

Introduction to Bayesian Inference

Robert W Rankin (Murdoch University, PhD Candidate)

November 18, 2015

Outline

Outline

Philosophical differences

- ▶ Frequentists vs. Bayesian

Priors

- ▶ densities, impacts

Practise: JAGS

Computation (e.g., Gibbs sampling, MCMC; if time)

- ▶ simulation-based approximation of the Posteriors

Advantages of Bayesian Inference

- ▶ inference statements: easy to understand (only Bayesians can make probabilistic statements about θ)
- ▶ small sample sizes: exact inference
- ▶ missing data: very easy to impute
- ▶ integrate other information, or calculate 'derived parameters'

Hierarchical Bayesian

- ▶ model dependences (space & time)
- ▶ "random-effects" models
- ▶ "model-selection" / "model-multi inference" (AIC, Lasso, etc., are just types of Bayesian models)
- ▶ shrinkage: deflate influence of outlier values

What is "Bayesian" inference?

what comes to mind when you think about "Bayesian"

- ▶ ???

What is "Bayesian" inference?

what comes to mind when you think about "Bayesian"

- ▶ Priors: most common ecologist's answer (not necessarily true)
- ▶ Posterior density $p(\theta|Y)$
- "(posterior) probability density of θ *given* the observed data Y ".
 - ▶ inference on θ *given* data
 - ▶ θ has a **distribution** of values

What is "Bayesian" inference

compare to the Likelihood

- ▶ Priors
- ▶ Posterior density $p(\theta|Y)$
 - "(posterior) probability density of θ *given* the observed data Y ".
 - *Only* Bayesian's have access to the Posterior
 - ▶ Likelihood: $p(Y; \theta)$
 - "the joint probability of a realization of the data *given* a particular value of θ ".

Maximum-Likelihood

- ▶ basis most Frequentist analysis
- ▶ Often (but not always) the MLE is the best estimator according to Frequentist's values (consistency, unbiased, etc)

The likelihood & Frequentism

- ▶ before we can talk about the posterior... what is the likelihood?

$$p(Y|\theta)$$

data is what is random; θ is given?

- ▶ find the value of θ that *maximizes* the probability of having observed the data
- ▶ Frequentist emphasize *repeated use*:

if repeat the experiment -> observed slightly different data. Want estimates that are optimal over all theoretical samples of data.

A little demotivation

Most Biologists are "Agnostic Bayesians"

- ▶ **Frequentist** vs. **Bayesian**: point estimates nearly identical (under certain conditions)

Example data:

- ▶ men's height, $n=20$ observations
- ▶ first run the Frequentist's $\text{glm}(y \sim 1)$ function

Frequentist Example

Example data:

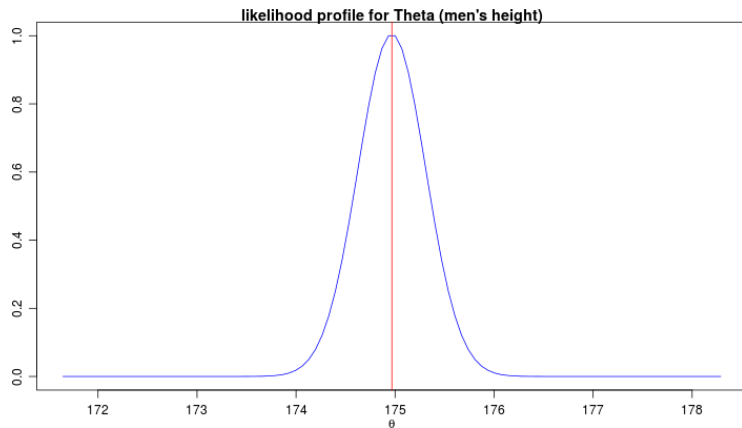
- ▶ men's height, $n=20$ observations
- ▶ first run the Frequentist's $\text{glm}(y \sim 1)$ function

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	174.9676	1.530233	114.3405	1.965619e-28

- ▶ Frequentist: start with a point-estimate, then estimate:

```
[1] "Frequentist:"  
      MLE      se    lo95CI    hi95CI  
174.967636  1.530233 171.968435 177.966837
```

Likelihood



- ▶ "It would be very (un)likely to have seen the data that I saw, if the value of θ were X"
- ▶ Choose θ : that which maximize's the likelihood seeing Y
- ▶ θ_{MLE} is NOT the "most probabilty value of θ "

Bayesians: The Posterior

- Frequentist: start with a point-estimate (MLE), then estimate S.E., 95% Confidence interval, etc

```
[1] "Frequentist:"
```

MLE	se	lo95CI	hi95CI
174.967636	1.530233	171.968435	177.966837

- Bayesian start with a distribution, and then summarize it with simple descriptive statistics

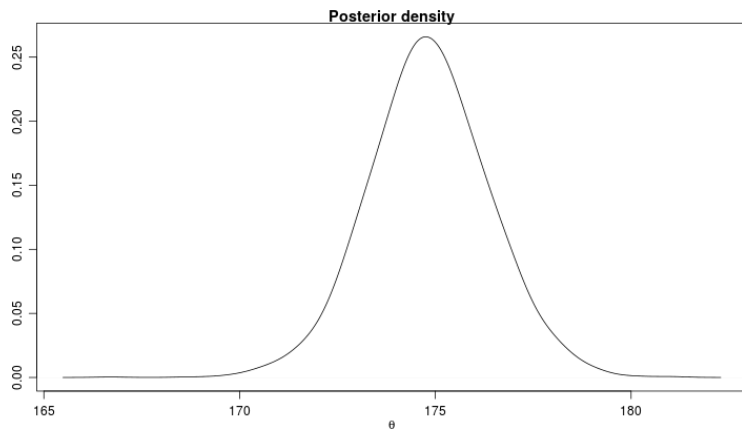
Mean, mode, S.E., 95% Credibility interval

```
[1] "Bayesian"
```

mu	se	lo95CI	hi95CI
174.83200	1.54682	171.75725	177.91146

Posterior density

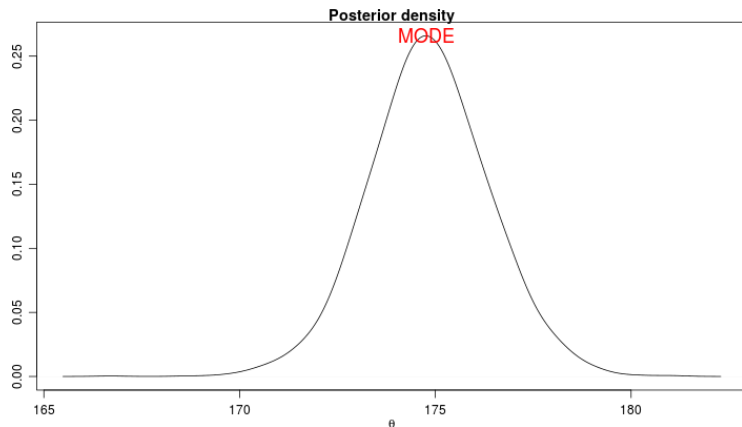
- IS a probability distribution



- easy to interpret

Posterior density

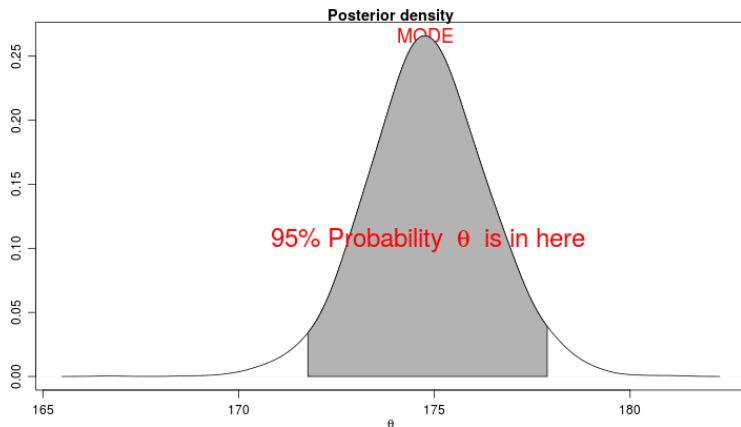
- ▶ IS a probability distribution



- ▶ Posterior mode: most probable value
- ▶ Posterior mean $\mathbb{E}[\theta] = \int p(\theta|Y)\theta d\theta$: expected value

Posterior density

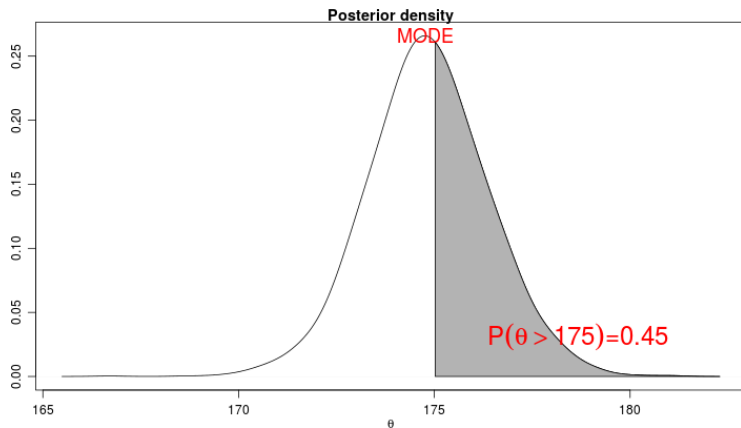
- ▶ IS a probability distribution



- ▶ Posterior mode: most probable value
- ▶ Posterior mean $\mathbb{E}[\theta] = \int p(\theta|Y)\theta d\theta$: expected value
- ▶ 95%CI of θ

Posterior density

- ▶ IS a probability distribution



- ▶ Posterior mode: most probable value
- ▶ Posterior mean $\mathbb{E}[\theta] = \int p(\theta|Y)\theta d\theta$: expected value
- ▶ What is the probability that $\theta > X$? Area of $p(\theta|Y) > X$

A little demotivation

Most Biologists are "Agnostic Bayesians"

- **Frequentist** vs. **Bayesian**: point estimates nearly identical (under certain conditions)

Example:

- men's height, $n=20$ observations S.E. and 95% CI

```
[1] "Frequentist:"
```

MLE	se	lo95CI	hi95CI
174.967636	1.530233	171.968435	177.966837

```
[1] "Bayesian"
```

mu	se	lo95CI	hi95CI
174.83200	1.54682	171.75725	177.91146

A little demotivation

Most Biologists are "Agnostic Bayesians"

- ▶ **Frequentist** vs. **Bayesian**: often nearly identical
- ▶ only true for: i) certain "priors", and ii) large-samples sizes
- ▶ key point: **Be a Master of Priors!**

Bayesians vs. Frequentism

Philosophy

- ▶ Bayesians: condition on the data, θ is random

think like a gambler

- ▶ Frequentism: data is random

think: had we repeated the experiment, we would get different data

Practical differences?

mostly, no. BUT, some important situations...

- ▶ priors!
- ▶ low-sample sizes, complex models
- ▶ missing data
- ▶ 'optional stopping'

Posterior Density

Posterior: the goal of Bayesian analysis...

- ▶ hard to evaluation
- ▶ Enter **Baye's Rule!**

$$p(\theta|Y) = \frac{p(Y|\theta)p(\theta)}{\int p(Y|\theta)p(\theta)d\theta}$$

Posterior \propto Likelihood \times Prior

- ▶ *likelihood*: easy to evaluate
- ▶ *prior*: express as easy distribution (Norm, Gamma, Beta)

Priors

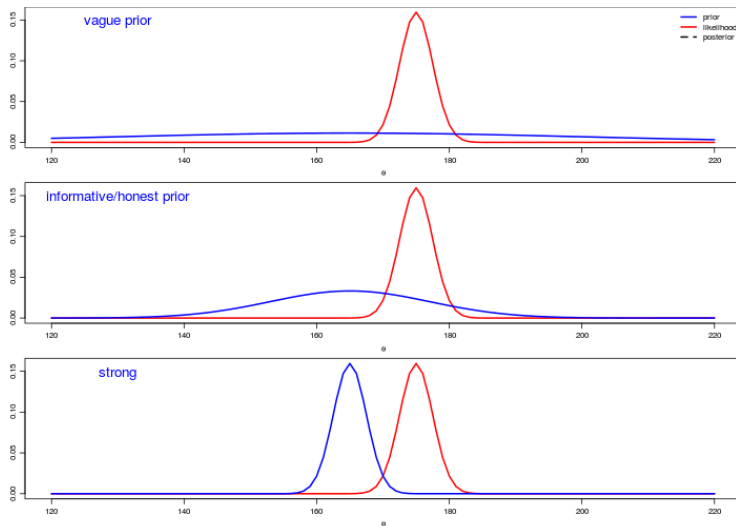
defn: "your belief about θ before observing data", or "a probability distribution about θ before observing data"

Posterior \propto Likelihood \times Prior

- ▶ The posterior: a mixture of "information in the data" (likelihood) and "information in the prior"
- ▶ **be a master of priors**

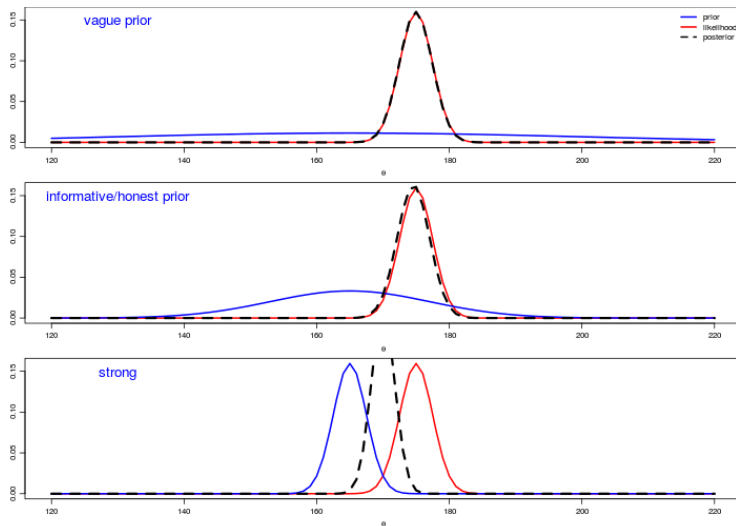
It is your responsibility to study and know how to express prior information in probabilistic terms

Posterior \propto Likelihood \times Prior



Competing information: priors vs. likelihood

Posterior \propto Likelihood \times Prior



Competing information: priors vs. likelihood

Types of Priors

non-informative priors

- ▶ desire Posterior estimates similar to MLE
- ▶ deliberately ignore prior knowledge
- ▶ Jeffrey's priors

'Subjective Bayes'

- ▶ honest representation of your actual knowledge
- ▶ inference: how the data (via likelihood) updates Prior -> Posterior

Strong Priors

- ▶ computational reasons
- ▶ 'fixing' parameters to a certain value
- ▶ non-identifiability of parameter

Types of Priors

Know the distributions and their parameters

Name	Usage	Density	Lower	Upper
Beta	<code>dbeta(a,b)</code> $a > 0, b > 0$	$\frac{x^{a-1}(1-x)^{b-1}}{\beta(a,b)}$	0	1
Chi-square	<code>dchisqr(k)</code> $k > 0$	$\frac{x^{\frac{k}{2}-1} \exp(-x/2)}{2^{\frac{k}{2}} \Gamma(\frac{k}{2})}$	0	
Double exponential	<code>ddexp(mu,tau)</code> $\tau > 0$	$\tau \exp(-\tau x - \mu)/2$		
Exponential	<code>dexp(lambda)</code> $\lambda > 0$	$\lambda \exp(-\lambda x)$	0	
F	<code>df(n,m)</code> $n > 0, m > 0$	$\frac{\Gamma(\frac{n+m}{2})}{\Gamma(\frac{n}{2})\Gamma(\frac{m}{2})} \left(\frac{n}{m}\right)^{\frac{n}{2}} x^{\frac{n}{2}-1} \left\{1 + \frac{nx}{m}\right\}^{-\frac{(n+m)}{2}}$	0	
Gamma	<code>dgamma(r, lambda)</code> $\lambda > 0, r > 0$	$\frac{\lambda^r x^{r-1} \exp(-\lambda x)}{\Gamma(r)}$	0	
Generalized gamma	<code>dgen.gamma(r, lambda, b)</code> $\lambda > 0, b > 0, r > 0$	$\frac{b \lambda^{br} x^{br-1} \exp\{-(\lambda x)^b\}}{\Gamma(r)}$	0	
Logistic	<code>dlogis(mu, tau)</code> $\tau > 0$	$\frac{\tau \exp\{(x - \mu)\tau\}}{[1 + \exp\{(x - \mu)\tau\}]^2}$		
Log-normal	<code>dlnorm(mu,tau)</code> $\tau > 0$	$\left(\frac{\tau}{2\pi}\right)^{\frac{1}{2}} x^{-1} \exp\{-\tau(\log(x) - \mu)^2/2\}$	0	
Noncentral Chi-square	<code>dnchisqr(k, delta)</code> $k > 0, \delta \geq 0$	$\sum_{r=0}^{\infty} \frac{\exp(-\frac{\delta}{2}) (\frac{\delta}{2})^r}{r!} \frac{x^{(k/2+r-1)} \exp(-\frac{x}{2})}{2^{(k/2+r)} \Gamma(\frac{k}{2}+r)}$	0	
Normal	<code>dnorm(mu,tau)</code> $\tau > 0$	$\left(\frac{\tau}{2\pi}\right)^{\frac{1}{2}} \exp\{-\tau(x - \mu)^2/2\}$		
Pareto	<code>dpar(alpha, c)</code> $\alpha > 0, c > 0$	$\alpha c^\alpha x^{-(\alpha+1)}$	c	

Figure : rjags Plummer 2015

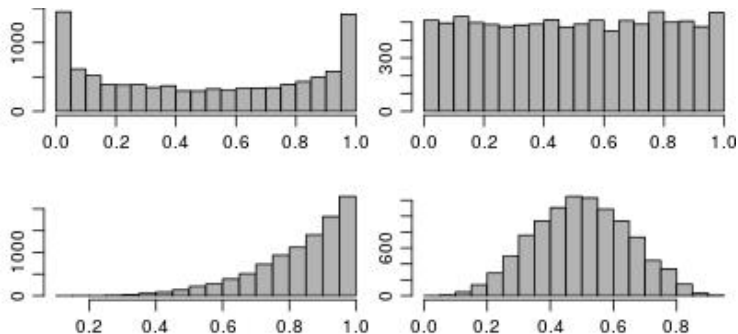
Types of Priors

Know the distributions and their parameters

Familiarize yourself with distributions: plot it, calculate some statistics

► Beta distribution example

```
r <- rbeta(10000, 0.5, 0.5)
```



Bayesian Analysis Example

Time to open up R and JAGS

'JAGS: Just Another Gibbs Sampler'

Uses BUGS-like syntax (similar to OpenBUGS, WinBUGS)

- ▶ rjags Package: R friendly JAGS interface
- ▶ easy easy easy Bayesian inference

Don't worry about 'samplers': JAGS does the hard work

- ▶ specify **likelihood** (how the data arose) and the **priors**

Bayesian Analysis Example

example model: height of 20 Australian

```
y <- c(183.46, 182.32, 178.31, 181.36, 165.12,  
185.68, 170.47, 178.11, 174.86, 182.03, 180.09,  
172.88, 177.94, 177.26, 182.58, 171, 173.74, 177.78,  
180.02, 163.05)
```

- ▶ lets estimate the mean height (μ) and the dispersion (sigma)

JAGS we estimate the 'precision' (τ): $\tau = \frac{1}{\sigma^2}$

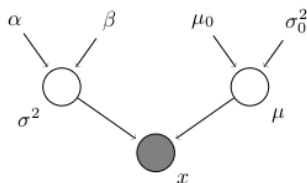


Figure : Prof Mike Jordan lecture notes

Bayesian Analysis Example 1

- ▶ open up R and rjags
- ▶ download and open the R file:

Bayesian Analysis Example 1

Jags model syntax: specify priors and likelihood

```
model.txt<-'model{  
  # Normal priors on mean height  
  mu0 <- 100  
  sigma0 <- 35  
  tau0 <- pow(sigma0,-2)  
  mu ~ dnorm(mu0,tau0)  
  # Gamma prior on precision  
  alpha0 <- 0.1  
  beta0 <- 0.1  
  tau ~ dgamma(alpha0,beta0)  
  # Likelihood: how the data arose  
  for(i in 1:length(y)){  
    y[i] ~ dnorm(mu,tau) T(0,) # truncated normal  
  }  
  sigma <- pow(tau,-0.5)  
}'
```

Sample-based inference

Posteriors

often no 'analytical' solution to $P(\theta|Y)$

Solution: Sampling

- ▶ it is a Probability Distribution!!!
- ▶ find a way to "sample" from posterior.
- ▶ with enough samples: $\text{mean}(\text{samples}) = \text{Posterior Expectation}$

Sampling Algorithms

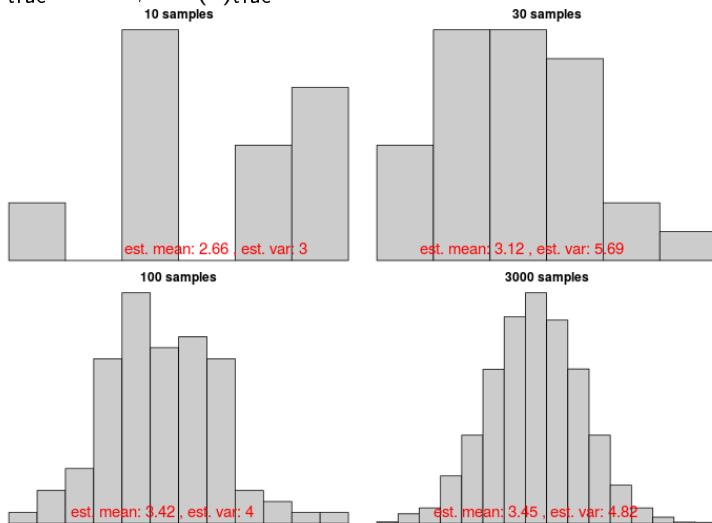
MCMC; Gibbs Sampling; Metropolis-Hastings; Slice-Sampling; Importance Sampling; "Conjugate Priors"; conditional probability

- ▶ all (sub)algorithms or concepts or techniques to help sample a posterior

Approximate the joint-posterior distribution"

example: estimate mean and variance of θ

$$\theta_{\text{true}} = 3.44; \text{Var}(\theta)_{\text{true}} = 4.89$$



Gibbs Sampling

break-down joint posterior into (simpler) conditional distributions

- ▶ difficult: sampling $P(\beta_0, \beta_1, \beta_2, \sigma^2 | Y)$
- ▶ easy: sampling $P(\beta_0, \beta_1, \beta_2, | \sigma^2, Y)$ then $P(\sigma^2 | \beta_0, \beta_1, \beta_2, Y)$
then repeat

approximates the joint posterior

algorithm

- ▶ initialize: $\beta_0^{(0)}, \beta_1^{(0)}, \beta_2^{(0)}, \sigma^{2(0)}$

$$\begin{aligned}\{\beta_0^{(1)}, \beta_1^{(1)}, \beta_2^{(1)}\} &\sim P(\beta | \sigma^{2(0)}, Y) \\ \sigma^{2(1)} &\sim P(\sigma^2 | \beta_0^{(1)}, \beta_1^{(1)}, \beta_2^{(1)}, Y) \\ \{\beta_0^{(2)}, \beta_1^{(2)}, \beta_2^{(2)}\} &\sim P(\beta | \sigma^{2(1)}, Y) \\ \sigma^{2(2)} &\sim P(\sigma^2 | \beta_0^{(2)}, \beta_1^{(2)}, \beta_2^{(2)}, Y)\end{aligned}\tag{1}$$

- ▶ repeat 1000's or 1000000 's times

BUGS to the rescue

Previously, Bayesian analysis demanded custom-coding MCMC algorithms

WinBUGS & OpenBUGS & JAGS

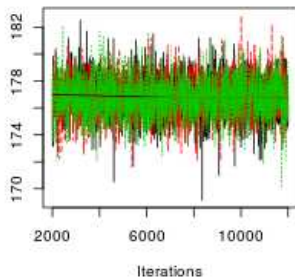
automatically use appropriate sampling techniques; so we don't have to worry

BUT you must: Monitor the MCMC!

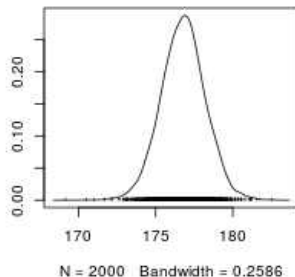
- ▶ give reasonable **initial values**
- ▶ ensure **convergence**: no trend; independent chains give same answer
- ▶ ensure adequate **mixing**: independent samples

MCMC: Good mixing

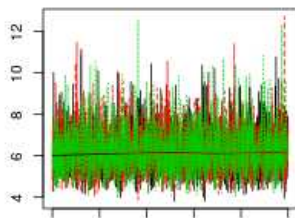
Trace of μ



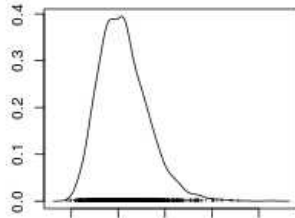
Density of μ



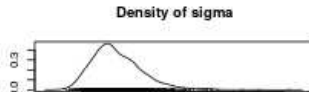
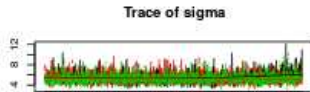
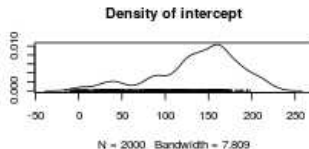
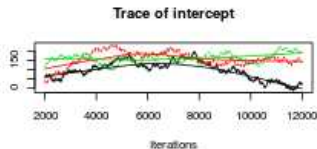
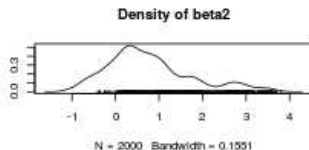
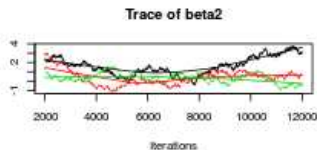
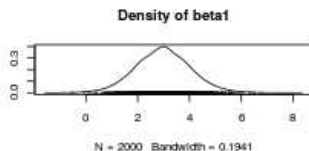
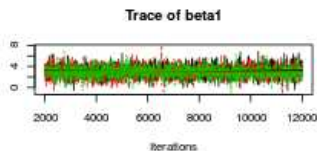
Trace of σ



Density of σ



MCMC: Poor convergence



MCMC

MCMC parameters in JAGS

- ▶ n.chains: num. of MCMC chains; more is better
- ▶ n.adapt: discard first samples; let algorithm 'adapt'
- ▶ n.burn: discard extra samples; allow algorithm to reach stationary distribution
- ▶ n.iter: total number of sample; more is better
- ▶ thin: take every k^{th} iteration for a sample; decorrelates one sample from the next; higher is better
- ▶ total samples: number of samples to approximate your Posterior; target at least 2000 to 5000

MCMC: what to do with bad mixing

- ▶ run longer chains
- ▶ ensure long enough adaption phase
- ▶ misspecified priors
- ▶ bad initial values?

Advantages of Bayesian Inference

- ▶ inference statements: easy to understand (only Bayesians can make probabilistic statements about θ)
- ▶ small sample sizes: exact inference
- ▶ missing data: very easy to impute
- ▶ integrate other information, or calculate 'derived parameters'

Hierarchical Bayesian

- ▶ model dependences (space & time)
- ▶ "random-effects" models
- ▶ "model-selection" / "model-multi inference" (AIC, Lasso, etc., are just types of Bayesian models)
- ▶ shrinkage: deflate influence of outlier values

Where to go from here?

some Bayesian learning resources

- ▶ learn about prior distributions!
- ▶ great R package for learning the fundamentals of Gibbs sampling, MCMC, conditional probability, etc.

LearnBayes: Functions for Learning Bayesian Inference!
See the Vignettes. <https://cran.r-project.org/web/packages/LearnBayes/index.html>

- ▶ OpenBUGS examples: read and run yourself

<http://www.openbugs.net/w/Examples>

- ▶ Textbook: WinBUGs for Ecologists, Marc Kery
- ▶ Blog: Andrew Gelman: <http://andrewgelman.com/>

Frequentism

- ▶ Excellent and accessible video lecture by Michael Jordan

http://videolectures.net/mlss09uk_jordan_bfway/