# Gibbs Sampling, More Bayesian Topics

Mark M. Fredrickson (mfredric@umich.edu)

Computational Methods in Statistics and Data Science (Stats 406)

#### Review

- Bayesian statistics (as compared to frequentist statistics):
  - Treats parameters as random variables and samples as fixed values
  - Captures beliefs about parameters with a prior distribution  $p(\theta)$ .
  - Models sample with conditional  $f(x \mid \theta)$  and marginal f(x) likelihoods
  - Combines using Bayes' Rule to form a posterior distribution:

$$\pi(\theta \mid x) = \frac{f(x \mid \theta)p(\theta)}{f(x)}$$

• Inference is performed using integration on posterior (or other properties of  $\pi$ ):

$$\mathsf{E}(\mathsf{g}(\theta) \mid \mathsf{x})$$

#### Review, cont.

- For simple problems (e.g., conjugate priors and likelihoods), we can draw directly from posterior
- More complicated problems require Markov Chain Monte Carlo
  - A Markov Chain is a stochastic process with  $X(t) \mid X(t-1), X(t-2), \ldots = X(t) \mid X(t-1)$
  - If we have algorithms that are stationary and ergodic, we can use those to draw from posterior.
  - Metropolis-Hastings (regular, independent, symmetric)
- Practical concerns:
  - Burn in to drop non-stationary portion of chain
  - Rejection rate trades off exploration for time to get a sufficient sample size
  - We frequently have to tune parameters to get samplers

**Non-Conjugate Prior** 

### Return to binomial example

Last time we consider a sample which we modeled as binomial:

$$f(x \mid \theta) = {30 \choose x} \theta^{x} (1 - \theta)^{30 - x}$$

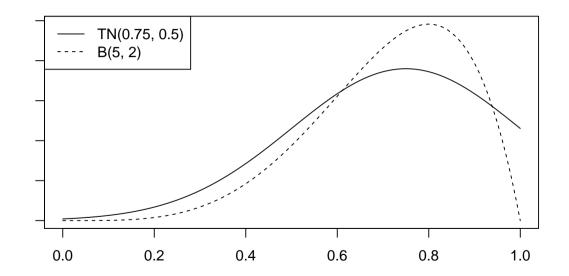
We saw that with a **beta prior** for  $\theta$ , the **posterior was also beta** (conjugate).

What about other priors? Suppose instead described out beliefs using a **truncated**Normal?:

$$p(\theta) \propto \phi((\theta - \mu)/\sigma)$$

where  $\phi$  is PDF of N(0,1). (Notice use of **proportionality**.)

#### **Truncated Normal Prior**



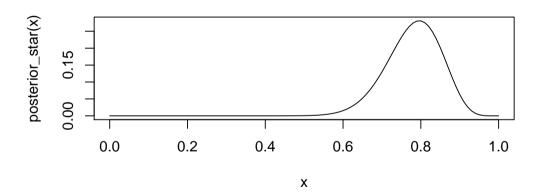
## Posterior after seeing X = 24

What is the posterior distribution (proportional to)? Dropping all terms not involving  $\theta$ ,

$$\pi(\theta \mid x) \propto \theta^{x} (1-\theta)^{x} \exp\left\{-\frac{(\theta-0.75)^{2}}{0.5}\right\}$$

```
> posterior_star <- function(theta) {
+   dbinom(24, 30, prob = theta) * dnorm(theta, 0.75, 0.25)
+ }</pre>
```

### **Unnormalized Posterior**



## Drawing from posterior with Metropolis-Hastings

Due the complexity of the posterior, let's use MCMC to draw from  $\pi$ .

We need a candidate distribution, let's a random walk (bounded by [0,1]):

$$\theta(t)^* \sim U\left[a(\theta(t-1)), b(\theta(t-1))\right], a(x) = \max(0, x-\delta), b(x) = \min(x+\delta, 1)$$

so  $\theta^*$  has density  $1/(b(\theta(t-1)) - a(\theta(t-1)))$ .

Recall, we will need to compute:

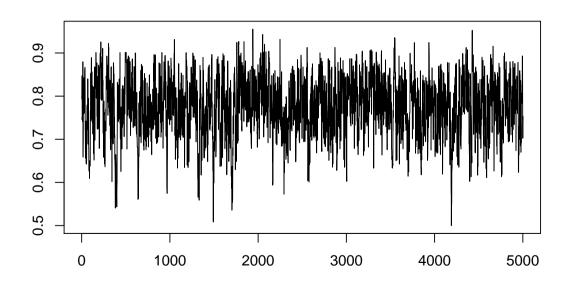
$$\frac{\pi^*(\theta^* \mid x)}{\pi^*(\theta(t-1) \mid x)} \frac{g(\theta(t-1) \mid \theta^*)}{g(\theta^* \mid \theta(t-1))} = \frac{\pi^*(\theta^* \mid x)}{\pi^*(\theta(t-1) \mid x)} \frac{\left\lfloor \frac{1}{b(\theta^*) - a(\theta^*)} \right\rfloor}{\left\lfloor \frac{1}{b(\theta(t-1)) - a(\theta(t-1))} \right\rfloor}$$
$$= \frac{\pi^*(\theta^* \mid x)}{\pi^*(\theta(t-1) \mid x)} \frac{b(\theta(t-1)) - a(\theta(t-1))}{b(\theta^*) - a(\theta^*)}$$

```
> findDeltas <- function(point, delta) {
+    c(max(0, point - delta), # must be positive
+    min(1, point + delta)) # must be less than 1
+ }
> drawCandidate <- function(previous, delta) {
+    ab <- findDeltas(previous, delta)
+    runif(1, ab[1], ab[2])
+ }</pre>
```

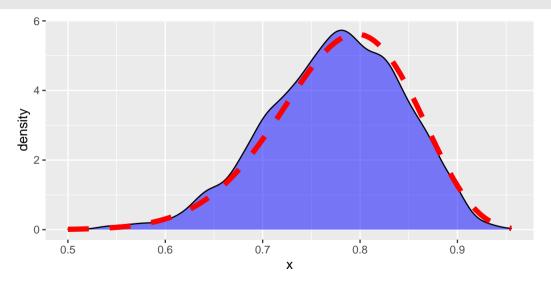
```
> nextDraw <- function(previous, delta = 0.1) {</pre>
      candidate <- drawCandidate(previous, delta)</pre>
+
+
      post_ratio <- posterior_star(candidate) / posterior_star(previous)</pre>
      cand_ratio <- diff(findDeltas(previous, delta)) /</pre>
                      diff(findDeltas(candidate, delta))
+
+
      u \leftarrow runif(1)
      if (u <= post_ratio * cand_ratio) {</pre>
           return(candidate)
      } else {
           return(previous)
```

```
> B <- 10000 ; chain <- numeric(B) ; chain[1] <- 0.75
> for(i in 2:B) {
+          chain[i] <- nextDraw(chain[i - 1], 0.1)
+ }
> half_chain <- chain[5001:B] # drop burn in
> mean(half_chain > 0.75) # probability of successful teaching
[1] 0.6544
```

# Chain (5000 to 10000)



# Density



**Multivariate Sampling** 

#### **Multidimensional Posterior**

So far, we've focused on univariate random number generation.

Goal: sample from multivariate posterior

$$\pi(\theta_1, \theta_2, \ldots, \theta_k \mid x)$$

- $\mu$  and  $\sigma^2$  from a Normal distribution
- $p_1, \ldots, p_k$  where  $\sum_{i=1}^k p_i = 1$  in a multinomial distribution
- $\beta_0$ ,  $\beta_1$  and  $\sigma^2$  from the model:

$$Y = \beta_0 + \beta_1 x + \epsilon, \quad \epsilon \sim N(0, \sigma^2)$$

• Mixture distributions with  $\sigma^2 > 0, \theta \in \{0, 1\}$ :

$$\theta \, \mathit{N}(0,\sigma^2) + (1- heta) \, \mathsf{Laplace}(0,\sigma^2)$$

# **Metropolis-Hastings**

Everything we've discussed for univariate sampling, also works for multivariate sampling.

We need to find a multivariate candidate distribution.

Example: Generating zero-mean bivariate Normals with variance-covariance matrix:

$$\begin{pmatrix} 1 & 0.8 \\ 0.8 & 1 \end{pmatrix}$$

As a candidate, we'll use a random walk with  $\epsilon = N(0, 0.25I_2)$ .

### Setup

```
> library(mvtnorm) # includes the multivariate normal density
> B <- 5000
> chain <- matrix(0, nrow = 2, ncol = B)
> S1 <- matrix(c(1, 0.8, 0.8, 1), ncol = 2)
> S2 <- matrix(c(0.25, 0, 0, 0.25), ncol = 2)</pre>
```

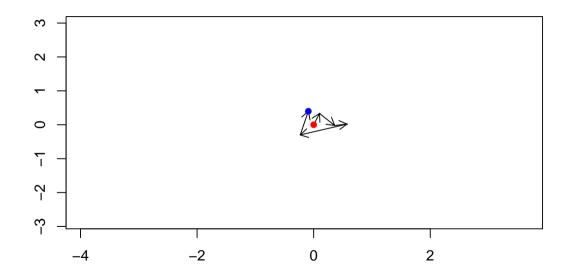
## **Computing Ratio**

```
> ratio <- function(candidate, previous) {</pre>
+
      ## evaluate pi(theta*) / pi(theta(t - 1))
+
      a <- dmvnorm(candidate, mean = c(0, 0), sigma = S1) /
+
           dmvnorm(previous, mean = c(0, 0), sigma = S1)
+
+
+
      ## evaluate the candidate density
      b <- dmvnorm(previous, mean = candidate, sigma = S2) /
+
           dmvnorm(candidate, mean = previous, sigma = S2)
+
      return(a * b)
+ }
```

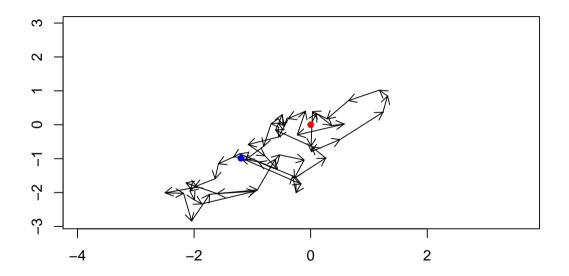
## Making the Chain

```
> for (i in 2:B) {
   ## generate 2, independent Normals at the previous point
  candidate <- rnorm(2, mean = chain[, i - 1],</pre>
                          sd = sqrt(0.25)
+
  r <- ratio(candidate, chain[, i - 1])
   if (runif(1) <= r) {
        chain[, i] <- candidate
+ } else {
  chain[, i] \leftarrow chain[, i - 1]
+ }
+ }
```

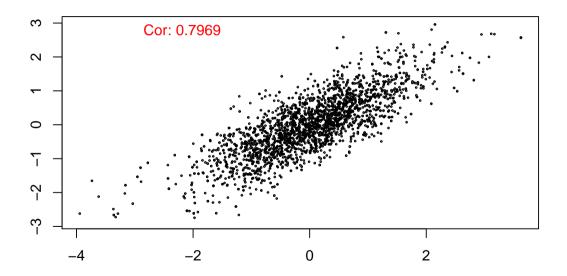
# Chain: 1:10



# Chain: 1:100



## Chain: 2000:5000



# **Gibbs sampling**

It may be difficult to find effective multivariate candidates.

Define the **full conditional posterior** for parameter  $\theta_i$ :

$$\pi(\theta_i | \theta_1, \theta_2, \dots, \theta_{i-1}, \theta_{i+1}, \dots, \theta_d, x) = \pi_i(\theta_i)$$

Gibbs sampler: Step through the  $\theta_i$  drawing from  $\pi_i$  conditional on the rest of the parameters.

Special case of Metropolis-Hastings that

- draws  $\theta_i^*$  directly from  $\pi_i$  (which is always accepted)
- sets  $\theta_j(t) = \theta_j(t-1)$  for all  $j \neq i$ .

### Gibbs for Multivariate Normal

If  $(\theta_1, \theta_2, ...)$  are MVN, all conditional distributions are also MVN.

Two dimensional case:

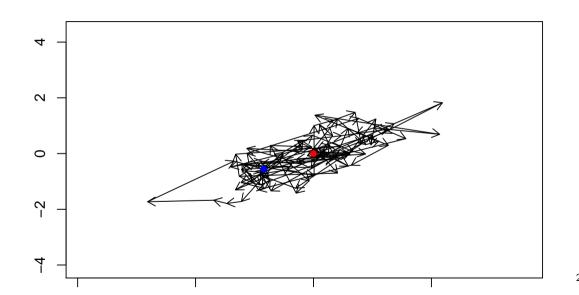
$$\theta_1 \mid \theta_2 = t \sim N \left( \mu_1 + \frac{\mathsf{Cov}(\theta_1, \theta_2)}{\mathsf{Var}(\theta_2)} (t - \mu_2), \mathsf{Var}(\theta_1) - \frac{\mathsf{Cov}(\theta_1, \theta_2)^2}{\mathsf{Var}(\theta_2)} \right)$$

$$\theta_2 \mid \theta_1 = t \sim N \left( \mu_2 + \frac{\mathsf{Cov}(\theta_2, \theta_1)}{\mathsf{Var}(\theta_1)} (t - \mu_1), \mathsf{Var}(\theta_2) - \frac{\mathsf{Cov}(\theta_2, \theta_1)^2}{\mathsf{Var}(\theta_1)} \right)$$

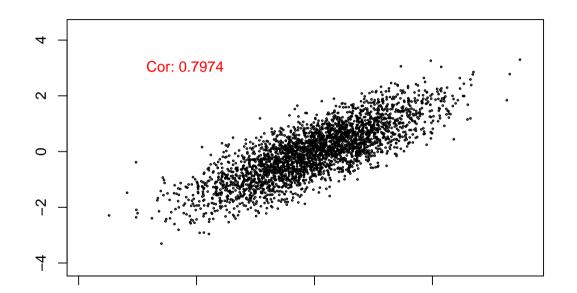
In our example,  $\mu_1 = \mu_2 = 0$ ,  $Var(\theta_1) = Var(\theta_2) = 1$ , and  $Cov(\theta_1, \theta_2) = 0.8$ .

```
> pi_i <- function(t) {
+    rnorm(1, mean = 0.8 * t, sd = sqrt(1 - 0.8^2))
+ }
> chain_gibbs <- matrix(0, ncol = B, nrow = 2)
> for (i in 2:B) {
+    chain_gibbs[1, i] <- pi_i(chain_gibbs[2, i - 1])
+    chain_gibbs[2, i] <- pi_i(chain_gibbs[1, i])
+ }</pre>
```

Gibbs: 1:100



Gibbs: 2000:5000



#### Remarks

- Must be able to draw from the full conditional posterior directly.
- Often use conjugate prior distributions to make this possible.
- Gibbs sampling is frequently the choice for hierarchical models in which pieces are built on top of each other.

#### Hierarchical Model: Normal mean

Suppose we are willing to assume that

$$X_i \sim N(\mu, \sigma^2), \quad i = 1, \ldots, n$$

We have two parameters, we'll attach two convenient priors (assumed independent):

$$\mu \sim N(\theta, \tau^2), \quad \sigma^2 \sim \text{Inv. Gamma}(a, b)$$

The Inverse Gamma distribution has density:

$$f(\sigma^2) = \frac{b^a}{(\sigma^2)^{a+1}} \frac{\exp(-b/\sigma^2)}{\Gamma(a)}$$

## Full conditional posteriors: useful tricks

Before we find the FCPs for this model, let's learn two useful tricks.

The full conditional posterior for any parameter is proportional to the joint posterior. Writing  $\theta_{-i}$  for all other parameters,

$$\pi(\theta_i \mid \theta_{-i}, \mathsf{x}, \ldots) = \frac{\pi(\theta_i, \theta_{-i} \mid \mathsf{x}, \ldots)}{\pi(\theta_{-i} \mid \mathsf{x}, \ldots)} \propto \pi(\theta_i, \theta_{-i} \mid \mathsf{x}, \ldots)$$

Remember that addition in exponents is mutiplicative:

$$g(a \mid b) = \exp(a + b) = \exp(a) \exp(b) \propto \exp(a)$$

#### Joint Posterior Distribution

$$\pi(\mu, \sigma^{2} \mid \theta, \tau^{2}, a, b, \mathbf{x}) \propto f(\mathbf{x} \mid \mu, \sigma^{2}) p(\mu, \sigma^{2})$$

$$\propto \exp\left\{-\frac{\sum_{i=1}^{n} (x_{i} - \mu)^{2}}{2\sigma^{2}}\right\} \frac{1}{(\sigma^{2})^{a+1}} \exp\left\{-b/\sigma^{2}\right\} \exp\left\{-\frac{(\mu - \theta)^{2}}{2\tau^{2}}\right\}$$

$$= \exp\left\{-\frac{\tau^{2} \sum_{i=1}^{n} (x_{i} - \mu)^{2} + \sigma^{2} (\mu - \theta)^{2}}{2\sigma^{2} \tau^{2}}\right\} \frac{1}{(\sigma^{2})^{a+1}} \exp\left\{-b/\sigma^{2}\right\}$$

## Full Conditional for $\mu$

$$\pi(\mu \mid \sigma^{2}, \theta, \tau^{2}, a, b, x) \propto \exp\left\{-\frac{\tau^{2} \sum_{i=1}^{n} (x - \mu)^{2} + \sigma^{2}(\mu - \theta)^{2}}{2\sigma^{2}\tau^{2}}\right\} \frac{1}{(\sigma^{2})^{a+1}} \exp\left\{-b/\sigma^{2}\right\}$$

$$\propto \exp\left\{-\frac{\tau^{2} \sum_{i=1}^{n} (x_{i} - \mu)^{2} + \sigma^{2}(\mu - \theta)^{2}}{2\sigma^{2}\tau^{2}}\right\}$$

$$= \exp\left\{-\frac{\tau^{2} \left(\left[\sum_{i=1}^{n} x_{i}^{2}\right] - 2n\bar{x}\mu + n\mu^{2}\right) + \sigma^{2}\mu^{2} - 2\sigma^{2}\mu\theta + \sigma^{2}\theta^{2}}{2\sigma^{2}\tau^{2}}\right\}$$

$$\propto \exp\left\{-\frac{(\tau^{2} + n\sigma^{2})\mu^{2} - 2(\sigma^{2}\mu\theta - \tau^{2}n\bar{x})\mu}{2\sigma^{2}\tau^{2}}\right\}$$

$$\propto \exp\left\{-\frac{(\mu - (\sigma^{2}\mu\theta - \tau^{2}n\bar{x})/(\tau^{2} + n\sigma^{2}))^{2}}{2\sigma^{2}\tau^{2}/(\tau^{2} + n\sigma^{2})}\right\}$$

#### **Full Conditionals**

After working through  $\pi(\mu, \sigma^2 \mid x)$ , we find:

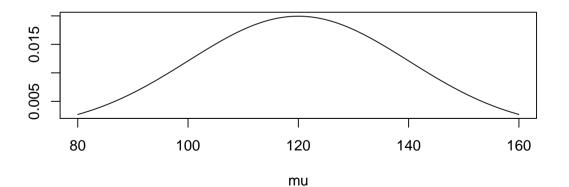
$$\mu \mid \sigma^2, x \sim N\left(rac{\sigma^2 heta + n au^2 ar{x}}{\sigma^2 + n au^2}, rac{\sigma^2 au^2}{\sigma^2 + n au^2}
ight)$$
 $\sigma^2 \mid \mu, x \sim ext{Inv. Gamma}\left(rac{n}{2} + a, rac{1}{2} \sum_{i=1}^n (x - \mu)^2 + b
ight)$ 

#### Prior for $\mu$

We'll work on the systolic blood pressure data again.

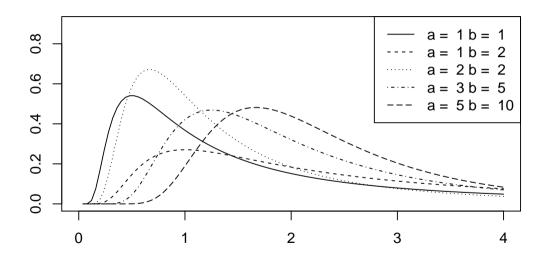
If we start from the idea that a **healthy systolic BP** is about 120, so  $\theta = 120$ .

We might not be very certain about that, so let's provide a wide variance:  $\tau = 20$ .



33

#### **Inverse Gamma**



### Prior for $\sigma^2$ , setup

For my subjective beliefs, I think a=2, b=5 best captures my position.

- > param\_a <- 3
- > param\_b <- 5
- > param\_theta = 120
- > param\_tau2 = 20^2
- > n <- dim(combined)[1] # the BP data

### Gibbs for BP: $\mu$ step

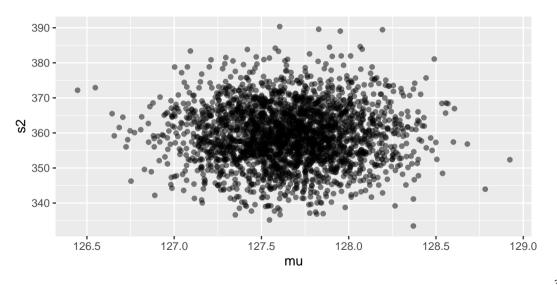
### **Gibbs for BP:** $\sigma^2$ **step**

```
\sigma^2 \mid \mu, x \sim \text{Inv. Gamma}\left(\frac{n}{2} + a, \frac{1}{2} \sum_{i=1}^{n} (x - \mu)^2 + b\right)
> shape_1 <- n/2 + param_a # doesn't depend on mu
> gibbs_s2 <- function(mu) {</pre>
    shape_2 \leftarrow (0.5) * sum((combined\$sys_mean - mu)^2) + param_b
+ g <- rgamma(1, shape_1, shape_2)
+ 1 / g # recall: inverse gamma
+ }
```

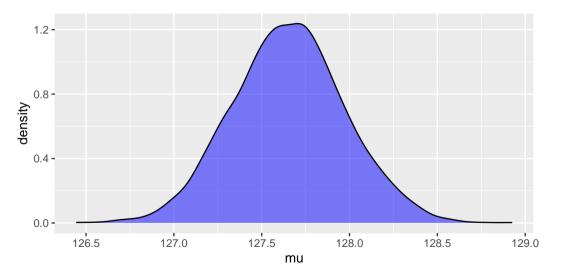
### Creating the chain

```
> gibbs_mu_sigma2 <- matrix(0, nrow = 2, ncol = B)</pre>
> ## draw from the prior to set up the chain
> gibbs_mu_sigma2[1, 1] <- rnorm(1, param_theta, sqrt(param_tau2))</pre>
> gibbs_mu_sigma2[2, 1] <- 1 / rgamma(1, param_a, param_b)</pre>
> for (i in 2:B) {
   chain[1, i] \leftarrow gibbs_mu(chain[2, i - 1])
   chain[2, i] \leftarrow gibbs_s2(chain[1, i])
+ }
```

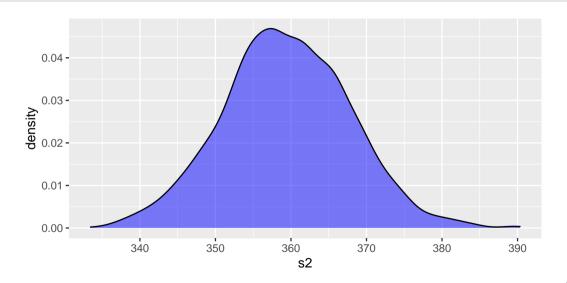
### Joint distribution (discarding first 1/2 chain)



## Marginal: $\mu$



# Marginal: $\sigma^2$



### How much did we decrease our uncertainty?

```
For \mu:
> 1 - var(chain[1, -(1:500)]) / 20^2 # recall, tau^2 = 20^2
[1] 0.9997
```

We've greatly increased our certainty on the mean.

For  $\sigma^2$ :

```
> prior_var <- param_b^2 / ((param_a - 1)^2 * (param_a - 2))
> 1 - var(chain[2, -(1:500)]) / prior_var
[1] -10.05
```

But now we are much less certain about the variance (perhaps we were over confident before!).

#### Inference

```
> # discard the first 500 draws
> stationary <- chain[, -(1:500)]</pre>
Bayes estimators (with regard to squared loss/MSE) for the parameters:
> # m11
> mean(stationary[1,])
[1] 127.7
> # sigma^2
> mean(stationary[2,])
[1] 359.2
```

#### More inference

95% credible intervals for the parameters (intervals that contain 95% of the mass for marginal posterior distributions:

```
> # m11
> quantile(stationary[1, ], c(0.025, 0.975))
2.5% 97.5%
127.0 128.3
> # sigma^2
> quantile(stationary[2, ], c(0.025, 0.975))
 2.5% 97.5%
343.0 375.3
```

### **Gibbs Sampling Summary**

- While MH can do multivariate, candidate distributions can be hard to find or inefficient
- Gibbs sampling draws parameters one at a time (much easier!)
- Downside: need to be able to draw from full conditional posteriors
- Algorithm for B MCMC steps
  - 1. Draw  $\theta_1$  conditional on  $\theta_2, \theta_3, \dots, \theta_k$ )
  - 2. Draw  $\theta_2$  conditional on  $\theta_1, \theta_3, \dots, \theta_k$ )
  - 3. ...
  - 4. Draw  $\theta_k$  conditional on  $\theta_1, \theta_2, \dots, \theta_{k-1}$ )
- Most of the work is getting the FPCs.

**Bayesian Computation with Stan** 

### Stan: A Bayesian Programming Language



- A programming language for specifying Bayesian models
- A library R, Python, and other languages
- A collection of advanced Bayesian algorithms

### **Example: BP Model**

$$X_i \sim \mathcal{N}(\mu, \sigma^2)$$
  
 $\mu \sim \mathcal{N}(120, 400)$   
 $\sigma^2 \sim \text{Inv. Gamma}(2, 5)$ 

#### **Data and Parameters**

```
data {
  int<lower=0> n;
  real y[n];
parameters {
  real mu;
  real<lower=0> sigmasq;
```

#### Model

```
model {
  mu ~ normal(120, 20);
  sigmasq ~ inv_gamma(3, 5);
  for (i in 1:n)
      y[i] ~ normal(mu, sqrt(sigmasq));
}
```

### Running the bp.stan

. . .

The data, parameters, and model sections are put into bp.stan. > library(rstan) > bp\_stan <- stan("bp.stan",</pre> data = list(n = dim(combined)[1],+ v = combined\$svs\_mean)) + After compiling bp. stan into its own executable, we see SAMPLING FOR MODEL 'bp' NOW (CHAIN 1). Chain 1: Chain 1: Iteration: 1 / 2000 [ 0%] (Warmup) Chain 1: Iteration: 200 / 2000 [ 10%] (Warmup)

#### **Results**

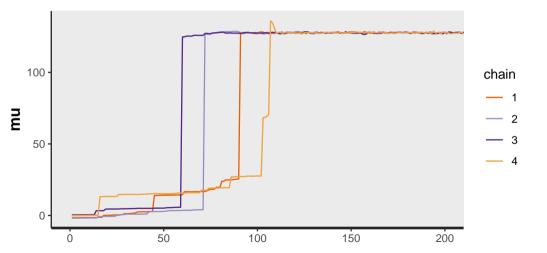
> print(bp\_stan)

```
Inference for Stan model: bp.
4 chains, each with iter=2000; warmup=1000; thin=1;
post-warmup draws per chain=1000, total post-warmup draws=4000.
```

|         | mean     | se_mean  | sd     | 2.5%     | 25%      | 50%      |
|---------|----------|----------|--------|----------|----------|----------|
| mu      | 127.6    | 0.01     | 0.31   | 127.0    | 127.4    | 127.6    |
| sigmasq | 358.6    | 0.15     | 8.37   | 342.4    | 353.0    | 358.4    |
| lp      | -12243.4 | 0.02     | 0.96   | -12246.0 | -12243.8 | -12243.1 |
|         | 75%      | 97.5%    | ‰ n_ef | f Rhat   |          |          |
| mu      | 127.8    | 128.2    | 364    | 14 1     |          |          |
| sigmasq | 364.1    | 375.4    | 308    | 36 1     |          |          |
| lp      | -12242.7 | -12242.5 | 205    | 55 1     |          |          |

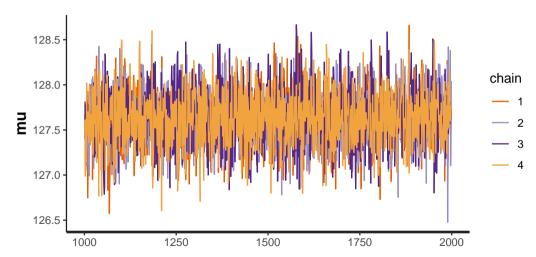
### Plotting chains, warmup period

> traceplot(bp\_stan, pars = "mu", inc\_warmup = TRUE, window = c(0, 200))



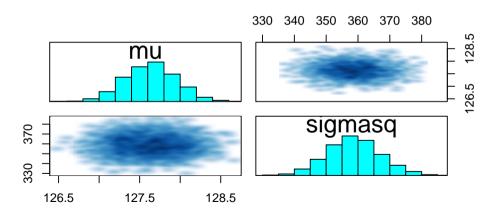
### Plotting chains, convergence

> traceplot(bp\_stan, "mu")



#### **Joint Posterior**

> pairs(bp\_stan, pars = c("mu", "sigmasq"))



#### A more involved model

We previously investigated the **effect of aspirin** on BP, comparing subjects who took to those who did not.

$$\mu_1 \sim \mathcal{N}(120, 20)$$
 $\delta \sim \mathcal{N}(0, 10)$ 
 $\sigma^2 \sim \text{Inv. Gamma}(3, 5)$ 
 $X_i \sim \mathcal{N}(\mu_1 + I(T_i = 0)\delta, \sigma^2)$ 

#### **Data and Parameters**

```
data {
  int<lower=1> n;
  int<lower=1> m;
  real takers[n];
  real nontakers[m];
parameters {
  real mu_1;
  real delta;
  real<lower=0> sigmasq;
```

### **Transformed Parameters and Model**

```
transformed parameters {
  real mu_2 = mu_1 + delta;
model {
  \mathtt{mu}_{-}1
            ~ normal(120, 20);
  delta
            ~ normal(0, 10);
            ~ inv_gamma(3, 5);
  sigmasq
            ~ normal(mu_1, sqrt(sigmasq));
  takers
  nontakers ~ normal(mu_2, sqrt(sigmasq));
```

### Running the model

```
> aspirin_effect <- stan("aspirin_effect.stan",
+ data = with(combined,
+ list(
+ n = sum(taking_aspirin),
+ m = sum(!taking_aspirin),
+ takers = sys_mean[taking_aspirin],
+ nontakers = sys_mean[!taking_aspirin])))</pre>
```

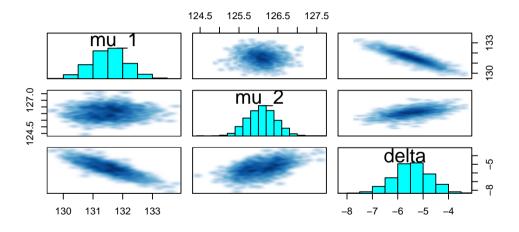
#### Results

Inference for Stan model: aspirin\_effect.
4 chains, each with iter=2000; warmup=1000; thin=1;
post-warmup draws per chain=1000, total post-warmup draws=4000.

|         | mean      | se_mean | sd      | 2.5%      | 25%      | 50%       |  |
|---------|-----------|---------|---------|-----------|----------|-----------|--|
| $mu_1$  | 131.53    | 0.02    | 0.59    | 130.37    | 131.1    | 131.54    |  |
| delta   | -5.45     | 0.02    | 0.70    | -6.86     | -5.9     | -5.44     |  |
| sigmasq | 352.93    | 0.16    | 8.24    | 337.06    | 347.3    | 352.75    |  |
| $mu_2$  | 126.08    | 0.01    | 0.37    | 125.39    | 125.8    | 126.08    |  |
| lp      | -12213.71 | 0.03    | 1.21    | -12216.65 | -12214.3 | -12213.41 |  |
|         | 75%       | 97.5    | 5% n_e: | ff Rhat   |          |           |  |
| $mu_1$  | 131.92    | 132.7   | 2 15    | 31 1      |          |           |  |
| delta   | -4.97     | -4.1    | .3 164  | 45 1      |          |           |  |
| sigmasq | 358.32    | 369.3   | 39 26   | 76 1      |          |           |  |

59

### **Posterior Distribution**



### Using the posterior distribution

```
> samples <- as.array(aspirin_effect)</pre>
> dimnames(samples)
$iterations
NUIT.I.
$chains
[1] "chain:1" "chain:2" "chain:3" "chain:4"
$parameters
[1] "mu_1" "delta" "sigmasq" "mu_2"
                                             "lp__"
```

```
> ## probability that the effect size is at least 5
> mean(abs(samples[,, "delta"]) >= 5)
[1] 0.7362
```

### **Installing Stan**

In theory, installing Stan should be as easy as:

> install.packages("rstan")

In practice, I've had **mixed success** (yes on my linux machine, no on my OS X machine).

We won't use Stan in class, but feel free to use on your final project.

# Convergence

**Example:** N(0,1)

Recall this example from last class:

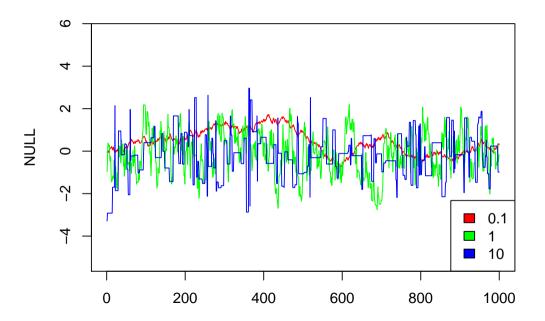
Generating draws from  $\mathcal{N}(0,1)$  using Metroplis-Hastings with

$$\theta^* = \theta(t-1) + U(-\delta, \delta)$$

as a proposal.

```
> unif chain <- function(delta. B = 5000) {</pre>
    chain <- numeric(B); chain[1] <- runif(1, -delta, delta) ; rejects <-</pre>
    for (i in 2:B) {
      candidate <- chain[i - 1] + runif(1, -delta, delta)</pre>
+
      ratio <- dnorm(candidate) / dnorm(chain[i - 1])
+
      if (runif(1) <= ratio) {</pre>
          chain[i] <- candidate
+
      } else {
          chain[i] <- chain[i - 1]</pre>
          rejects <- rejects + 1
+
    list(reject_rate = rejects / B, chain = chain)
+ }
```

- > n01\_chain\_0.1 <- unif\_chain(0.1)</pre>
- > n01\_chain\_1 <- unif\_chain(1)</pre>
- > n01\_chain\_10 <- unif\_chain(10)</pre>



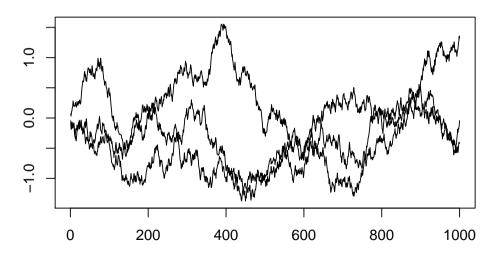
### Convergence

We can see that for  $\delta = 0.1$ , the chain did not converge.

This conclusion was made easier generating multiple chains.

To check convergence for a single  $\delta$ , we will need to generate several chains. Luckily, we can do this in parallel.

- > library(parallel)
- > RNGkind("L'Ecuyer-CMRG") # parallel safe PRNG
- > chains\_0.1 <- mclapply(rep(0.1, 3), unif\_chain, mc.cores = 3, B = 1000)</pre>



#### **Gelman-Rubin Method**

Suppose we have k Markov Chains from 1 up to n:

$$X_1(0), X_1(2), \dots, X_1(n)$$
  
 $\vdots$   
 $X_k(0), X_k(1), \dots, X_k(n)$ 

Let  $\psi$  be a function of n arguments. We can compute:

$$\psi_{1n} = \psi_n(X_1(0), \dots, X_1(n))$$

$$\vdots$$

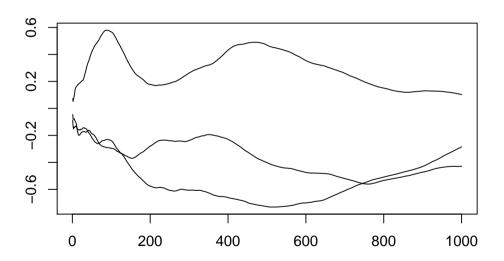
$$\psi_{kn} = \psi_n(X_k(0), \dots, X_k(n))$$

Observation: If the chains are converging to the same distribution, then all  $\psi_{in}$  should converge as well.

#### **Example: Mean**

One common choice for  $\psi_n$  is the **mean of the chain up** n:

```
> psi <- function(chain) {
+    n <- length(chain)
+    cumsum(chain) / (1:n) # cumulative mean
+ }
> psi_1 <- psi(chains_0.1[[1]]$chain)
> psi_2 <- psi(chains_0.1[[2]]$chain)
> psi_3 <- psi(chains_0.1[[3]]$chain)</pre>
```



#### Within and Between Variances

Define the following:

$$B = \frac{n}{k-1} \sum_{i=1}^{l} (\bar{\psi}_{i.} - \bar{\psi}_{..})^{2}$$

$$W = \frac{1}{nk} \sum_{i=1}^{k} \sum_{t=1}^{n} (\psi_{it} - \bar{\psi}_{i.})^{2}$$

where the "dot" notation means taking the mean over that index.

B measures how much each chain's average varies about the overall average.

W measures the within chain variance.

## Variance of $\psi$

An unbiased estimate of the variance of  $\psi$  (with respect to the true posterior) is

$$V = \frac{n-1}{n}W + \frac{1}{n}B$$

However, if the chains are overdispersed (i.e., tending to cover more of the sample space than the posterior suggests) V overestimates the true variance.

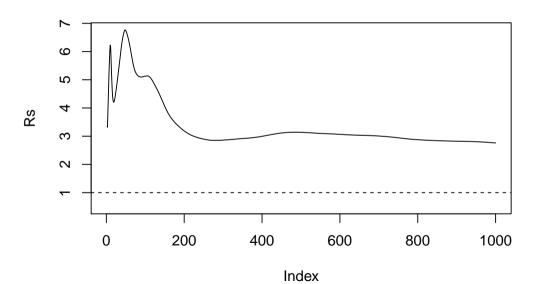
Conversely, W (on its own) underestimates the variance, but converges to the true variance.

This suggests:

$$\hat{R} = \sqrt{rac{V}{W}} pprox 1 \iff ext{the chains have converged}$$

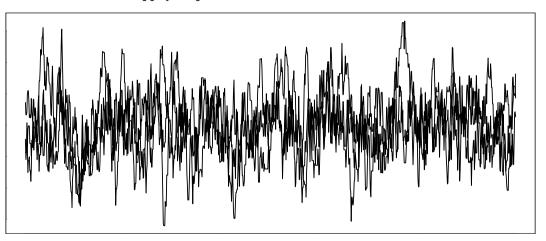
# Computing $\hat{R}$

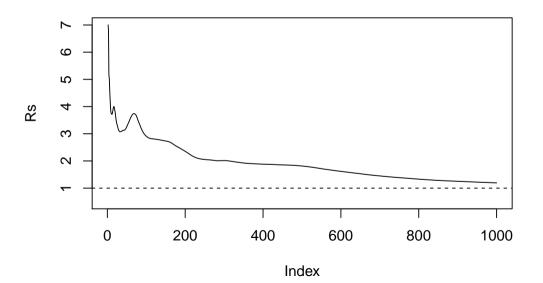
```
> Rs <- numeric(1000)
> for (t in 1:1000) {
      p1 <- psi_1[1:t] ; p2 <- psi_2[1:t] ; p3 <- psi_3[1:t]
      psi_bars \leftarrow c(mean(p1), mean(p2), mean(p3))
      psi_bar_bar \leftarrow mean(c(p1, p2, p3))
+
+
      B \leftarrow (t / 2) * sum((psi_bars - psi_bar_bar)^2)
+
      W = (1 / (2 * t))*(sum((p1 - psi_bars[1])^2) +
+
                           sum((p2 - psi_bars[2])^2) +
+
                           sum((p2 - psi_bars[2])^2))
+
     Rs[t] \leftarrow sqrt(((t-1) / t * W + 1 / t * B) / W)
+
+ }
```



# Repeat with better mixing

> chains\_1 <- mclapply(rep(1, 3), unif\_chain, mc.cores = 3, B = 1000)</pre>





### **Monitoring Convergence and Stan**

Computing the  $\hat{R}$  values can be somewhat tedious. Luckily, **Stan will compute them** for us:

```
> summary(bp_stan)$summary[, c("mean", "sd", "n_eff", "Rhat")]

mean sd n_eff Rhat

mu 127.6 0.3149 3644 1.0006

sigmasq 358.6 8.3742 3086 0.9998

lp__ -12243.4 0.9593 2055 1.0019
```