q}]$$

$$D_{KL}(q, p) = -E_q[\log \frac{p(x, z|\theta)}{q p(x|\theta)}]$$

$$D_{KL}(q, p) = - \left(E_q[\log \frac{p(x, z|\theta)}{q}] - E_q[\log p(x|\theta)] \right)$$

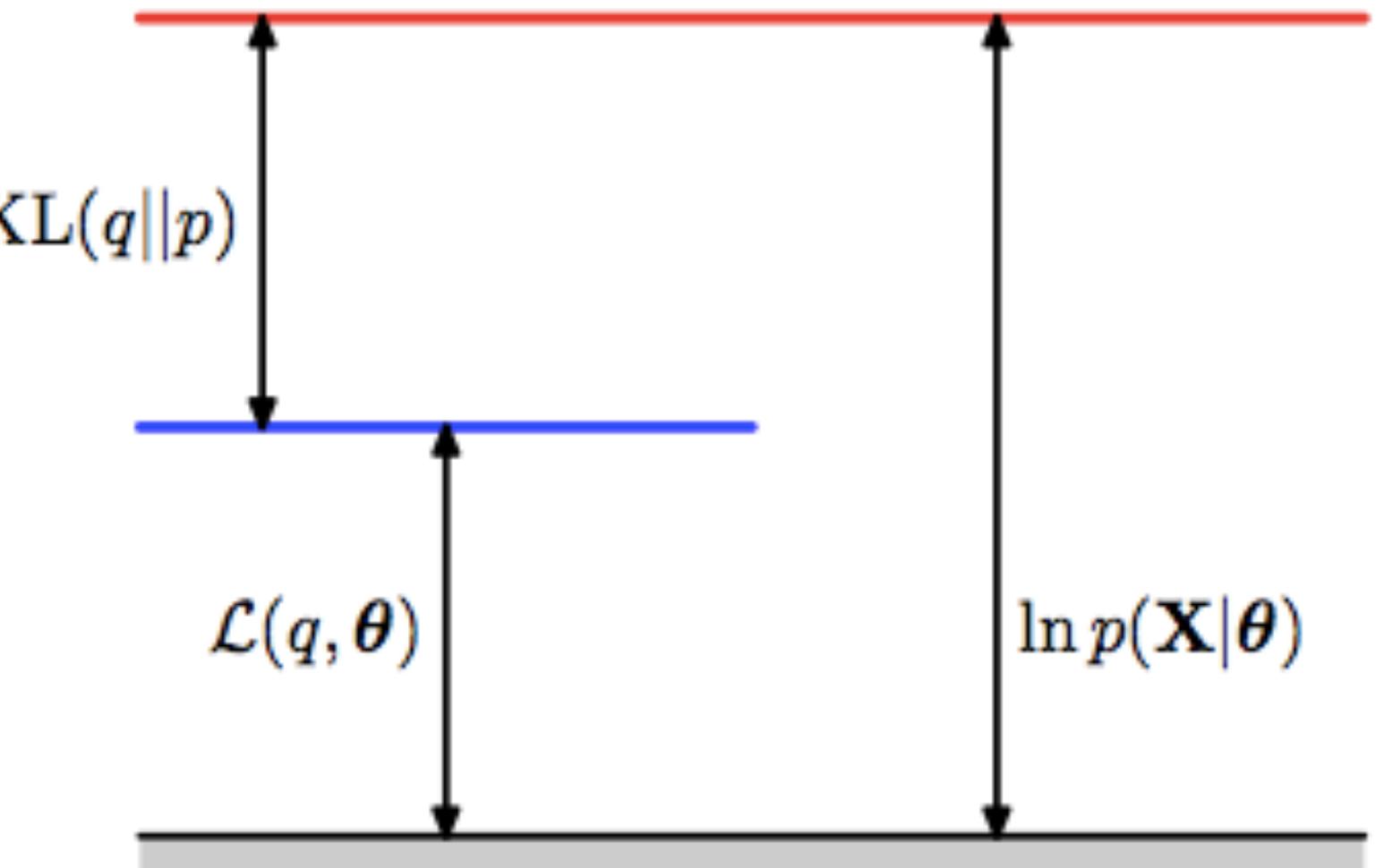
x-data likelihood

$$\log p(x|\theta) = E_q[\log \frac{p(x, z|\theta)}{q}] + D_{KL}(q, p)$$

If we define the ELBO or Evidence Lower bound as:

$$\mathcal{L}(q, \theta) = E_q[\log \frac{p(x, z|\theta)}{q}]$$

then $\log p(x|\theta) = \text{ELBO} + \text{KL-divergence}$



- KL divergence only 0 when $p = q$ exactly everywhere
- minimizing KL means maximizing ELBO
- ELBO $\mathcal{L}(q, \theta)$ is a lower bound on the log-likelihood.
- ELBO is average full-data likelihood minus entropy of q :

$$\mathcal{L}(q, \theta) = E_q[\log \frac{p(x, z|\theta)}{q}] = E_q[\log p(x, z|\theta)] - E_q[\log q]$$

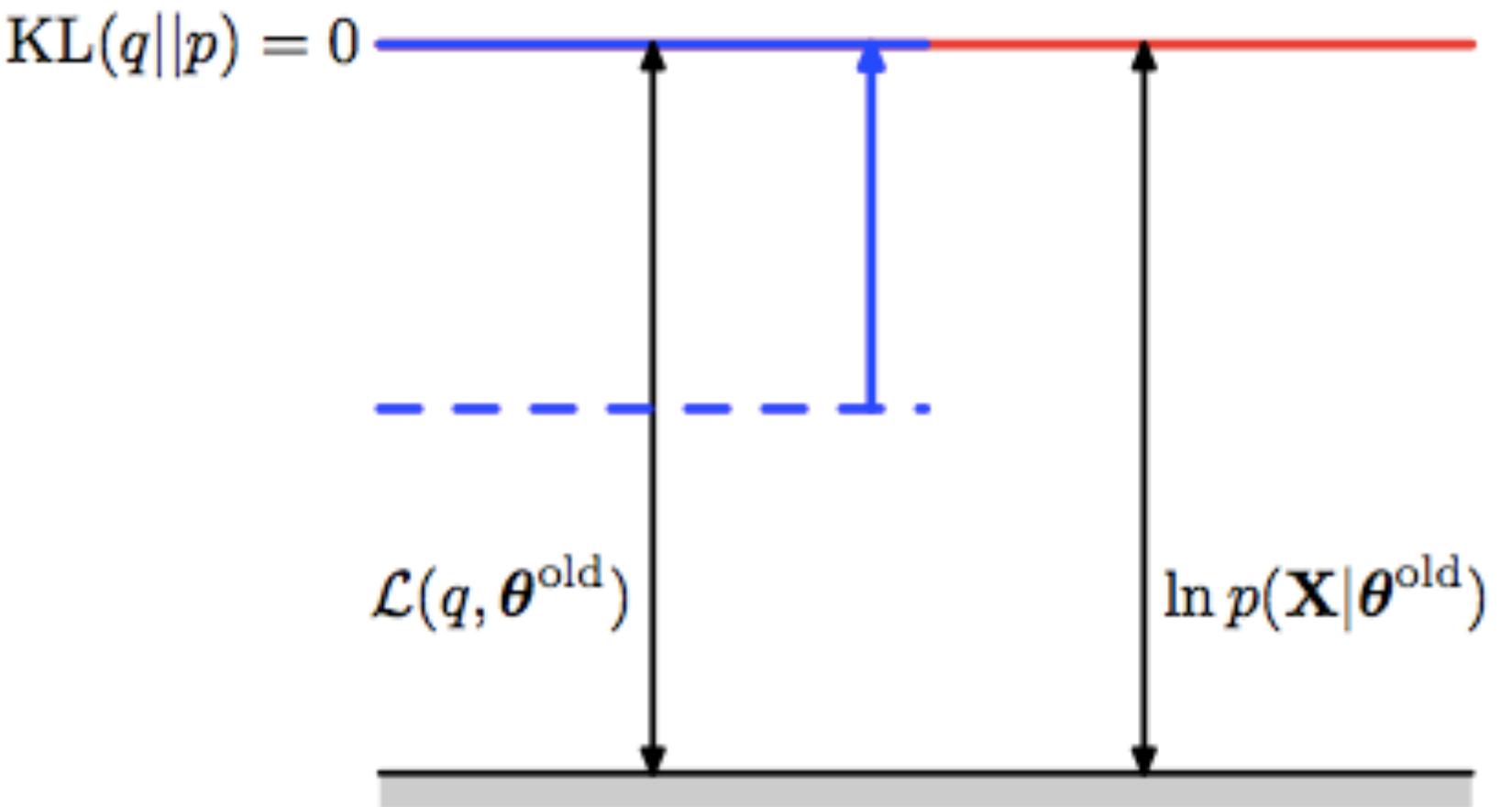
E-step

Choose at some (possibly initial) value of the parameters θ_{old} ,

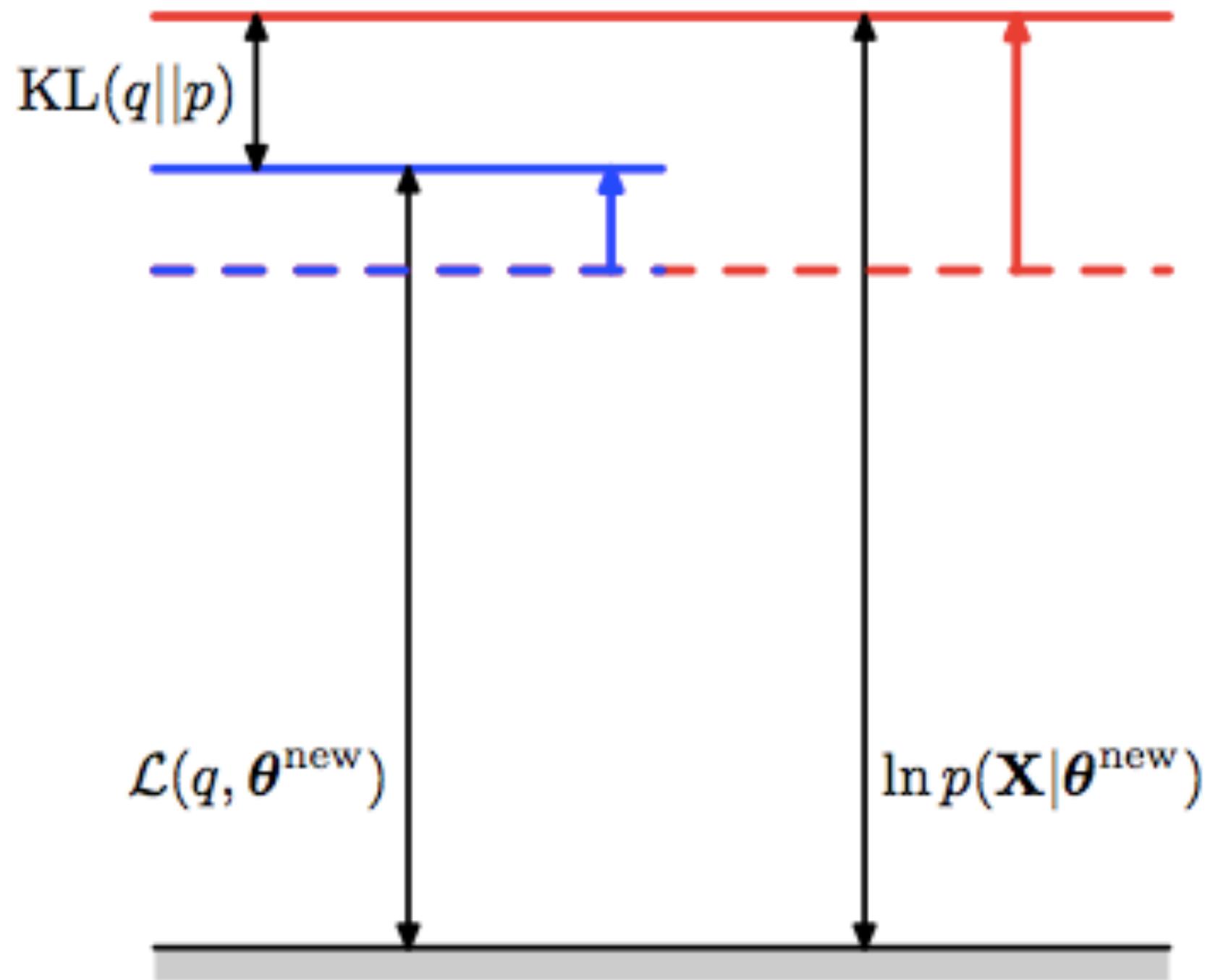
$$q(z) = p(z|x, \theta_{old}),$$

then KL divergence = 0, and thus $\mathcal{L}(q, \theta) =$ log-likelihood at θ_{old} , maximizing the ELBO.

Conditioned on observed data, and θ_{old} , we use q to compute the expectation of the missing data.



M-step



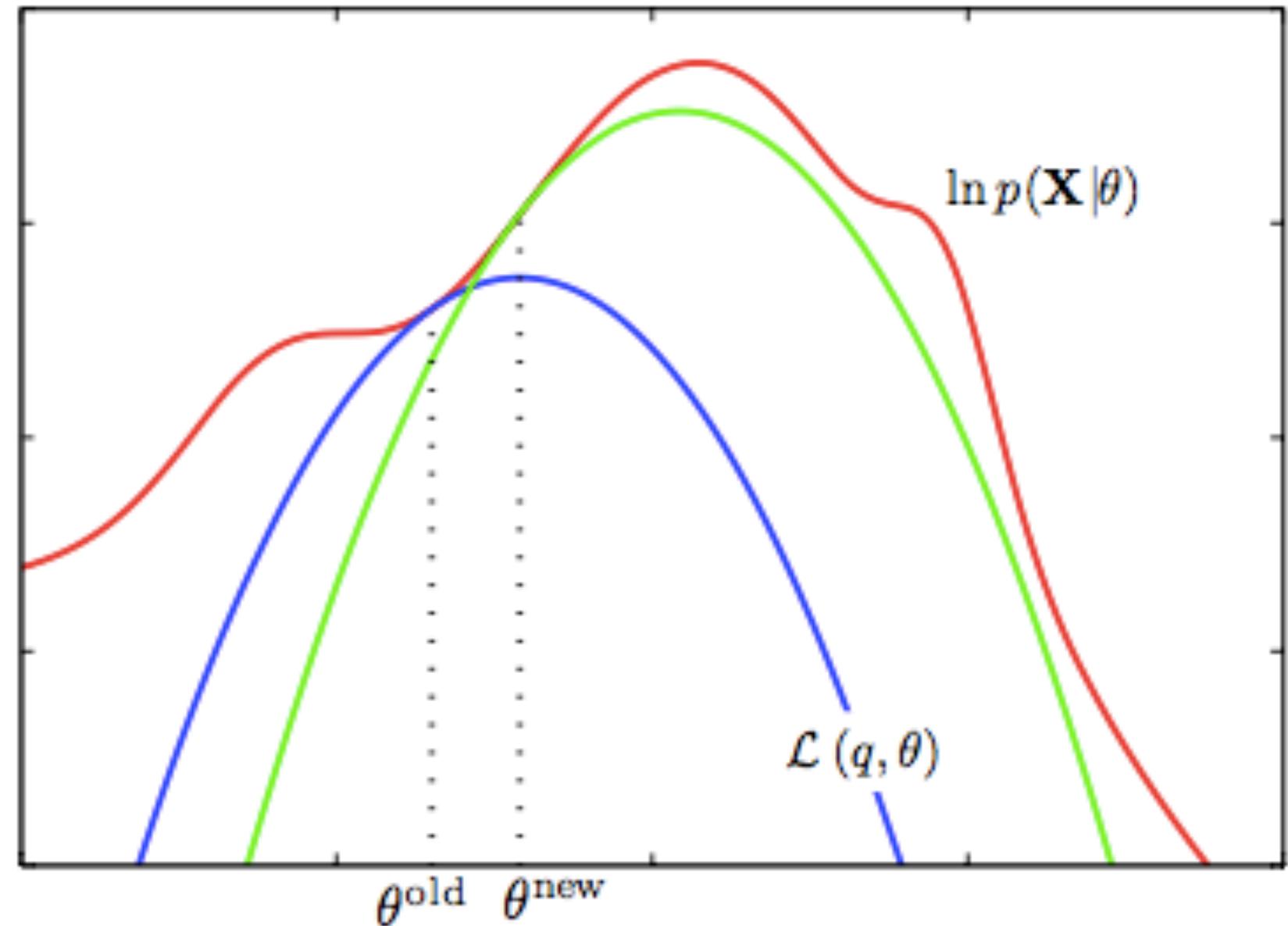
After E-step, ELBO touches $\ell(x|\theta)$, any maximization from ELBO's current value wrt θ will also “push up” on likelihood, thus increasing it.

Thus hold $q(z)$ fixed at the z-posterior calculated at θ_{old} , and maximize $\mathcal{L}(q, \theta)$ wrt θ to obtain new θ_{new} .

In general $q(\theta_{old}) \neq p(z|x, \theta_{new})$, hence $\text{KL} \neq 0$. Thus increase in $\ell(x|\theta) \geq$ increase in ELBO.

Process

1. Start with $\ln p(x|\theta)$ (red curve), θ_{old} .
2. Until convergence:
 1. E-step: Evaluate
$$q(z, \theta_{old}) = p(z|x, \theta_{old})$$
 which gives rise to ELBO(θ): $\mathcal{L}(q(z, \theta_{old}), \theta)$ (blue curve) whose value equals the value of $\ln p(x|\theta)$ at θ_{old} .
 2. M-step: maximize ELBO wrt θ to get θ_{new} .
 3. Set $\theta_{old} = \theta_{new}$



An iteration:

$$\ell(\theta_{t+1}) \geq \mathcal{L}(q(z, \theta_t), \theta_{t+1}) \geq \mathcal{L}(q(z, \theta_t), \theta_t) = \ell(\theta_t)$$

The first equality follows since \mathcal{L} is a lower bound on ℓ , the second from the M-step's maximization of \mathcal{L} , and the last from the vanishing of the KL-divergence after the E-step.

As a consequence, you **must** observe monotonic increase of the observed-data log likelihood ℓ across iterations. **This is a powerful debugging tool for your code.**

EM is local only!

Note that as shown above, since each EM iteration can only improve the likelihood, you are guaranteeing convergence to a local maximum. Because it IS local , you must try some different initial values of θ_{old} and take the one that gives you the largest ℓ .

GMM

E-step: Calculate $w_{i,j} = q_i(z_i = j) = p(z_i = j|x_i, \lambda, \mu, \Sigma)$

M-step: maximize: $\mathcal{L} = \sum_i \sum_{z_i} q_i(z_i) \log \frac{p(x_i, z_i | \lambda, \mu, \Sigma)}{q_i(z_i)}$

$$\mathcal{L} = \sum_i \sum_{j=i}^k q_i(z_i = j) \log \frac{p(x_i | z_i = j, \mu, \Sigma)p(z_i = j | \lambda)}{q_i(z_i = j)}$$

$$\mathcal{L} = \sum_{i=1}^m \sum_{j=i}^k w_{i,j} \log \left[\frac{\frac{1}{(2\pi)^{n/2} |\Sigma_j|^{1/2}} \exp\left(-\frac{1}{2}(x_i - \mu_j)^T \Sigma_j^{-1} (x_i - \mu_j)\right) \lambda_j}{w_{i,j}} \right]$$

M-step

Taking derivatives yields following updating formulas:

$$\lambda_j = \frac{1}{m} \sum_{i=1}^m w_{i,j}$$

$$\mu_j = \frac{\sum_{i=1}^m w_{i,j} x_i}{\sum_{i=1}^m w_{i,j}}$$

$$\Sigma_j = \frac{\sum_{i=1}^m w_{i,j} (x_i - \mu_j)(x_i - \mu_j)^T}{\sum_{i=1}^m w_{i,j}}$$

E-step

We are basically calculating the posterior of the z 's given the x 's and the current estimate of our parameters. We can use Bayes rule

$$w_{i,j} = p(z_i = j|x_i, \lambda, \mu, \Sigma) = \frac{p(x_i|z_i = j, \mu, \Sigma) p(z_i = j|\lambda)}{\sum_{l=1}^k p(x_i|z_i = l, \mu, \Sigma) p(z_i = l|\lambda)}$$

Where $p(x_i|z_i = j, \mu, \Sigma)$ is the density of the Gaussian with mean μ_j and covariance Σ_j at x_i and $p(z_i = j|\lambda)$ is simply λ_j .

```
def Estep(x, mu, sigma, lam):
    a = lam * norm.pdf(x, mu[0], sigma[0])
    b = (1. - lam) * norm.pdf(x, mu[1], sigma[1])
    return b / (a + b)

def Mstep(x, w):
    lam = np.mean(1.-w)

    mu = [np.sum((1-w) * x)/np.sum(1-w), np.sum(w * x)/np.sum(w)]

    sigma = [np.sqrt(np.sum((1-w) * (x - mu[0])**2)/np.sum(1-w)),
             np.sqrt(np.sum(w * (x - mu[1])**2)/np.sum(w))]

    return mu, sigma, lam
```

```
0.4 [2, 5] [0.6, 0.6]
Initials, mu: [-4.85176052  5.51133343]
Initials, sigma: [ 2.02807915  3.58912888]
Initials, lam: 0.5418931691319009
Iterations 71
A: N(2.0261, 0.5936)
B: N(5.0083, 0.6288)
lam: 0.5884
```

```
0.4 [2, 5] [0.6, 0.6]
Initials, mu: [ 11.09643621 -4.48315085]
Initials, sigma: [ 4.31750531  0.95518757]
Initials, lam: 0.5767814041950222
Iterations 103
A: N(5.0083, 0.6288)
B: N(2.0261, 0.5936)
lam: 0.4116
```

Compared to supervised classification

- M-step formulas vs GDA we can see that are very similar except that instead of using δ functions we use the w 's.
- Thus the EM algorithm corresponds here to a weighted maximum likelihood and the weights are interpreted as the 'probability' of coming from that Gaussian
- Thus we have achieved a **soft clustering** (as opposed to k-means in the unsupervised case and classification in the supervised case).

Oceanic Tools

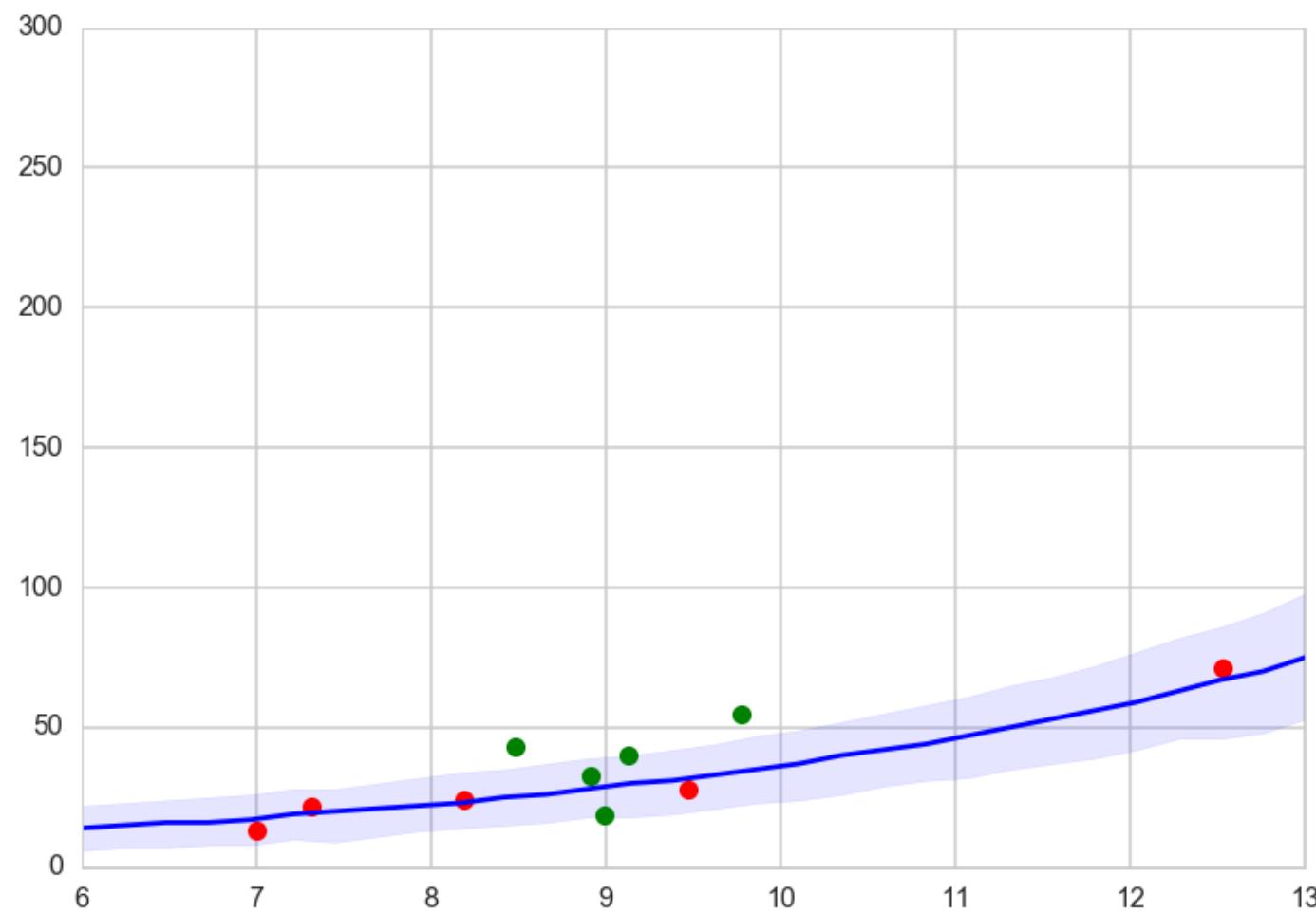
From Mcelreath:

The island societies of Oceania provide a natural experiment in technological evolution. Different historical island populations possessed tool kits of different size. These kits include fish hooks, axes, boats, hand plows, and many other types of tools. A number of theories predict that larger populations will both develop and sustain more complex tool kits. So the natural variation in population size induced by natural variation in island size in Oceania provides a natural



Overdispersion for only p

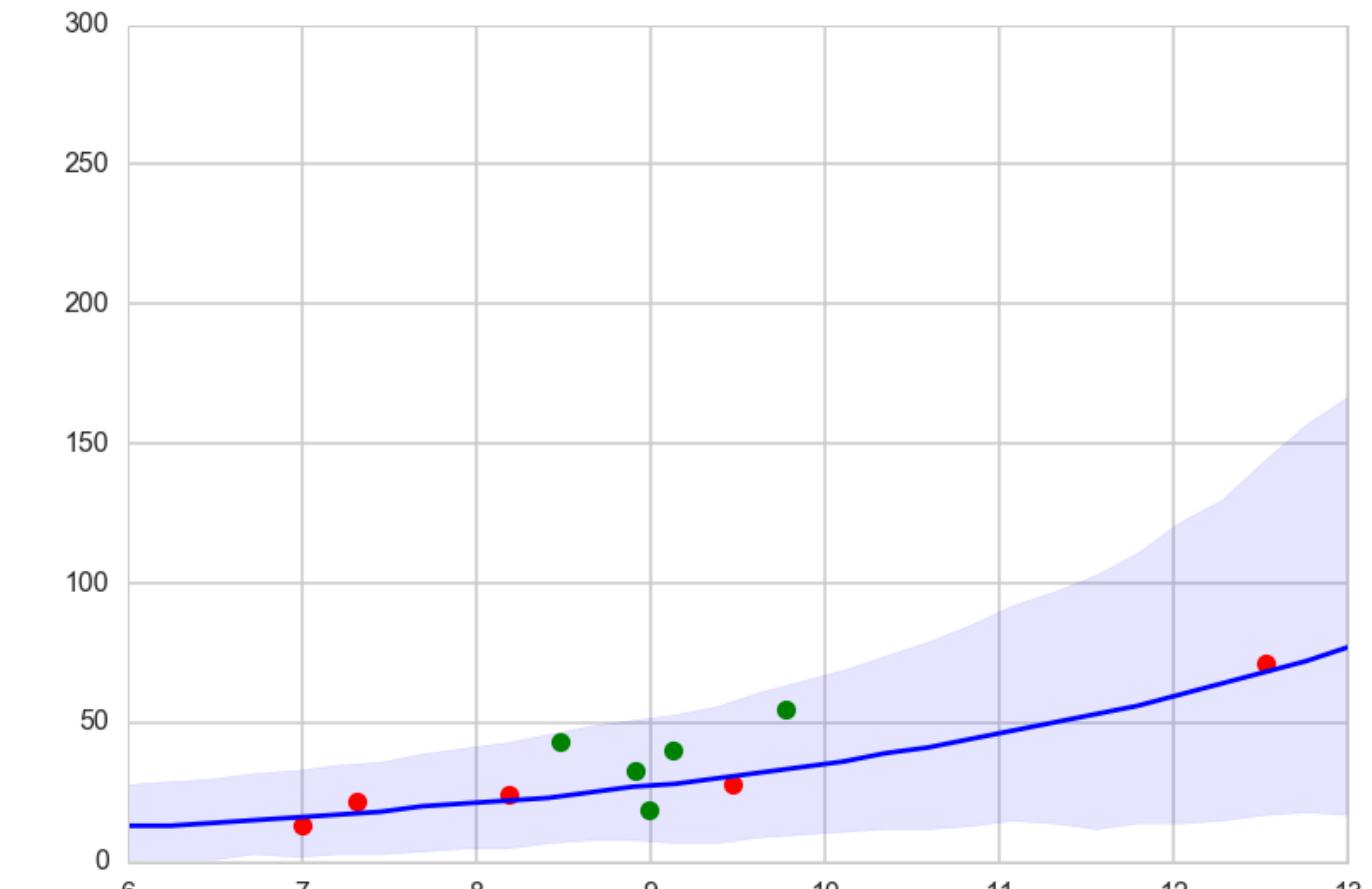
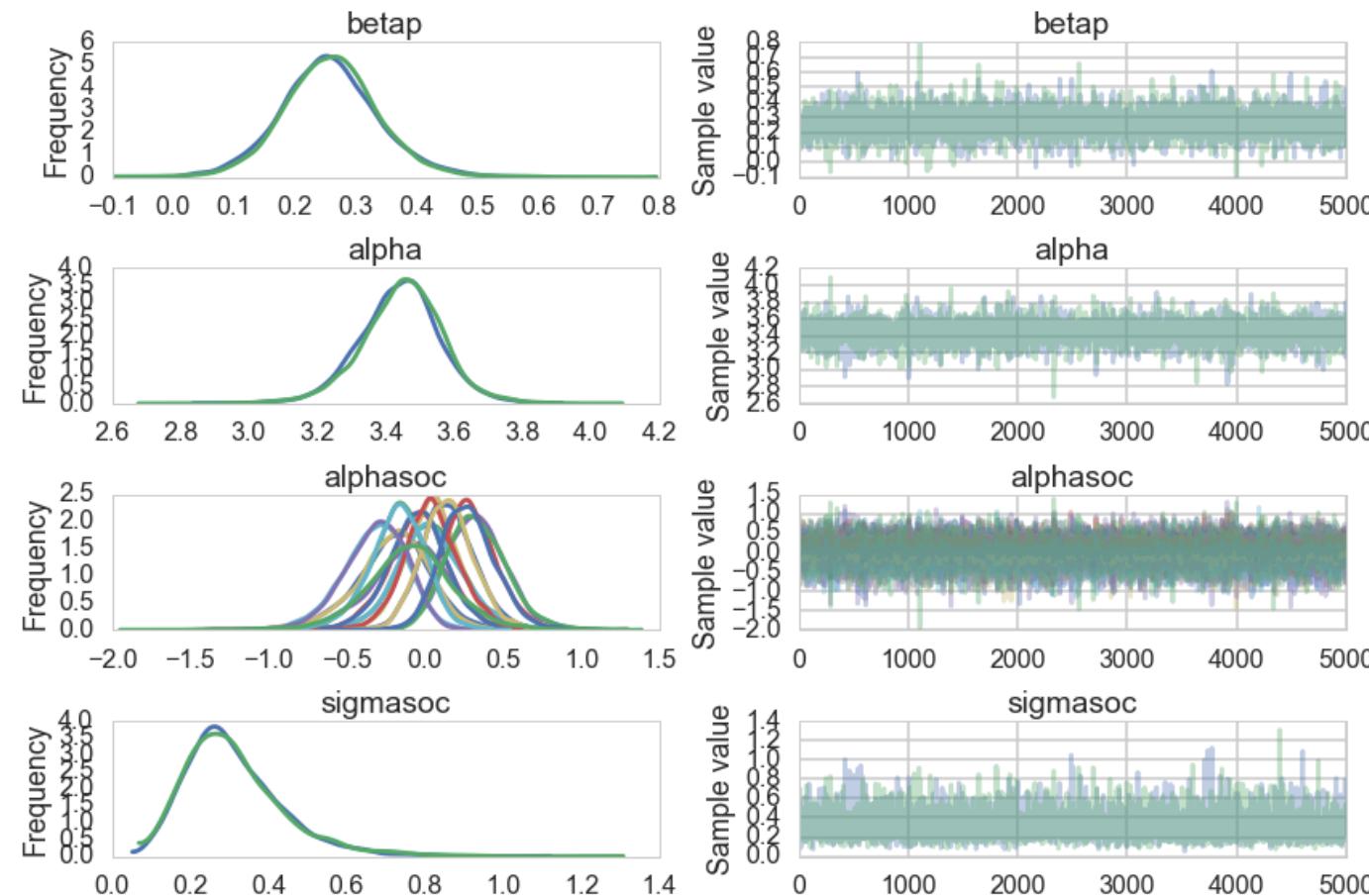
```
m2c_onlyp: loglam = alpha + betap*df.logpop_c
```



Varying hierarchical intercepts model

```
with pm.Model() as m3c:  
    betap = pm.Normal("betap", 0, 1)  
    alpha = pm.Normal("alpha", 0, 100)  
    sigmasoc = pm.HalfCauchy("sigmasoc", 1)  
    alphasoc = pm.Normal("alphasoc", 0, sigmasoc, shape=df.shape[0])  
    loglam = alpha + alphasoc + betap*df.logpop_c  
    y = pm.Poisson("ntools", mu=t.exp(loglam), observed=df.total_tools)
```

Hierarchical Model Posterior predictive



much wider, includes data areas

What if we model the correlation between societies based on the distance between them?

How?

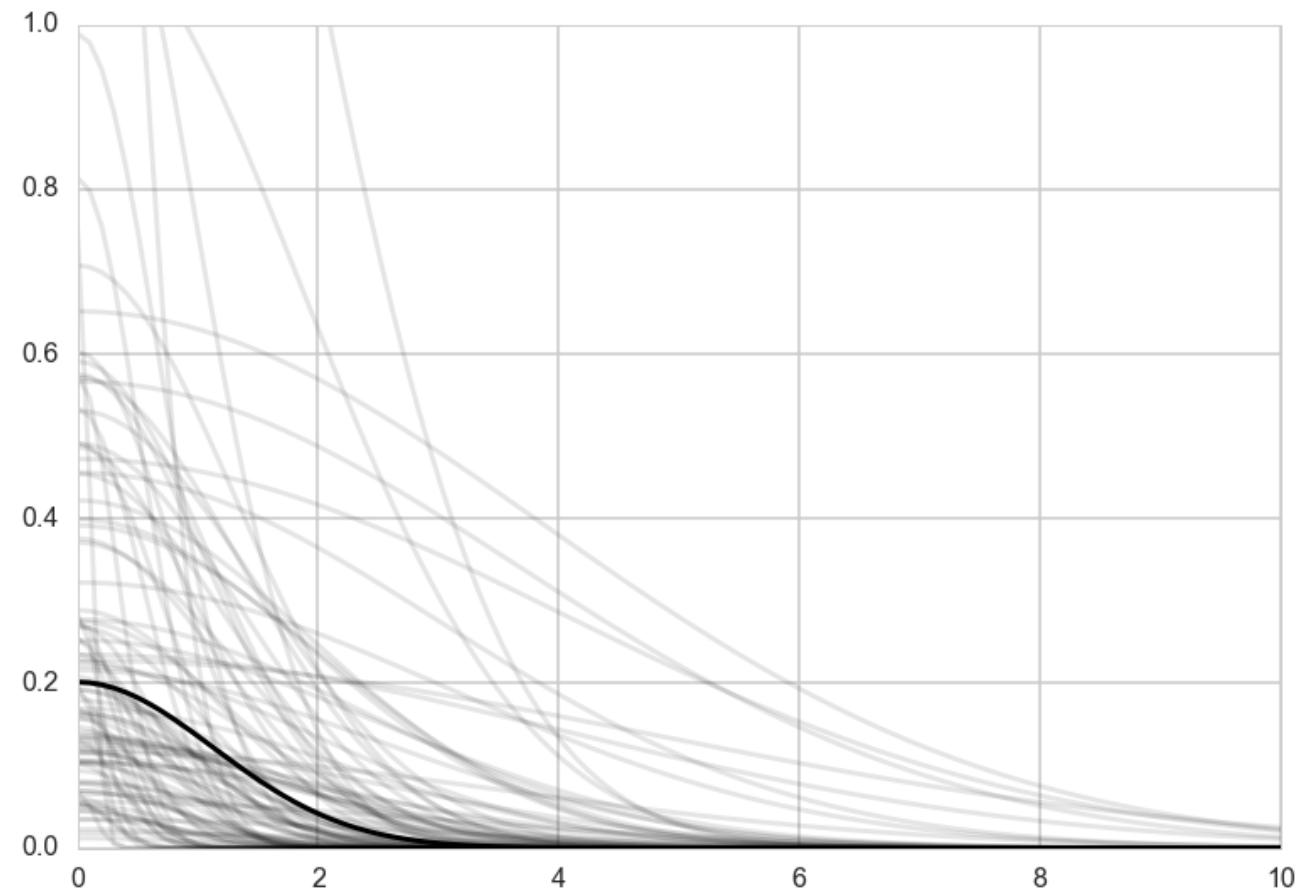
Replace independent intercepts by correlated ones.

Draw from a Multivariate Normal with a modeled covariance matrix.

The idea sounds familiar!

We can model society specific intercepts for oceanic tools as draws from a 0 mean MVN.

Covariance posteriors:



$$T_i \sim \text{Poisson}(\lambda_i)$$

$$\log \lambda_i = \alpha + \gamma_{\text{SOCIETY}[i]} + \beta_P \log P_i$$

$$\gamma \sim \text{MVNormal}((0, \dots, 0), \mathbf{K})$$

$$\mathbf{K}_{ij} = \eta^2 \exp(-\rho^2 D_{ij}^2) + \delta_{ij}(0.01)$$

$$\alpha \sim \text{Normal}(0, 10)$$

$$\beta_P \sim \text{Normal}(0, 1)$$

$$\eta^2 \sim \text{HalfCauchy}(0, 1)$$

$$\rho^2 \sim \text{HalfCauchy}(0, 1)$$

