MCMC Sampling and JAGS

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology

Learning objectives:

- Gain insights into how MCMC sampling works
- Be able to implement your first Bayesian model in JAGS

Will borrow from. . .

MCMC

In our moose sighting example, we could determine the posterior distribution using calculus.

In many cases, there will be no closed form solution to:

$$p(\theta|y) = \frac{L(y|\theta)\pi(\theta)}{\int_{-\infty}^{\infty} L(y|\theta)\pi(\theta)}$$

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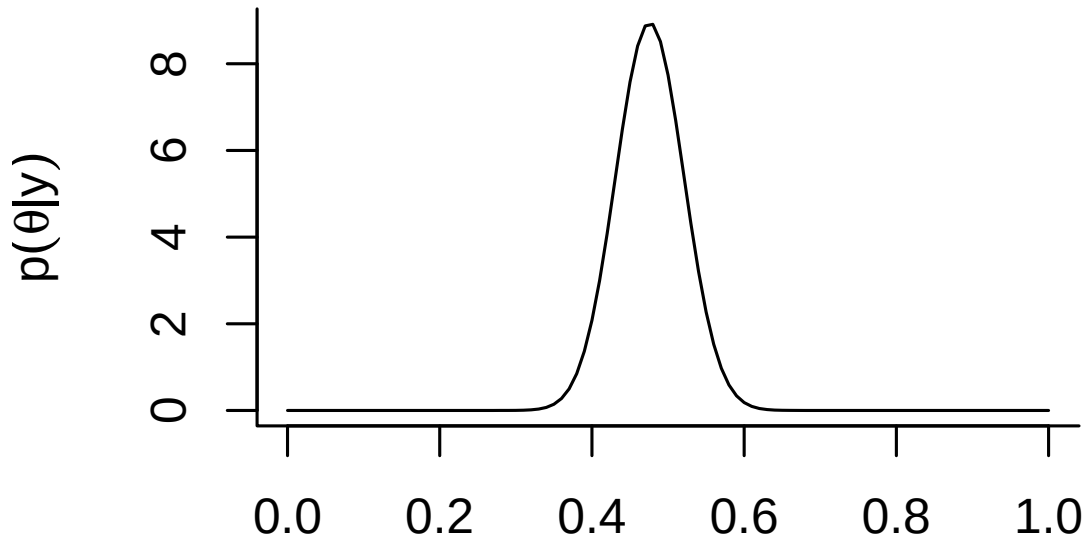
MCMC = Markov Chain Monte Carlo is a way to draw a sequence of random variables that will converge in distribution to $p(\theta|y)$

MCMC Sampling

Goal: generate samples that we can use to summarize the posterior distribution, $p(\theta|y)$



- Once we have these samples, we can estimate θ by the mean (or median) of the samples.
- We can compute credible intervals using quantiles of the samples.

Samplers

There are a variety of MCMC algorithms and samplers. We are going to consider 1 approach to gain some general insights into how these methods work.

Metropolis Algorithm

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Consider two possible values of $\theta = \{\theta_1$ and $\theta_2\}$. Without the denominator, we cannot evaluate $p(\theta_1|y)$ or $p(\theta_2|y)$.

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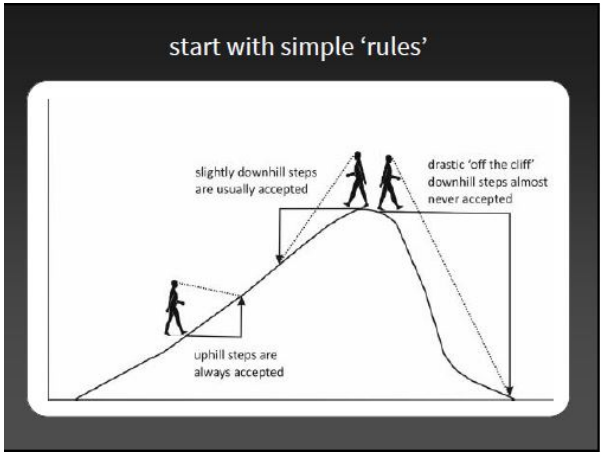
We can, however, evaluate the relative likelihood of θ_1 and θ_2:

$$\text{R} = \frac{p(\theta_2|y)}{p(\theta_1|y)} = \frac{L(y|\theta_2)\pi(\theta_2)}{L(y|\theta_1)\pi(\theta_1)}$$

Metropolis Algorithm



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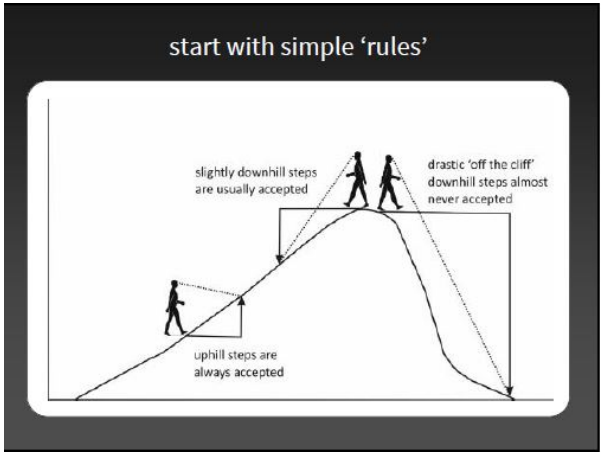
Metropolis Algorithm



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2. Generate a new, proposed, value of θ from a symmetric distribution centered on θ_0 (e.g., $\theta' = \text{rnorm}(\theta_0)$).

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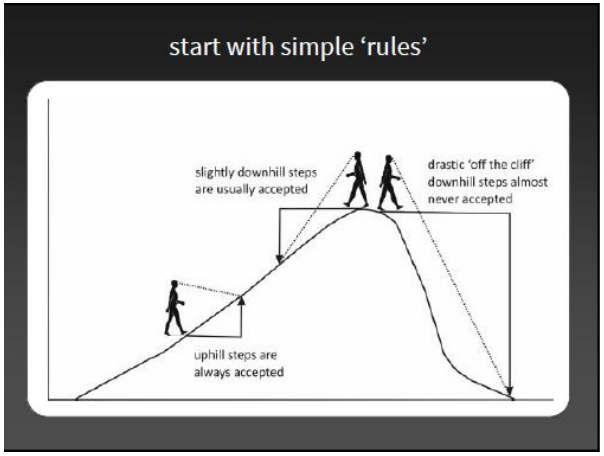

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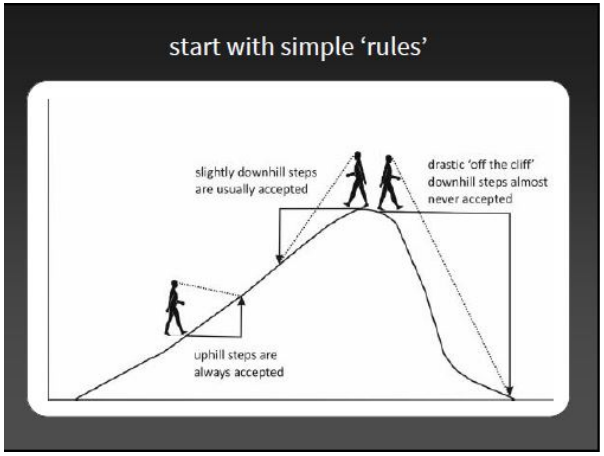

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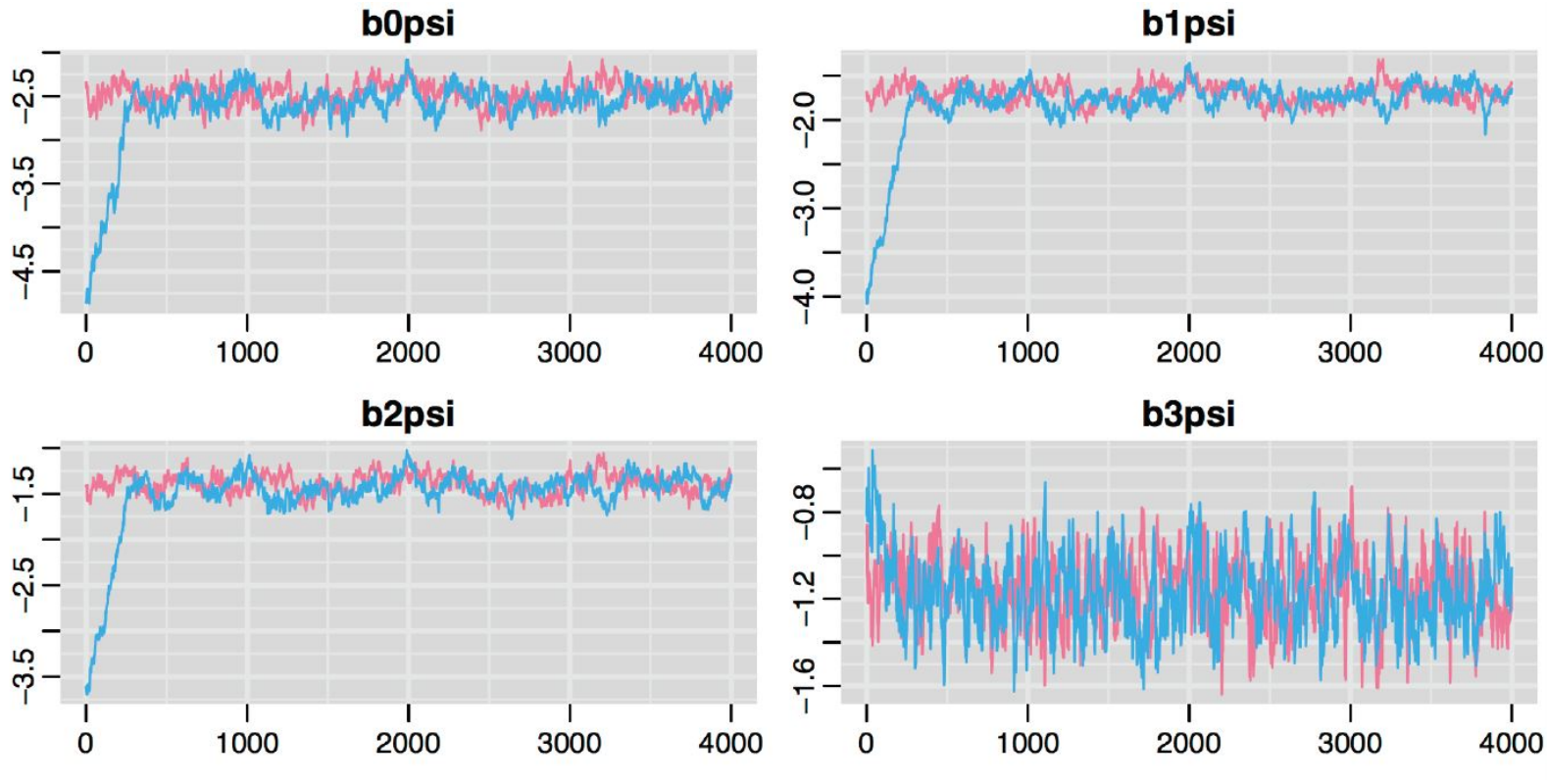
   - If R = $\frac{p(\theta'|y)}{p(\theta_0|y)} > 1$: Accept and set $\theta_1 = \theta'$!
   - If R < 1 accept θ' with probability = R. Otherwise (i.e., if reject), set $\theta_1 = \theta_0$
4. Back to step 2, and ...

Continue to sample until:

1. The distribution of $\theta_1, \theta_2, \ldots, \theta_M$ appears to have reached a steady state (i.e., reached convergence).
2. The MCMC sample, $\theta_1, \theta_2, \ldots, \theta_M$ is sufficiently large to summarize $p(\theta|data)$



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- Discard the first n_{burnin} iterations (where the sampler has not yet converged)
- Calculate the Gelman-Rubin Statistic, Rhat = compares variance of between chains to within chains
  - Values near 1 suggest likely convergence
  - Should be less than 1.1 (general rule)

Details

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JAGS will attempt to determine how best to sample once we give it a likelihood and set of prior distributions (one for each parameter).

JAGS

Steps:

- Specify prior distributions and the likelihood of the data.
- Call JAGS from R to generate samples.
- Evaluate whether or not we think the samples have converged in distribution to $p(\theta|y)$
- Use our samples to characterize the posterior distribution, $p(\theta|data)$

T-test

Mandible lengths in mm:

- 10 male and 10 female golden jackals
- From British Museum (Manly 1991)

```
males<-c(120, 107, 110, 116, 114, 111, 113, 117, 114, 112)
females<-c(110, 111, 107, 108, 110, 105, 107, 106, 111, 111)
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Do males and females have, on average, different mandible lengths?

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$$H_0 : \mu_m = \mu_f \text{ versus } H_a : \mu_m \neq \mu_f$$

\end{center}

JAGS

Likelihood:

- $y_{males} \sim N(\mu_m, \sigma^2)$
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Priors:

- $\mu_m \sim N(100, 0.001)$
- $\mu_f \sim N(100, 0.001)$
- $\sigma \sim$ Uniform(0,30)

JAGS

JAGS/BUGS (hereafter JAGS) code looks just like R code, but with some differences:

- JAGS code is not executed (just defines the model)
- Order does not matter (prior before likelihood, likelihood after prior, etc)

JAGS

There are 6 types of objects

1. **Modeled data** defined with a $\sim$ ("distributed as"). For example y $\sim$ followed by a probability distribution. The variable y here is the response in our regression model.
2. **Unmodeled data**: objects that are not assigned probability distributions. Examples include predictors, constants, and index variables.
3. **Modeled parameters**: these are given informative "priors" that themselves depend on parameters called hyperparameters. These are what a frequentist would call random effects. We won't consider till later in the course.
4. **Unmodeled parameters**: these are given uninformative priors. [So in truth all parameters are modeled].
5. **Derived quantities**: these objects are typically defined with the assignment arrow, <-
6. **Looping indexes**: i, j, etc.

JAGS

Types of objects for JAW example

1. **Modeled data** = males, females
2. **Unmodeled data** = nmales, nfemales
3. **Modeled parameters** (none in this example)
4. **Unmodeled parameters** = mu.male, mu.female, sigma
5. **Derived quantities** = tau, mu.diff
6. **Looping indexes**: i (used twice)

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Lots of good tricks and tips in the Appendix of Kery's Introduction to WinBugs for Ecologists, especially:

Numbers: 2, 3, 4, 9, 11, 12 (use %T% in JAGS), 14, 16, 17, 20, 23,24, 25, 26, 27

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Googling error messages is often useful for diagnosing problems.

JAGS

Work with jags_template.R file to fit your first model in JAGS