

Lecture 9

Bayesian Stats and Sampling

Last Time

- Bayesian Stats in detail
- Posterior, Posterior predictive
- Bayesian Stats

Today:

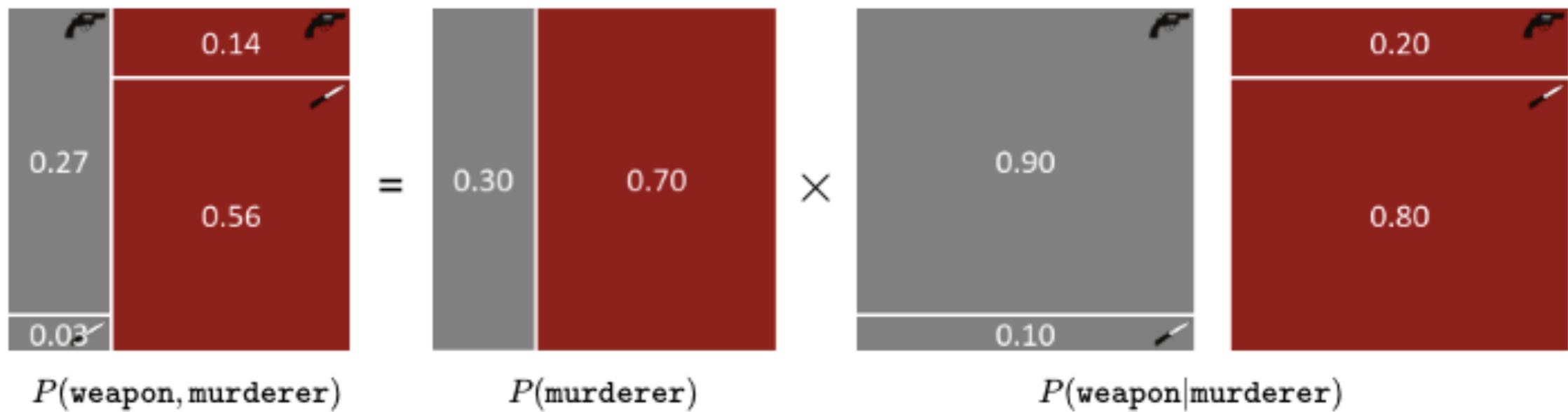
- Exchangeability and the exponential model
- Prior predictive
- Bayesian Regression
- Logistic Regression
- Inverse Transform Sampling
- Rejection Sampling

Bayesian Stats

- assume sample IS the data, no stochasticity
- parameters θ are stochastic random variables
- associate the parameter θ with a prior distribution $p(\theta)$
- The prior distribution generally represents our belief on the parameter values when we have not observed any data yet (to be qualified later)
- obtain posterior distributions
- predictive distribution from the posterior

Basic Idea

Get the joint Probability distribution



Now we condition on some random variables and learn the values of others.

Rules

$$1. P(A, B) = P(A | B)P(B)$$

$$2. P(A) = \sum_B P(A, B) = \sum_B P(A | B)P(B)$$

$P(A)$ is called the **marginal** distribution of A,
obtained by summing or marginalizing over B .

Posterior

$$p(\theta|D = \{x, y\}) = \frac{p(\{y\}|\theta, \{x\}) p(\theta)}{p(\{y\} | \{x\})}$$

Posterior: $p(\theta|D) \propto p(\{y\}|\theta, \{x\}) p(\theta)$

Evidence:

$$p(\{y\} | \{x\}) = \int d\theta p(\theta, D) = \int d\theta p(\{y\}|\theta, \{x\})p(\theta).$$

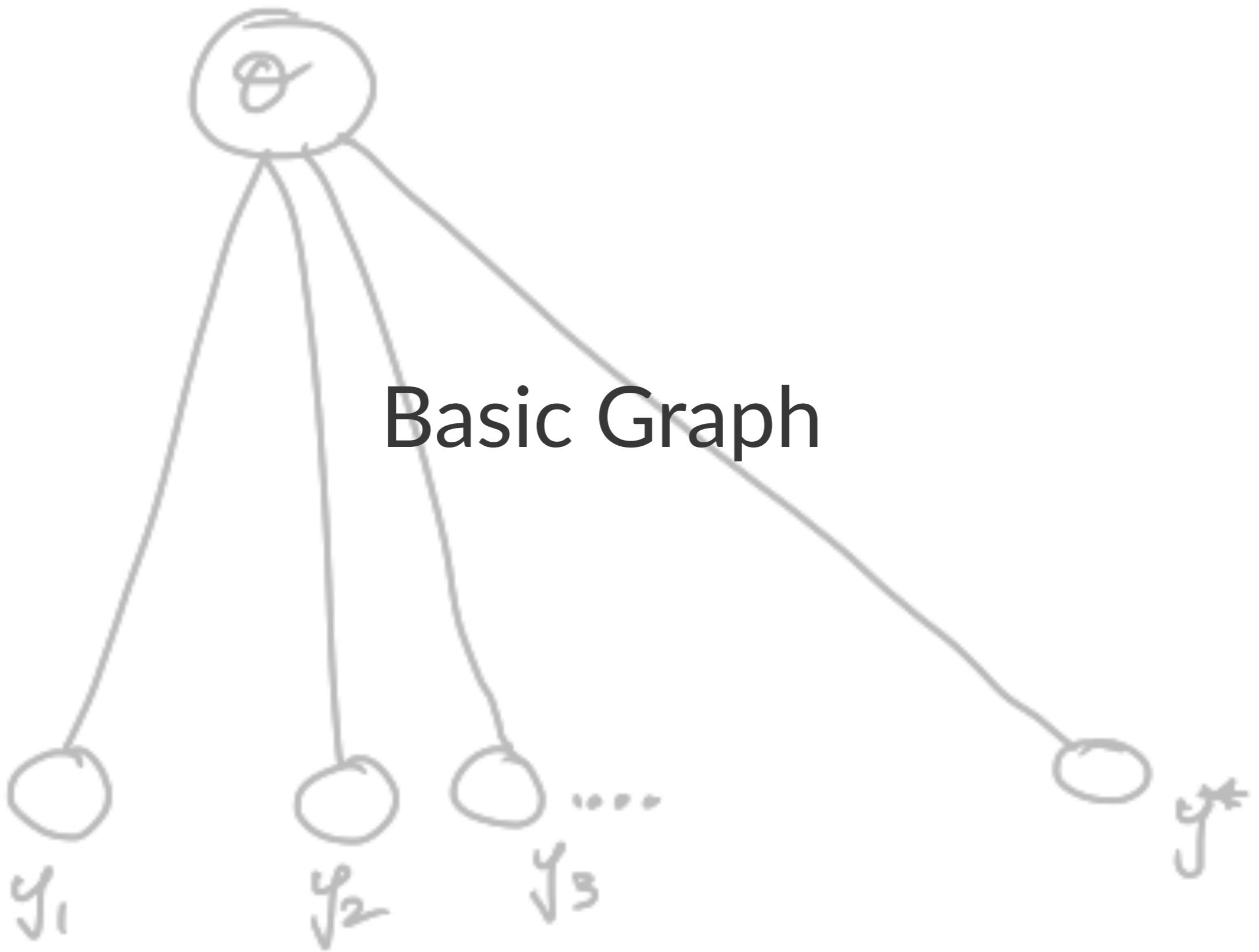
Marginalization

Marginal posterior: $p(\theta_1 | D) = \int d\theta_{-1} p(\theta | D).$

Posterior Predictive:

$p(y^* | D = \{x, y\}) = \int d\theta p(y^*, \theta | \{x, y\}).$

Basic Graph



Replicative Posterior Predictive

$$p(\{y^*\} \mid \{x^*\}) = \int p(\{y^*\} \mid \theta, \{x^*\}) p(\theta \mid \mathcal{D}) d\theta, \text{ observed}$$

data: $\mathcal{D} = \{x, y\}$

Replicated Data: $\{y_r\}$: data seen tomorrow if experiment replicated with same model and value of θ producing todays data $\{y\}$.

$\{y_r\}$ comes from posterior predictive. The idea is to make as many replications as the size of your dataset.

Another way to sample

```
ppc_rep=np.empty((dataset_size, num_samples))
for i in range(dataset_size):
    ppc_rep[i,:] = distrib.rvs(param=posterior_samples)
```

For each data point, sample using the likelihood(sampling distribution) from S samples of the posterior. Gives an S sized posterior predictive at each "data point".

You can then slice the other way to get a dataset sized posterior-predictive

n_D

'sampling-distrib'

θ_1	y_{11}	y_{12}	y_{13}	\dots	$-$	y_{1n_D}	{
θ_2	y_{21}	y_{22}	\vdots				
\vdots	y_{31}	y_{32}					
\vdots	y_{41}						
\vdots	y_{51}						
θ_{s-1}	y_{s1}						
θ_s	y_{s1}	y_{s2}	y_{s3}	\dots	$-$	y_{sn_D}	}

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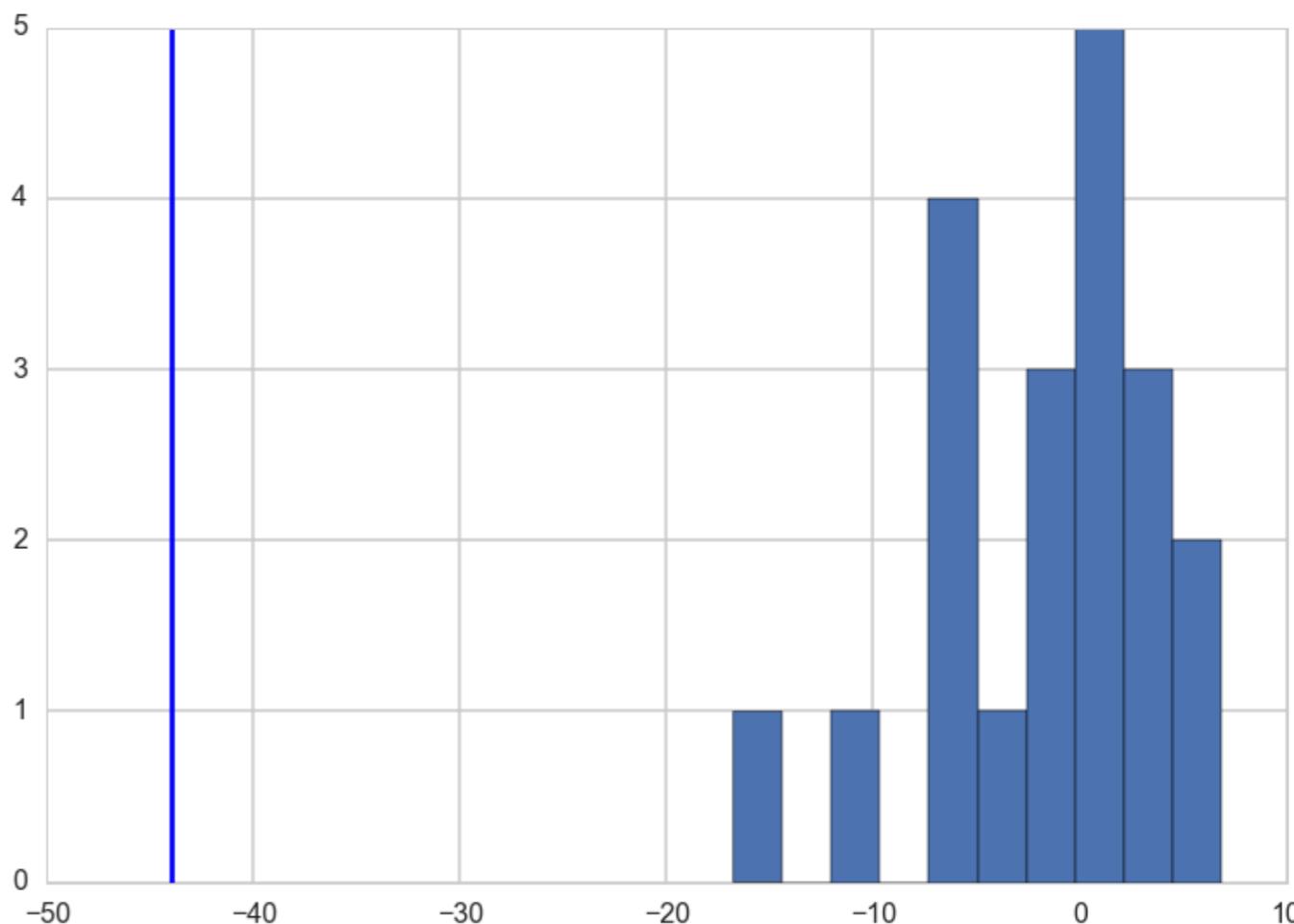
Departure from usual predictive sampling

Sample an entire $\{y_r\}$ at each θ from trace.

This allows to compute distributions from the posterior predictive replications for informal test statistics.

These processes are called **Posterior Predictive Checks**.

Replicative prior predictives are also useful for calibration.



Sufficient Statistics and the exponential family

$$p(y_i|\theta) = f(y_i)g(\theta)e^{\phi(\theta)^T u(y_i)}.$$

Likelihood:

$$p(y|\theta) = \left(\prod_{i=1}^n f(y_i) \right) g(\theta)^n \exp \left(\phi(\theta) \sum_{i=1}^n u(y_i) \right)$$

$\sum_{i=1}^n u(y_i)$ is said to be a **sufficient statistic** for θ

Poisson Gamma Example

The data consists of 155 women who were 40 years old. We are interested in the birth rate of women with a college degree and women without. We are told that 111 women without college degrees have 217 children, while 44 women with college degrees have 66 children.

Let $Y_{1,1}, \dots, Y_{n_1,1}$ children for the n_1 women without college degrees, and $Y_{1,2}, \dots, Y_{n_2,2}$ for n_2 women with college degrees.

Exchangeability

Lets assume that the number of children of a women in any one of these classes can me modelled as coming from ONE birth rate.

The in-class likelihood for these women is invariant to a permutation of variables.

This is really a statement about what is IID and what is not.

It depends on how much knowledge you have...

Poisson likelihood

$$Y_{i,1} \sim Poisson(\theta_1), Y_{i,2} \sim Poisson(\theta_2)$$

$$p(Y_{1,1}, \dots, Y_{n_1,1} | \theta_1) = \prod_{i=1}^{n_1} p(Y_{i,1} | \theta_1) = \prod_{i=1}^{n_1} \frac{1}{Y_{i,1}!} \theta_1^{Y_{i,1}} e^{-\theta_1}$$

$$= c(Y_{1,1}, \dots, Y_{n_1,1}) (n_1 \theta_1)^{\sum Y_{i,1}} e^{-n_1 \theta_1} \sim Poisson(n_1 \theta_1)$$

$$Y_{1,2}, \dots, Y_{n_1,2} | \theta_2 \sim Poisson(n_2 \theta_2)$$

Posterior

$$c_1(n_1, y_1, \dots, y_{n_1}) (n_1 \theta_1)^{\sum Y_{i,1}} e^{-n_1 \theta_1} p(\theta_1) \\ \times c_2(n_2, y_1, \dots, y_{n_2}) (n_2 \theta_2)^{\sum Y_{i,2}} e^{-n_2 \theta_2} p(\theta_2)$$

$\sum Y_i$, total number of children in each class of mom,
is sufficient statistics

Conjugate prior

Sampling distribution for θ : $p(Y_1, \dots, y_n | \theta) \sim \theta^{\sum Y_i} e^{-n\theta}$

Form is of *Gamma*. In shape-rate parametrization
(wikipedia)

$$p(\theta) = \text{Gamma}(\theta, a, b) = \frac{b^a}{\Gamma(a)} \theta^{a-1} e^{-b\theta}$$

Posterior:

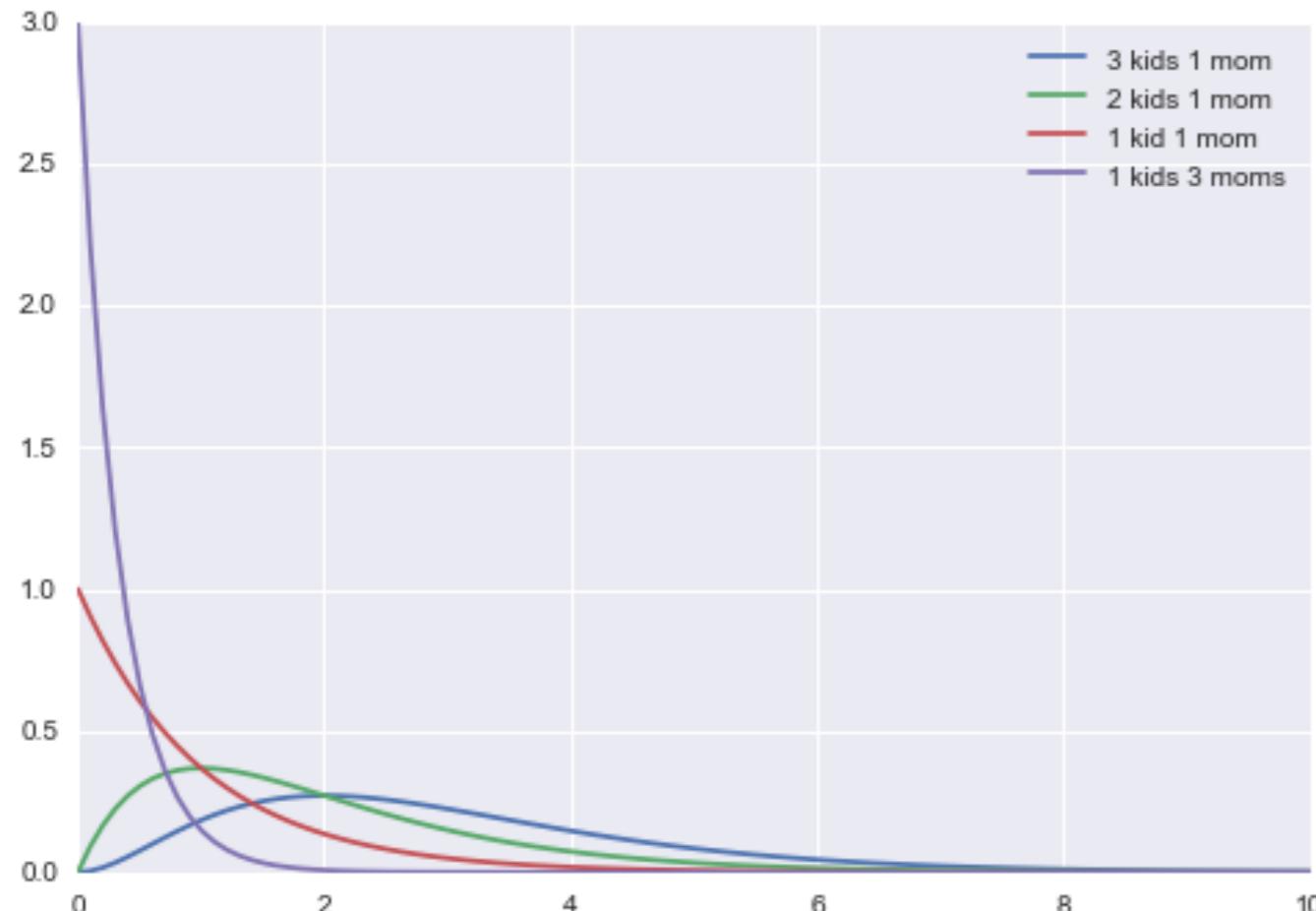
$$p(\theta | Y_1, \dots, Y_n) \propto p(Y_1, \dots, y_n | \theta) p(\theta) \sim \text{Gamma}(\theta, a + \sum Y_i, b + n)$$

Complete Posterior

Multiplies the 2 posteriors

Priors and Posteriors

We choose 2,1 as our prior.



$$p(\theta_1 | n_1, \sum_i^{n_1} Y_{i,1}) \sim \text{Gamma}(\theta_1, 219, 112)$$

$$p(\theta_2 | n_2, \sum_i^{n_2} Y_{i,2}) \sim \text{Gamma}(\theta_2, 68, 45)$$

Prior mean, variance:
 $E[\theta] = a/b, var[\theta] = a/b^2$.

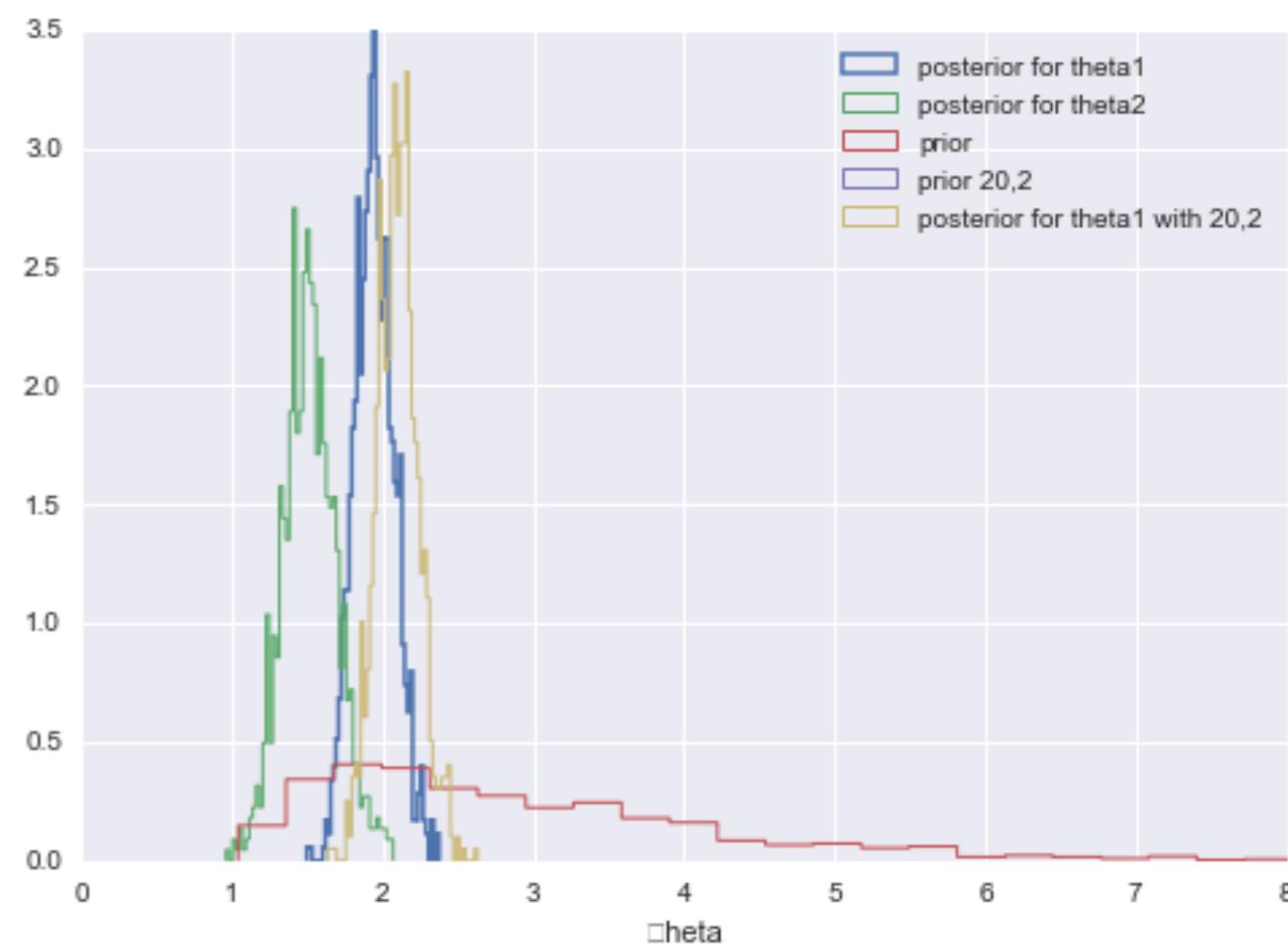
Posteriors

$$E[\theta] = (a + \sum y_i)/(b + N)$$

$$\text{var}[\theta] = (a + \sum y_i)/(b + N)^2.$$

```
np.mean(theta1),  
np.var(theta1) =  
(1.9516881521791478,  
0.018527204185785785)
```

```
np.mean(theta2),  
np.var(theta2) =  
(1.5037252100213609,  
0.034220717257786061)
```



Posterior Predictives

$$p(y^*|D) = \int d\theta p(y^*|\theta)p(\theta|D)$$

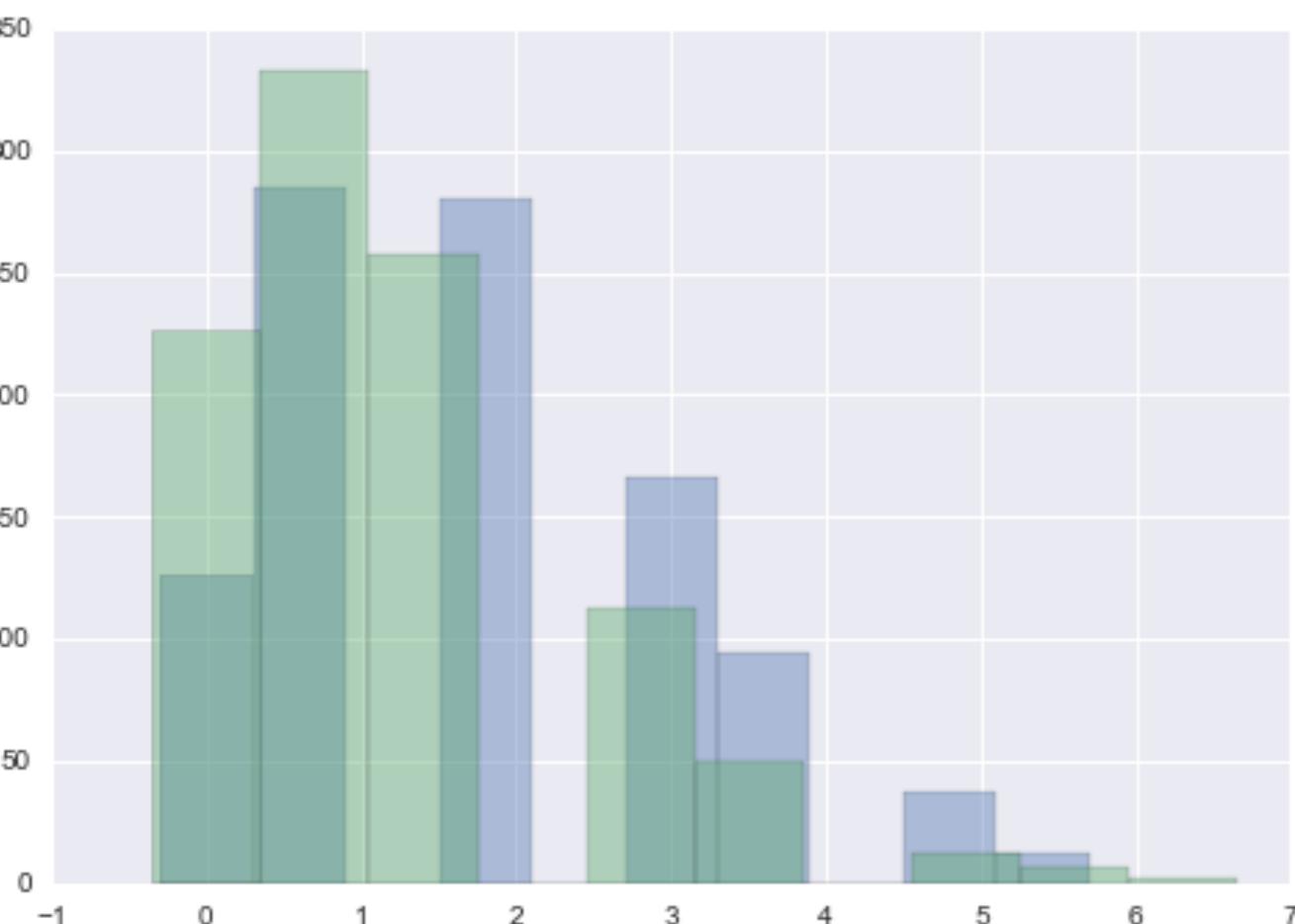
Sampling makes it easy:

```
postpred1 = poisson.rvs(theta1)
postpred2 = poisson.rvs(theta2)
```

Negative Binomial:

$$E[y^*] = \frac{(a + \sum y_i)}{(b + N)}$$

$$var[y^*] = \frac{(a + \sum y_i)}{(b + N)^2} (N + b + 1).$$

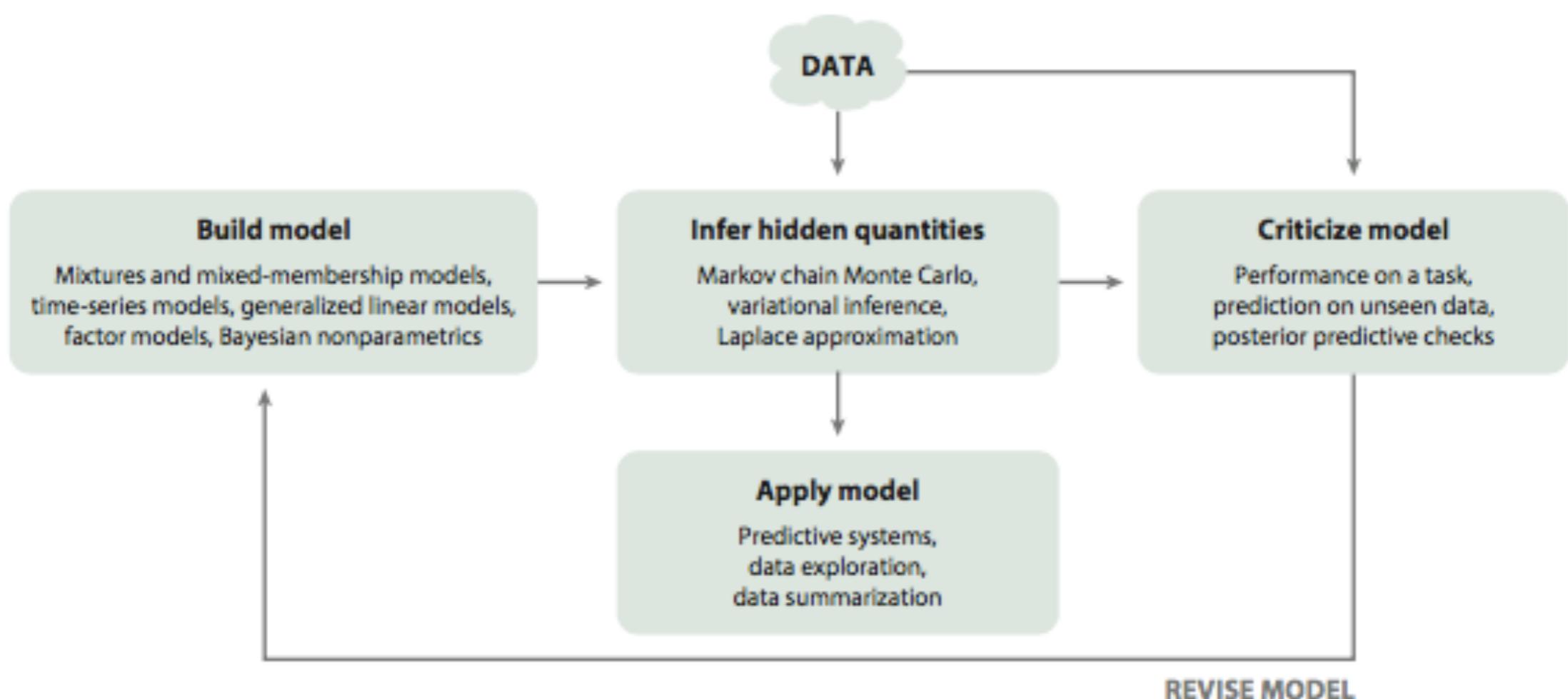


But see width:

```
np.mean(postpred1),  
np.var(postpred1)=(1.976,  
1.8554239999999997)
```

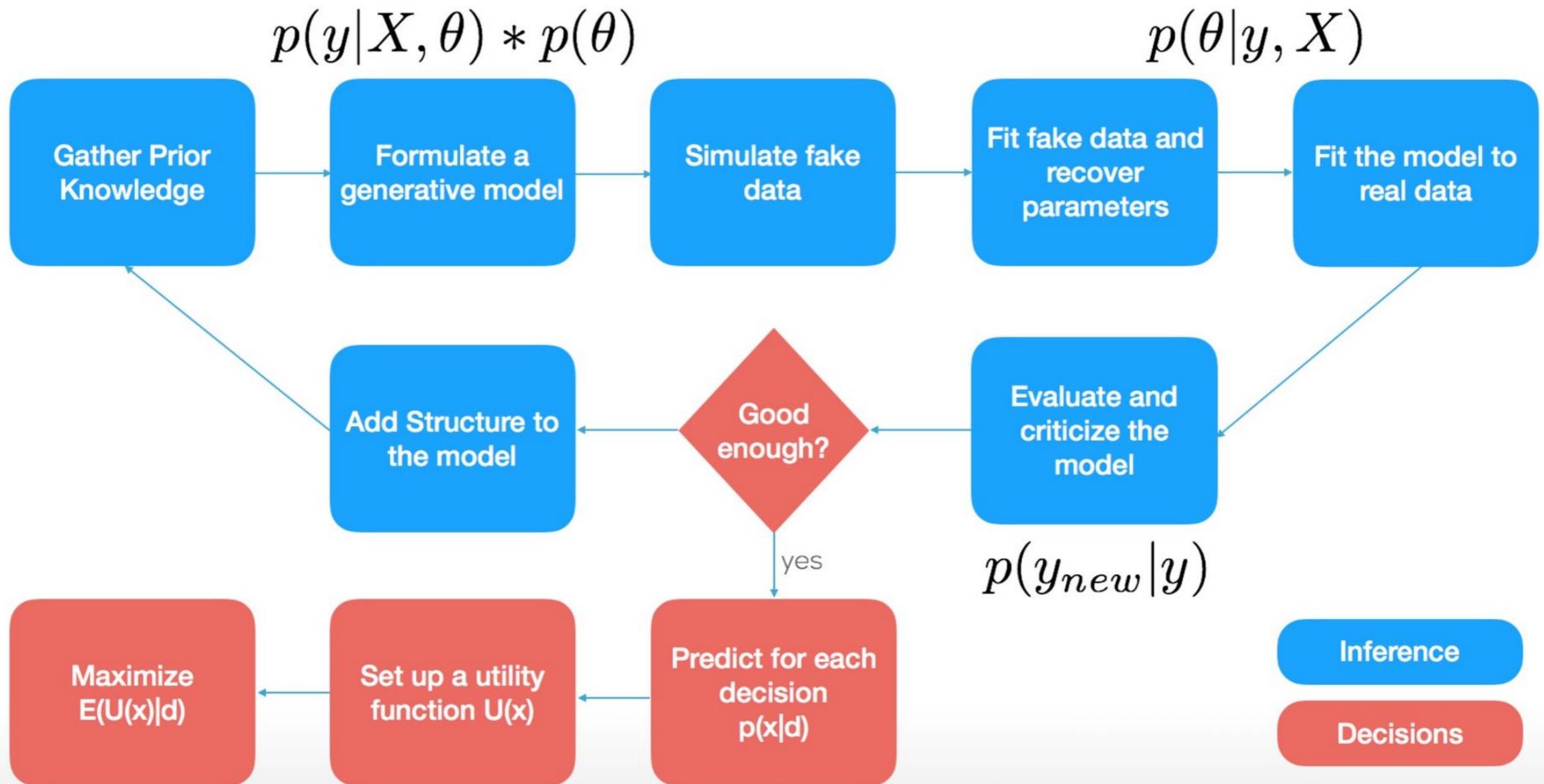
Posterior predictive smears out posterior error with sampling distribution

Box's loop



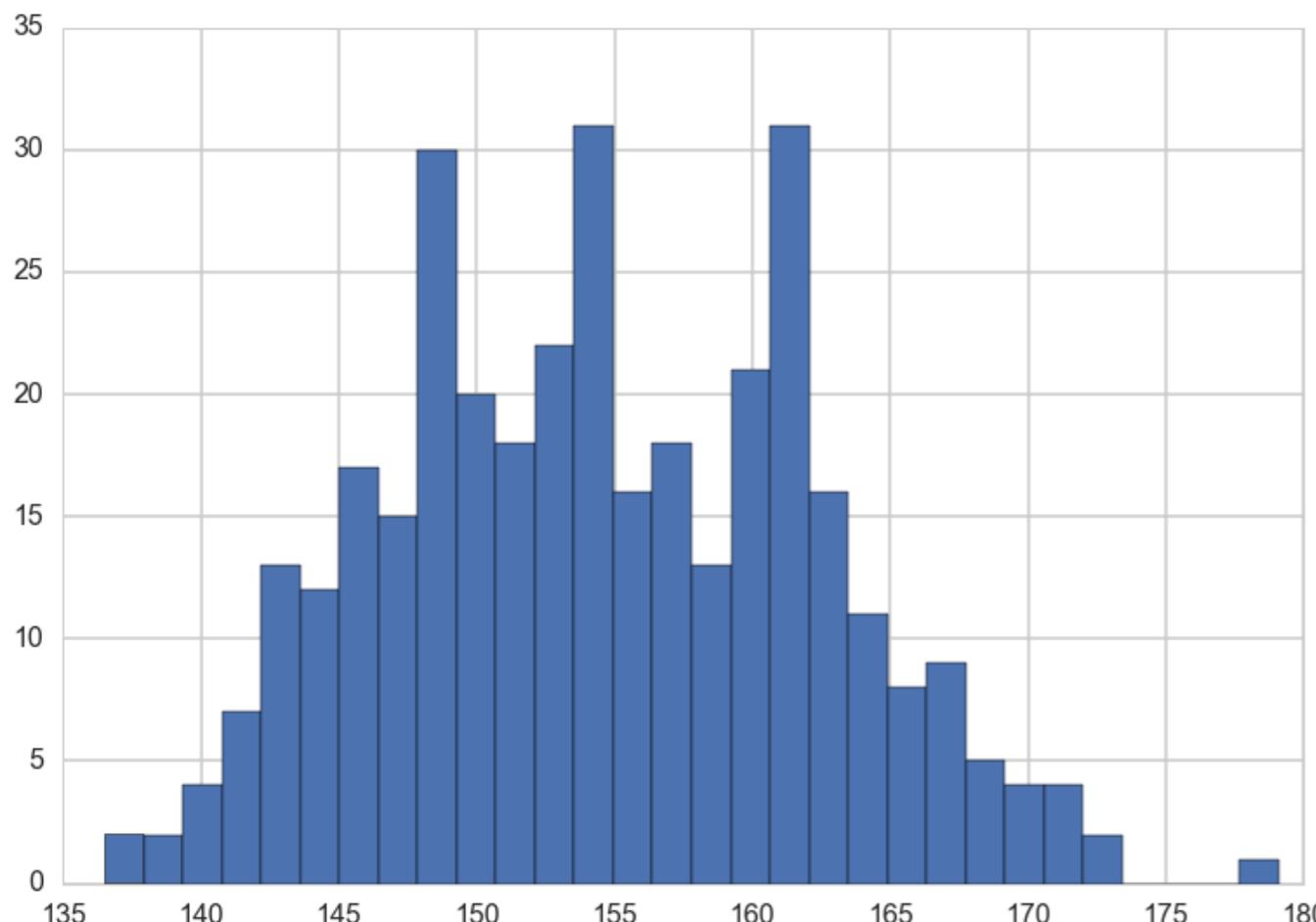
(from @ericnovik)

Bayesian Workflow



Howell's data

- These are census data for the Dobe area !Kung San people
- Nancy Howell conducted detailed quantitative studies of this Kalahari foraging population in the 1960s.



	height	weight	age	male
0	151.765	47.825606	63.0	1
1	139.700	36.485807	63.0	0
2	136.525	31.864838	65.0	0
3	156.845	53.041915	41.0	1
4	145.415	41.276872	51.0	0

Model

$$\begin{aligned} h &\sim N(\mu, \sigma) \\ \mu &\sim Normal(148, 20) \\ \sigma &= samplestd \end{aligned}$$

Normal-Normal Model

Posterior for a gaussian likelihood:

$$p(\mu, \sigma^2 | y_1, \dots, y_n, \sigma^2) \propto \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2\sigma^2} \sum (y_i - \mu)^2} p(\mu, \sigma^2)$$

What is the posterior of μ assuming we know σ^2 ?

Prior for σ^2 is $p(\sigma^2) = \delta(\sigma^2 - \sigma_0^2)$

$$p(\mu|y_1, \dots, y_n, \sigma^2 = \sigma_0^2) \propto p(\mu|\sigma^2 = \sigma_0^2) e^{-\frac{1}{2\sigma_0^2} \sum (y_i - \mu)^2}$$

The conjugate of the normal is the normal itself.

Say we have the prior

$$p(\mu|\sigma^2) = \exp\left\{-\frac{1}{2\tau^2} (\hat{\mu} - \mu)^2\right\}$$

posterior: $p(\mu|y_1, \dots, y_n, \sigma^2) \propto \exp\left\{-\frac{a}{2}(\mu - b/a)^2\right\}$

Here

$$a = \frac{1}{\tau^2} + \frac{n}{\sigma_0^2}, \quad b = \frac{\hat{\mu}}{\tau^2} + \frac{\sum y_i}{\sigma_0^2}$$

Define $\kappa = \sigma^2 / \tau^2$

$$\mu_p = \frac{b}{a} = \frac{\kappa}{\kappa + n} \hat{\mu} + \frac{n}{\kappa + n} \bar{y}$$

which is a weighted average of prior mean and sampling mean.

The variance is

$$\tau_p^2 = \frac{1}{1/\tau^2 + n/\sigma^2}$$

or better

$$\frac{1}{\tau_p^2} = \frac{1}{\tau^2} + \frac{n}{\sigma^2}.$$

as n increases, the data dominates the prior and the posterior mean approaches the data mean, with the posterior distribution narrowing...

Normal-Normal Posterior Predictive

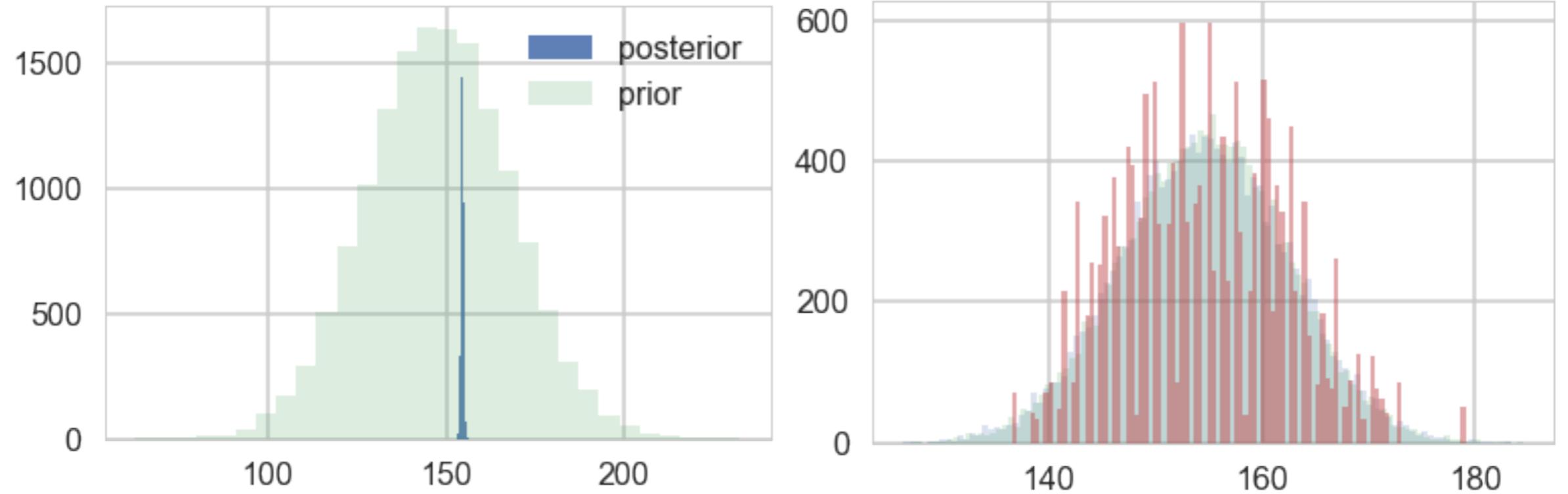
So the posterior is

$$p(\mu \mid \{y\}, \sigma^2) = N(\mu_p, \tau_p^2)$$

The corresponding posterior predictive is:

$$p(y^* \mid \{y\}) = N(\mu_p, \tau_p^2 + \sigma^2)$$

Predictive variance is uncertainty due to the obsv.
noise plus uncertainty due to the parameters.



Bayesian Formulation of Regression

Data

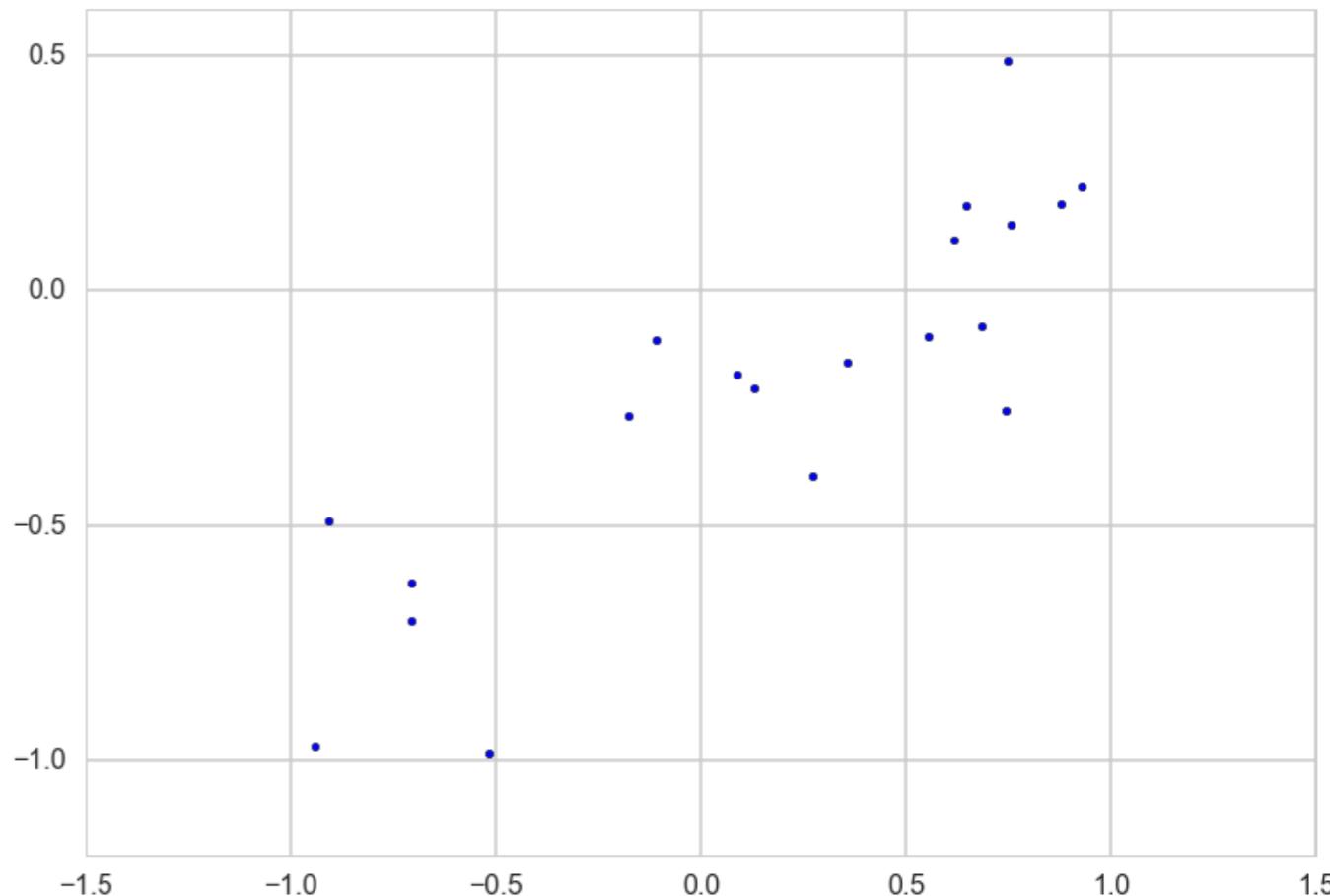
$$D = \{(\mathbf{x}_1, y_1), (\mathbf{x}_2, y_2), \dots, (\mathbf{x}_n, y_n)\}$$

All data points are combined into a $D \times n$ matrix X .

Model:

$$y = \mathbf{x}^T \mathbf{w} + \epsilon$$

$$\epsilon \sim N(0, \sigma_n^2)$$

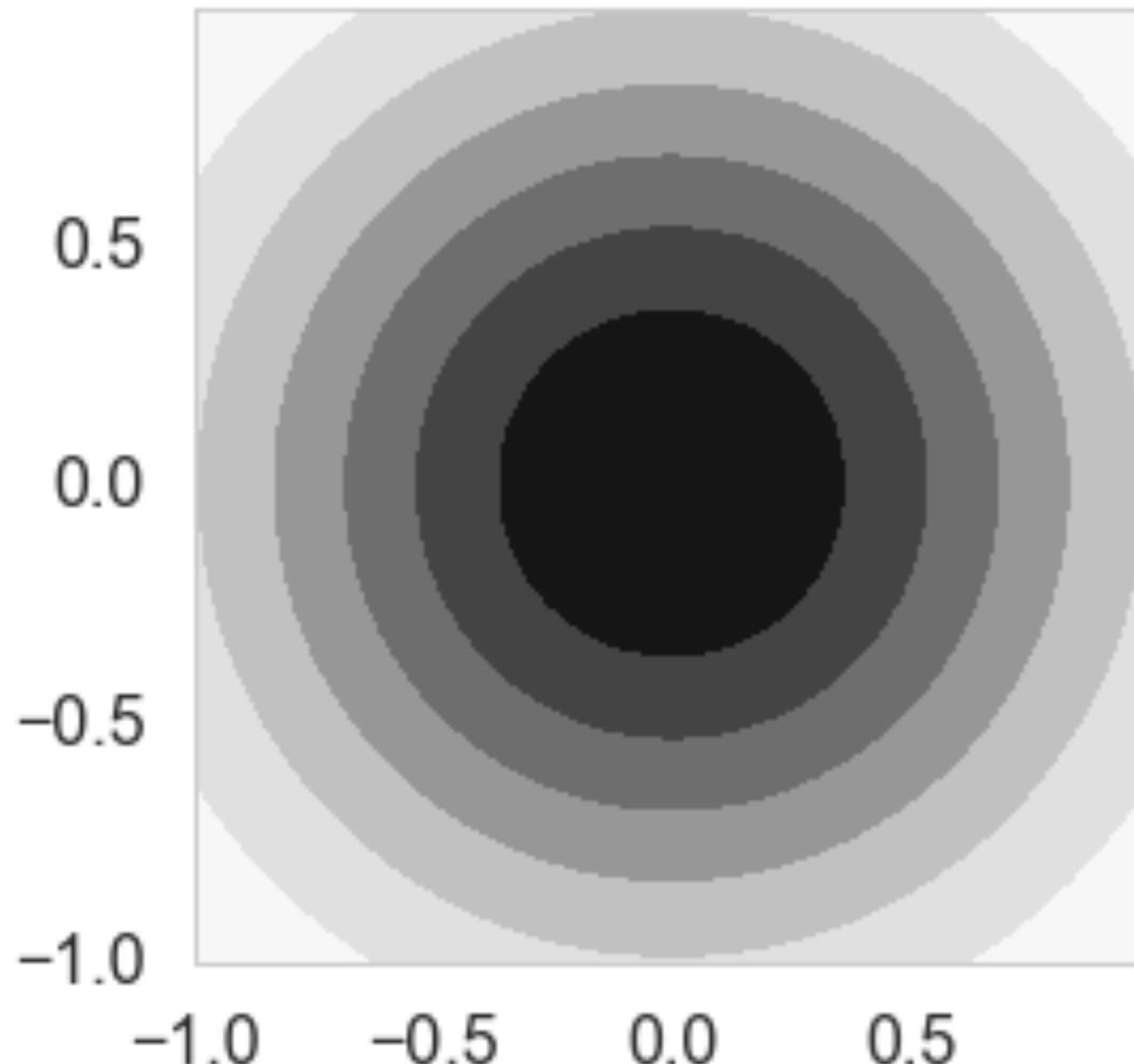


Likelihood

The likelihood is, because we assume independency, the product

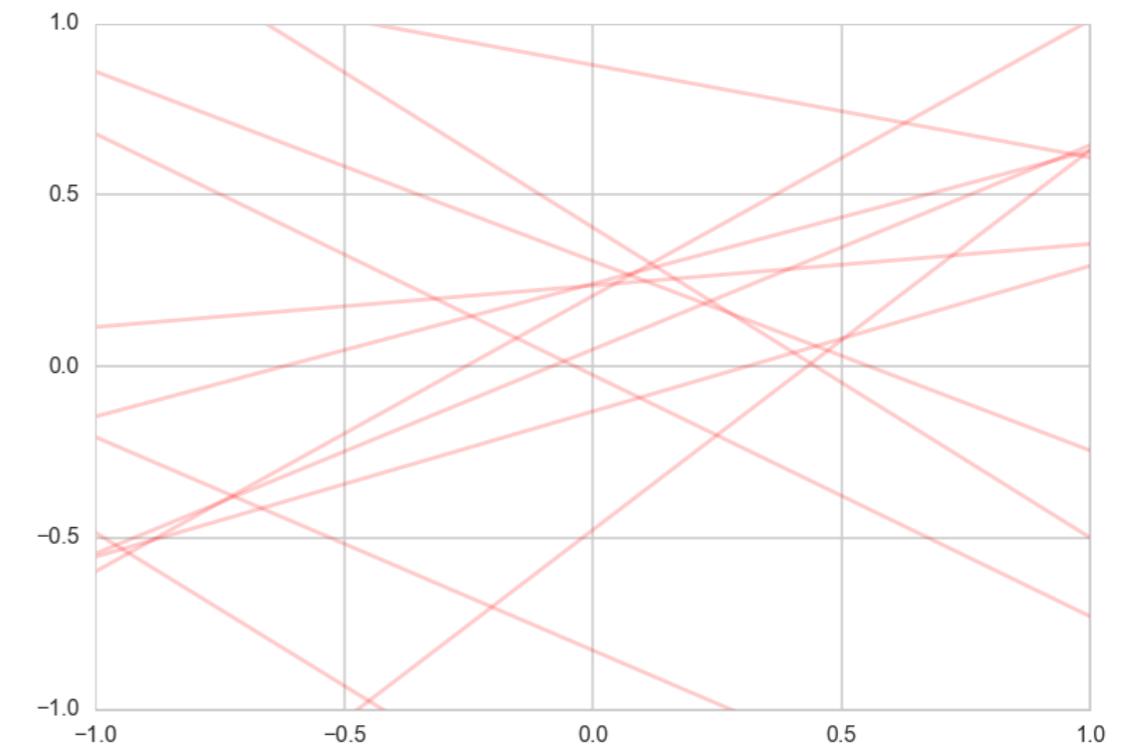
$$\begin{aligned}\mathcal{L} = p(\mathbf{y}|\mathbf{X}, \mathbf{w}) &= \prod_{i=1}^n p(y_i|\mathbf{X}_i, \mathbf{w}) = \prod_{i=1}^n \frac{1}{\sqrt{2\pi}\sigma_n} \exp\left(-\frac{(y_i - \mathbf{X}_i^T \mathbf{w})^2}{2\sigma_n^2}\right) \\ &\propto \exp\left(-\frac{|\mathbf{y} - \mathbf{X}^T \mathbf{w}|^2}{2\sigma_n^2}\right) \propto N(\mathbf{X}^T \mathbf{w}, \sigma_n^2 \mathbf{I})\end{aligned}$$

Prior $\mathbf{w} \sim \mathbf{N}(\mathbf{w}_0, \Sigma)$



$$\mathbf{w} \sim \mathbf{N}(\mathbf{w}_0, \boxed{\tau^2 \mathbf{I}})$$

Circular Variance:
\Sigma is diagonal & same value at each entry
=> No correlation across weight params



Posterior

$$p(\mathbf{w}|\mathbf{y}, \mathbf{X}) \propto p(\mathbf{y}|\mathbf{X}, \mathbf{w}) p(\mathbf{w})$$

$$\propto \exp\left(-\frac{1}{2\sigma_n^2}(\mathbf{y} - \mathbf{X}^T \mathbf{w})^T (\mathbf{y} - \mathbf{X}^T \mathbf{w})\right) \exp\left(-\frac{1}{2}\mathbf{w}^T \Sigma^{-1} \mathbf{w}\right)$$

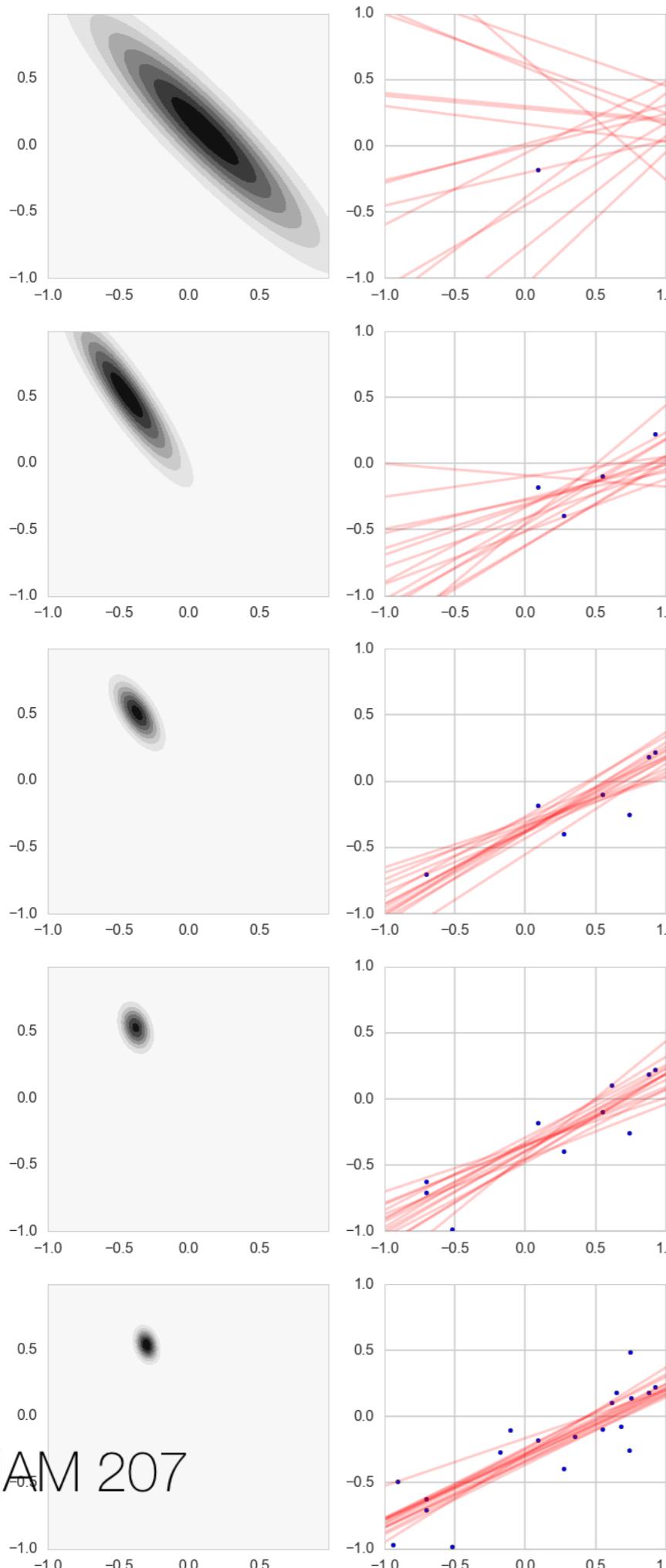
$$p(\mathbf{w}|\mathbf{y}, \mathbf{X}) \propto \exp\left(-\frac{1}{2}(\mathbf{w} - \bar{\mathbf{w}})^T \left(\frac{1}{\sigma_n^2} \mathbf{X} \mathbf{X}^T + \Sigma^{-1}\right) (\mathbf{w} - \bar{\mathbf{w}})\right)$$

$$\text{Inverse covariance } A = \sigma_n^{-2} \mathbf{X} \mathbf{X}^T + \Sigma^{-1}$$

where the new mean is

$$\bar{\mathbf{w}} = A^{-1} \Sigma^{-1} \mathbf{w}_0 + \sigma_n^{-2} (A^{-1} \mathbf{X}^T \mathbf{y})$$

Bayesian updating



```
def update(x,y,likelihoodPrecision,priorMu,priorCovariance):
    postCovInv = np.linalg.inv(priorCovariance) +
        likelihoodPrecision*np.outer(x.T,x)
    postCovariance = np.linalg.inv(postCovInv)
    postMu =
        np.dot(
            np.dot(postCovariance,
                   np.linalg.inv(priorCovariance))
        ),
    priorMu)
    +likelihoodPrecision*
        np.dot(postCovariance,np.outer(x.T,y)).flatten()
postW = lambda w: multivariate_normal.pdf(
    w, postMu, postCovariance)
return postW, postMu, postCovariance
```

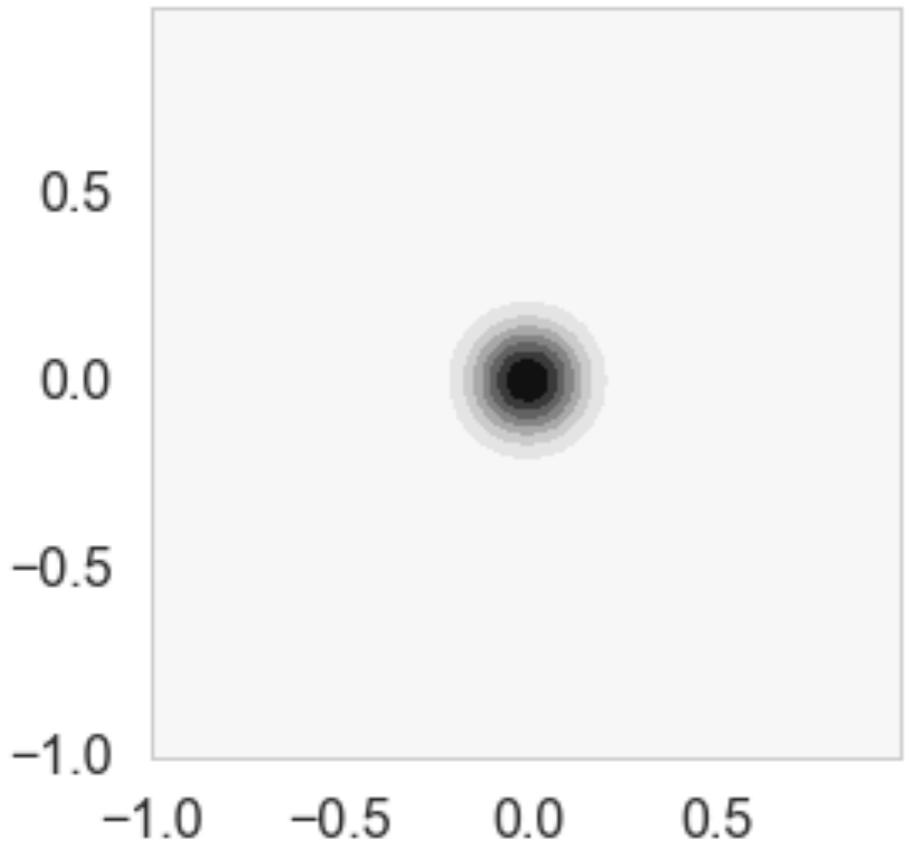
Posterior Predictive

$$p(y^* | x^*, \mathbf{x}, \mathbf{y}) =$$

$$\int p(\mathbf{y}^* | \mathbf{x}^*, \mathbf{w}) p(\mathbf{w} | \mathbf{X}, \mathbf{y}) d\mathbf{w}$$

$$= \mathcal{N}\left(y | \bar{\mathbf{w}}^T \mathbf{x}^*, \sigma_n^2 + \mathbf{x}^{*^T} A^{-1} \mathbf{x}^*\right)$$

Regularization



priorPrecision/likelihoodPrecision

4.0 **posterior:**
 `p(slope, intercept, alpha | D)`

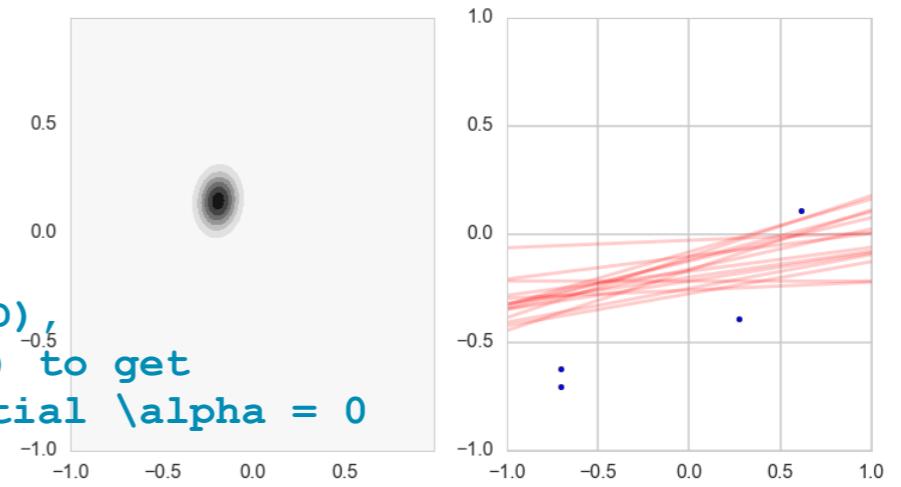
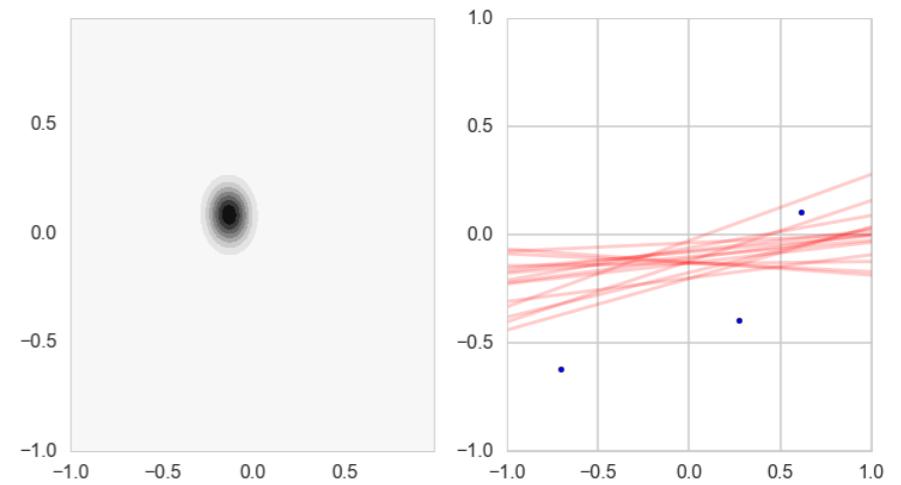
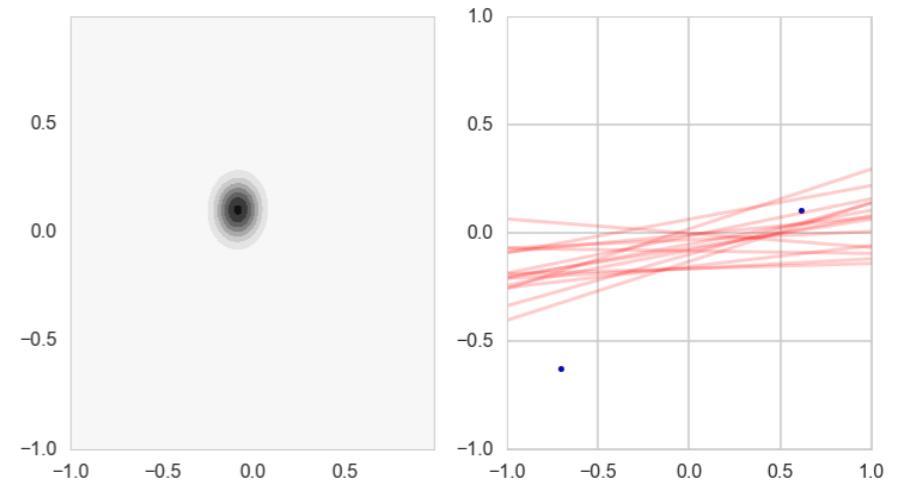
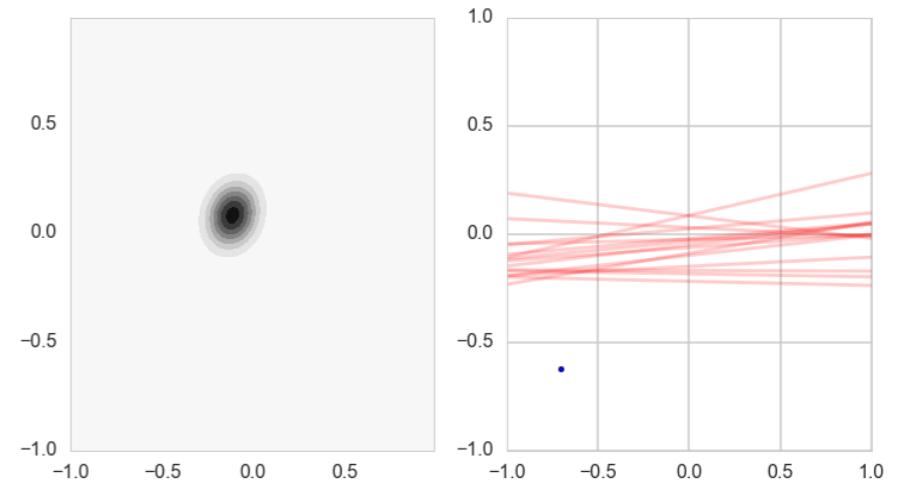
This ratio is the ridge α .

How to choose alpha?

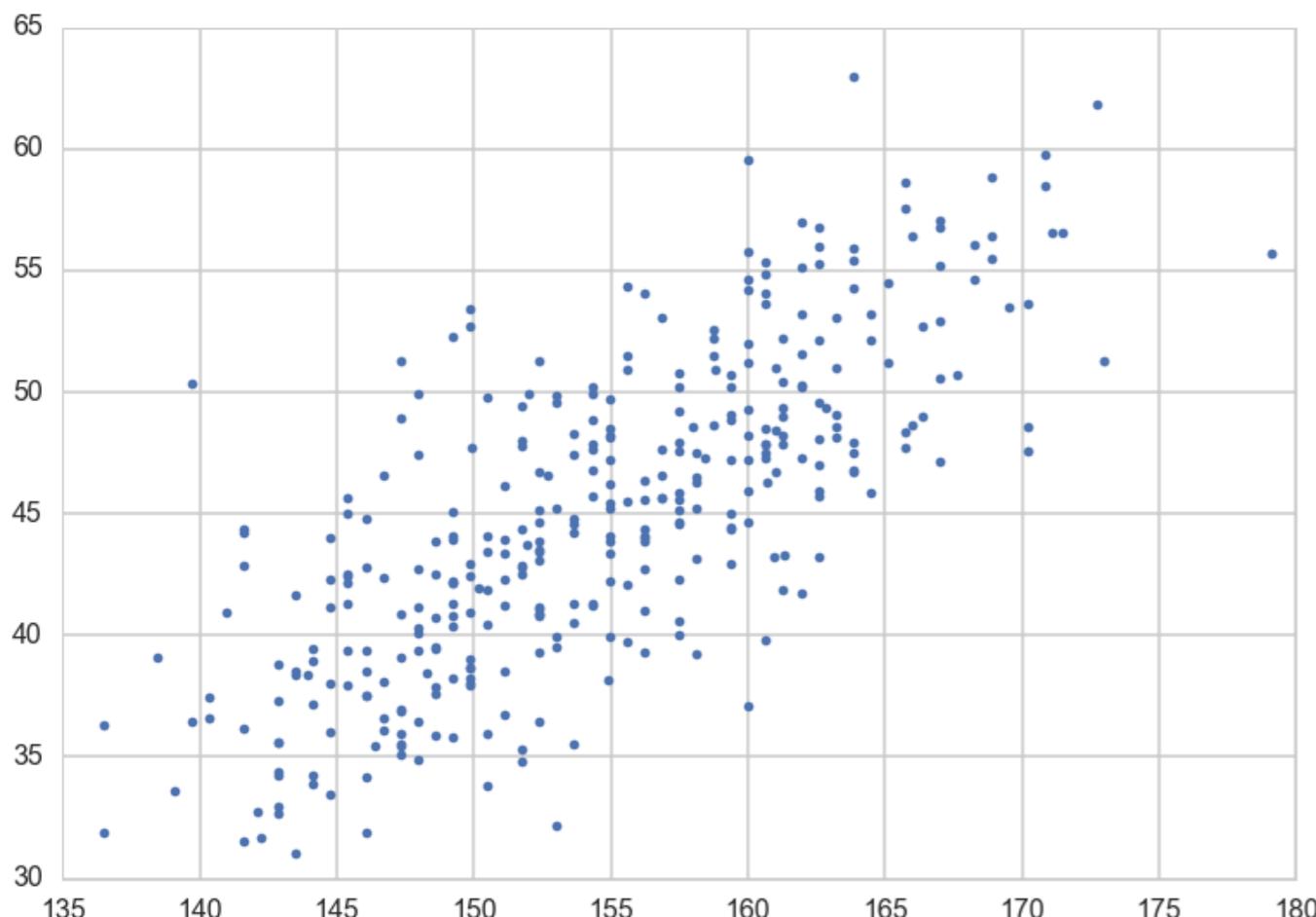
1. Marginalize `p(slope, intercept, alpha | D)`,
2. maximize this `posterior(slope, intercept)` to get
`\partial posterior(slope, intercept) / \partial alpha = 0`



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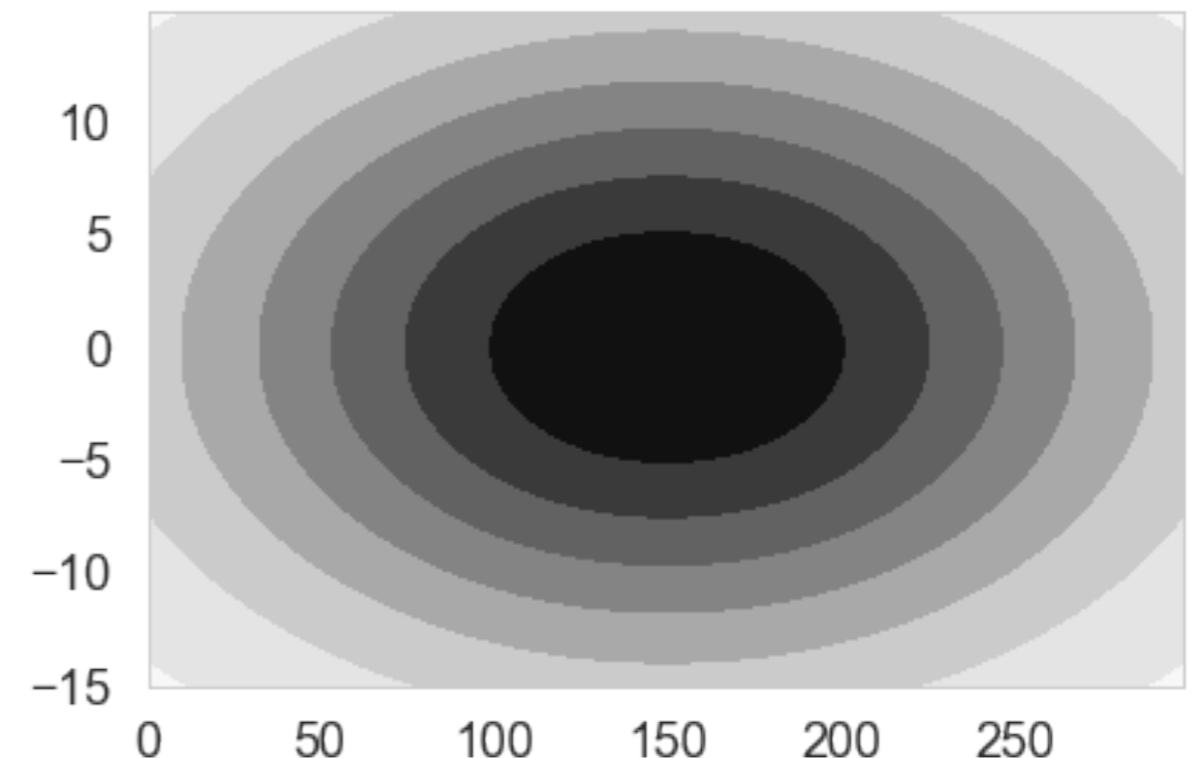
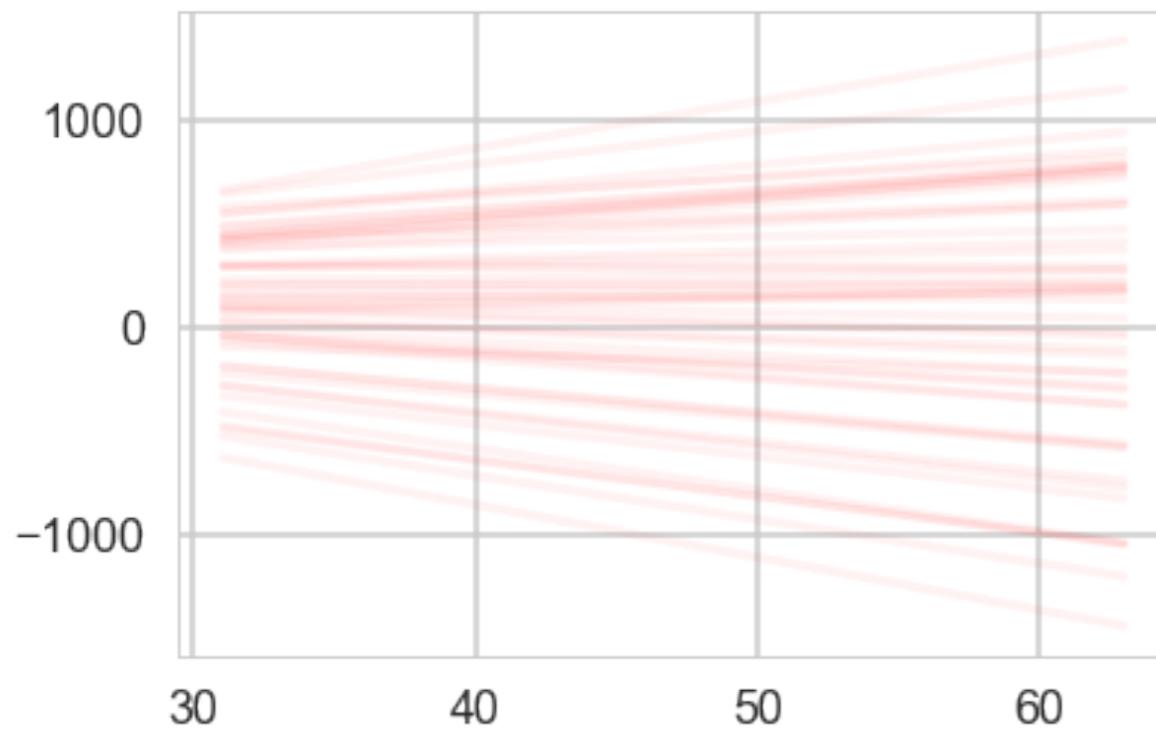


Regression, adding a predictor, weight

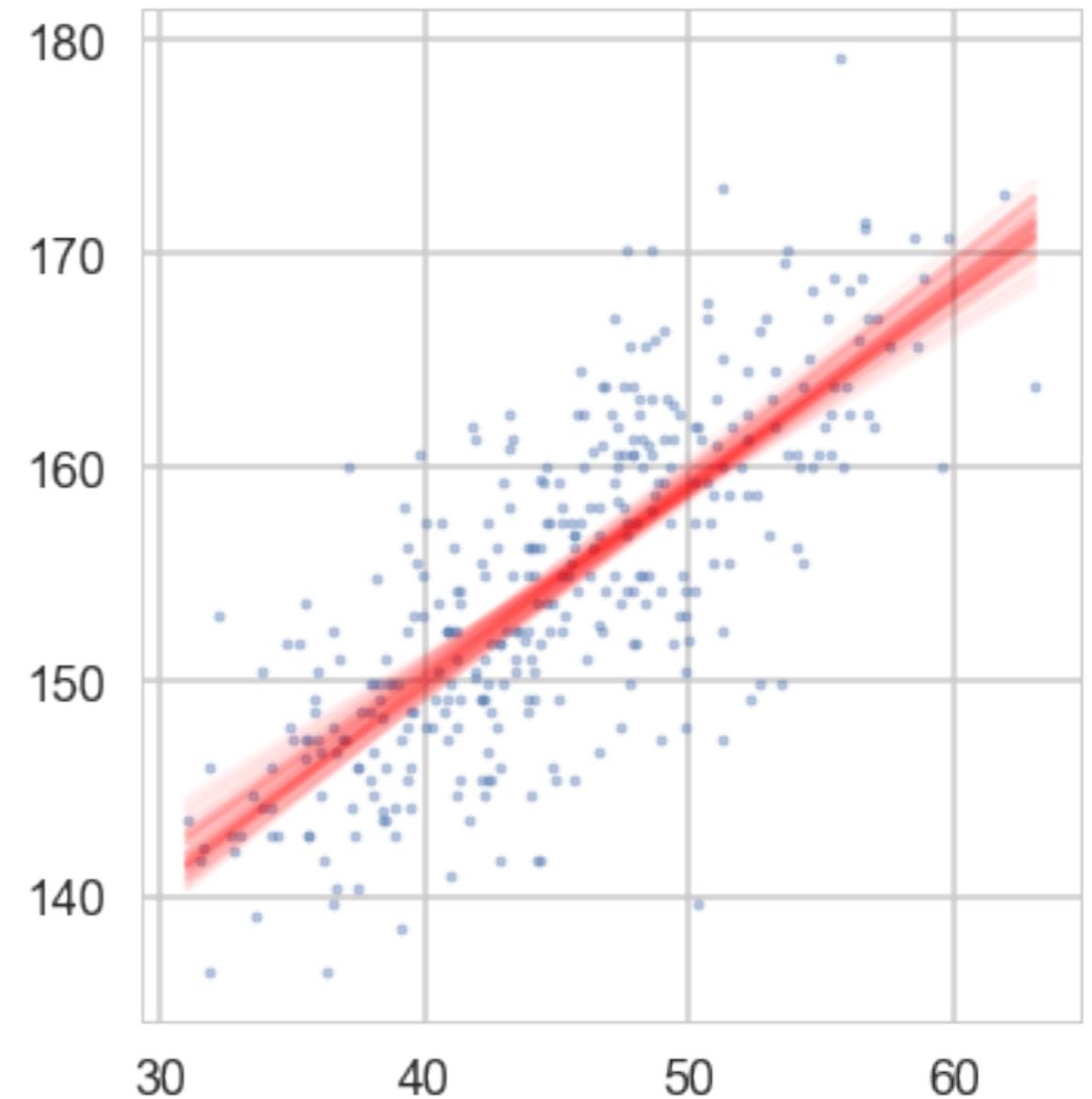
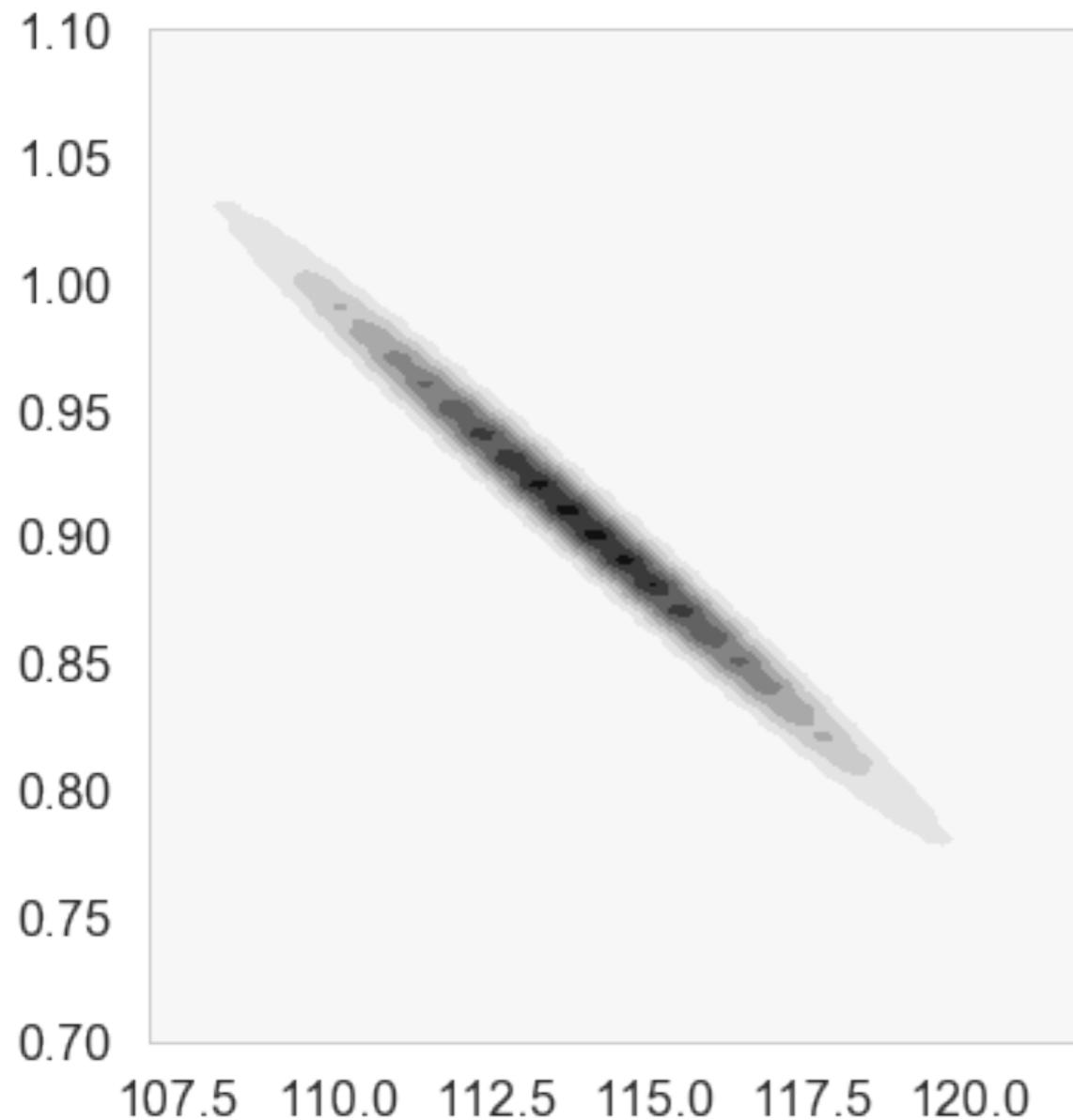


$h \sim N(\mu, \sigma)$
 $\mu = \text{intercept} + \text{slope} \times \text{weight}$
 $\text{intercept} \sim N(150, 100)$
 $\text{slope} \sim N(0, 10)$
 $\sigma = \text{std. dev}$

Priors

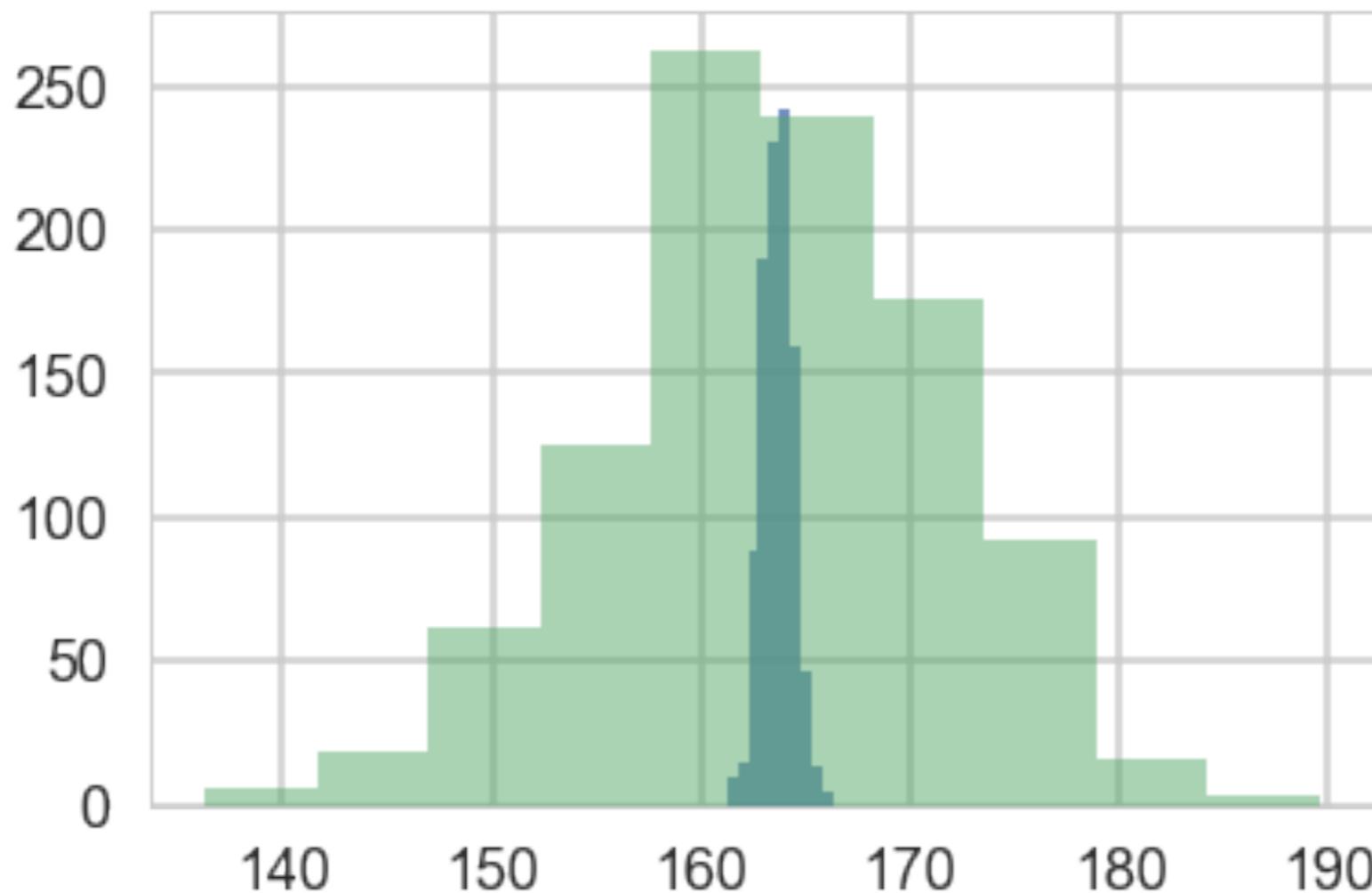


Posteriors

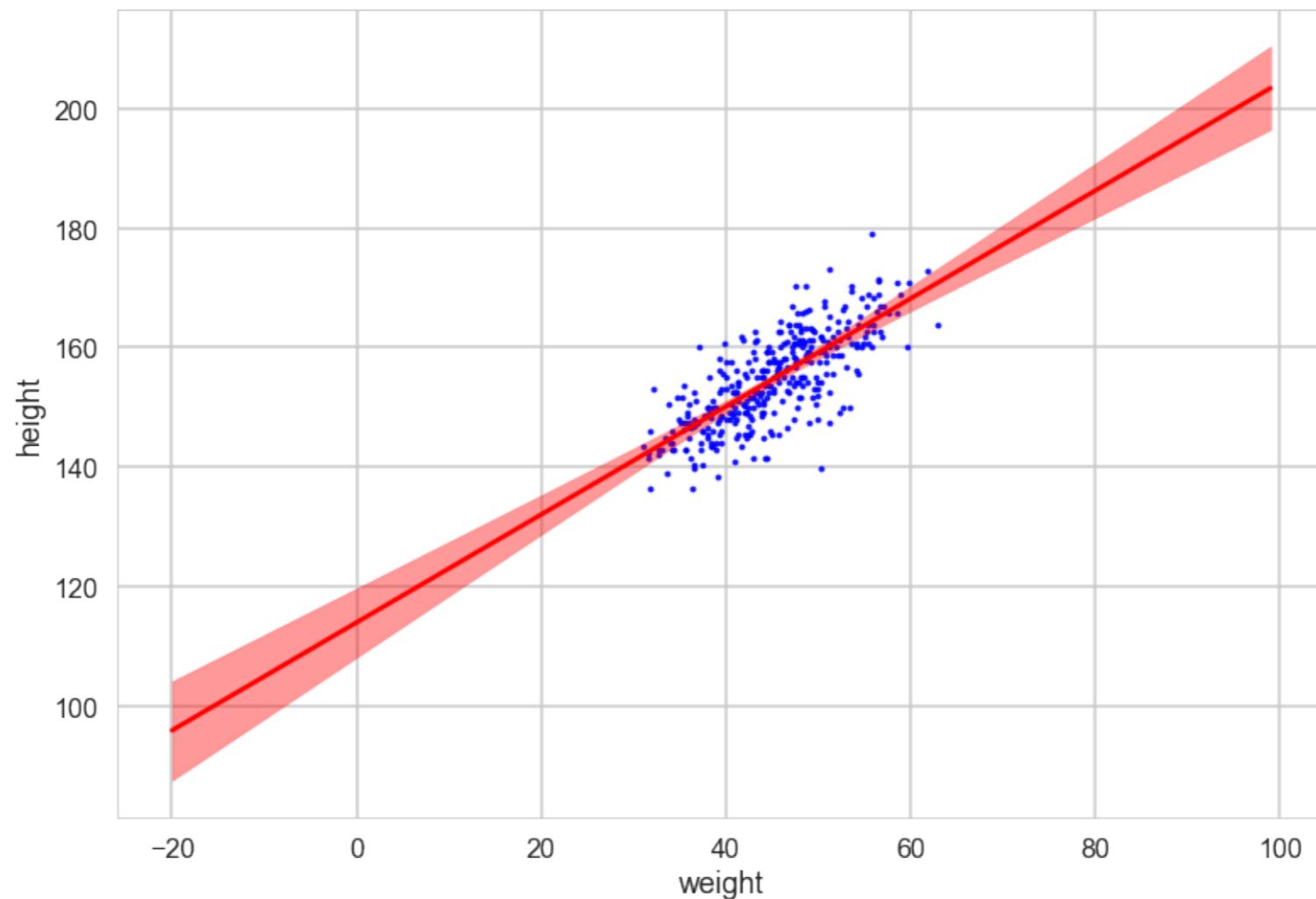


Posterior at weight 55

DO INTERCEPT SLOPE, AND WEIGHT 55

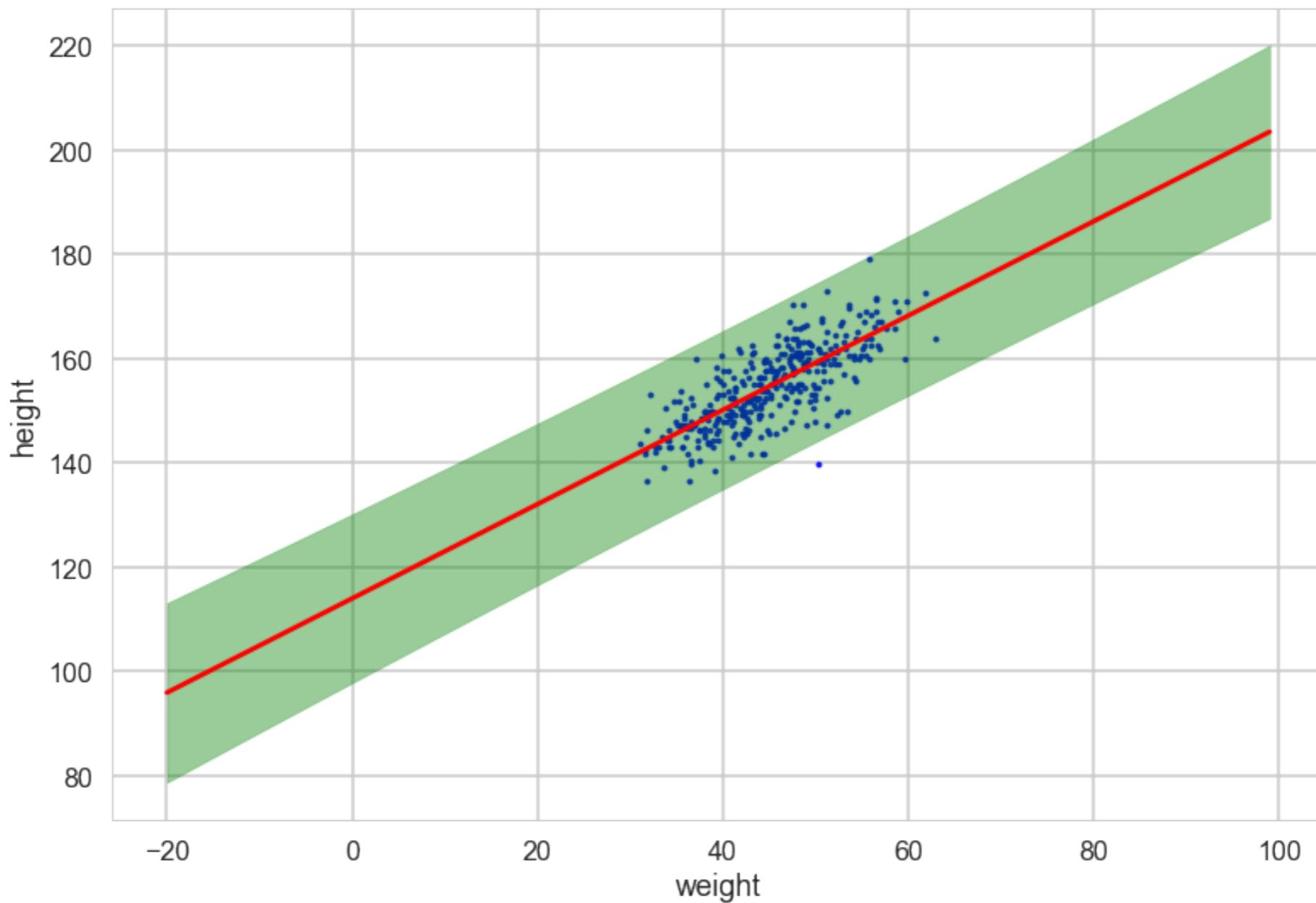


Posteriors on a grid



Why so tight?

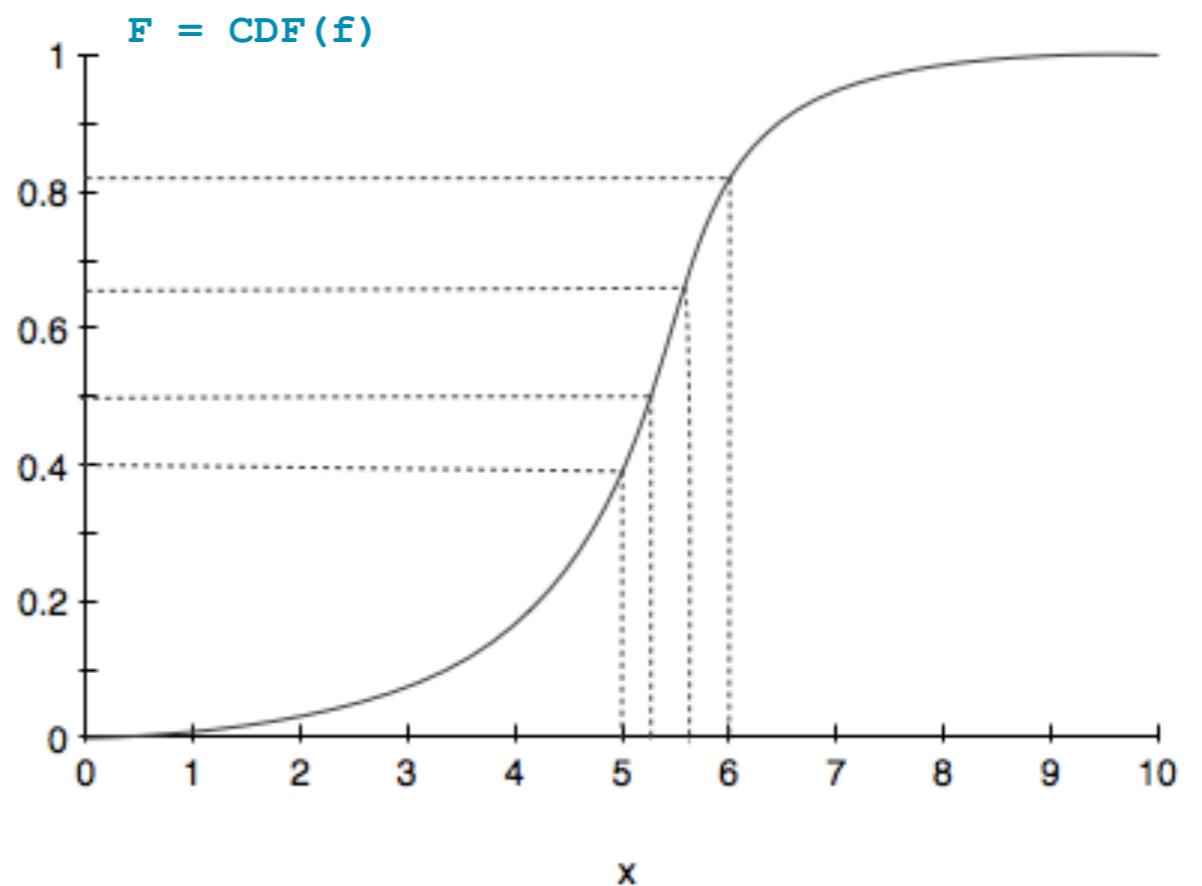
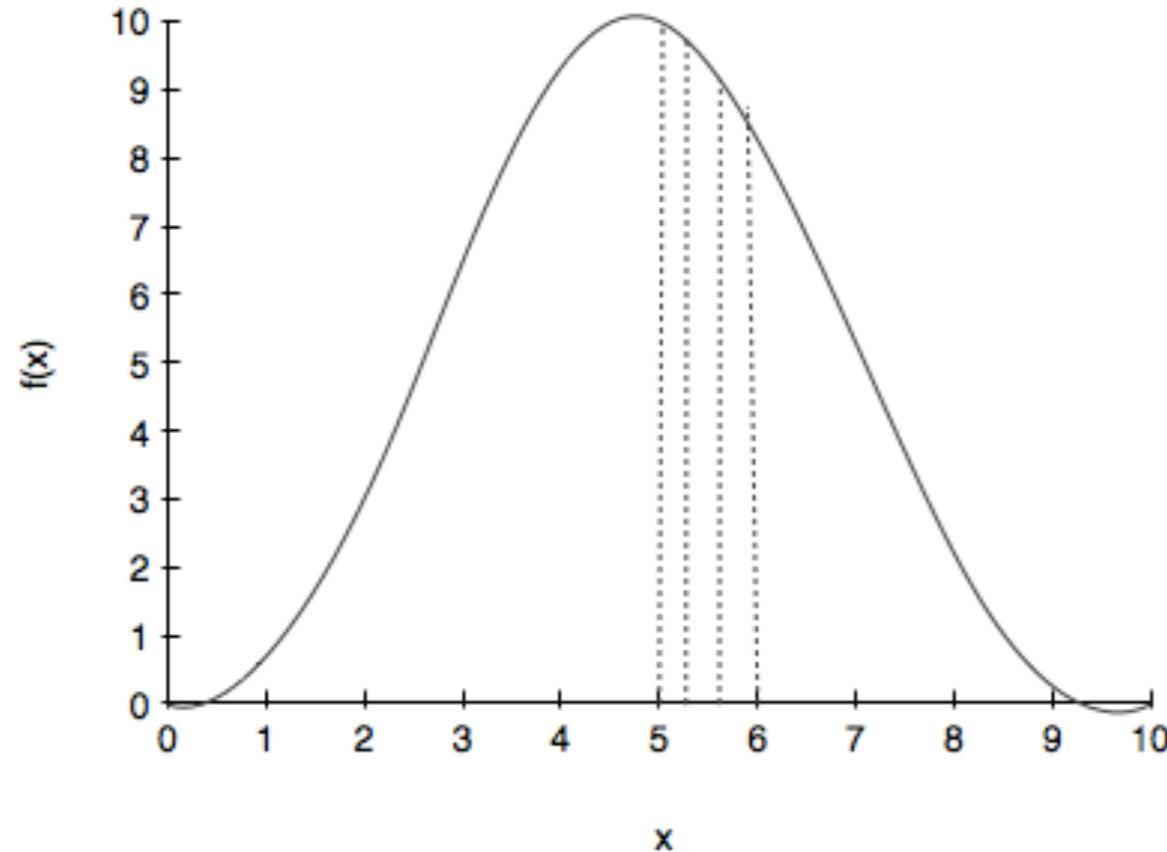
Predictives on grid



Ok. We need Samples

- to compute expectations, integrals and do statistics, we need samples
- we start that journey today
- inverse transform
- rejection sampling
- importance sampling: a direct, low-variance way to do integrals and expectations

Inverse transform



algorithm

The CDF F must be invertible!

1. get a uniform sample u from $Unif(0, 1)$
2. solve for x yielding a new equation $x = F^{-1}(u)$
where F is the CDF of the distribution we desire.
3. repeat.

Why does it work?

$F^{-1}(u) = \text{smallest } x \text{ such that } F(x) \geq u$

What distribution does random variable $y = F^{-1}(u)$ follow?

The CDF of y is $p(y \leq x)$. Since F is monotonic:

$$p(y \leq x) = p(F(y) \leq F(x)) = p(u \leq F(x)) = F(x)$$

F is the CDF of y , thus f is the pdf.

Example: exponential

pdf: $f(x) = \frac{1}{\lambda} e^{-x/\lambda}$ for $x \geq 0$ and $f(x) = 0$ otherwise.

$$u = \int_0^x \frac{1}{\lambda} e^{-x'/\lambda} dx' = 1 - e^{-x/\lambda}$$

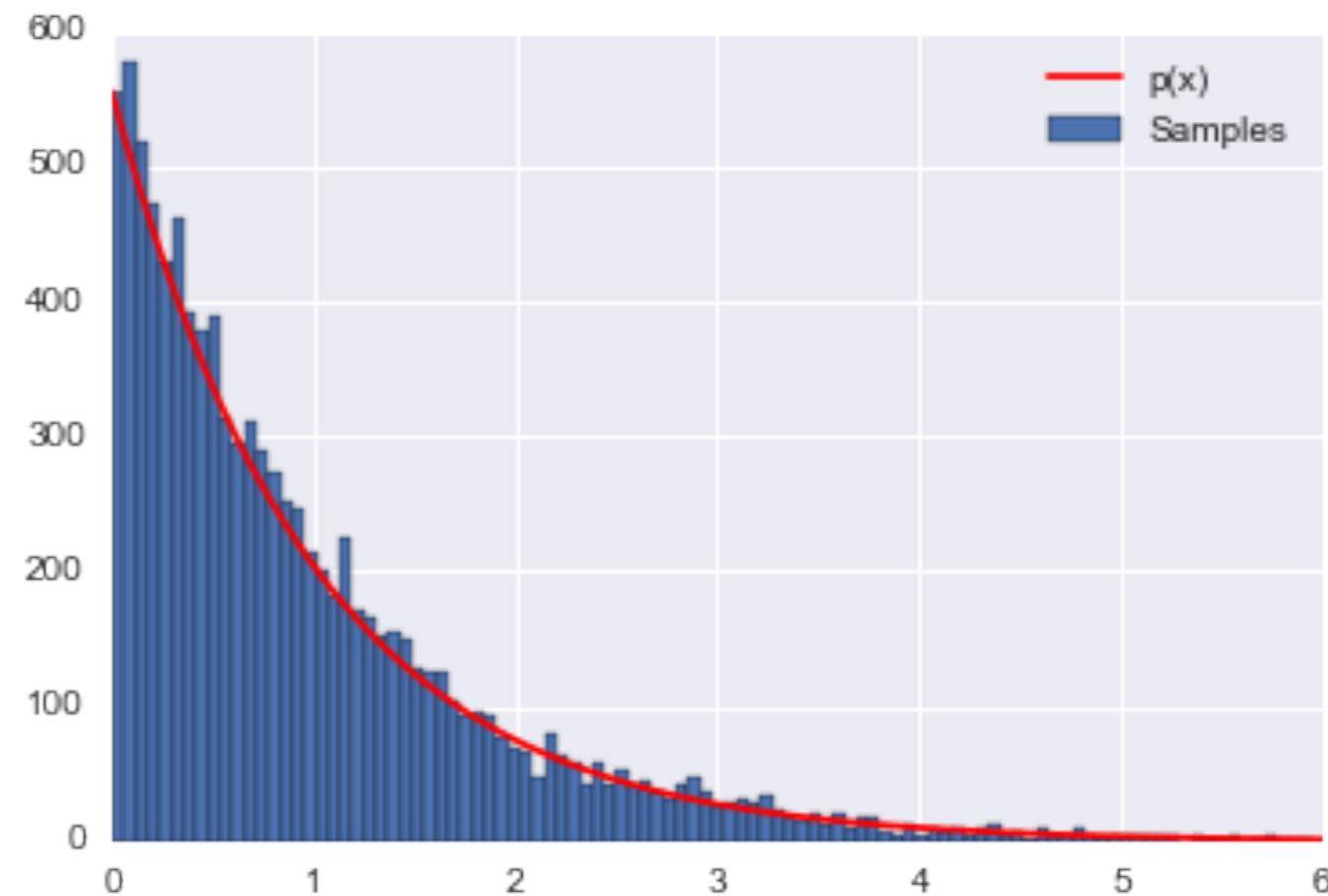
Solving for x

$$x = -\lambda \ln(1 - u)$$

code

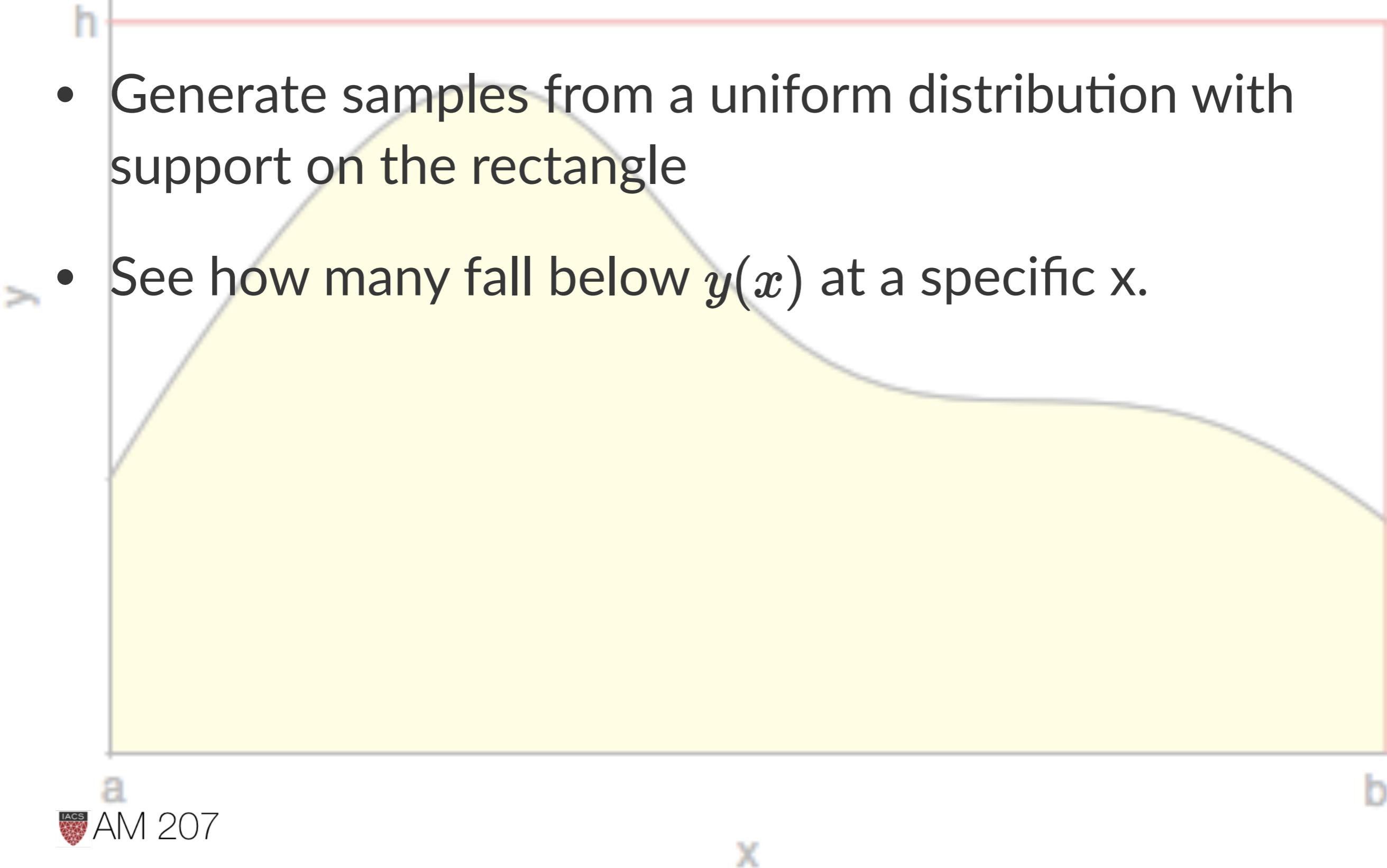
to get an empirical samples distribution from a theoretical pdf/cdf

```
p = lambda x: np.exp(-x)
CDF = lambda x: 1-np.exp(-x)
invCDF = lambda r: -np.log(1-r) # invert the CDF
xmin = 0 # the lower limit of our domain
xmax = 6 # the upper limit of our domain
rmin = CDF(xmin)
rmax = CDF(xmax)
N = 10000
# generate uniform samples in our range then invert the CDF
# to get samples of our target distribution
R = np.random.uniform(rmin, rmax, N)
X = invCDF(R)
hinfo = np.histogram(X, 100)
plt.hist(X, bins=100, label=u'Samples');
# plot our (normalized) function
xvals=np.linspace(xmin, xmax, 1000)
plt.plot(xvals, hinfo[0][0]*p(xvals), 'r', label=u'p(x)')
plt.legend()
```



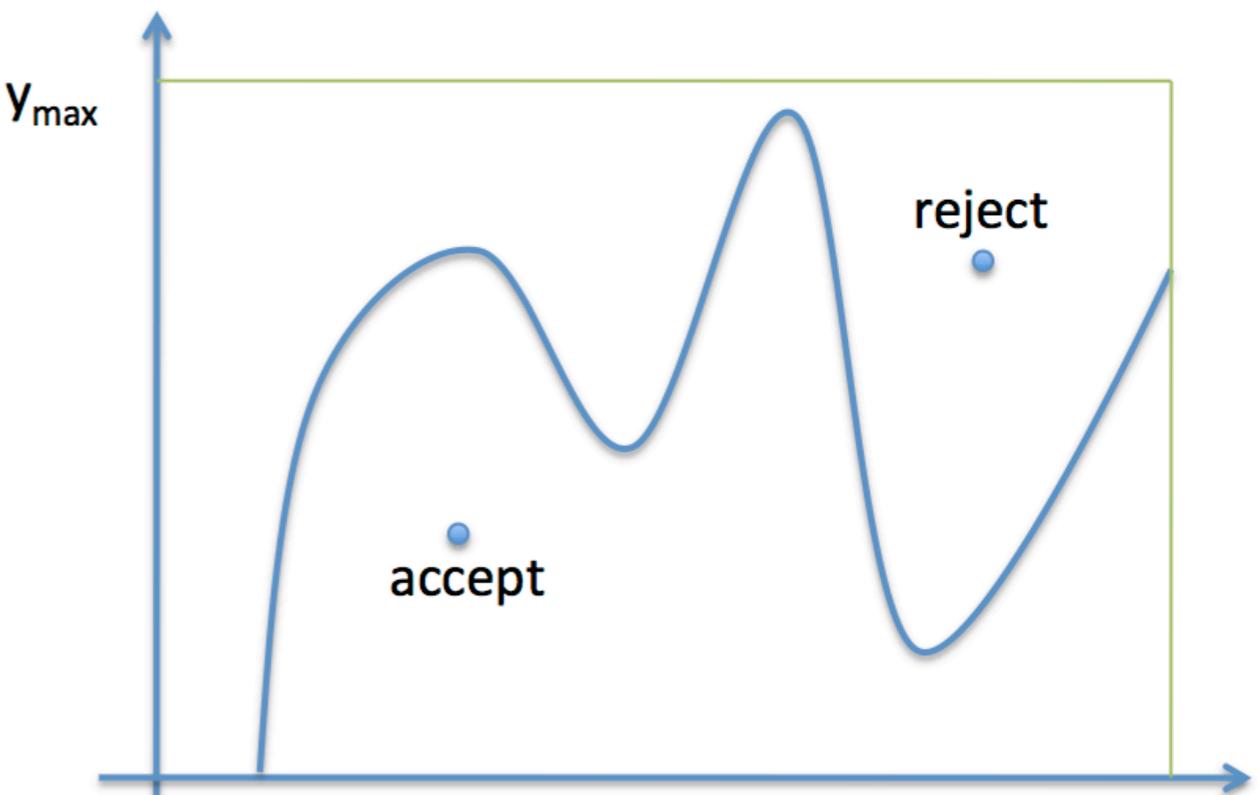
Rejection Sampling

- Generate samples from a uniform distribution with support on the rectangle
- See how many fall below $y(x)$ at a specific x .



Algorithm

1. Draw x uniformly from $[x_{min}, x_{max}]$
2. Draw y uniformly from $[0, y_{max}]$
3. if $y < f(x)$, accept the sample
4. otherwise reject it
5. repeat



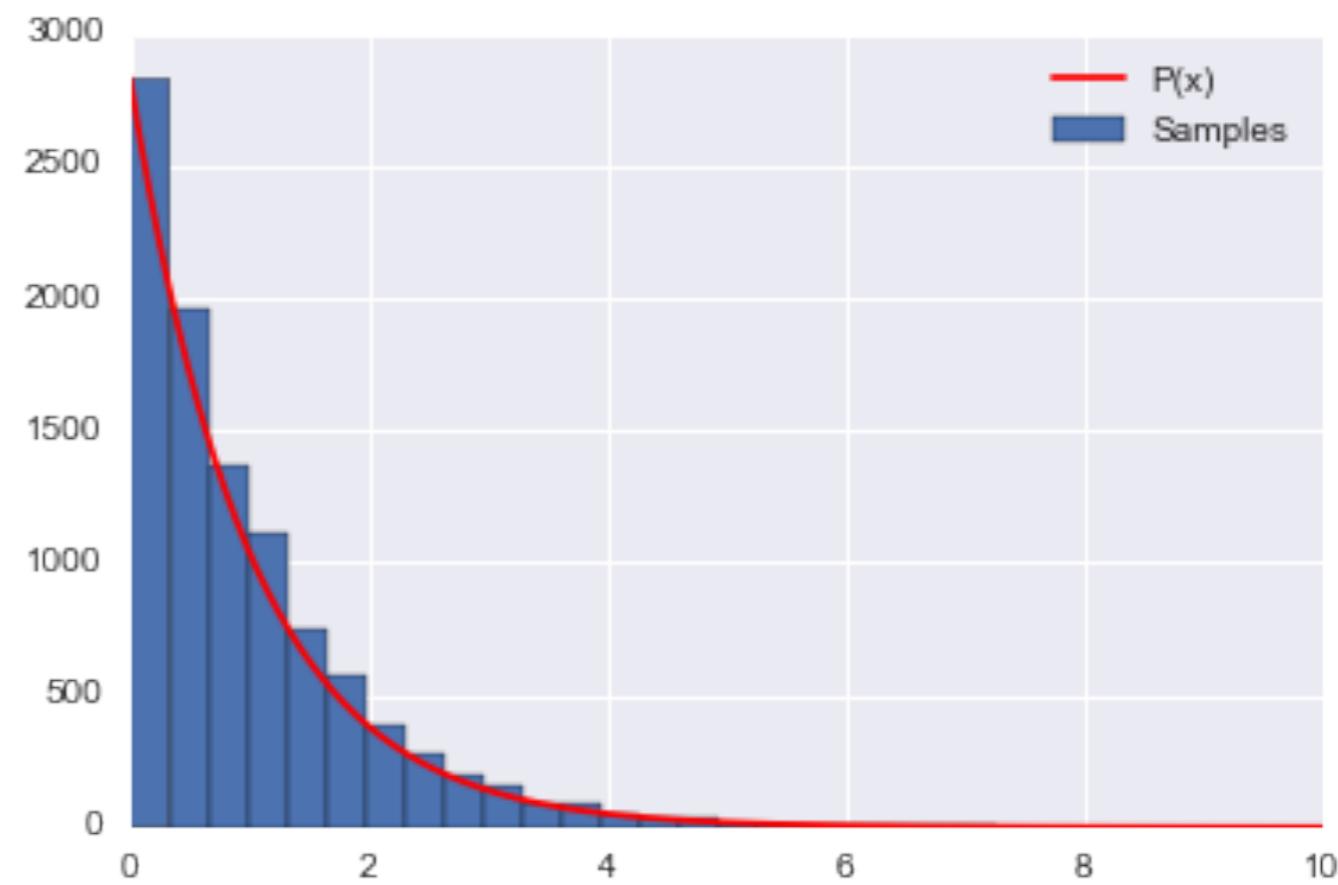
example

```
P = lambda x: np.exp(-x)
xmin = 0 # the lower limit of our domain
xmax = 10 # the upper limit of our domain
ymax = 1
#you might have to do an optimization to find this.
N = 10000 # the total of samples we wish to generate
accepted = 0 # the number of accepted samples
samples = np.zeros(N)
count = 0 # the total count of proposals

while (accepted < N):
    # pick a uniform number on [xmin, xmax) (e.g. 0...10)
    x = np.random.uniform(xmin, xmax)
    # pick a uniform number on [0, ymax)
    y = np.random.uniform(0,ymax)
    # Do the accept/reject comparison
    if y < P(x):
        samples[accepted] = x
        accepted += 1

    count +=1

print("Count",count, "Accepted", accepted)
hinfo = np.histogram(samples,30)
plt.hist(samples,bins=30, label=u'Samples');
xvals=np.linspace(xmin, xmax, 1000)
plt.plot(xvals, hinfo[0][0]*P(xvals), 'r', label=u'P(x)')
plt.legend()
```



Count 100294 Accepted 10000

problems

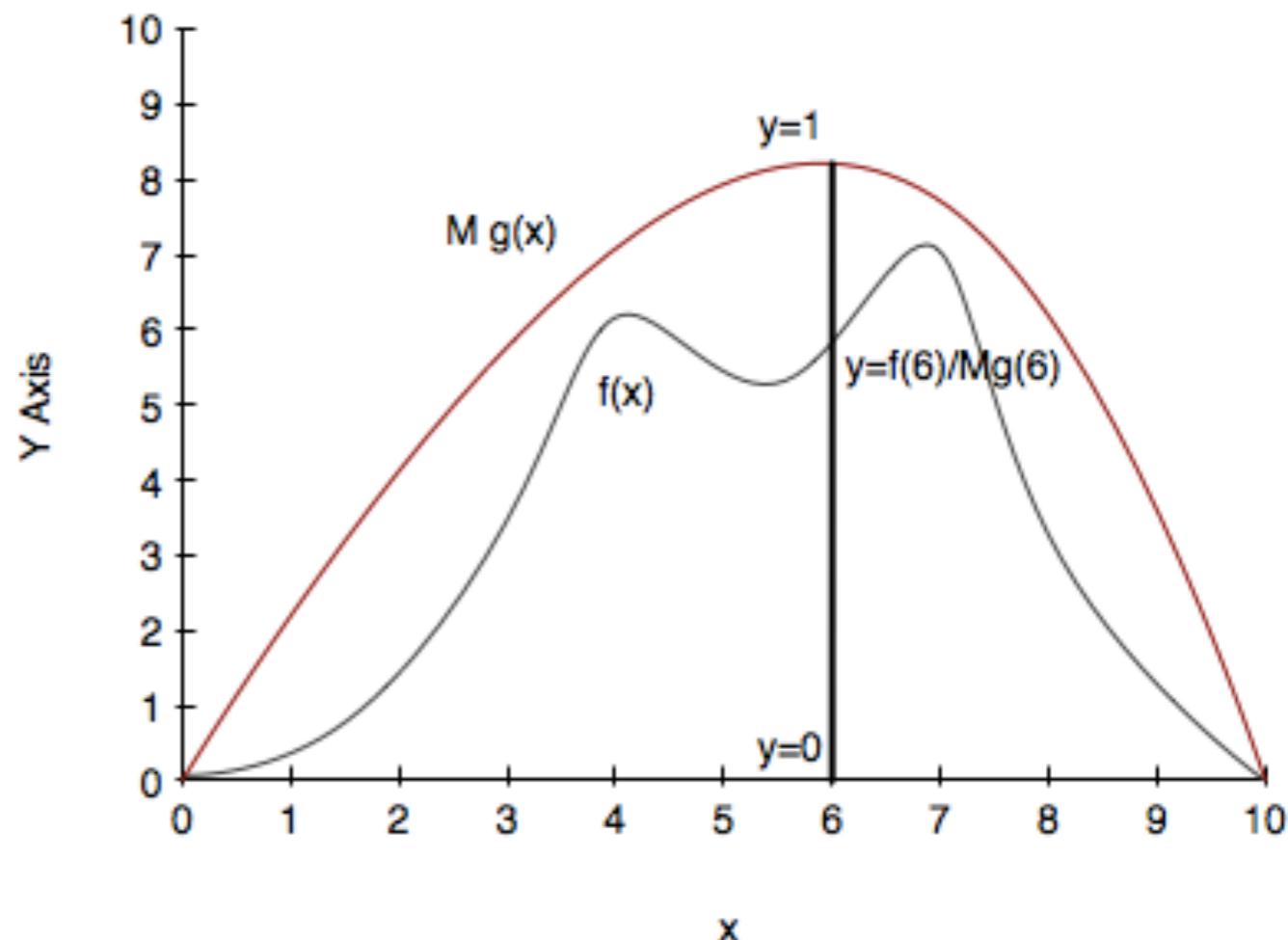
- determining the supremum may be costly
- the functional form may be complex for comparison
- even if you find a tight bound for the supremum, basic rejection sampling is very inefficient: **low acceptance probability**
- infinite support

Variance Reduction

Rejection on steroids

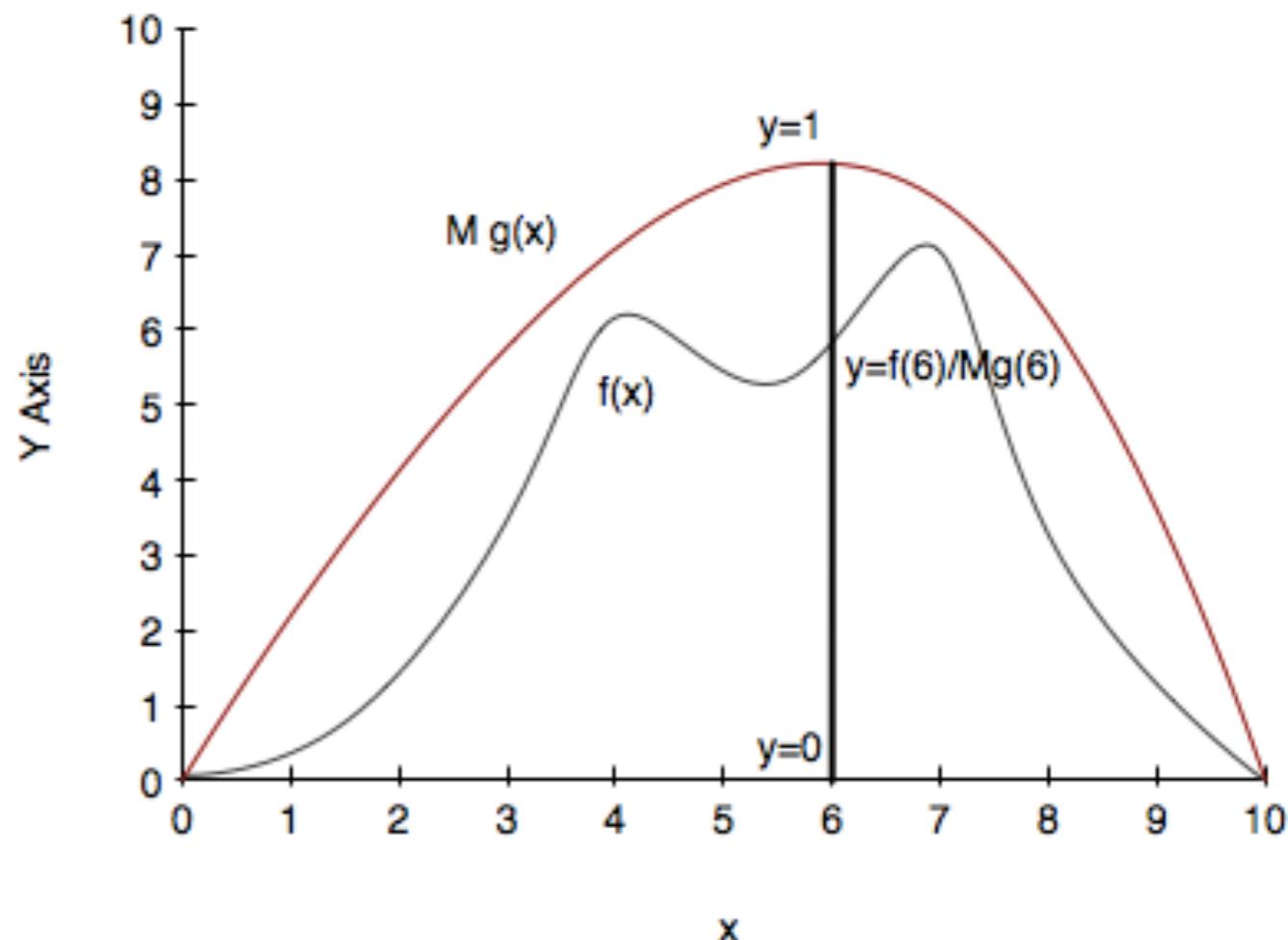
Introduce a **proposal density** $g(x)$.

- $g(x)$ is easy to sample from and (calculate the pdf)
- Some M exists so that $M g(x) > f(x)$ in your entire domain of interest
- ideally $g(x)$ will be somewhat close to f
- optimal value for M is the supremum over your domain



Algorithm

1. Draw x from your proposal distribution $g(x)$
2. Draw y uniformly from $[0,1]$
3. if $y < f(x)/M g(x)$, accept the sample
4. otherwise reject it
5. repeat



Example

```
p = lambda x: np.exp(-x) # our distribution
g = lambda x: 1/(x+1) # our proposal pdf (we're thus choosing M to be 1)
invCDFg = lambda x: np.log(x +1) # generates our proposal using inverse sampling
xmin = 0 # the lower limit of our domain
xmax = 10 # the upper limit of our domain
# range limits for inverse sampling
umin = invCDFg(xmin)
umax = invCDFg(xmax)
N = 10000 # the total of samples we wish to generate
accepted = 0 # the number of accepted samples
samples = np.zeros(N)
count = 0 # the total count of proposals

while (accepted < N):

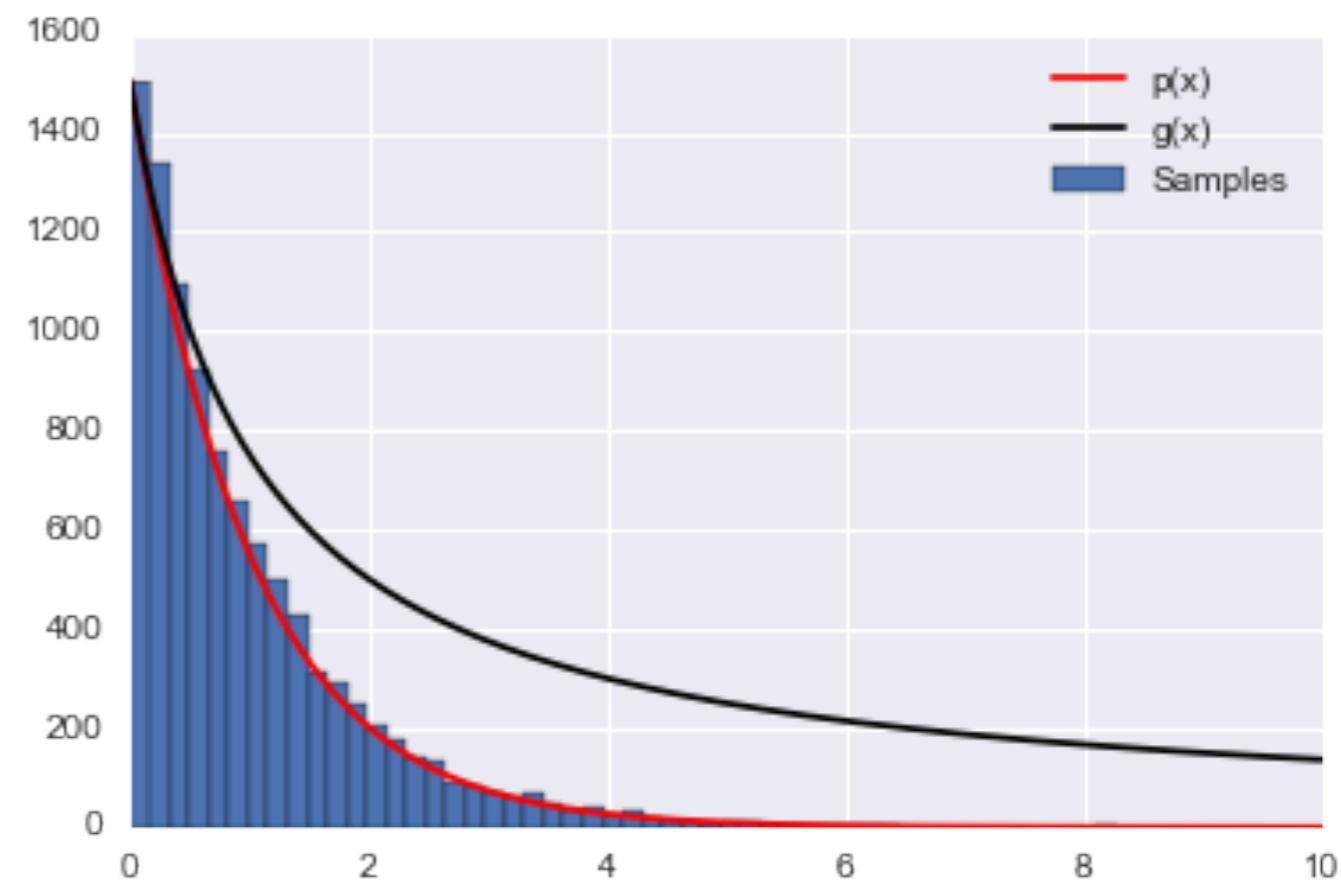
    # Sample from g using inverse sampling
    u = np.random.uniform(umin, umax)
    xproposal = np.exp(u) - 1

    # pick a uniform number on [0, 1)
    y = np.random.uniform(0,1)

    # Do the accept/reject comparison
    if y < p(xproposal)/g(xproposal):
        samples[accepted] = xproposal
        accepted += 1

    count +=1

print("Count", count, "Accepted", accepted)
# get the histogram info
hinfo = np.histogram(samples,50)
plt.hist(samples,bins=50, label=u'Samples');
xvals=np.linspace(xmin, xmax, 1000)
plt.plot(xvals, hinfo[0][0]*p(xvals), 'r', label=u'p(x)')
plt.plot(xvals, hinfo[0][0]*g(xvals), 'k', label=u'g(x)')
plt.legend()
```



Count 23809 Accepted 10000

MLE for Logistic Regression

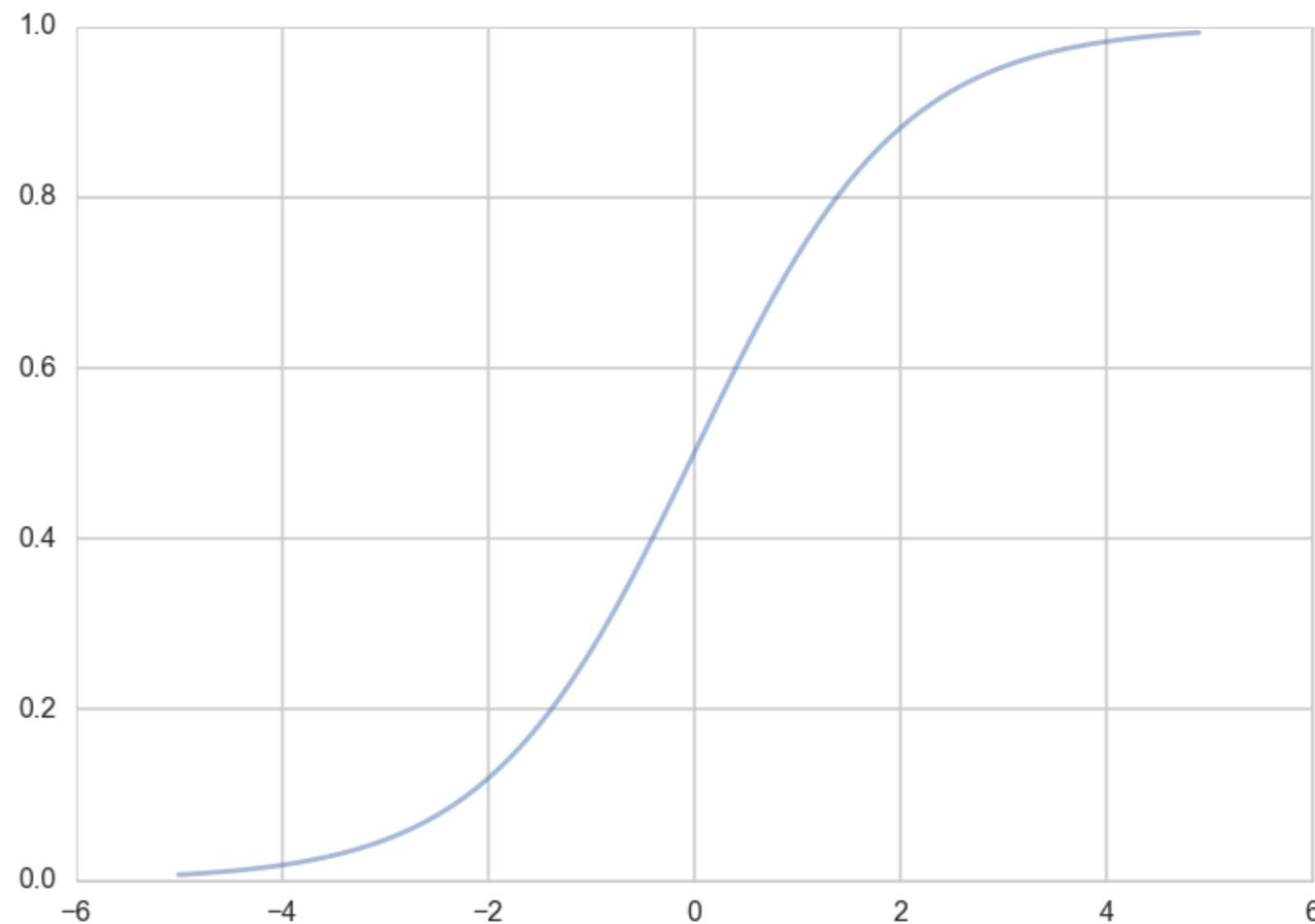
- example of a Generalized Linear Model (GLM)
- "Squeeze" linear regression through a **Sigmoid** function
- this bounds the output to be a probability
- What is the sampling Distribution?

Sigmoid function

This function is plotted below:

```
h = lambda z: 1./(1+np.exp(-z))  
zs=np.arange(-5,5,0.1)  
plt.plot(zs, h(zs), alpha=0.5);
```

Identify: $z = \mathbf{w} \cdot \mathbf{x}$ and $h(\mathbf{w} \cdot \mathbf{x})$
with the probability that the
sample is a '1' ($y = 1$).



Then, the conditional probabilities of $y = 1$ or $y = 0$ given a particular sample's features \mathbf{x} are:

$$P(y = 1|\mathbf{x}) = h(\mathbf{w} \cdot \mathbf{x})$$

$$P(y = 0|\mathbf{x}) = 1 - h(\mathbf{w} \cdot \mathbf{x}).$$

These two can be written together as

$$P(y|\mathbf{x}, \mathbf{w}) = h(\mathbf{w} \cdot \mathbf{x})^y (1 - h(\mathbf{w} \cdot \mathbf{x}))^{(1-y)}$$

BERNOULLI!!

Multiplying over the samples we get:

$$P(y|\mathbf{x}, \mathbf{w}) = P(\{y_i\}|\{\mathbf{x}_i\}, \mathbf{w}) = \prod_{y_i \in \mathcal{D}} P(y_i|\mathbf{x}_i, \mathbf{w}) = \prod_{y_i \in \mathcal{D}} h(\mathbf{w} \cdot \mathbf{x}_i)^{y_i} (1 - h(\mathbf{w} \cdot \mathbf{x}_i))^{(1-y_i)}$$

A noisy y is to imagine that our data \mathcal{D} was generated from a joint probability distribution $P(x, y)$. Thus we need to model y at a given x , written as $P(y | x)$, and since $P(x)$ is also a probability distribution, we have:

$$P(x, y) = P(y | x)P(x),$$

Indeed its important to realize that a particular sample can be thought of as a draw from some "true" probability distribution.

maximum likelihood estimation maximises the **likelihood of the sample y** ,

$$\mathcal{L} = P(y \mid \mathbf{x}, \mathbf{w}).$$

Again, we can equivalently maximize

$$\ell = \log(P(y \mid \mathbf{x}, \mathbf{w}))$$

Thus

$$\begin{aligned}\ell &= \log \left(\prod_{y_i \in \mathcal{D}} h(\mathbf{w} \cdot \mathbf{x}_i)^{y_i} (1 - h(\mathbf{w} \cdot \mathbf{x}_i))^{(1-y_i)} \right) \\ &= \sum_{y_i \in \mathcal{D}} \log \left(h(\mathbf{w} \cdot \mathbf{x}_i)^{y_i} (1 - h(\mathbf{w} \cdot \mathbf{x}_i))^{(1-y_i)} \right) \\ &= \sum_{y_i \in \mathcal{D}} \log h(\mathbf{w} \cdot \mathbf{x}_i)^{y_i} + \log (1 - h(\mathbf{w} \cdot \mathbf{x}_i))^{(1-y_i)} \\ &= \sum_{y_i \in \mathcal{D}} (y_i \log(h(\mathbf{w} \cdot \mathbf{x})) + (1 - y_i) \log(1 - h(\mathbf{w} \cdot \mathbf{x})))\end{aligned}$$