Lecture 13 Bayesian Regression and pymc3



Last time: Bayes

- Gibbs Sampling samples from conditionals
- Hierarchical models have a graph structure
- Makes conditional sampling easy
- Best to use log posteriors
- Gibbs can have strong correlations



Today

- the normal-normal model with MCMC
- then with pymc3
- bayesian regression and updating
- regularization and the ridge
- from the normal model to regression using pymc
- posterior vs predictive in regression problems



The levels of Bayesian analysis (from last time)

Method	Definition
Maximum Likelihood	$\hat{ heta} = argmax_{ heta} p(D heta)$
MAP estimation	$\hat{ heta} = argmax_{ heta} p(D heta) p(heta \eta)$
ML-2 (Empirical Bayes)	$\hat{\eta} = argmax_{\eta} \int d\theta p(D \theta) p(\theta \eta) = argmax_{\eta} p(D \eta)$
MAP-2	$\hat{\eta} = argmax_{\eta} \int d\theta p(D \theta) p(\theta \eta) p(\eta) = argmax_{\eta} p(D \eta) p(\eta)$
Full Bayes	$p(\theta, \eta D) \propto p(D \theta)p(\theta \eta)p(\eta)$



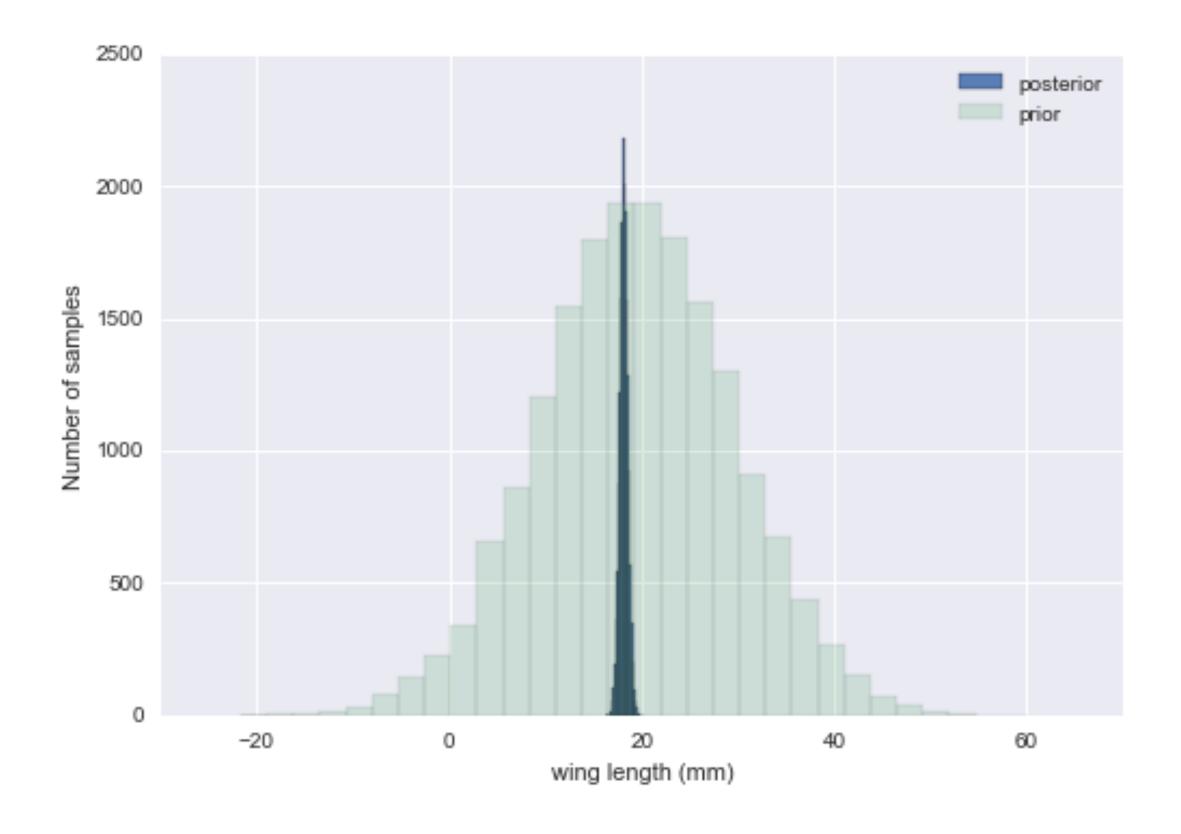
Normal-normal model

We have data on the wing length in millimeters of a nine members of a particular species of moth. We wish to make inferences from those measurements on the population mean μ .

Other studies show the wing length to be around 19 mm. We also know that the length must be positive. We can choose a prior that is normal and most of the density is above zero (μ =19.5, τ =10).

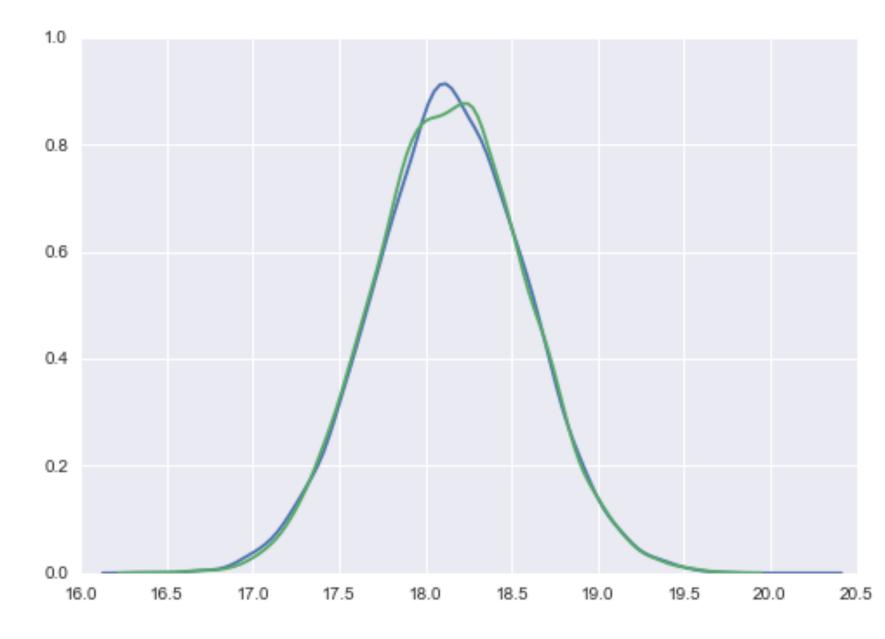
$$Y = [16.4, 17.0, 17.2, 17.4, 18.2, 18.2, 18.2, 19.9, 20.8]$$







```
def metropolis(logp, qdraw, stepsize, nsamp, xinit):
    samples=np.empty(nsamp)
   x prev = xinit
    accepted = ∅
    for i in range(nsamp):
        x_star = qdraw(x_prev, stepsize)
        logp_star = logp(x_star)
        logp_prev = logp(x_prev)
        logpdfratio = logp_star -logp_prev
       u = np.random.uniform()
        if np.log(u) <= logpdfratio:</pre>
            samples[i] = x_star
            x_prev = x_star
            accepted += 1
        else:#we always get a sample
            samples[i]= x_prev
   return samples, accepted
logprior = lambda mu: norm.logpdf(mu, loc=19.5, scale=10)
loglike = lambda mu: np.sum(norm.logpdf(Y, loc=mu, scale=np.std(Y)))
logpost = lambda mu: loglike(mu) + logprior(mu)
```





Sampling with pymc

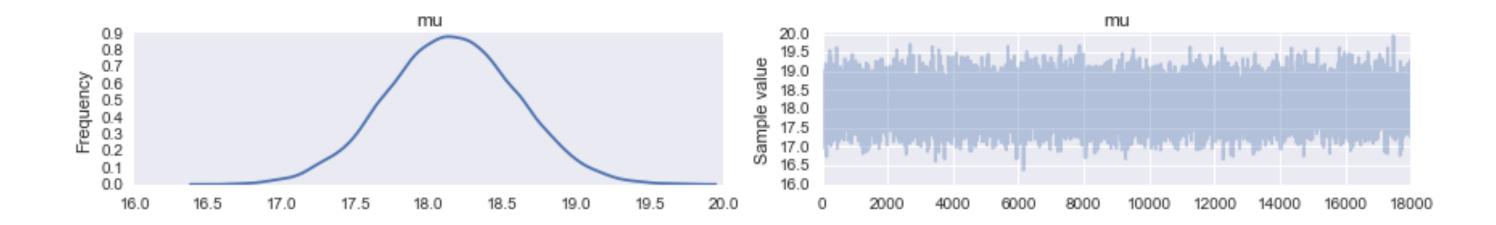
conda install pymc3 patsy

Installed 3.0rc4 for me.

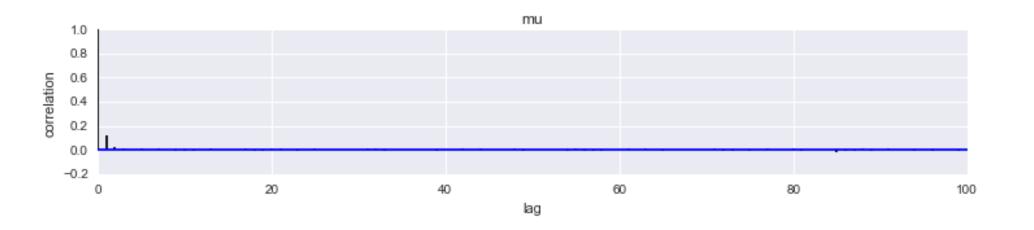
```
import pymc3 as pm
with pm.Model() as model1:
    mu = pm.Normal('mu', mu=19.5, sd=10)#parameter's prior
    wingspan = pm.Normal('wingspan', mu=mu, sd=np.std(Y), observed=Y)#likelihood
    stepper=pm.Metropolis()
    tracemodel1=pm.sample(100000, step=stepper)
100%
```



pm.traceplot(tracemodel1[10000::5]);



pm.autocorrplot(tracemodel1[10000::5]);





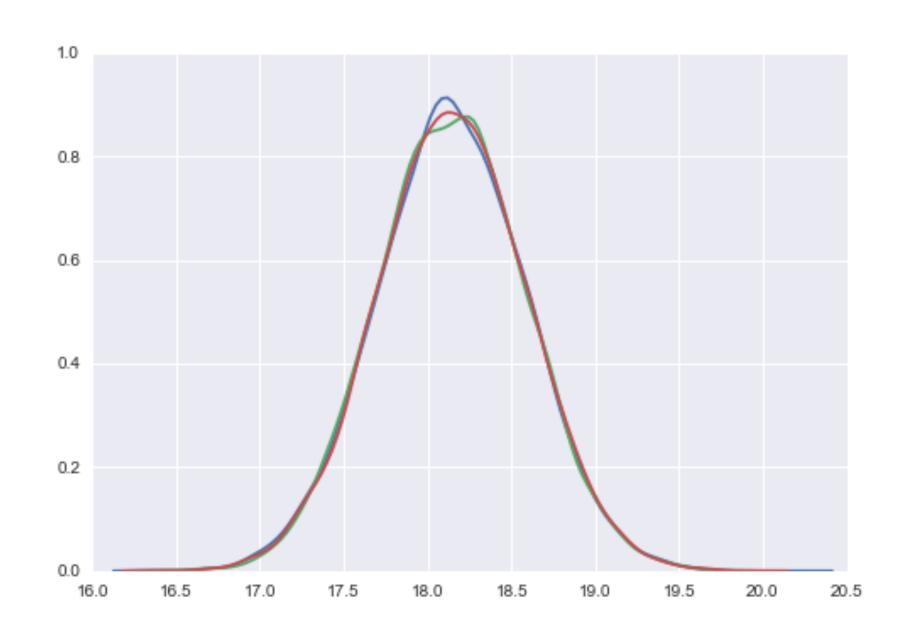
HPD: The highest-posterior-density smallest width Bayesian Credible Interval.

pm.summary(tracemodel1)
mu:

Mean	SD	MC Error	95% HP	D interval
18.148	0.443	0.003	[17.28	5, 19.019]
Posterior qu 2.5 	antiles: 25 ======	50 ==== ======	75 ===	97.5
17.277	17.849	18.146	18.446	19.012



Posteriors all match up!





Posterior predictives

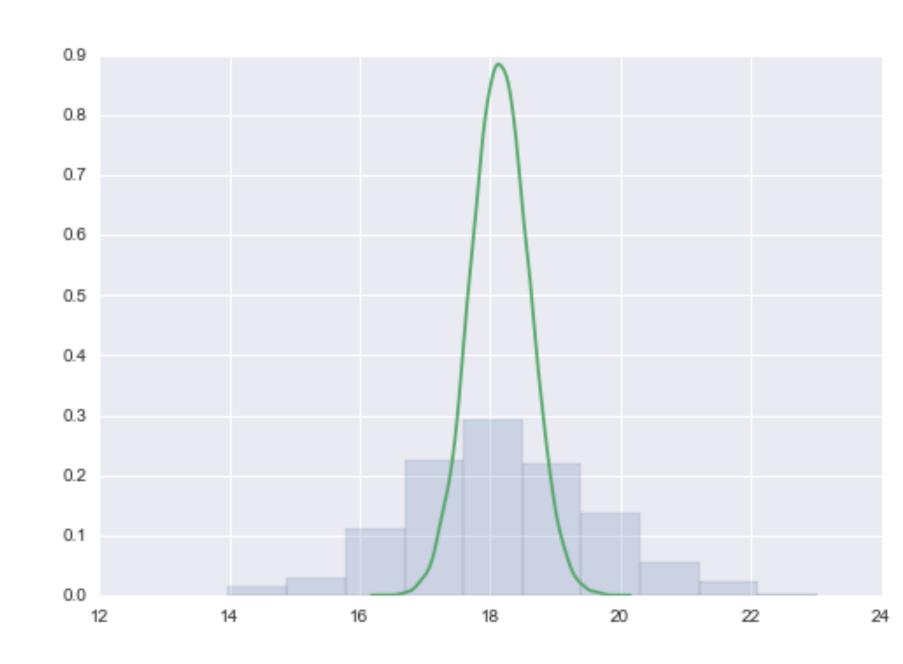
The posterior predictive is accessed via the sample_ppc function:

model1.observed_RVs

[wingspan]

```
tr1 = tracemodel1[10000::5]
postpred = pm.sample_ppc(tr1, 1000, model1)
```

100%| | 1000/1000 [00:01<00:00, 510.20it/s] | 25/1000 [00:00<00:03, 244.20it/s]





Bayesian Formulation of Regression

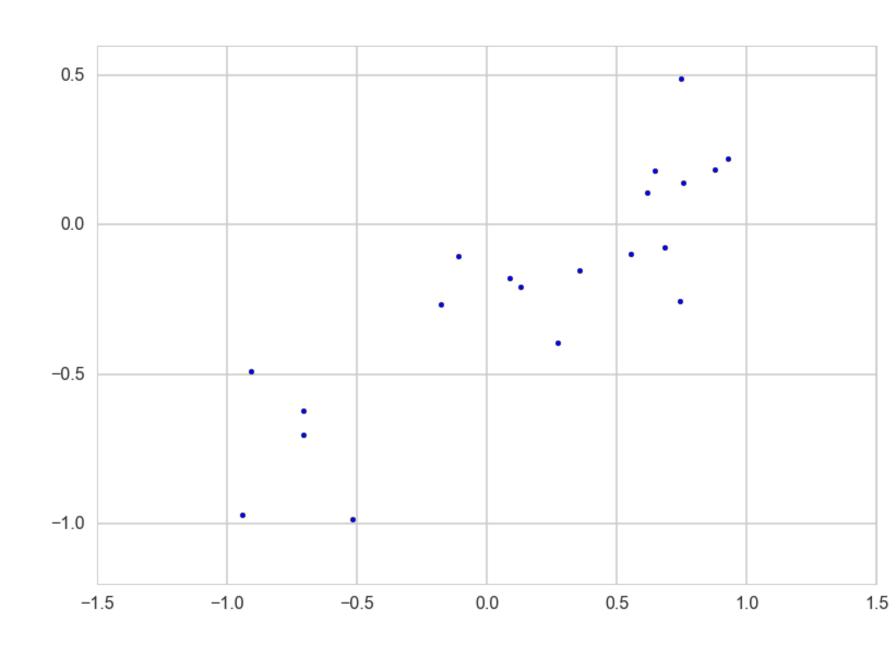
Data

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

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

Model:

$$y = \mathbf{x^T}\mathbf{w} + \epsilon$$
 $\epsilon \sim N(0, \sigma_n^2)$



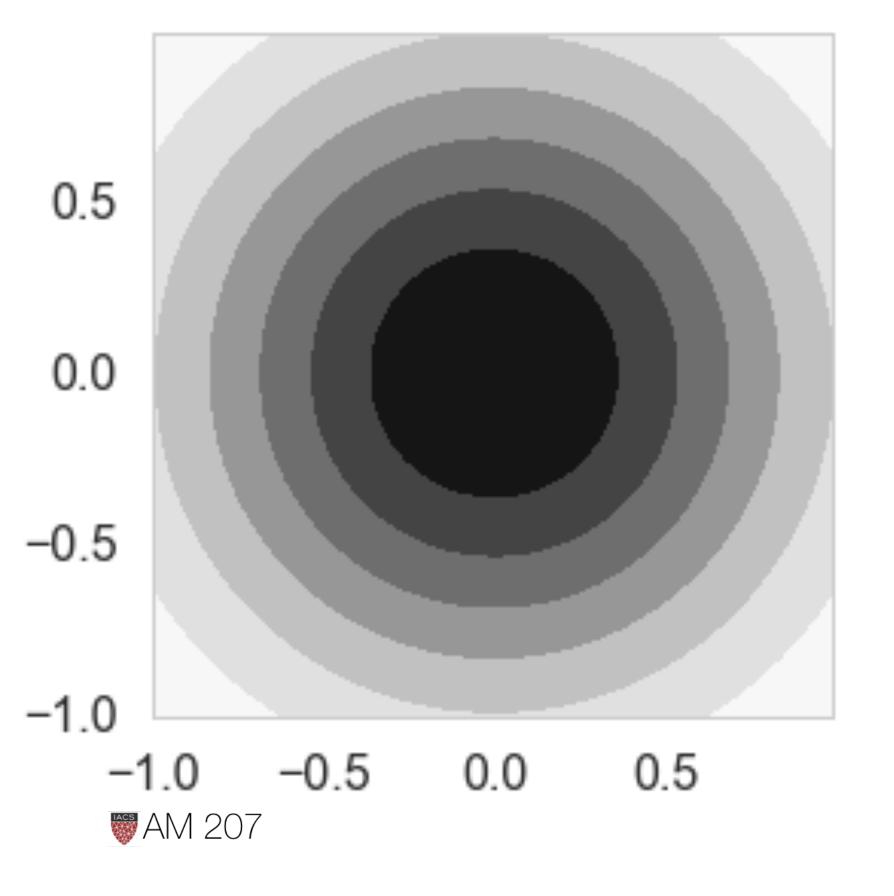


Likelihood

The likelihood is, because we assume independency, the product

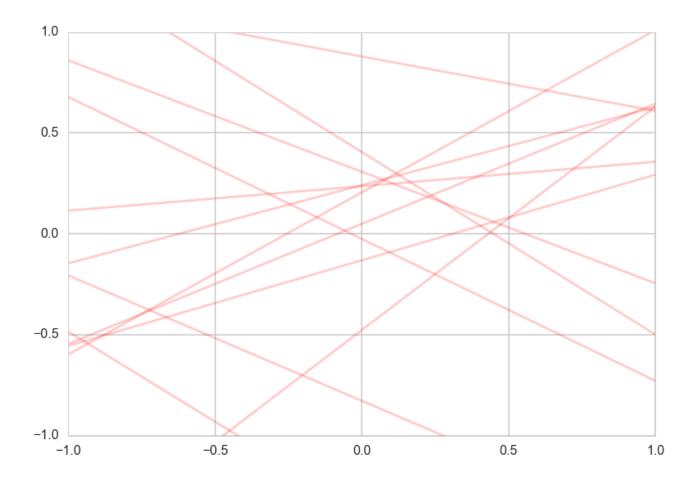
$$\mathcal{L} = p(\mathbf{y}|\mathbf{X}, \mathbf{w}) = \prod_{i=1}^{n} \mathbf{p}(\mathbf{y}_{i}|\mathbf{X}_{i}, \mathbf{w}) = \prod_{i=1}^{n} \frac{1}{\sqrt{2\pi}\sigma_{n}} \exp\left(-\frac{(\mathbf{y}_{i} - \mathbf{X}_{i}^{T}\mathbf{w})^{2}}{2\sigma_{n}^{2}}\right)$$

$$\propto \exp\left(-\frac{|\mathbf{y} - \mathbf{X}^{T}\mathbf{w}|^{2}}{2\sigma_{n}^{2}}\right) \propto N(X^{T}\mathbf{w}, \sigma_{n}^{2}\mathbf{I})$$



Prior $\mathbf{w} \sim \mathbf{N}(\mathbf{w_0}, \boldsymbol{\Sigma})$

$$\mathbf{w} \sim \mathbf{N}(\mathbf{w_0}, au^2 \mathbf{I})$$



Posterior

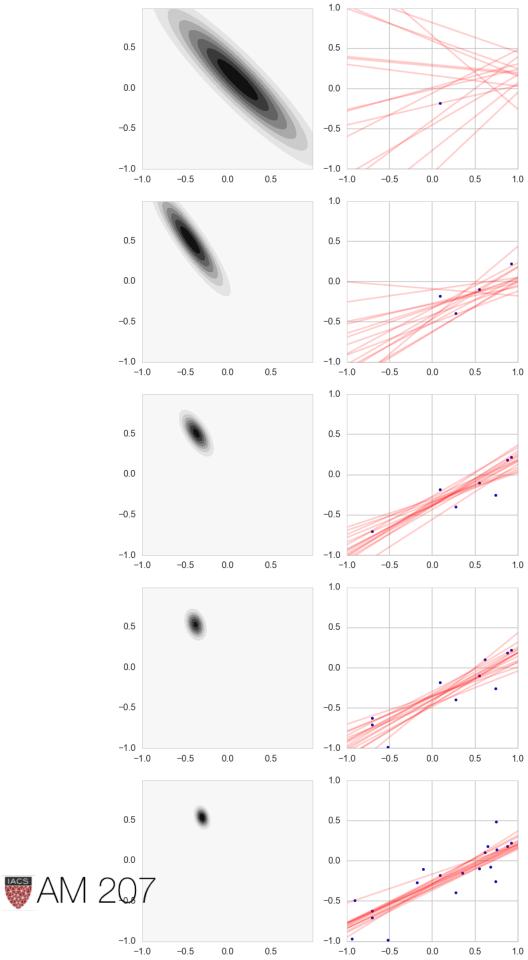
$$p(\mathbf{w}|\mathbf{y}, \mathbf{X}) \propto p(\mathbf{y}|\mathbf{X}, \mathbf{w}) \mathbf{p}(\mathbf{w})$$

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

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

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

where the new mean is $\bar{\mathbf{w}} = A^{-1}\Sigma^{-1}\mathbf{w_0} + \sigma_n^{-2}(A^{-1}X^T\mathbf{y})$

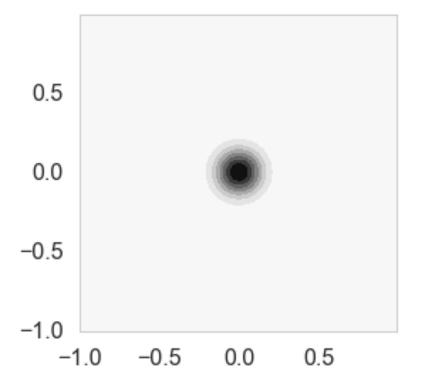


Bayesian updating

Posterior predictive

$$egin{aligned} p(y^*|x^*,\mathbf{x},\mathbf{y}) &= \int p(\mathbf{y}^*|\mathbf{x}^*,\mathbf{w})p(\mathbf{w}|\mathbf{X},\mathbf{y})\mathbf{dw} \ &= \mathcal{N}\left(y|ar{\mathbf{w}}^Tx^*,\sigma_n^2 + x^{*^T}A^{-1}x^*
ight), \end{aligned}$$

Regularization

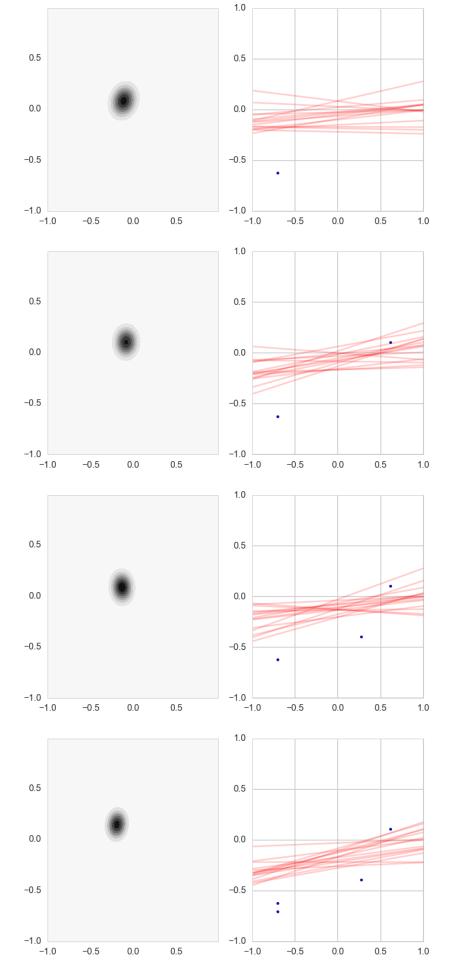


priorPrecision/likelihoodPrecision

4.0

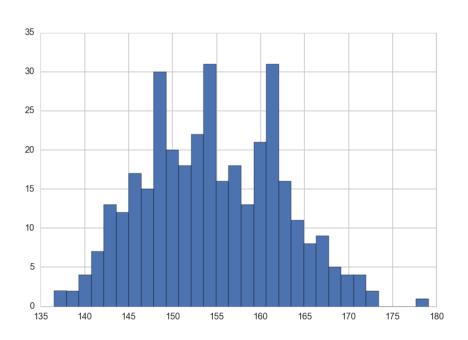
This ratio is the ridge α .





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.



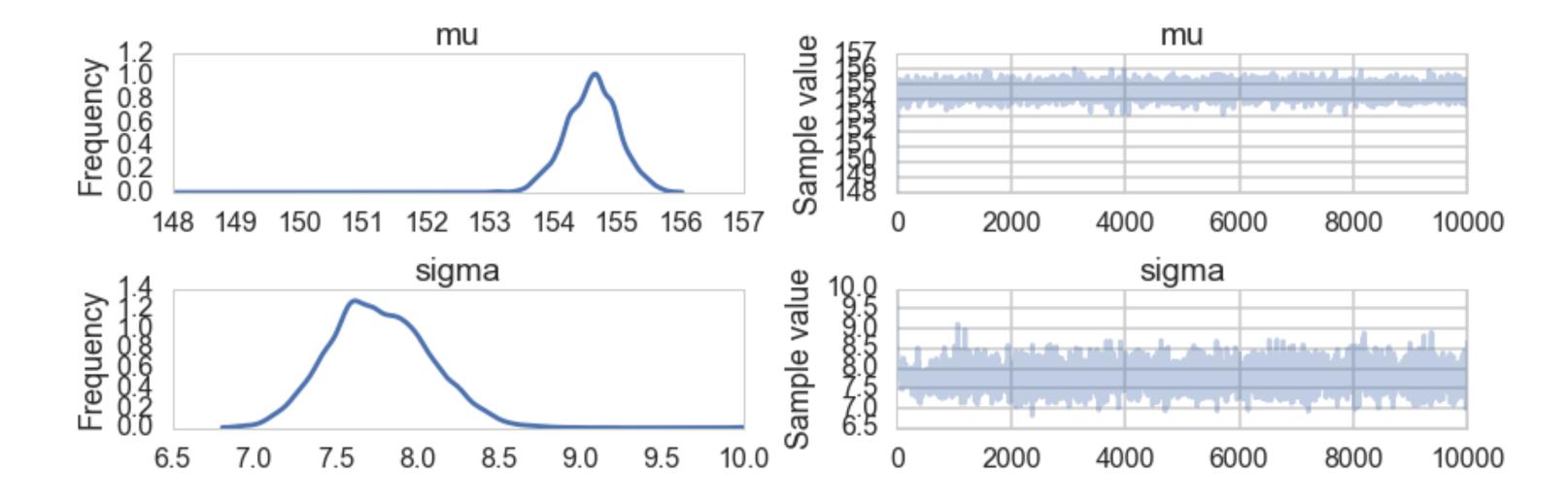
	height	weight	age	male
0	151.765	47.825606	63.0	1
1	139.700	36.485807	63.0	0
2	136.525	31.864838	65.0	0
3	156.845	53.041915	41.0	1
4	145.415	41.276872	51.0	0



Model

```
h \sim N(\mu, \sigma) \ \mu \sim Normal(148, 20) \ \sigma \sim Unif(0, 50)
```

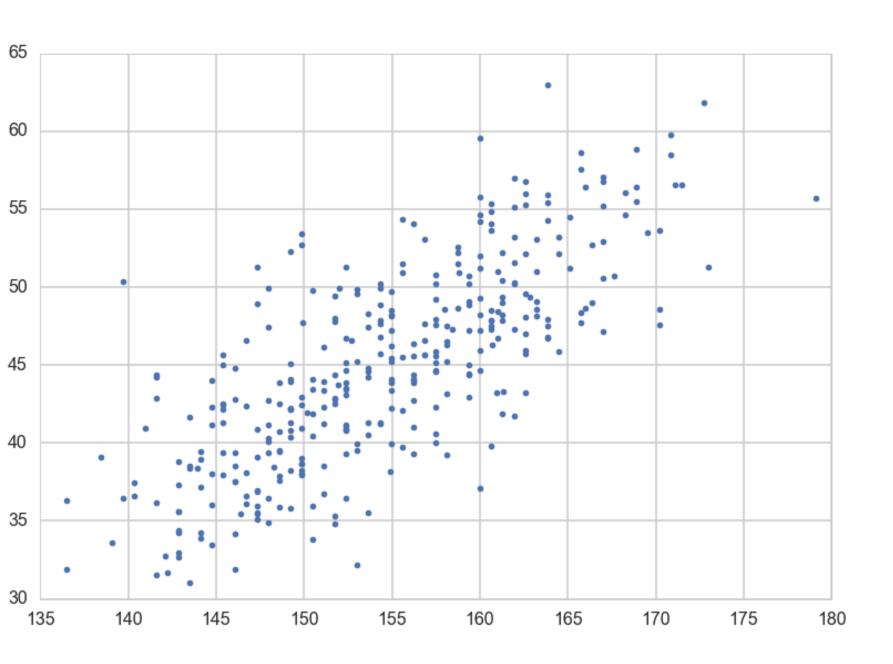




```
def acceptance(trace, paramname):
    accept = np.sum(trace[paramname][1:] != trace[paramname][:-1])
    return accept/trace[paramname].shape[0]

acceptance(tracehm1, 'mu'), acceptance(tracehm1, 'sigma')
(0.3896, 0.30009999999999999)
```





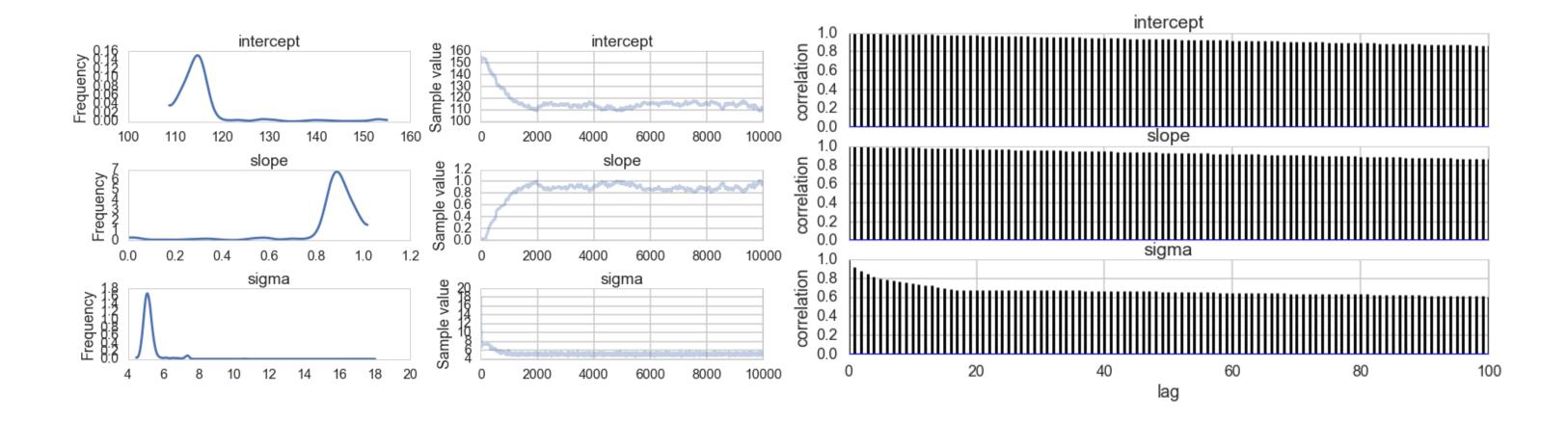
Regression, adding a predictor, weight

```
h \sim N(\mu, \sigma) \ \mu = intercept + slope 	imes weight \ intercept \sim N(150, 100) \ slope \sim N(0, 10) \ \sigma \sim Unif(0, 50)
```

```
with pm.Model() as hm2:
    intercept = pm.Normal('intercept', mu=150, sd=100)
    slope = pm.Normal('slope', mu=0, sd=10)
    sigma = pm.Uniform('sigma', lower=0, upper=50)
# below is a deterministic
mu = intercept + slope * df2.weight
height = pm.Normal('height', mu=mu, sd=sigma, observed=df2.height)
    stepper=pm.Metropolis()
    tracehm2 = pm.sample(10000, step=stepper)
```



Traces are awful



The slope and intercept are very highly correlated: -0.99!

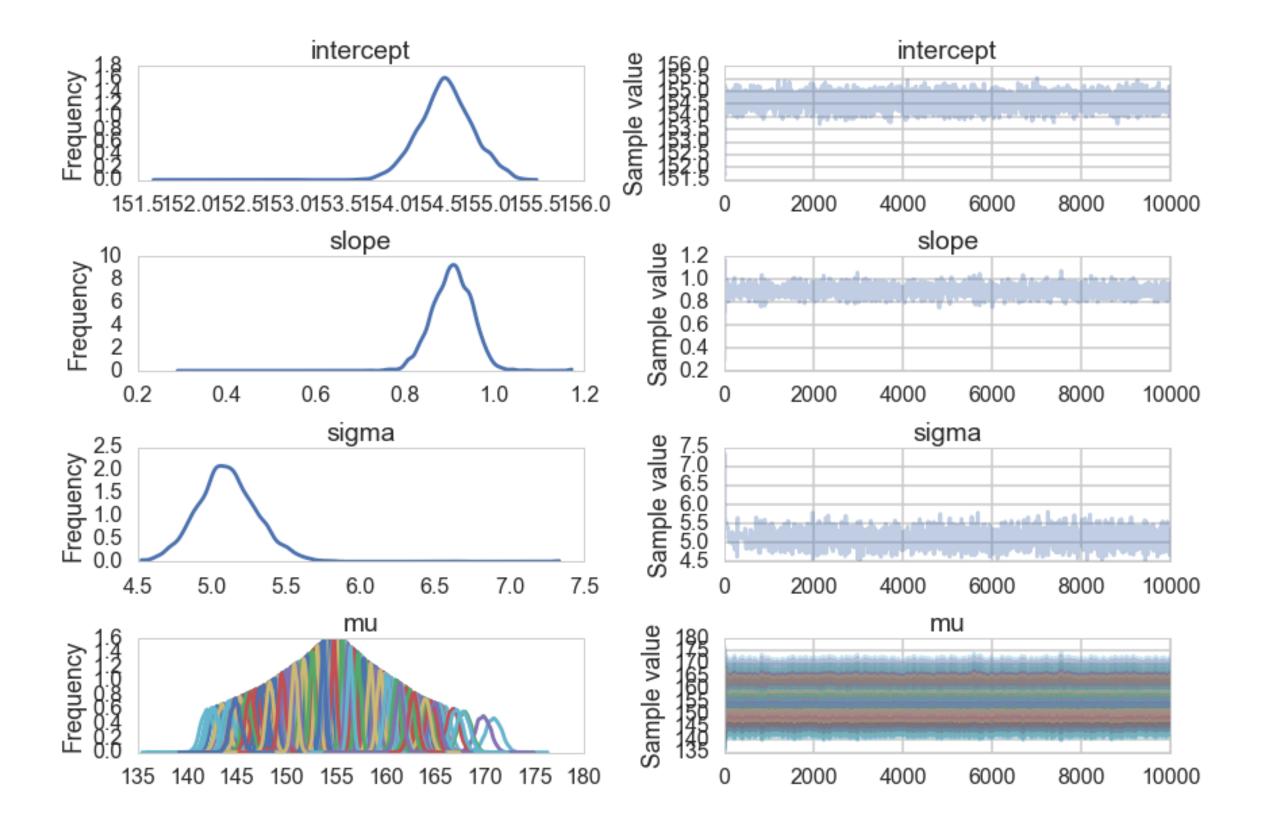


Sympton of shared information and identifiability

fix by centering. intercept then gives response when predictor=mean.

```
with pm.Model() as hm2c:
    intercept = pm.Normal('intercept', mu=150, sd=100)
    slope = pm.Normal('slope', mu=0, sd=10)
    sigma = pm.Uniform('sigma', lower=0, upper=50)
    # below is a deterministic
    #mu = intercept + slope * (df2.weight -df2.weight.mean())
    mu = pm.Deterministic('mu', intercept + slope * (df2.weight -df2.weight.mean()))
    height = pm.Normal('height', mu=mu, sd=sigma, observed=df2.height)
    stepper=pm.Metropolis()
    tracehm2c = pm.sample(10000, step=stepper)
```

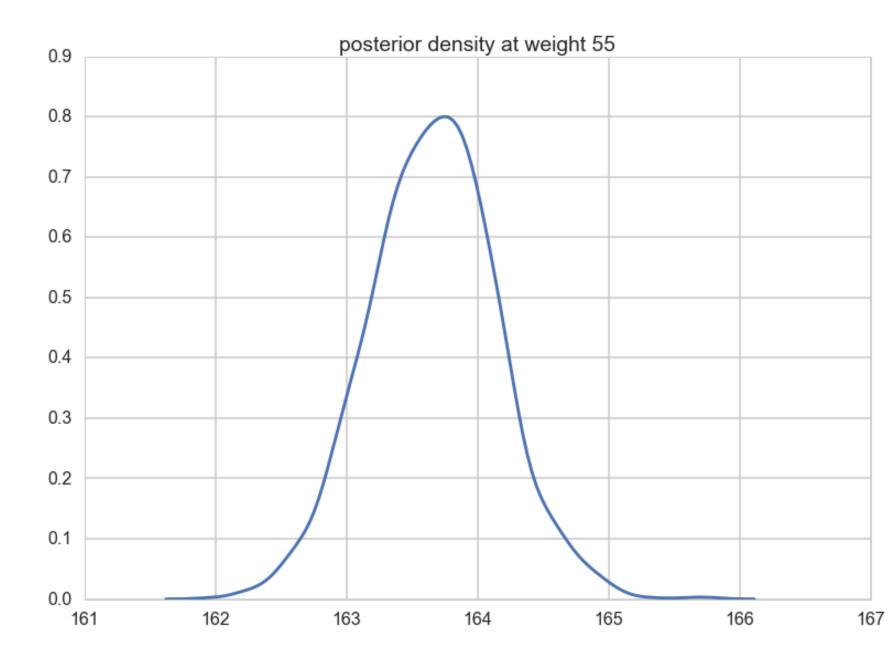




Posteriors

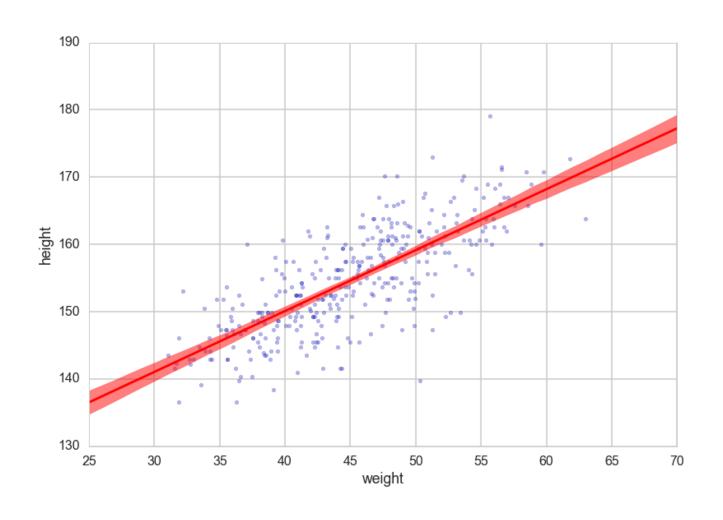
```
meanweight = df2.weight.mean()
weightgrid = np.arange(25, 71)
mu_pred = np.zeros((len(weightgrid), len(tr2c)))
for i, w in enumerate(weightgrid):
    mu_pred[i] = tr2c['intercept'] + tr2c['slope'] * (w - meanweight)

mu_mean = mu_pred.mean(axis=1)
mu_hpd = pm.hpd(mu_pred.T)
```





Posteriors on a grid



Why so tight?



Posterior predictive

At data:

```
postpred = pm.sample_ppc(tr2c, 1000, hm2c)

100%| | 1000/1000 [00:19<00:00, 57.56it/s] | 1/1000 [00:00<08:17, 2.01it/s]
```

On a full grid:

```
n_ppredsamps=1000
weightgrid = np.arange(25, 71)
meanweight = df2.weight.mean()
ppc_samples=np.zeros((len(weightgrid), n_ppredsamps))

for j in range(n_ppredsamps):
    k=np.random.randint(len(tr2c))#samples with replacement
    musamps = tr2c['intercept'][k] + tr2c['slope'][k] * (weightgrid - meanweight)
    sigmasamp = tr2c['sigma'][k]
    ppc_samples[:,j] = np.random.normal(musamps, sigmasamp)
```



Predictives at data and on grid

