Overview of the course

Day 1

Lecture 1: Introduction to Bayesian Inference

Lecture 2: Bayesian analysis for single parameter models

Lecture 3: Prior distributions: univariate
Day 2

**Lecture 4:** Bayesian analysis for multiple parameter models with R

**Lecture 5:** An introduction to WinBUGS

**Lecture 6:** Multivariate models with WinBUGS

Day 3

**Lecture 7:** An introduction to MCMC computations

**Lecture 8:** Bayesian regression with WinBUGS

**Lecture 9:** Introduction to Hierarchical Statistical modeling

---

**Learning objectives**

- Understanding of the potential role of Bayesian methods for making inference about real-world problems

- Insight into modern computations techniques used for Bayesian analysis

- Learning Bayesian statistical analysis with R and WinBUGS

- An interest in using Bayesian methods in your own field of work
Style and emphasis

- Immediately applicable methods rather than latest theory
- Attention to real problems: case studies
- Implementation in R and WinBUGS (although not a full tutorial)
- Focus on statistical modeling rather than running code, checking convergence etc.
- Make more emphasis to the complementary aspects of Bayesian Statistics to Classical Statistics rather than one vs. the other

Recommended bibliography

- **The BUGS Book: A Practical Introduction to Bayesian Analysis.** David Lunn; Chris Jackson; Nicky Best; Andrew Thomas; David Spiegelhalter. CRC Press, *October 3, 2012.*

- **Bayesian Data Analysis (Second edition).** Andrew Gelman, John Carlin, Hal Stern and Donald Rubin. 2004 Chapman & Hall/CRC.


- **An introduction of Bayesian data analysis with R and BUGS: a simple worked example.** Verde, P.E. Estadistica (2010), 62, pp. 21-44
Lecture 1:

Introduction to Modern Bayesian Inference

"I shall not assume the truth of Bayes' axiom (...) theorems which are useless for scientific purposes."


How did it all start?

In 1763, Reverend Thomas Bayes wrote:

PROBLEM.

Given the number of times in which an unknown event has happened and failed: Required the chance that the probability of its happening in a single trial lies somewhere between any two degrees of probability that can be named.

In modern language, given $r \sim \text{Binomial}(\theta, n)$, what is $Pr(\theta_1 < \theta < \theta_2 | r, n)$?
**Example:** surgical procedure

- Suppose a hospital is considering a new high-risk operation

- Experience in other hospitals indicates that the risk $\theta$ for each patient is around 10%.

- It would be surprising to be less than 3% or more than 20%.

- We can directly express uncertainty about the patient risk $\theta$ with a probability distribution.

Probability that mortality risk is greater than 15% is $\Pr(\theta > 0.15) = 0.17$. 
Why a direct probability distribution?

- Tells us what we want: what are plausible values for the parameter of interest?
- No P-values: just calculate relevant tail areas
- No confidence intervals: just report central area that contains 95% of distribution
- Easy to make predictions (see later)
- Fits naturally into decision analysis / risk analysis / cost-effectiveness analysis
- There is a procedure for adapting the distribution in the light of additional evidence: i.e. Bayes theorem allows us to learn from experience

What about disadvantages?

- Requires the specification of what we thought before new evidence is taken into account: the prior distribution
- Explicit allowance for quantitative subjective judgment in the analysis
- Analysis may be more complex than a traditional approach
- Computation may be more difficult
- Currently no established standards for Bayesian reporting
Why does Bayesian statistics is popular today?

- Bayesian methods optimally combine multiple sources of information in a common model

- The computational revolution produced by the rediscovery of Markov chain Monte Carlo (MCMC) techniques in statistics

- Free available software implementation of MCMC (e.g. WinBUGS, JAGS, STAN, large number of packages in R, etc.)

- As a result, we can routinely construct sophisticated statistical models that may reflect the complexity for phenomena of interest

Bayes theorem for observable quantities

Let A and B be events; then it is provable from axioms of probability theory that

\[ P(A|B) = \frac{P(B|A)P(A)}{P(B)} \]

- \( P(A) \) is the marginal probability of A, i.e., \textbf{prior} to taking account of the information in \( B \)

- \( P(A|B) \) is the conditional probability of A given B, i.e., \textbf{posterior} to taking account of the value of \( B \)

- \( P(B|A) \) is the conditional probability of B given A

- \( P(B) \) is the marginal probability of \( B \)

- Sometimes is useful to work with \( P(B) = P(A)P(B|A) + P(\bar{A})P(B|\bar{A}) \), which is curiously called "extending the conversation" (Lindley 2006, pag. 68)
Example: Problems with statistical significance (Simon, 1994)

- Suppose that a priory only 10% of clinical trials are truly effective treatments

- Assume each trial is carried out with a design with enough sample size such that $\alpha = 5\%$ and power $1 - \beta = 80\%$

**Question:** What is the chance that the treatment is true effective given a significant test results?

$$p(H_1 | \text{"significant results"})?$$

- Let $A$ be the event that $H_1$ is true, then $p(H_1) = 0.1$

- Let $B$ be the event that the statistical test is significant

- We want $p(A|B) = p(H_1 | \text{"significant results"})$

- We have: $p(B|A) = p(\text{"significant results"}|H_1) = 1 - \beta = 0.8$

- We have: $p(B|\bar{A}) = p(\text{"significant results"}|H_0) = \alpha = 0.05$

- Now, Bayes theorem says

$$p(H_1 | \text{"significant results"}) = \frac{(1 - \beta) \times 0.1}{(1 - \beta) \times 0.1 + \alpha \times 0.9} = \frac{0.8 \times 0.1}{0.8 \times 0.1 + 0.05 \times 0.9} = 0.64$$

**Answer:** This says that if truly effective treatments are relatively rare, then a "statistically significant" results stands a good chance of being a false positive.
Bayesian inference for unknown quantities

- **Makes fundamental distinction between:**
  - Observable quantities $y$, i.e., data.
  - Unknown quantities $\theta$, that can be statistical parameters, missing data, predicted values, mismeasured data, indicators of variable selected, etc.
  - Technically, in the Bayesian framework parameters are treated as values of random variables.

- **Differences with classical statistical inference:**
  - In Bayesian inference, we make probability statements about model parameters
  - In the classical framework, parameters are *fixed* non-random quantities and the probability statements concern the data

### Bayesian Inference

- Suppose that we have observed some data $y$
- We want to make inference about unknown quantities $\theta$: model parameters, missing data, predicted values, mismeasured data, etc.
- The Bayesian analysis starts like a classical statistical analysis by specifying the sampling model:
  $$p(y|\theta)$$
  this is the **likelihood function**.
- From a Bayesian point of view, $\theta$ is unknown so should have a *probability distribution* reflecting our *uncertainty* about it *before* seeing the data. We need to specify a **prior distribution**
  $$p(\theta)$$
- Together they define a full **probability model**:
  $$p(y, \theta) = p(y|\theta)p(\theta)$$
Then we use the Bayes theorem to obtain the conditional probability distribution for unobserved quantities of interest given the data:

\[ p(\theta|y) = \frac{p(\theta)p(y|\theta)}{\int p(\theta)p(y|\theta)d\theta} \propto p(\theta)p(y|\theta) \]

This is the posterior distribution for \( \theta \),

\[ \text{posterior} \propto \text{likelihood} \times \text{prior} . \]

### Inference with binary data

**Example:** Inference on proportions using a discrete prior

- Suppose I have 3 coins in my pocket:
  1. A biased coin: \( p(\text{heads}) = 0.25 \)
  2. A fair coin: \( p(\text{heads}) = 0.5 \)
  3. A biased coin: \( p(\text{heads}) = 0.75 \)

- I randomly select one coin, I flip it once and it comes a head.

- What is the probability that I have chosen coin number 3?
Inference with binary data

1. Let \( y = 1 \) the event that I observed a head.
2. Let \( \theta \) denote the probability of a head: \( \theta \in (0.25, 0.5, 0.75) \).
3. Prior: \( p(\theta = 0.25) = p(\theta = 0.5) = p(\theta = 0.75) = 1/3 \).
4. Sampling distribution: 
   \[ y|\theta \sim \text{Binomial}(\theta, 1), \]
   with likelihood 
   \[ p(y|\theta) = \theta^y(1-\theta)^{1-y}. \]

If we observe a single positive response \( (y = 1) \), how is our belief revised?

| Coin | \( \theta \) | Prior \( p(\theta) \) | Likelihood \( p(y = 1|\theta) \) | Likelihood \( \times \) prior \( p(y = 1|\theta)p(\theta) \) | Posterior \( p(\theta|y = 1) \) |
|------|-------------|----------------|----------------|----------------|----------------|
| 1    | 0.25        | 0.33           | 0.25           | 0.0825         | 0.167          |
| 2    | 0.50        | 0.33           | 0.50           | 0.1650         | 0.333          |
| 3    | 0.75        | 0.33           | 0.75           | 0.2475         | 0.500          |
| \( \sum \) | 1.0       | 1.50           | 0.495          | 1.0            |

So, observing a head on a single flip of the coin means that there is now a 50% probability that the chance of heads is 0.75 and only a 16.7% that the chance of heads is 0.25.

Note that if we normalize the likelihood \( p(y = 1|\theta) \) we have exactly the same results.
Example: Three coins by simulation

We can approximate the results of the three coins example with the following computer simulation algorithm:

1. Generate a random index \( i^* \) from \((1, 2, 3)\) with prior probability \( 1/3 \) for each component

2. Evaluate the probability of \( y = 1 \) at \( \theta^* = \theta(i^*) \)

3. Generate a Binomial \( y^* \) with probability \( \theta^* \)

4. Repeat 1 to 3 a large number of times

5. Average and normalize the outcomes of \( y^* \)

Example: Three coins by simulation in R

```r
> coin.pri <- rep(1/3, 3)  # prior for coins 1, 2, 3.
> theta <- c(0.25, 0.5, 0.75)  # pr. heads under 1, 2, 3.
> sim <- 100000  # number of simulations
> y <- rep(0, 3*sim)
> dim(y) <- c(sim, 3)
> for( i in 1:sim)
> {
>   ind <- sample(c(1,2,3), size = 1, prob = coin.pri, replace = TRUE)
>   y.new <- rbinom(1, 1, prob = theta[ind])
>   y[i, ind] <- y.new
> }
> # average each class and normalize
> apply(y, 2, mean) / sum( apply(y, 2, mean))
[1] 0.1661 0.3306 0.5034
```
Monte Carlo error: How accurate are the empirical estimation by simulation?

- Suppose that we obtain empirical mean $\hat{E}(g(X))$ and variance $\hat{V} = \hat{\text{Var}}(g(X))$ based on $T$ simulations.

- Then since $\hat{E}$ is a sample mean based on $T$ independent samples, it has true sample variance $V = Var(g(X))/T$ which may be estimated by $\hat{V} / T$

- Hence $\hat{E}$ has estimated standard error $\sqrt{\hat{V} / T}$, which is known as **Monte Carlo error**.

```r
> th.post <- apply(y, 2, mean)/sum( apply(y, 2, mean))
> # monte carlo error
> V <- th.post * (1 - th.post)/sim
> sqrt(V)
[1] 0.001177 0.001488 0.001581
```

Posterior predictive distributions

The predictive posterior distribution for a new observation $y^{\text{new}}$ is given by

$$p(y^{\text{new}}|y) = \int p(y^{\text{new}}|y, \theta)p(\theta|y)d\theta.$$ 

Assuming that past and future observations are conditionally independent given $\theta$, this simplify to

$$p(y^{\text{new}}|y) = \int p(y^{\text{new}}|\theta)p(\theta|y)d\theta.$$ 

For the discrete case of $\theta$, integrals are replaced by sums:

$$p(y^{\text{new}}|y) = \sum_{\theta_i} p(y^{\text{new}}|\theta_i)p(\theta_i|y)$$

where the $p(\theta_i|y)$ can be thought of as "posterior weights".
**Example:** Three coins continue ...

Suppose we want to predict the probability that in the next toss is a head. We have:

\[
p(y^{\text{new}} = 1 | y = 1) = \sum_{\theta_i} \theta_i \cdot p(\theta_i | y = 1)
\]

\[
= (0.25 \times 0.167) + (0.50 \times 0.333) + (0.75 \times 0.5)
\]

\[
= 0.5833
\]

By using the previous simulation results in R we have:

```r
> sum(theta * apply(y, 2, mean)/sum(apply(y, 2, mean)))
[1] 0.5843
> 
```

Sequential learning

Suppose we obtain data \(y_1\) and form the posterior \(p(\theta | y_1)\) and then we obtain further data \(y_2\). The posterior based on \(y_1, y_2\) is given by:

\[
p(\theta | y_1, y_2) \propto p(y_2 | \theta) \times p(\theta | y_1).
\]

**Today’s posterior is tomorrow’s prior!**

The resultant posterior is the same as if we have obtained the data \(y_1, y_2\) together:

\[
p(\theta | y_1, y_2) \propto p(y_1, y_2 | \theta) \times p(\theta).
\]
Example: Three coins continue ...

- Now suppose that after observing $y_1 = 1$ we observe $y_2 = 1$, how is our belief revised?

| Coin | $\theta$ | Prior $p(\theta)$ | Likelihood $p(y = 1|\theta)$ | Likelihood $\times$ prior $p(y = 1|\theta)p(\theta)$ | Posterior $p(\theta|y = 1)$ |
|------|----------|-------------------|-----------------------|---------------------------------|---------------------------|
| 1    | 0.25     | 0.167             | 0.25                  | 0.042                           | 0.071                     |
| 2    | 0.50     | 0.333             | 0.50                  | 0.167                           | 0.286                     |
| 3    | 0.75     | 0.500             | 0.75                  | 0.375                           | 0.644                     |
| $\sum$ | 1.0      | 1.50              | 0.583                 |                                 | 1.0                       |

- After observing a second head, there is now a 64.4% probability that the chance of heads is 0.75 and only a 7.1% that the chance of heads is 0.25.

A bit of philosophy: Probability ”for” and probability ”of”

- The prior distribution $p(\theta)$, expresses our uncertainty about $\theta$ before seeing the data, that could be objective or subjective

- The Bayesian inference allows the combination of different types of probabilities

- Subjective probability implied a mental construct where probabilities are used to express our uncertainty. This is why we use a pedantic: ”probability for an event…”

- In the classical setting probabilities are defined in terms of long run frequencies and are interpreted as physical properties of systems. In this way we use: ”probability of…”

- In general we follow Bayesian Statistical Modeling, which is dynamic view of data analysis, which includes model building and model checking as well as statistical inference
Summary

Bayesian statistics:

▶ Formal combination of external information with data model by the Bayesian rule
▶ Uses of subjective probability to make inductive inference
▶ Straightforward inference by manipulating probabilities
▶ No need of repeated sampling ideas
▶ Specification of prior or external evidence may be difficult or controversial
▶ Prediction and sequential learning is straightforward.

Lecture 2:

Bayesian Inference for Single Parameter Models
Summary

1. Conjugate Analysis for:
   - Binomial model
   - Normal model known variance
   - Normal model known mean
   - Poisson model

2. Using R for:
   - Graphical visualization of posteriors
   - Direct Monte Carlo Simulation Methods
   - Calculations of posteriors for functional parameters

Inference of proportions using a continuous prior

Suppose we observe \( r \) positive responses out of \( n \) patients. Assuming patients are independent, with common unknown response rate \( \theta \), leads to a binomial likelihood

\[
p(r|n, \theta) = \binom{n}{r} \theta^r (1 - \theta)^{n-r} \propto \theta^r (1 - \theta)^{n-r}
\]

We consider the response rate \( \theta \) to be a **continuous parameter**, i.e., we need to give a continuous prior distribution.

Suppose that before the data is observed we believe all values for \( \theta \) are equally likely (very unrealistic!), then we give \( \theta \sim \text{Unif}(0, 1) \), i.e., \( p(\theta) = 1 \).

Posterior is then

\[
p(\theta|r, n) \propto \theta^r (1 - \theta)^{n-r} \times 1
\]

this has a form of the *kernel* of a \( \text{Beta}(r + 1, n - r + 1) \).
To represent external evidence that some response rates are more plausible than others, it is mathematical convenient to use a $\text{Beta}(a, b)$ prior distribution for $\theta$

$$ p(\theta) \propto \theta^{a-1}(1 - \theta)^{b-1} $$

Combining this with the binomial likelihood gives a posterior distribution

$$ p(\theta | r, n) \propto p(r | \theta, n)p(\theta) \propto \theta^{r+a-1}(1 - \theta)^{n-r+b-1} \propto \text{Beta}(r + a, n - r + b). $$

- When the prior and posterior come from the same family of distributions the prior is said to be **conjugate** to the likelihood

- A $\text{Beta}(a, b)$ distribution has

$$ E(\theta) = a/(a + b) \quad \text{var}(\theta) = ab/[(a + b)^2(a + b + 1)] $$

Hence the posterior mean is $E(\theta | r, n) = (r + a)/(n + a + b)$

- $a$ and $b$ are equivalent to observing a prior $a - 1$ successes in $a + b - 2$ trials, then it can be elicited.

- With fixed $a$ and $b$, as $r$ and $n$ increase, $E(\theta | r, n) \rightarrow r/n$ (the MLE).

- A $\text{Beta}(1,1)$ is equivalent to Uniform(0,1).
**Example:** Shape of the Beta density function

The Beta($a$, $b$) prior is a flexible distribution. We can explore its shape by using the following lines in R:

```r
# Beta flexibility
par(mfrow=c(2,2))
curve(dbeta(x, 1, 1), from =0, to=1, lty = 1, lwd=2,
     main="Beta(1, 1)", xlab=expression(theta))
curve(dbeta(x, 1/2, 1/2), from = 0, to = 1, lty = 2,
     lwd=2, col="red", main="Beta(1/2, 1/2)", xlab=expression(theta))
curve(dbeta(x, 2, 5), from = 0, to = 1, lty = 2, lwd=2,
     col="blue", main="Beta(2, 5)", xlab=expression(theta))
curve(dbeta(x, 2, 2), from = 0, to = 1, lty = 2, lwd=2,
     col="green", main="Beta(2, 2)", xlab=expression(theta))
par(mfrow=c(1,1))
```
Example: drug investigation

- Consider an early investigation of a new drug
- Experience with similar compounds has suggested that response rates between 0.2 and 0.6 could be feasible
- Interpret this as a distribution with mean=0.4 and standard deviation 0.1
- A Beta(9.2, 13.8) distribution has these properties
- Suppose we treat \( n = 20 \) volunteers with the compound and observe \( r = 15 \) positive responses.
- Then we update the prior and the posterior is Beta(15 + 9.2, 5 + 13.8)

R script to perform the analysis:

```
> par(mfrow=c(3,1))  # graphical output: 3 by 1 panels
# draw a curve for a beta density
> curve(dbeta(x,9.2, 13.8),from=0, to =1,
   xlab= "prob of success",main="Prior")
# draw a curve for a binomial density
> curve(dbinom(15, 20,x),from=0, to =1,
   col="blue", xlab="prob of sucess", main="Likelihood")
# draw the posterior
> curve(dbeta(x, 24.2, 18.8),from=0, to =1,
   col="red", xlab="prob of sucess", main="Posterior")
```

> par(mfrow=c(1,1))
Monte Carlo Simulation

- If we are able to sample values $\theta^*$ from the posterior $p(\theta | r, n)$, then we can extend the inferential scope.

- For example, one important application of this simulation process is when we need to estimate the posterior of a functional parameter, e.g., the odds ratio:

  $$\phi = f(\theta) = \frac{\theta}{1 - \theta}$$

- For simple models we can directly simulate from the posterior density and use this values to empirically approximate the posterior quantiles.
Example: Posterior for the odds ratio

The posterior of

\[ \phi = \frac{\theta}{1 - \theta} \]

is calculated in R as follows:

```r
> theta.star <- rbeta(20000, 24.2, 18.8)
> odds.star <- theta.star/(1-theta.star)
> quantile(odds.star, prob = c(0.05, 0.5, 0.75, 0.95))
  5%  50%  75%  95%
0.7730276 1.2852558 1.5784318 2.1592678
```

```r
> hist(odds.star, breaks=100, xlab="odds ratio", freq=FALSE, xlim=c(0, 4))
> lines(density(odds.star), lwd =2, lty = 1, col ="red")
```

Histogram of odds.star
Making predictions for binary data

- Suppose that we want to make predictions from the model

- The predictive posterior distribution for \( r_{\text{new}} \) (the number of successes in \( m \) trials) follows a **Beta-Binomial** distribution with density:

\[
p(r_{\text{new}}) = \frac{\Gamma(a + b)}{\Gamma(a)\Gamma(b)} \binom{m}{r_{\text{new}}} \frac{\Gamma(a + r_{\text{new}})\Gamma(b + m - r_{\text{new}})}{\Gamma(a + b + m)}
\]

- In R:

```r
# Beta-binomial density
betabin <- function(r, a, b, m)
{
    gamma(a+b)/(gamma(a)*gamma(b)) * choose(m,r) *
    gamma(a+r)*gamma(b+m-r)/gamma(a+b+m)
}
```

**Example:** drug investigation continue ...

- Suppose that we are interested in the predictive posterior of the number of success in the next 40 trials:

- Using the betabin function in R we have:

```r
# Beta-binomial distribution of the number of successes x in the next
# 40 trials with mean 22.5 and standard deviation 4.3

x <- 0:40; px <- betabin(0:40, a=24.2, b=18.8, m=40)

plot(x, px, type="h", xlab="number of successes out of 40", main="Predictive Posterior")
```
Example: drug investigation continue ...

- Suppose that we would consider continuing a development program if the drug managed to achieve at least a further 25 successes out of these 40 future trials.

- In R we can calculate:

```r
# probability of at least 25 successes out of 40 further trials
> sum(betabin(25:40,24.2,18.8,m=40))
[1] 0.3290134
>
```
Simulations for predictive data

Instead of using the analytical approximation based on the Beta-Binomial distribution, we can simulate predicted observations in the following way:

- We simulate $\theta_1^*, \ldots, \theta_B^*$ from the posterior Beta(24.2, 18.8)
- Then we simulate $y^*$ from a binomial distribution with rate $\theta^*$ and $n = 40$.
- We tabulate and normalize predictive frequencies.

In R notation

```r
> # Simulation of predictive data with a Beta-Binomial model ...
> theta.star <- rbeta(10000, 24.2, 18.8)
> y <- rbinom(10000, 40, theta.star)
> freq.y <- table(y)
> ys <- as.integer(names(freq.y))
> predprob <- freq.y/sum(freq.y)
> plot(ys, predprob, type = "h", xlab = "y",
+     ylab = "Predictive Probability")
>
> # Probability of at least 25 out of future 40 trials.
> sum(predprob[ys>24])
[1] 0.3244
```
Bayesian analysis for Normal data

**Known variance, unknown mean**

Suppose we have a sample of Normal data

\[ y_i \sim N(\mu, \sigma^2), \quad i = 1, \ldots, n \]

where \( \sigma^2 \) is known and \( \mu \) is unknown. The conjugate prior of \( \mu \) is

\[ \mu \sim N(\mu_0, \tau^2). \]

It is convenient to write \( \tau^2 \) as \( \sigma^2 / n_0 \), where \( n_0 \) represents the "effective number of observations" in the prior distribution.
Then the posterior distribution for $\mu$ is given by

$$p(\mu|y) = \mathcal{N}\left(\frac{n_0 \mu_0 + n \bar{y}}{n_0 + n}, \frac{\sigma^2}{n_0 + n}\right)$$

- Prior variance is based on an "implicit" sample size $n_0$
- As $n_0$ tends to 0, the distribution becomes "flatter"
- Posterior mean is a weighted average of the prior mean $\mu_0$ and parameter estimate $\bar{x}$, weighted by their precisions, i.e., relative sample sizes.
- Posterior variance is based on an implicit sample size $n_0$ and the data sample size $n$.

Alternative expressions for the posterior mean $\mu_n$ are:

$$\mu_n = w \mu_0 + (1-w)\bar{y} \quad \text{where} \quad w = \frac{n_0}{n + n_0},$$

$$\mu_n = \mu_0 + (\bar{y} - \mu_0)\frac{n}{n + n_0},$$

$$\mu_n = \bar{y} - (\bar{y} - \mu_0)\frac{n_0}{n + n_0}.$$ 

That shows "shrinkage" towards prior mean.
Prediction

Denoting the posterior mean and variance as $\mu_n$ and $\sigma^2_n = \sigma^2/(n_0 + n)$, the *predictive posterior distribution* for a new observation $y^*$ is

$$ p(y^*|y) = \int p(y^*|\mu, \mu|y) \rho(\mu|y) d\mu $$

which is generally equal to

$$ p(y^*|y) = \int p(y^*|\mu) \rho(\mu|y) d\mu $$

which can be shown to give

$$ p(y^*|y) \sim N(\mu_n, \sigma^2_n + \sigma^2) $$

The predictive posterior distribution is centered around the posterior mean $\mu_n$ with variance equal to sum of the posterior variance of $\mu$ plus the data variance.

Bayesian inference for Normal data

**Unknown variance, know mean**

Suppose we have sample of Normal data

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

where $\mu$ is *known* and $\sigma^2$ is *unknown*.

It is convenient to change parameterization to the precision $w = 1/\sigma^2$. The conjugate prior for $w$ is then

$$ w \sim \text{Gamma}(\alpha, \beta), $$

where

$$ \rho(w) \propto w^{\alpha-1} \exp(-\beta w). $$

Then $\sigma^2$ is then said to have an inverse-gamma distribution.
The posterior distribution for \( w \) takes the form

\[
p(w|\mu, y) \propto w^{\alpha-1} \exp(-\beta w) \times w^{\frac{n}{2}} \exp \left[ -\frac{w}{2} \sum_{i=1}^{n} (y_i - \mu)^2 \right].
\]

Collecting terms gives

\[
p(w|\mu, y) = \text{Gamma} \left( \frac{\alpha + n}{2}, \beta + \frac{1}{2} \sum_{i=1}^{n} (y_i - \mu)^2 \right).
\]

- Clearly we can think of \( \alpha = n_0/2 \), where \( n_0 \) is the "effective prior sample size".
- Since \( \sum_{i=1}^{n} (y_i - \mu)^2 / n \) estimate \( \sigma^2 = 1/w \), then we interpret \( 2\beta \) as representing \( n_0 \times \) prior estimate of \( \sigma_0^2 \).
- Alternative, we can write our conjugate prior as

\[
w \sim \text{Gamma} \left( \frac{n_0}{2}, \frac{n_0 \sigma_0^2}{2} \right),
\]

which can be seen as a scale \( \chi^2_{n_0} \) distribution. This is useful when assessing prior distributions for sample variances.
Bayesian inference with count data

Suppose we have an independent sample of counts \(y_1, \ldots, y_n\) which can be assumed to follow a Poisson distribution with unknown mean \(\mu t_i\), where \(\mu\) is the rate per unit \(t\):

\[
p(y | \mu) = \prod_i (\mu t_i)^{y_i} \exp(-\mu t_i)
\]

The kernel of the Poisson likelihood as a function of \(\mu\) has the same form as a Gamma\((a, b)\) prior for \(\mu\):

\[
p(\mu) \propto \mu^{a-1} \exp(-b\mu).
\]

This implies the following posterior

\[
p(\mu | y) \propto p(\mu)p(y | \mu) \\
\propto \mu^{(a-1)} e^{-b\mu} \prod_{i=1}^n e^{-\mu t_i} \mu_i^{y_i} \\
\propto \mu^{a+Y_n-1} e^{-(b+T_n)\mu} \\
= \text{Gamma}(a + Y_n, b + T_n).
\]

where \(Y_n = \sum_{i=1}^n y_i\) and \(T_n = \sum_{i=1}^n t_i\).
The posterior mean is:

\[ E(\mu|y) = \frac{a + Y_n}{b + T_n} = \frac{Y_n}{T_n} \left( \frac{n}{n+b} \right) + \frac{a}{b} \left( 1 - \frac{n}{n+b} \right). \]

The posterior mean is a compromise between the prior mean \( a/b \) and the MLE \( \frac{Y_n}{T_n} \).

Thus \( b \) can be interpreted as an effective exposure and \( a/b \) as a prior estimate of the Poisson mean.

**Example: Annual number of cases of haemolytic uraemic syndrome Henderson and Matthews, (1993)**

Annual numbers of cases were available from two a specialist center at Birmingham, from 1970 to 1988. For analysis we consider observed values from the first decade.

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>cases, ( x_i )</td>
<td>1</td>
<td>5</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

Because we are interested in counts of disease over time, a simple model is a Poisson process.

\[ y_i|\mu \sim \text{Poisson}(\mu) \quad i = 1, \ldots, 10. \]
Similar data is collected by another centre, given a mean rate of 2.3 with s.d. 2.79.

- with prior mean $a/b = 2.3$
- prior sd $\sqrt{a/b} = 2.79$
- Solving for $a$ and $b$, this information can be translated to a prior Gamma(0.679, 0.295) distribution

Then

$$p(\mu|y) = \text{Gamma}(\sum_i x_i + 0.679, 10 + 0.295) = \text{Gamma}(16.679, 10.295)$$

$$E(\mu|y) = \frac{16.679}{10.295} = 1.620; \quad sd(\mu|y) = \frac{\sqrt{16.679}}{10.295} = 0.396$$
The predictive posterior distribution for a new count $y^*$ is

$$y^* | y \sim \text{Negative-Binomial}(a + n\bar{y}, b + n)$$

If we ask what is the probability to observe 7 or more cases in the next year we have

```r
> sum(dnbinom(6:17, prob=10.295/(1+10.295), size=16.679))
[1] 0.0096
```

Note: the observed values for the following years were 7,11,4,7,10,... Indicating a possible structural break.

We can visualize the density by

```r
plot(dnbinom(0:10, prob=p, size=16.679, type="h",
   lwd=2, col="red", xlab= "counts")
```
Some comments

For all these examples, we see that

- the posterior mean is a compromise between the prior mean and the MLE
- the posterior s.d. is less than each of the prior s.d. and the s.e. (MLE)
- As $n \to \infty$,
  - the posterior mean $\to$ the MLE
  - the posterior s.d. $\to$ the s.e. (MLE)
  - the posterior does not depend on the prior.

These observations are generally true, when the MLE exists and is unique.

Priors

- When the posterior is in the same family as the prior then we have what is known as conjugacy.

- Conjugate models have the advantage that:
  - Prior parameters can usually be interpreted as implied prior sample size: $n_0$
  - They involve simple mathematical models, examples include:

<table>
<thead>
<tr>
<th>Distribution of $y$</th>
<th>Parameter</th>
<th>conjugate prior</th>
</tr>
</thead>
<tbody>
<tr>
<td>Binomial</td>
<td>Prob. of success</td>
<td>Beta</td>
</tr>
<tr>
<td>Poisson</td>
<td>Mean</td>
<td>Gamma</td>
</tr>
<tr>
<td>Exponential</td>
<td>Reciprocal of mean</td>
<td>Gamma</td>
</tr>
<tr>
<td>Normal</td>
<td>Mean (variance known)</td>
<td>Normal</td>
</tr>
<tr>
<td>Normal</td>
<td>Variance (mean known)</td>
<td>Inverse Gamma</td>
</tr>
</tbody>
</table>

- Unfortunately conjugate priors only exists for small catalog of likelihoods.
Practical

**Exercise:** Conjugate inference for a binomial experiment

Drug investigation example from this Lecture

We treat \( n = 20 \) volunteers with a new compound and observe \( r = 15 \) positive responses. We use as prior \( \theta \sim \text{Beta}(9.2, 13.8) \):

1. What is the posterior mean and median for the response rate?
2. What are the 2.5th and 97.5th percentiles of the posterior?
3. What is the probability that the true response rate is greater than 0.6?
4. How is this value affected if a uniform prior is adopted?
5. Using the original Beta(9.2, 13.8) prior, suppose 40 more patients were entered into the study. What is the chance that at least 25 of them respond positively?

Solution

```r
# 1) Posteriors mean and median
# The posterior mean is: (r+a) / (n + a+b)
> (15 + 9.2) / (20 + 9.2 + 13.8)
[1] 0.5627907

# the posterior median is
> qbeta(0.5, 24.2, 18.8)
[1] 0.5637731

# 2) Posterior percentiles:
> qbeta(0.025, 24.2, 18.8) # 2.5%
[1] 0.4142266
> qbeta(0.975, 24.2, 18.8) # 97.5%
[1] 0.7058181
```

Dr. Pablo E. Verde
# 3) Posterior prob that the rate is greater than 0.6
> 1 - pbeta(0.6, 24.2, 18.8)
[1] 0.3156323

# 4) Uniform prior is beta(1,1) then the posterior is beta( r+1, n-r+1)
> 1 - pbeta(0.6, 15+1, 20-15+1)
[1] 0.9042598

# 5) Posterior probability of at least 25 successes out of 40 further trials:
> sum(betabin(25:40, 24.2, 18.8, m=40))
[1] 0.3290134
Summary

▶ Misunderstandings about prior distributions

▶ Non-informative Priors and Jeffreys invariance priors

▶ Sensitivity analysis and making priors predictions

▶ Adjustment of priors based on historical data and judgement

▶ Mixture of priors

Misunderstandings about prior distributions

It is worth pointing out some misunderstanding regarding prior distributions:

▶ The name prior suggests a temporal relationship, however, this is misleading. The prior distribution models the uncertainty given by the external evidence. Cox (1999)

▶ The prior is not necessarily unique! In a recent article Lambert et. al. (2005) analyze the use of 13 different priors for the between study variance parameter in random-effects meta-analysis.

▶ There is no such thing as the correct prior. Bayesian analysis is regarded as transforming prior into posterior opinion, rather than producing the posterior distribution.

▶ The prior may not be completely specified. In Empirical Bayes inference priors have unknown parameters that are estimated from the data.
\textbf{Priors can be overparametrized.} Sometimes we intentionally overparametrized the priors in order to accelerate convergence of simulation methods, see Gelman, Carlin, Stern and Rubin (2004) Chapter 6.

\textbf{Inference may rely only on priors.} There are situations where no further data are available to combine with our priors or there is no intention to update the priors. This is the typical case of \textit{risk analysis, sample size determination in experiments, simulation of complex process}, etc. In these analytical scenarios priors are usually used to simulate hypothetical data and we refer to that \textit{prior predictive analysis}.

\textbf{Finally, priors are not necessarily important!} In many scientific applications, as the amount of data increases, the prior is overwhelmed by the likelihood and the influence of the prior disappears, see Box and Tiao (1973) (pag. 20-25).

\textbf{Non-informative Priors: Classical Bayesian Perspective}

We may be interested to introduce an initial state of "ignorance" in our Bayesian analysis.

But representing ignorance raises formidable difficulties!

There has been a long and complex search for various "\textbf{non-informative}, "\textbf{reference}" or "\textbf{objective}" priors during the last century. A sort of "\textbf{off-the-shelf objective prior}" that can be applied in all circumstances.

The synthesis of this search is that those \textit{magic priors do not exists}, although useful guidance exists (Berger, 2006).
Problems with uniform priors for continuous parameters

Example: uniform prior on proportions

Let $\theta$ be the chance that a bias coin comes down heads, we assume

$$\theta \sim \text{Uniform}(0,1).$$

Let $\phi = \theta^2$ the chance that it coming down heads in both of the next 2 throws.

Now, the density of $\phi$ is

$$p(\phi) = \frac{1}{2\sqrt{\phi}},$$

which corresponds to a Beta(0.5,1) distribution and is certainly not uniform!

Jeffreys' invariance priors

Consider a 1-to-1 transformation of $\theta : \phi = g(\theta)$

Transformation of variables: prior $p(\theta)$ is equivalent to prior on $\phi$ of $p(\phi) = p(\theta) \left| \frac{d\theta}{d\phi} \right|$

Jeffreys proposed defining a non-informative prior for $\theta$ as

$$p(\theta) \propto I(\theta)^{1/2}$$

where $I(\theta)$ is Fisher information for $\theta$

$$I(\theta) = -E_{x|\theta} \left[ \frac{\partial^2 \log p(X|\theta)}{\partial \theta^2} \right] = E_{x|\theta} \left[ \left( \frac{\partial \log p(X|\theta)}{\partial \theta} \right)^2 \right].$$
Non-informative priors for proportions

**Data model is Binomial:** we consider \( r \) successes from \( n \) trials

\[
r|\theta \sim \text{Binomial}(\theta, n)
\]

we have

\[
\log p(x|\theta) = r \log(\theta) + (n - r) \log(1 - \theta) + C
\]

then

\[
I(\theta) = \frac{n}{\theta(1 - \theta)}.
\]

So the Jeffreys' prior is

\[
p(\theta) \propto (\theta(1 - \theta))^{-1/2},
\]

which is a Beta(1/2, 1/2).

---

Non-informative priors for location parameters

A location parameter \( \theta \) is such that \( p(\theta|y) \) is a function of \((y - \theta)\) and so the distribution of \((y - \theta)\) is independent of \( \theta \).

**Example:** data model is Normal with unknown mean \( \theta \) and known variance \( \nu \)

\[
x_1, x_2, \ldots, x_n|\theta \sim \text{Normal}(\theta, \nu)
\]

then we have

\[
\log p(x|\theta) = -\sum \frac{(x_i - \theta)^2}{2\nu} + C
\]

with

\[
I(\theta) = \frac{n}{\nu}.
\]

So the Jeffreys' prior is

\[
p(\theta) \propto 1
\]

which is the Uniform distribution for \( \theta \).
Non-informative priors for scale parameters

A scale parameter $\theta$ is such that $p(y|\theta)$ is a function of $1/\theta f(y/\theta)$ and so the distribution of $(y/\theta)$ is independent of $\theta$.

**Example: data model is Normal with known mean $m$ and unknown variance $\theta$**

$$x_1, x_2, \ldots, x_n | \theta \sim \text{Normal}(m, \theta)$$

then we have

$$\log p(x|\theta) = -n/2 \log(\theta) - \frac{s}{2\theta},$$

where $s = \sum(x_i - m)^2$, then

$$I(\theta) = \frac{n}{2\theta^2}.$$

So the Jeffreys’ prior on variance is

$$p(\theta) \propto \frac{1}{\theta}.$$

This Jeffreys’ improper prior is approximated by a Gamma$(\epsilon, \epsilon)$ with $\epsilon \to 0$.

---

**Priors for counts and rates**

**Data model is Poisson:** $x | \theta \sim \text{Poisson}(\theta)$, then we have

$$\log p(x|\theta) = -\theta + x \log \theta + C$$

with

$$I(\theta) = 1/\theta.$$

So the Jeffreys’ prior is

$$p(\theta) \propto \theta^{-1/2}.$$

This improper prior is approximated by a Gamma distribution with $\alpha = 1/2$ and $\beta \to 0$. 
Comments Jeffreys’ rule

- They are invariant, whatever the scale we choose to measure the unknown parameter, the same prior results when the scale is transformed to any particular scale.

- Some inconsistencies associated with Jeffreys’ priors have been discussed:
  - Applying this rule to the normal case with both mean and variance parameters unknown does not lead to the same prior as applying separately the rule for the mean and the variance and assuming a priori independence between these parameters.

- Although Jeffreys’ rule is suggestive, it cannot be applied blindly. It should be thought of as guideline to consider particularly if there is no other obvious way of finding a prior distribution.

Predictive Prior Analysis

In practice it is not necessary to adopt a full Bayesian approach. Sometimes is very useful to use Bayesian methods for some analyzes and classical approaches for others.

Example: predictive distribution of the power in sample size calculations

- a randomize trial is planned with $n$ patients in each of two arms.

- the response within each treatment arm is assumed to have between-patient standard deviation $\sigma$.

- the treatment estimate $\hat{\theta} = \bar{y}_1 - \bar{y}_2$ is approximately distributed as $\text{Normal}(\theta, 2\sigma^2/n)$.

- a trial designed to have two-sided Type I error $\alpha$ and Type II error $\beta$ in detecting a true difference of $\theta$ in mean response between the groups will require a sample size per group of

$$n = \frac{2\sigma^2}{\theta^2} \left( z_{1-\beta} - z_{1-\alpha/2} \right)^2,$$
Alternatively, for fixed $n$, the power of this experiment is

\[
\text{Power} = \Phi \left( \sqrt{\frac{n\theta^2}{2\sigma^2} - z_{1-\alpha/2}} \right).
\]

If we assume $\theta/\sigma = 0.5$, $\alpha = 0.05$ and $\beta = 0.2$, we have $z_{1-\beta} = 0.84$, $z_{1-\alpha/2} = 1.96$, then the power of the trial is 80% and $n = 63$ in each trial arm.

However, we accept uncertainty about $\theta$ and $\sigma$ and we wish to include this feature into the sample size and power calculations.

We assume from previous studies that it is reasonable that

\[
\theta \sim N(0.5, 1) \quad \text{and} \quad \sigma \sim N(1, 0.3^2)I(0, \infty).
\]

Then

1. Simulate values $\theta^* \sim N(0.5, 1)$ and $\sigma^* \sim N(1, 0.3^2)$ (subject to the constrain of $\sigma$ being positive).
2. Substitute them in the formulae and generate $n^*$ and $\text{Power}^*$.
3. Use the histogram of $n^*$ and $\text{Power}^*$ as their corresponding predictive distribution.
4. In R we have

```r
## predictive prior distribution for sample size and power
set.seed(123)
theta <- rnorm(10000, 0.5, 0.1)
sigma <- rnorm(10000, 1, 0.3)
 sigma <- ifelse(sigma < 0, -1*sigma, sigma)
n <- 2*sigma^2 /(theta^2)*(0.84 + 1.96)^2
pow <- pnorm( sqrt( 63/2) * theta /sigma - 1.96)
par(mfrow=c(1,2))
hist(n, xlim = c(0, 400), breaks=50)
hist(pow)
par(mfrow=c(1,1))
```
It is clear that there is huge uncertainty to the appropriate sample size.

For n=63 the median power is 81% and a trial of 63 patients per group could be seriously underpowered. There is a 37% chance that the power is less than 70%.
Mixture of priors for proportions

- We may want to express a more complex prior opinion that cannot be encapsulated by a beta distribution.

- A prior which is a mixture of beta distributions

\[ p(\theta) = qp_1(\theta) + (1-q)p_2(\theta) \]

where \( p_i = \text{Beta}(a_i, b_i) \).

- Now if we observe \( r \) successes out of \( n \) trials, the posterior is

\[ p(\theta | r, n) = q^*p_1(\theta | r, n) + (1-q^*)p_2(\theta | r, n) \]

where

\[ q^* = \frac{qp_1(r | n)}{qp_1(r | n) + (1-q)p_2(r | n)} \]

- \( p_i(r | n) \) is a beta-binomial predictive probability or \( r \) successes in \( n \) trials assuming \( \theta \) has distribution \( \text{Beta}(a_i, b_i) \).

- The posterior is a mixture of beta posteriors, with mixture weights adapted to support prior that provides best prediction for the observed data.

- In R:

```r
# mixture of betas
mixbeta <- function(x,r,a1,b1,a2,b2,q,n)
{
  qstar <- q*betabin(r,a1,b1,n)/
  (q*betabin(r,a1,b1,n)+(1-q)*betabin(r,a2,b2,n))

  p1 <- dbeta(x,a1+r,n-r+b1)
  p2 <- dbeta(x,a2+r,n-r+b2)
  posterior <- qstar*p1 + (1-qstar)*p2
}
```
Example: drug investigation continue ...

- We want to combine:
  - an informative Beta(9.2, 13.8)
  - a non-informative Beta(1, 1)
  - we give 80% of prior weight to the informative prior

- Suppose we treat $n = 20$ volunteers with the compound and observe $r = 15$ positive responses.

We can visualize this analysis in R as follows:

```r
par(mfrow=c(2,1))
# informative beta prior
curve(dbeta(x, 9.2, 13.8), from=0, to=1, col="red",
     xlab="probability of response", main="priors")
# mixture beta prior with 80% informative and 20% flat
  curve(0.8*dbeta(x, 9.2, 13.8)+0.2*dbeta(x, 1, 1), from=0, to=1, col="blue", add=T)
# beta posterior
  curve(dbeta(x, 24.2, 18.8), from=0, to=1, col="red",
       xlab="probability of response", main="posteriors")
# posterior from a mixture prior
  curve(mixbeta(x, r=15, a1=9.2, b1=13.8, a2=1, b2=1, q=.8, 20),
       from=0, to=1, col="blue", add=T)
par(mfrow=c(1,1))
```
Further topics on priors:

- Adjustment of priors based on historical data and judgement
  1. Power priors (Ibrahim and Shen, 2000)
  2. Bias modelling

- Hierarchical priors for large dimensional problems (e.g. regression with more predictors than observations)

Summary:

- The need for priors distributions should not be an embarrassment

- It is reasonable that the prior should influence the analysis, as long as the influence is recognized and justified

- Importance of transparency and sensitivity analysis
Practical

**Exercise:** Conjugate mixture priors inference for a binomial experiment

- Suppose that most drugs (95%) are assumed to come from the stated Beta(9.2, 13.8) prior, but there is a small chance that the drug might be a "winner".

- Winners are assumed to have a prior distribution with mean 0.8 and standard deviation 0.1.

1. What Beta distribution might represent the "winners" prior? (Hint: Use the formulas of the mean and the variance for a Beta(a, b) distribution from lecture 2. This can be re-arranged to

   \[ a = m(m(1 - m)/v - 1) \]

   and

   \[ b = (1 - m)(m(1 - m)/v - 1), \]

   where \( m \) and \( v \) are the mean and the variance of a Beta(a, b) distribution).

2. Enter this mixture prior model into the R code for mixtures and plot it.

3. Calculate the posterior mixture model based on 15 success out of 20 trials and plot it.

4. What is the chance that the drug is a winner?
Solution

# 1) to workout the a and b for the winner drug prior use the realtionship of the mean and variance of the beta distribution and its parameters
> m <- 0.8
> v <- 0.1^2
> a <- m*(m*(1-m)/v -1)
> a
[1] 12
> b <- (1-m)*(m*(1-m)/v -1)
> b
[1] 3
# 2) plot for the mixture prior
curve(dbeta(x, 12, 3)*0.05 + dbeta(x, 9.2, 13.8)*0.95, from = 0, to = 1, main = "prior", xlab = "rate")

# 3) plot for the mixture posterior with 15 success out of 20 trials
# mixture posterior of betas
mixbeta <- function(x,r,a1,b1,a2,b2,q,n)
{
    qstar <- q*betabin(r,a1,b1,n)/(q*betabin(r,a1,b1,n)+(1-q)*betabin(r,a2,b2,n))
    p1 <- dbeta(x,a1+r,n-r+b1)
    p2 <- dbeta(x,a2+r,n-r+b2)
    posterior <- qstar*p1 + (1-qstar)*p2
}
# then the mixture beta has parameters:
# a = 12, b = 3 with probability 5%
# a = 9.2, b = 13.8 with probailty 95%
# r = 15, n = 20
curve(mixbeta(x, r = 15, a1 = 12, b1 = 3, a2 = 9.2, b2 = 13.8, q = 0.05, n = 20), from = 0, to = 1, main = "posterior", xlab = "rate")
The probability that the drug is a winner is given by the posterior weight to belong to the winner class.

```r
qstar <- 0.05*betabin(15, 12, 3, 20)/(0.05*betabin(15, 12, 3, 20)
+ (1-0.05)*betabin(15, 9.2, 13.8, 20))

> qstar
[1] 0.3951545
```
Summary

▶ Introduction to multiparameter inference
▶ Normal model with unknown mean and variance: standard non-informative priors
▶ Using R for predictive model checking
▶ Multinomial Model conjugate analysis and its application in R
▶ Comparing classical and Bayesian multiparameter models

Introduction

▶ The basic ideas is similar to one parameter models:
  ▶ We have a model for the observed data which defines a likelihood $p(y|\theta)$ on the vector parameter $\theta$
  ▶ We specify a joint prior distribution $p(\theta)$ for the possible values of $\theta$
  ▶ We use Bayes’ rule to obtain the posterior of $\theta$,
    $$p(\theta|y) \propto p(\theta) \times p(y|\theta)$$
  
▶ Problems:
  ▶ In many applications is difficult to specify priors on multivariate $\theta$
  ▶ Computations could be very difficult, they involve multivariate integration
**Example: Normal with unknown mean $\mu$ and variance $\sigma^2$**

- In this example we use `marathontimes` in the R package `LearnBayes`

- The observations are the mean times (in minutes) for men running Marathon with age classes between 20 to 29 years old:

  ```r
data(marathontimes)
martathontimes$time
```

- We assume a Normal model for the data given the mean $\mu$ and the variance $\sigma^2$:

  \[
y_1, \ldots, y_{20} \mid \mu, \sigma^2 \sim N(\mu, \sigma^2)
  \]

- We use a non-informative Jeffreys’ prior assuming independence between location and scale:

  \[
p(\mu, \sigma) \propto \frac{1}{\sigma},
  \]

- Then posterior density for the mean and the variance $p(\mu, \sigma \mid y)$ is called the Normal-$\chi^2$ distribution
  - This posterior delivers same results as classical analysis: $E(\mu \mid y) = \bar{y}$, $E(\sigma^2 \mid y) = S^2$
  - The posterior $p(\mu \mid y)$ is proportional to a t-distribution with $n - 1$ df, and so on
  - Direct simulation from these posteriors is straightforward
The Normal-$\chi^2$ posterior is implemented in the function `normchi2post` in LearnBayes, which computes the logarithm of the joint posterior density of $(\mu, \sigma^2)$.

We can visualize the $\alpha\%$ levels contours with the function `mycontour`. The arguments include the log-density to plot, the rectangular area $(x_{lo}, x_{hi}, y_{lo}, y_{hi})$ and the data:

```r
> mycontour(normchi2post, c(220,330,500,9000), time,
  xlab = "mean", ylab = "var")
```

We can simulate directly form the marginal posteriors of $\mu$ and $\tau$:

```r
> SS <- sum((time - mean(time))^2)
> n <- length(time)
> sigma2 <- SS/rchisq(1000, n - 1)
> mu <- rnorm(1000, mean = mean(time), sd = sqrt(sigma2)/sqrt(n))
> points(mu, sigma2, col="blue")
> quantile(mu, c(0.025, 0.975)) # 95% posterior interval for mu
2.5%   97.5%
253.1121 301.1133
```
Predictive model checking

Is the statistical model consistent with the data?

We answer this question by simulating predictive $y^*$ values from the model and comparing some data features with the predictive data.

We start by looking at some histograms between the original data and the simulated data with the same sample size.

```r
y.star <- rnorm(1000, mean = mu, sd = sqrt(sigma2))  #predictive data
par(mfrow=c(3,4))
hist(time, breaks=10, xlim =c(150, 400), main="Original Data", col="green")
for(i in 1:11){
  y.sim <- sample(y.star, 20)
hist(y.sim,breaks=10,xlim=c(150, 400),main="Simulated Data",col="blue")
}
```

![Histograms of original and simulated data](image)
Predictive model checking

We define the following features between the observed data $y$ and the predictive data $y^*$:

$$T_1^* = \min(y^*), \quad T_2^* = \max(y^*), \quad T_3^* = q_{75}(y^*) - q_{25}(y^*)$$

and for asymmetry

$$T_4^* = |y_{(18)}^* - \mu^*| - |y_{(2)}^* - \mu^*|$$

where the 18th and 2sd order statistics approximate the 90% and 10% respectively.

These measures are compared with the corresponding values based on the observed data:

$$T_1 = \min(y), \quad T_2 = \max(y), \quad T_3 = q_{75}(y) - q_{25}(y)$$

and

$$T_4 = |y_{(18)} - \mu^*| - |y_{(2)} - \mu^*|.$$
To display this quantities

```r
par(mfrow =c(2,2))
hist(min.y, breaks = 50, col="blue", main = "Minimum y*")
abline(v=min(time), lwd=3, lty=2)
hist(max.y, breaks = 50, col="red", main = "Maximum y")
abline(v=max(time), lwd=3, lty=2)
hist(inter.q, breaks = 50, col="magenta", main = "Variability y")
abline(v=quantile(time,prob=0.75)-quantile(time,prob=0.25), lwd=3,lty=2)
plot(asy1, asy2, main ="Asymmetry", xlab="Asymmetry predicted data",
ylab ="Asymmetry original data")
abline(a=0, b=1, lwd=2)
par(mfrow=c(1,1))
```

This analysis shows that the data and the model are compatibles and deviations can be easily explained by sampling variation.
Multinomial distribution with unknown cell probabilities

In this model we observe \( n \) independent trials each of which has \( p \) possible outcomes with associated probabilities

\[
\theta = (\theta_1, \ldots, \theta_p).
\]

Letting \( y = (y_1, \ldots, y_p) \) be the number of times each outcome is observed we have

\[
y|\theta \sim \text{Multinomial}(n, \theta),
\]

with likelihood

\[
p(y|\theta) = \frac{(\sum y_i)!}{\prod y_i!} \prod \theta_i^{y_i}, \quad \sum y_i = n, \sum \theta_i = 1.
\]

The kernel of this likelihood is proportional to a Dirichlet distribution. If a-priori we assume

\[
\theta \sim \text{Dirichlet}(a_1, \ldots, a_p), \quad a_i > 0,
\]

then

\[
p(\theta) \propto \prod \theta_i^{a_i-1}
\]

and the posterior for \( \theta \) is

\[
p(\theta|y) \propto \prod \theta_i^{y_i+a_i-1}
\]

so taking \( \alpha_i = a_i + y_i \), then the posterior for \( \theta \) is

\[
p(\theta|y) = \text{Dirichlet}(\alpha_1, \ldots, \alpha_p).
\]
Some comments

- The prior distribution is equivalent to a likelihood resulting from $\sum a_i$ observations, with $a_i$ observations in the $i$th category.

- A uniform density is obtained by setting $a_i = 1$ for all $i$. This distribution assigns equal probability to each $\theta_i$.

- In general it is very difficult to work with this distribution in practice. Proportions are in general not independent and modeling prior information in this context it is very difficult.

- We are going to use for contingency tables a surrogate Poisson model for the multinomial distribution.

- Moments and properties for the Dirichlet distribution are in Appendix A of Gelman et.al.

Example: A model for a two by two contingency table

<table>
<thead>
<tr>
<th></th>
<th>Intervention</th>
<th>Control</th>
</tr>
</thead>
<tbody>
<tr>
<td>Death</td>
<td>$\theta_{1,1}$</td>
<td>$\theta_{1,2}$</td>
</tr>
<tr>
<td>No death</td>
<td>$\theta_{2,1}$</td>
<td>$\theta_{2,2}$</td>
</tr>
</tbody>
</table>

Data model:

$$p(y|\theta) \propto \prod_{j=1}^{2} \prod_{i=1}^{2} \theta_{i,j}^{y_{i,j}}$$

Prior model:

$$p(\theta) \propto \prod_{j=1}^{2} \prod_{i=1}^{2} \theta_{i,j}^{a_{i,j} - 1}$$

Posterior model:

$$p(\theta|y) \propto \prod_{j=1}^{2} \prod_{i=1}^{2} \theta_{i,j}^{y_{i,j} + a_{i,j} - 1}$$
We are interested in making inference for the Odds ratio:

\[
\psi = \frac{\theta_{1,1} \theta_{2,2}}{\theta_{1,2} \theta_{2,1}}.
\]

We use direct simulation methods:

- Simulate a large number of values for the vector \( \theta \) from its posterior.
- For each simulated value calculate \( \psi^* \).
- Inference for \( \psi \) is based on the histogram of \( \psi^* \).

**Example:** GREAT trial, Spiegelhalter et.al. pag 69.

**Intervention:** Thrombolytic therapy after myocardial infarction, given at home by general practitioners.

**Aim of study:** to compare a new drug treatment to be given at home as soon as possible after a myocardial infarction and placebo.

**Outcome measure:** Thirty-day mortality rate under each treatment, with the benefit of the new treatment measured by the odds ratio, i.e., the ratio of the odds of death following the new treatment to the odds of death on the conventional: \( OR < 1 \) therefore favors the new treatment.

**Prospective Bayesian analysis:** NO. It was carried out after the trial reported its results.
**Example:** GREAT trial continue

<table>
<thead>
<tr>
<th></th>
<th>Intervention</th>
<th></th>
<th>Control</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>New</td>
<td>Death</td>
<td>13</td>
<td>23</td>
<td>36</td>
</tr>
<tr>
<td></td>
<td></td>
<td>No death</td>
<td>150</td>
<td>125</td>
<td>275</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>163</td>
<td>148</td>
<td>311</td>
</tr>
</tbody>
</table>

We use a Dirichlet prior with parameters $a_{1,1} = a_{1,2} = a_{2,1} = a_{2,2} = 1$, which corresponds to a uniform distribution for $(\theta_{1,1}, \theta_{1,2}, \theta_{2,1}, \theta_{2,2})$.

We can simulate from a Dirichlet distributions with the function `rdirichlet()` from the package LearnBayes:

```r
> library(LearnBayes)
> draws <- rdirichlet(10000, c(13, 23, 150, 125))
> odds <- draws[,1]*draws[,4]/(draws[,2]*draws[,3])
> hist(odds, breaks = 100, xlab="Odds Ratio", freq = FALSE)
> lines(density(odds), lty = 2, lwd = 2, col = "blue")
> abline(v = quantile(odds, prob = c(0.025, 0.5, 0.975)), lty = 3, col = "red")
> quantile(odds, prob = c(0.025, 0.5, 0.975))
  2.5%  50%  97.5%
0.2157422 0.4649921 0.9698272
```
Now suppose that we want to calculate the "p-value" of

\[ H_0 : \Psi \geq 1 \quad \text{vs.} \quad H_1 : \Psi < 1 \]

then,

\begin{verbatim}
> sum(odds > 1)/10000
[1] 0.0187
\end{verbatim}

It is interesting to compare this results with the exact Fisher test:

\begin{verbatim}
> fisher.test(matrix(c(13, 23, 150, 125), nrow=2, byrow=TRUE),
alternative="less")
Fisher's Exact Test for Count Data
p-value = 0.02817
\end{verbatim}

Thus, the uniform prior on \((\theta_{1,1}, \theta_{1,2}, \theta_{2,1}, \theta_{2,2})\) does not corresponds to a standard statistical analysis.
Now, if we work with a prior with parameters $a_{1,1} = 2, a_{1,2} = 1, a_{2,1} = 1$ and $a_{2,2} = 2$, with density
\[
p(\theta_{1,1}, \theta_{1,2}, \theta_{2,1}, \theta_{2,2}) \propto \theta_{1,1} \theta_{2,2}
\]
we get the following results

```r
> param <- c(2,1,1,2) # parameter of the dirichlet
> draws <- rdirichlet(10000, c(13,23,150,125)+param )
> odds <-draws[,1]*draws[,4]/(draws[,2]*draws[,3])
> sum(odds>1)/10000
[1] 0.0277
```

This shows (empirically) that the Fisher test is NOT based in a non-informative prior. Some weakly information of association is implied in the test.

However, there is a difference in interpretation between the Bayesian and sampling theory results.
Practical

Exercise: Normal data with unknown mean and variance

- Review the Bayesian analysis presented in this lecture
- Generate predictive posterior data and check model fitness
- Now, change the first observation of the marathon times and generate an outlier as follows:

  ```r
  > library(LearnBayes)
  > data(marathontimes)
  > marathontimes$time
  [1] 182 201 221 234 237 251 261 266 267 273 286 291 292 ...
  >
  > # generate an outlier in the first observation:
  > data1 <- marathontimes$time
  > data1[1] <- 82
  ```
- Make the same analysis for the contaminated data
- Which is the effect of this outlier in the analysis?
Summary

- Introduction to BUGS
- The BUGS language
- Some simple examples
- Making predictions
- Connecting WinBUGS with R

Introduction to BUGS

The BUGS project began at the Medical Research Council Biostatistics Unit in Cambridge in 1989, before the classic Gibbs sampling paper by Gelfand and Smith in 1990. An excellent review and future directions of the BUGS project is given in Lunn et al. (2009).

BUGS stands for Bayesian inference using Gibbs sampling, reflecting the basic computational techniques originally adopted.

BUGS has been just one part of the tremendous growth in the application of Bayesian ideas over the last 20 years.

At this time BUGS has approximately over 30,000 registered users worldwide, and an active on-line community comprising over 8,000 members.

Typing "WinBUGS" in Google generates over 100,000 hits; in Google scholars over 5,000; and searching in Statistics in Medicine on-line gives about 100 hits.
Think different ...

The modelling philosophy of BUGS was strongly influenced by developments in artificial intelligence in the 1980’s. In particular the focus was on Expert systems, where a basic principle was to separate:

- **Knowledge base:**
  - assumed model for the world
  - makes use of a declarative form of programming
  - structures described using a series of local relationships

- **Inference engine:**
  - used to draw conclusions in specific circumstances

This approach forces to think first about the model use to describe the problem at hand. The declarative programming approach, sometimes, confuses statistical analysts used to work with procedural or functional statistical languages (SAS, SPSS, R, etc).

The BUGS language:

- Language for specifying complex Bayesian models.
- Constructs object-oriented internal representation of the model graph by identifying parents and children. This is done with a DAG (Directed Acyclic Graph).
- Builds up an arbitrary complex model through specification of local structure.
- Simulation from full conditionals using Gibbs sampling.
- Current version is WinBUGS 1.4.3, it runs in Windows, and incorporates the DoodleBUGS graphical model editor and a script language for running in batch mode.

**WinBUGS is freely available from** [http://www.mrc-bsu.cam.ac.uk/bugs](http://www.mrc-bsu.cam.ac.uk/bugs)

An open source version of BUGS called OpenBUGS is under development, and includes versions of BUGS that run under LINUX (LinBUGS) and that can be run directly from R (BRugs). See [http://www.rni.helsinki.fi/openbugs](http://www.rni.helsinki.fi/openbugs)
**Example:** Drug

In $n = 20$ patients we observed $r = 15$ positive responses.

$$y \sim \text{Bin}(\theta, n)$$

and we assume a conjugate prior for $\theta$:

$$\theta \sim \text{Beta}(a, b)$$

Of course, we know the posterior distribution is

$$\theta \mid y \sim \text{Beta}(a + y, n - r + b)$$

and no simulation is necessary. But just to illustrate WinBUGS ...
Directed Acyclic Graph (DAG) representation:

- **Ovals nodes** represent random variables
- **Rectangular nodes** represent constants
- **Arrows** parent child relationships

1. Write BUGS code to specify the model ...
   ```
   model {
     y ~ dbin(theta, n)
     theta ~ dbeta(a, b)
   }
   ```
2. Check the model syntax ...
3. Load the data ...
   ```
   list(n=20, y = 15, a = 3, b =2)
   ```
   ... and compile.
4. Then load initial values ...
   ```
   list(theta = 0.5)
   ```
5. Select the nodes (variables) to monitor (just one in this case)...
6. Set the trace for all selected nodes (*) to monitor the MCMC simulations ...
7. Using the Update tools, select 10,000 simulations ...
8. Results ...
**Example:** Drug continue ...

Now we assume a different prior. A logit transform of

\[ \phi = \log \left( \frac{\theta}{1 - \theta} \right), \]

so that \(-\infty < \phi < \infty\)

We assume a normal prior for \(\phi\):

\[ \phi \sim \text{Normal}(\mu, \tau) \]

for suitable mean \(\mu\) and precision \(\tau = 1/\sigma^2\).

This is a non-conjugate prior with no simple form for the posterior.

Straightforward in WinBUGS!

Double arrows represent a logical node or a mathematical functional relationship.
The BUGS code for the model is ...

```r
model
{
  y ~ dbin(theta, n)
  logit(theta) <- phi
  phi ~ dnorm(0, 0.001)
}
```

Making predictions

- Important to be able to predict unobserved quantities for
  - 'filling-in" missing or censored data
  - model checking - are predictions 'similar' to observed data?
  - making predictions!

- Easy in MCMC/WinBUGS, just specify a stochastic node without a data value - it automatically predicted

- Provides automatic imputation of missing data

- Easiest case is where there is no data at all!! Just 'forwards sampling' from prior to make a Monte Carlo analysis.
**Example: making predictions**

The BUGS code for the model is...

```plaintext
model
{
  y ~ dbin(theta, n)
  logit(theta) <- phi
  phi ~ dnorm(mu, tau)
  y.pred ~ dbin(theta, n)  # defines a stochastic node for
                         # predictions
}
```

The prediction node `y.pred` is conditionally independent of the data node `y` given rate `θ`. 
Summary: Running WinBUGS

1. Open Specification tool and Update from Model menu, and Samples from Inference menu.

2. Highlight model by double-click. Click on Check model.

3. Highlight start of data. Click on Load data.

4. Click on Compile.

5. Highlight start of initial values. Click on Load inits.

6. Click on Gen Inits if model initials values are needed.

7. Click on Update to burn in.

8. Type nodes to be monitored into Sample Monitor, and click set after each.

9. Perform more updates.

10. Type * into Sample Monitor, and click stats, etc. to see results on all monitored nodes.

The R2WinBUGS package in R

The R package R2WinBUGS offers a versatile approach for making MCMC computations within WinBUGS and returning them to R.

Let see a step by step example of linking R and WinBUGS with R2WinBUGS.

Example: non-conjugate priors inference for a binomial experiment

First save the following file with WinBUGS code in your working directory ...

```r
# WinBUGS code: binary problem non-conjugate analysis
model{
  y ~ dbin(theta, n)
  logit(theta) <- phi
  phi ~ dnorm(0,0.001)
  y.pred ~ dbin(theta,n) # making prediction
}
```
Then in R console ...

```r
# load R2WinBUGS package
library(R2WinBUGS)

# setup WinBUGS directory and your working directory
bugsdir <- "C:/Programme/WinBUGS14"
workdir <- getwd()

# define you data nodes
n <- 20
y <- 15
data1 <- list("n", "y")

# define parameters of interest
par1 <- c("theta", "y.pred")

# run the bugs() function:
m1 <- bugs(data1, inits=NULL, par1, "model1.txt",
n.chains = 1, n.iter = 2000, n.thin=1,
bugs.directory = bugsdir,
workingdirectory = getwd(),
debug=TRUE)
```
> print(m1, digits.summary = 3)
Inference for Bugs model at "model1.txt", fit using WinBUGS, 
1 chains, each with 2000 iterations (first 1000 discarded) 
n.sims = 1000 iterations saved

<table>
<thead>
<tr>
<th></th>
<th>mean</th>
<th>sd</th>
<th>2.5%</th>
<th>25%</th>
<th>50%</th>
<th>75%</th>
<th>97.5%</th>
</tr>
</thead>
<tbody>
<tr>
<td>theta</td>
<td>0.749</td>
<td>0.096</td>
<td>0.543</td>
<td>0.690</td>
<td>0.760</td>
<td>0.819</td>
<td>0.914</td>
</tr>
<tr>
<td>y.pred</td>
<td>14.962</td>
<td>2.733</td>
<td>9.000</td>
<td>13.000</td>
<td>15.000</td>
<td>17.000</td>
<td>19.000</td>
</tr>
<tr>
<td>deviance</td>
<td>4.277</td>
<td>1.584</td>
<td>3.198</td>
<td>3.286</td>
<td>3.667</td>
<td>4.551</td>
<td>9.014</td>
</tr>
</tbody>
</table>

DIC info (using the rule, pD = Dbar-Dhat)
pD = 1.1 and DIC = 5.3
DIC is an estimate of expected predictive error (lower deviance is better).

The R object m1 generated in this analysis belong to the class bug and can be further manipulated, transformed, etc.

> class(m1)
[1] "bugs"

> names(m1)
[1] "n.chains" "n.iter" "n.burnin"
[4] "n.thin" "n.keep" "n.sims"
[7] "sims.array" "sims.list" "sims.matrix"
[10] "summary" "mean" "sd"
[13] "median" "root.short" "long.short"
[16] "dimension.short" "indexes.short" "last.values"
[19] "isDIC" "DICbyR" "pD"
[22] "DIC" "model.file" "program"
The object `m1` is a list in R, so we can extract elements of the list by using the "$" operator, for example:

```r
> m1$pD
[1] 1.065
> m1$n.chains
[1] 1
> m1$sims.array[1:10, , "theta"]
[1] 0.8389 0.9124 0.7971 0.8682 0.7025 0.7696 0.8417 0.6782 0.6146
[10] 0.8647
> m1$sims.array[1:10, , "y.pred"]
[1] 15 19 19 20 15 20 18 17 10 17
> theta <- m1$sims.array[1:1000, , "theta"]
> hist(theta, breaks = 50, prob = TRUE)
> lines(density(theta), col = "blue", lwd = 2)
```
Some aspects of the BUGS language

- \( \leftarrow \) represents logical dependence, e.g. \( m \leftarrow a + b \times x \)

- \( ~ \) represents stochastic dependence, e.g. \( r \sim \text{dunif}(a,b) \)

- Can use arrays and loops
  ```plaintext
  model{
    ....
    for (i in 1:N){
      r[i] ~ dbin(p[i], n[i])
    }
    ....
  }
  ```

A for loop is represented as a "plate" in the DAG's model
Some aspects of the BUGS language

- Some functions can appear on the left-hand-side of an expression, e.g.

\[
\begin{align*}
\text{logit}(p[i]) & \leftarrow a + b*x[i] \\
\log(m[i]) & \leftarrow c + d*y[i]
\end{align*}
\]

- \text{mean}(p[]) to take mean of whole array, \text{mean}(p[m:n]) to take mean of elements m to n. Also for \text{sum}(p[])

- \text{dnorm}(0, 1)I(0,) means the random variable will be restricted to the range (0, \infty).

Functions in the BUGS language

- \text{p} \leftarrow \text{step}(0.05 - x) = 1 \text{ if } x \leq 0.05, 0 \text{ otherwise. Hence monitoring p and recording its mean will give the probability that } x \leq 0.05. \text{ This is useful to calculate Bayesian p-values.}

- \text{p} \leftarrow \text{equals}(x, 0.7) = 1 \text{ if } x = 0.7, 0 \text{ otherwise.}

- \text{tau} \leftarrow 1/\text{pow}(s, 2) \text{ sets } \tau = 1/s^2.

- \text{s} \leftarrow 1/\text{sqrt}(\text{tau}) \text{ sets } s = 1/\sqrt(\tau)

- \text{p}[i,k] \leftarrow \text{inprod}(p[], \text{Lambda}[i,k]) \text{ sets } p_{ik} = \sum_j \pi_j \Lambda_{ij}.

- See 'Model Specification/Logical nodes' in the manual for full syntax.
Data transformations

Although transformations of data can always be carried out before using WinBUGS, it is convenient to be able to try various transformations of dependent variables within a model description.

For example, we may wish to try both $y$ and $\sqrt{y}$ as dependent variables without creating a separate variable $z = \sqrt{y}$ in the data file.

The BUGS language therefore permits the following type of structure to occur:

```plaintext
for (i in 1:N) {
  z[i] <- sqrt(y[i])
  z[i] ~ dnorm(mu, tau)
}
```

Strictly speaking, this goes against the declarative structure of the model specification.

Some common distributions

- Binomial: $r \sim \text{dbin}(p, n)$
- Normal: $x \sim \text{dnorm}(\mu, \tau)$
- Poisson: $r \sim \text{dpois}(\lambda)$
- Uniform: $x \sim \text{dunif}(a, b)$
- Gamma: $x \sim \text{dgamma}(a, b)$

Note: The normal distribution is parameterized in terms of its mean and precision $= 1/\text{variance} = 1/\sigma^2$.

Functions cannot be used as arguments in distributions. You need to create new nodes.
The WinBUGS data formats

WinBUGS accepts data files in:

1. Rectangular format
   
   ```
   n[] r[]
   50 2
   ....
   20 4
   END
   ```

2. R list format:
   
   ```
   list(N =12, n = c(50,12,...), r = c(2, 1,...))
   ```

Double indexing: Specifying categorical explanatory variables

```r
y[] x[]
12 1 #subject with x=level 1
34 2 #subject with x=level 2
...
for( i in 1:N) {
   y[i] ~dnorm(mu[i], tau)
   mu[i] <- alpha + beta[x[i]]
}
alpha ~ dunif(-100,100)
beta[1] <- 0  # alias first level of beta
beta[2] ~ dunif(-100, 100)
beta[3] ~ dunif(-100, 100)
tau ~ dgamma(0.1,0.1)
```
Practical

**Exercise: Survival data**

Aitchison & Dunsmore (1975) give data on survival times (in weeks) of 20 patients after treatment for a particular carcinoma. The data set is

```r
list(survtime=c(25, 45, 238, 194, 16, 23, 30, 16,
                22, 123, 51, 412, 45, 162,
                14, 72, 5, 43, 45, 91), N=20)
```

1. Write a WinBUGS script for the following model:

   \[ y_i = \log(\text{survival}[i]) \]

   \[ y_i | \mu, \tau \sim N(\mu, \tau), \quad \tau = 1/\sigma^2 \]

   with non-informative priors for \( \mu \sim N(0, 10^{-3}) \) and \( \tau \sim \text{Gamma}(10^{-3}, 10^{-3}) \).

2. Use as initial values

   ```r
   list( mu = 0, tau = 1)
   ```

3. Draw a DAG for this model.

4. Run the model with 10,000 iterations and discard the first 5,000. Analyze visually convergence.

5. Estimate the probability that a new patient has survival time more than 150 weeks.
Solution

# WinBUGS script:
model{
  for ( i in 1:N)
  {
    y[i] <- log(survtime[i])  #data transform
    y[i] ~ dnorm(mu, tau)     #sampling model
  }
  sigma <- 1/sqrt(tau)       #standard deviation
  mu ~ dnorm(0, 1.0E-3)      #prior for mu
  tau ~ dgamma(1.0E-3, 1.0E-3) #prior for tau
  y.new ~ dnorm(mu, tau)     #predicted data
  y.dif <- step(y.new - log(150)) #pr(survival>150)
}
Multivariate Normal Distribution

Multivariate Normal for $p$-dimensional vector $y$

$$y \sim \text{Normal}_p(\mu, \Sigma)$$

The conjugate prior for $\mu$ is also a MVN. WinBUGS follows parametrization using the precision matrix $\Omega = \Sigma^{-1}$.

In BUGS notation we have

$$y[1:p] \sim \text{dmnorm}(\mu[], \Omega[,])$$
$$\mu[1:p] \sim \text{dmnorm}(\mu.prior[], \Omega.prior[])$$
$$\text{Sigma}[1:p, 1:p] \leftarrow \text{inverse}(\Omega[],)$$
Conjugate prior is the Wishart distribution, which is analogous to Gamma or $\chi^2$.

Arises in classical statistics as the distribution of the sum-of-squares and products matrix in multivariate normal sampling.

The Wishart distribution $W_p(k, R)$ for a symmetric positive definite $p \times p$ matrix $\Omega$ has density

$$p(\Omega) \propto |R|^{k/2} |\Omega|^{(k-p-1)/2} \exp\left(-\frac{1}{2} \text{tr}(R\Omega)\right),$$

defined for a real scalar $k > p - 1$ and a symmetric positive definite matrix $R$.

Some characteristics

- When $p = 1$

  $$W_1(k, R) \equiv \text{Gamma}(k/2, R/2) \equiv \frac{\chi_k^2}{R}.$$

- The expectation of the $W_p(k, R)$ is

  $$E[\Omega] = kR^{-1}.$$

- Jeffreys prior is

  $$p(\Omega) \propto |\Sigma|^{-(p+1)/2},$$

  equivalent to $k \to 0$. This is not currently implemented in WinBUGS.

- For "weakly informative" we can set $R/k$ to be a rough prior guess at the unknown true covariance matrix and taking $k = p$ indicates minimal "effective prior sample size".
Known problems

- Every element must have same precision

- Incomprehensible! It is a good idea to make some prior predictions in practice to understand what we are doing.


- If do not use Wishart priors for precision matrices in BUGS, you need to make sure that the covariance matrix at each iteration is positive-definite, otherwise may crash.

Exercise 1: Correlation Analysis with missing data

The following is an artificial data from the book Tools for Statistical Inference (Tanner pag 63.(1994)):

```r
Y [,1] [,2]
[1,] 1  1
[2,] 1 -1
[3,] -1  1
[4,] -1 -1
[5,]  2 NA
[6,]  2 NA
[7,] -2 NA
[8,] -2 NA
...```
The following script in WinBUGS implement a Bayesian analysis for this problem.

model
{
  for (i in 1 : 12){
    Y[i, 1 : 2] ~ dmnorm(mu[], tau[ , ])
  }
  mu[1] <- 0
  mu[2] <- 0
  tau[1 : 2,1 : 2] ~ dwish(R[ , ], 2)
  R[1, 1] <- 0.001
  R[1, 2] <- 0
  R[2, 1] <- 0
  R[2, 2] <- 0.001
  Sigma2[1 : 2,1 : 2] <- inverse(tau[ , ])
  rho <- Sigma2[1, 2] / sqrt(Sigma2[1, 1] * Sigma2[2, 2])
}

Using predictive posterior values in each iteration WinBUGS impute the missing values.
Multinomial model: non-conjugate analysis

In some applications the cell probabilities of contingency tables can be made function of more basic parameters.

**Example:** Population genetics example

<table>
<thead>
<tr>
<th>Maternal genotype</th>
<th>Offspring genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>AA</td>
</tr>
<tr>
<td></td>
<td>427</td>
</tr>
<tr>
<td>AB</td>
<td>108</td>
</tr>
<tr>
<td>BB</td>
<td>-</td>
</tr>
</tbody>
</table>

The model equations are given by the following table:

<table>
<thead>
<tr>
<th>Maternal genotype</th>
<th>Offspring genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>(1 - (\sigma))p + (\sigma)</td>
</tr>
<tr>
<td>AB</td>
<td>(1 - (\sigma))p/2 + (\sigma)/4</td>
</tr>
<tr>
<td>BB</td>
<td>-</td>
</tr>
</tbody>
</table>

where \(p\) is the frequency of \(A\) in outcross pollen, \(\sigma\) is the rate of self-fertilization and \(q = 1 - p\).
To implement this model in WinBUGS, we equate cell probabilites with required function:

```
model{
  XAB[1]<-(1-sigma)*p/2 +sigma/4; XAB[2]<-0.5; XAB[3]<-(1-sigma)*q/2 +sigma/4
  KAA <- sum(NAA[]); KAB <- sum(NAB[]); KBB <- sum(NBB[])

  NAA[1:3] ~ dmulti(XAA[], KAA)
  NAB[1:3] ~ dmulti(XAB[], KAB)
  NBB[1:3] ~ dmulti(XBB[], KBB)

  p ~ dunif(0, 1)      # uniform prior for p
  sigma ~ dunif(0, 1)  # uniform prior for sigma
  q <- 1 -p
}
list(NAA = c(427, 95, 0), NAB=c(108, 161, 71), NBB=c(0, 64, 74))
```

```
> print(m.popgen, digits=3)
Inference for Bugs model at "popgen.bug", fit using WinBUGS,
2 chains, each with 10000 iterations (first 5000 discarded)
n.sims = 10000 iterations saved
    mean   sd 2.5%  25% 50%  75% 97.5%   Rhat  n.eff
p   0.705 0.024 0.655 0.690 0.706 0.721 0.749    1.0   10000
sigma 0.371 0.042 0.288 0.343 0.371 0.400 0.451    1.0   10000
deviance 27.151 1.972 25.210 25.730 26.540 27.960 32.410    1.0   10000

For each parameter, n.eff is a crude measure of effective sample size,
and Rhat is the potential scale reduction factor (at convergence, Rhat=1).

DIC info (using the rule, pD = Dbar-Dhat)
pD = 2.0 and DIC = 29.1
```
Lecture 7:
Bayesian Computations with MCMC Methods
Why is computation important?

- Bayesian inference centers around the posterior distribution

\[ p(\theta | y) \propto p(y | \theta) \times p(\theta) \]

where \( \theta \) may be a vector of thousand components!

- \( p(y | \theta) \) and \( p(\theta) \) are usually available in closed form, but \( p(\theta | y) \) is usually not analytical tractable. Also, we may want to obtain
  
  \( \text{marginal posteriors} \ p(\theta_1 | y) = \int p(\theta | y) d\theta_{(-1)} \)
  
  \( \text{calculate properties of} \ p(\theta_1 | y), \text{such as mean} \ E(\theta_1 | y) = \int \theta_1 p(\theta | y) d\theta_{(-1)}, \text{tail areas, etc.} \)

- We see that numerical integration becomes crucial in Bayesian inference!
General Monte Carlo integration

If we have algorithms for sampling from arbitrary (typically high-dimensional) posterior distributions, we could use 'Monte Carlo' methods for Bayesian inference:

▶ Suppose we can draw samples from the joint posterior distribution for $\theta$, i.e.

$$\theta^{(1)}, \theta^{(2)}, \ldots, \theta^{(N)} \sim p(\theta|y)$$

▶ Then Monte Carlo integration

$$E(g(\theta)) = \int g(\theta)p(\theta|y)d\theta \approx \frac{1}{N} \sum_{i=1}^{N} g(\theta^{(i)})$$

▶ Theorems exist which prove convergence even if the sample is dependent, i.e.

$$\frac{1}{N} \sum_{i=1}^{N} g(\theta^{(i)}) \rightarrow E(g(\theta)) \quad \text{as} \quad n \rightarrow \infty$$

Markov Chain Monte Carlo (MCMC)

▶ **Independent sampling** from $p(\theta|y)$ may be very difficult in high dimensions

▶ Alternative strategy based on **dependent sampling**:

▶ We know $p(\theta|y)$ up to a normalizing constant

▶ Then, we design a **Markov chain** which has $p(\theta|y)$ as its stationary distribution

▶ A sequence of random variables $\theta^{(0)}, \theta^{(1)}, \theta^{(3)}, \ldots$ forms a Markov chain if

$$\theta^{(i+1)} \sim p(\theta|\theta^{(i)})$$

i.e. conditional on the value of $\theta^{(i)}$, $\theta^{(i+1)}$ is independent of $\theta^{(i-1)}, \ldots, \theta^{(0)}$. 

Dr. Pablo E. Verde
Run the chain until it appears to have settled down to equilibrium, say

\[ \theta^{(k)}, \theta^{(k+1)}, \ldots, \theta^{(K)} \sim p(\theta | y) \]

Use these sampling values to empirically estimate the posterior of \( \theta \), say,

\[ \hat{p}(\theta | y) \]

**Problem:** Design a Markov chain with \( p(\theta | y) \) as its unique stationary distribution?

**Answer:** This is surprisingly easy and several standard recipes are available

- Metropolis *et al.* (1953) showed how to do it
- Hastings (1970) generalized Metropolis algorithm
- Geman and Geman (1984) introduced the Gibbs Sampling algorithm
- Gelfand and Smith (1990) popularized Gibbs sampling in statistics
- See Gilks, Richardson and Spiegelhalter (1996) for a gentle introduction and many worked examples.
- Robert and Casella (2004) for more detailed theoretical reference
The Gibbs sampler

Let our vector of unknowns $\theta$ consist of $k$ sub-components $\theta = (\theta_1, \ldots, \theta_k)$

1. Choose starting values $\theta_1^0, \ldots, \theta_k^0$

2. Sample from

$$
\theta_1^{(1)} \sim p(\theta_1^{(0)} | \theta_2^0, \ldots, \theta_k^0, y) \\
\theta_2^{(1)} \sim p(\theta_2^{(1)} | \theta_1^{(1)}, \theta_3^0, \ldots, \theta_k^0, y) \\
\vdots \\
\theta_k^{(1)} \sim p(\theta_k^{(1)} | \theta_1^{(1)}, \theta_2^{(1)}, \ldots, \theta_{k-1}^{(1)}, y)
$$

3. Repeat step 2 many 1000s of times. Eventually we obtain samples from $p(\theta | y)$

Example: Normal distribution with unknown mean and variance

- Suppose that the observations $y_1, \ldots, y_n \sim N(\mu, \tau^{-1})$

- We assume that $y_i$ are conditionally independent given $\theta$ and precision $\tau$, and $\theta$ and $\tau$ are themselves independent.

- We put conjugate priors on $\mu$ and $\tau$:

$$
\mu \sim N(\theta_0, \phi_0^{-1}), \quad \tau \sim \text{Gamma}(a, b)
$$

- Then the full conditionals for $\mu$ and $\tau$ are:

$$
p(\mu | \tau, y) = N\left(\frac{\mu_0\phi_0 + n\bar{y}\tau}{\phi_0 + n\tau}, \frac{1}{\phi_0 + n\tau}\right)
$$

$$
p(\tau | \mu, y) = \text{Gamma}\left(\frac{n}{2}, b + \frac{1}{2} \sum (y_i - \mu)^2\right)
$$
Programming the Gibbs sampler in R

**Example:** Normal distribution with unknown mean and variance

```r
gibbsNormal <- function(y, mu1, tau1, N, mu0, phi0, a, b) {
  mu <- numeric(N+1) # N = number of iterations
  mu[1] <- mu1 # the initial value for mu
  tau <- numeric(N+1)
  tau[1] <- tau1 # the initial value for tau
  n <- length(y); ybar <- mean(y)
  for(i in 2:(N+1)) { # generate samples from full conditional
    mu[i] <- rnorm(1, (mu0*phi0 + n*ybar*tau[i-1])/(phi0 + n*tau[i-1]),
                   1/sqrt(phi0 + n*tau[i-1]))
    tau[i] <- rgamma(1, (n+2*a)/2, (sum((y-mu[i])^2) + 2*b)/2)
  }
  output <- cbind(mu, tau)
}
```

Four independent sequences of the Gibbs sampler for a normal distribution with unknown mean and variance.

Left panel: first 10 steps. Right panel: last 500 iterations in each chain.
Traces of one sequence of Gibbs simulations. Upper panels: 500 iterations from the posterior of $\mu$. Lower panels: 500 iterations from the posterior of $\tau$.

General properties of a MCMC algorithm

- **Reversibility:**
  - The key property is *reversibility* or *detailed balance*, i.e., a balance in the flow of transition probabilities between the states of the Markov chain
  - A Markov chain which is reversible has **stationary distribution**
  - Thus we build a kernel or transition matrix $P$ such that it ensures reversibility
    $$p(x)P(y|x) = p(y)P(x|y)$$
    where $P(y|x)$ represents the flow of probability $x \to y$
Lecture 7 - MCMC-Short-version

- **Irreducibility:**
  - An irreducible chain is one in which for any point \( \theta^{(k)} \) in the parameter space, it is possible to move from \( \theta^{(k)} \) to other point \( \theta^{(l)} \) in a finite number of steps.
  - This guarantees the chain can visit all possible values of \( \theta \) irrespective of the starting value \( \theta^{(0)} \).

- **Aperiodicity:**
  - A chain is aperiodic if does not exhibit periodic behavior.
  - If \( R_1, R_2, \ldots, R_k \) are disjoint regions in parameter space the chain does not cycle around them.

To sample from \( p(\theta|y) \) we construct a Markov chain with transition matrix \( P \) which satisfies **reversibility**, **irreducibility** and **aperiodicity**.

**Metropolis algorithm**

The algorithm proceeds as follows:

- Start with a preliminary guess, say \( \theta^0 \).
- At iteration \( t \) sample a proposal \( \theta^t \sim P(\theta^t|\theta^{t-1}) \).
- The jumping distribution must be symmetric, satisfying the condition \( P(\theta_a|\theta_b) = P(\theta_b|\theta_a) \) for all \( \theta_a \) and \( \theta_b \).
- If \( p(\theta^t|y) > p(\theta^{t-1}|y) \) then accept \( \theta^t \)
- If not, flip a coin with probability \( r = \frac{p(\theta^t|y)}{p(\theta^{t-1}|y)} \), if it comes up heads, accept \( \theta^t \).
- If the coin toss comes up tails, stay at \( \theta^{t-1} \)

The algorithm continues, until we sample from \( p(\theta|y) \). The coin tosses allow it to go to less plausible \( \theta^t \)'s, and keep it from getting stuck in local maxima.
Some samplers for the Metropolis algorithm

The following are commonly implemented samplers for the proposal distribution \( P(\theta^t|\theta^{t-1}) \)

- Random walk sampler, observations are generated by \( \theta_t = \theta_{t-1} + z_t \) with \( z_t \sim f \). There are many common choices for \( f \), including the uniform in the unit disc, a multivariate normal or a t - distribution.

- The independent sampler, the candidate observation is sample independently from the current state of the chain.

- The Gibbs sampler. The Gibbs transition can be regarded as a special case of a Metropolis transition.

- The STAN software implements samplers based on Hamiltonian dynamics.

Metropolis in R

- The package MCMCpack implements Metropolis for a large number of statistical models.

- The current implementation uses a random walk Metropolis with proposal density multivariate Normals.

- The proposal density is centered at the current \( \theta^{(t)} \) with variance-covariance matrix given by the user or automatically calculated proportional to the Hessian of the posterior evaluated at its mode.
**Example:** an interesting bivariate distribution

- It is well know that the pair of *marginal distributions doest not uniquely determine a bivariate distribution*. For example, a bivariate distribution with normal marginal distributions need not be jointly normal (Feller 1966, p. 69)

- In contrast, *the conditional distribution functions uniquely determine a joint density* function (Arnold and Press 1989).

- A natural question arises: Must a bivariate distribution with normal conditionals be jointly normal?

The answer is NO!

Gelman and Meng (1991) introduced an interesting distribution, where the join distribution is non-normal:

\[ f(x, y) \propto \exp \left( -\frac{1}{2} \left[ Ax^2 y^2 + x^2 + y^2 - 2Bxy - 2C_1 - 2C_2y \right] \right). \]

But it has conditional distributions which are normals:

\[ x|y \sim N(\frac{By + C_1}{Ay^2 + 1}, \frac{1}{Ay^2 + 1}), \quad y|x \sim N(\frac{Bx + C_1}{Ax^2 + 1}, \frac{1}{Ax^2 + 1}). \]

**The question is how to sample form** \( f(x, y) \)?
Here we show an example where the parameters are $A = 1$, $B = 0$, $C_1 = 3$ and $C_2 = 3$. 

Gelman–Meng distribution $A=1$, $B=0$, $C_1=3$ and $C_2=3$
We implement a Metropolis sampling algorithm based on a random walk and bivariate normals as proposals.

```r
## Gelman and Meng (1991) kernel function:
f.g.m <- function(xy, A = 1, B = 0, C1 = 3, C2 = 3)
  { x <- xy[1]; y <- xy[2]
    r <- -.5 * (A * x^2 + y^2 + x^2 + y^2
              - 2 * B * x * y - 2 * C1 * x - 2 * C2 * y)
    as.vector(r) }

## Metropolis sampling with MCMCpack
res <- MCMCmetrop1R(f.g.m, theta.init=c(0, 1), mcmc=10000, burnin=5000,
                     logfun=FALSE)
```

The Metropolis acceptance rate was 0.47580
Performance of MCMC methods

There are three main issues to consider

▶ Convergence: How quickly does the distribution of $\theta^{(t)}$ approach $p(\theta|x)$?

▶ Efficiency: How well are functionals of $p(\theta|x)$ estimated from $\theta^{(t)}$?

▶ Simplicity: How convenient is the method to use?

In general computer effort should be measured in seconds, not iterations!
Checking convergence

- Convergence is to target distribution and not to a single value

- Once convergence is reached, samples should look like a random scatter about a stable mean value.

- One approach is to run many long chains with widely differing starting values.

- Plot traces of the simulated chain

- Plot ACF, etc.

Lecture 8: Bayesian Regression Models
Modeling Examples

- Multiple linear regression: model diagnostics and variable selection
- ANOVA models: an alternative to multiple testing
- Logistic regression: combining multiple information in Risk analysis

Introduction

Standard (and non standard) regression models can be easily formulated within a Bayesian framework.

- Specify probability distribution for the data
- Specify form of relationship between response and explanatory variables
- Specify prior distribution for regression coefficients and any other unknown (nuisance) parameters
Some advantages of a Bayesian formulation in regression modeling include:

- Easy to include parameter restrictions and other relevant prior knowledge
- It is simple to extended to non-linear regression
- We can easily robustified a model
- Easy to make inference about functions of regression parameters and/or predictions
- We can handle missing data and covariate measurement error
- Transparent variable selection by prior modeling regression coefficients

**Example:** Stack loss data, WinBUGS Volume 1

In this example, we illustrate a more complete regression analysis including outlier checking, model adequacy and variable selection methods.

This is a very often analyzed data of Brownlee (1965, p. 454).

- 21 daily responses of stack loss, $y_i$ the amount of ammonia escaping from industrial chimneys
- Covariates: air flow $x_1$, temperature $x_2$ and acid concentration $x_3$
- Transformed covariates: $z_{k,i} = (x_{k,i} - \bar{x}_k)/sd(x_k)$ for $k = 1, 2, 3$. 

Linear regression
Model 1 specification:

\[
\begin{align*}
  y_i & \sim \text{Normal}(\mu_i, \tau) \quad i = 1, \ldots, 21 \\
  \tau & = 1/\sigma^2 \\
  \mu_i & = \beta_0 + \beta_1 z_{1,i} + \beta_2 z_{2,i} + \beta_3 z_{3,i} \\
  \sigma & \sim \text{Uniform}(0.01, 100) \\
  \beta_k & \sim \text{Normal}(0, 0.001), \quad k = 0, \ldots, 3.
\end{align*}
\]
In these model we also calculate some diagnostic quantities:

By analogy to the classical regression analysis we calculate the \textit{standardized residuals} as

\[ d_i = \frac{y_i - E(y_i|z)}{\sqrt{\text{Var}(y_i|z)}}. \]

In a Bayesian setting these residuals have posterior distributions as well. They can be used similarly to residual analysis in classical statistics.

We specify the model in WinBUGS as:

\begin{verbatim}
model{
    # Model 1
    for (i in 1 : N) {
        y[i] ~ dnorm(mu[i], tau)
                beta[3] * z[i, 3]
        stres[i] <- (y[i] - mu[i]) / sigma
    }
    # Priors
    beta0 ~ dnorm(0, 0.001)
    for (j in 1 : p) {
        beta[j] ~ dnorm(0, 0.001) } # coefficients independent
    tau <- 1/(sigma*sigma)
    sigma ~ dunif(0.01, 100) # Gelman’s prior
}
\end{verbatim}
We run the model in WinBUGS, we look at the possible outliers.

As an alternative model we replace the Normal likelihood by a t-distribution with $\nu = 4$ degrees of freedom. The idea is to have a more robust model against outliers in the $y$'s.

**Model 2:**

\[
\begin{align*}
y_i & \sim t(\mu_i, \tau, \nu) \quad i = 1, \ldots, 21 \\
\tau & = 1/\sigma^2 \\
\mu_i & = \beta_0 + \beta_1 z_{1,i} + \beta_2 z_{2,i} + \beta_3 z_{3,i} \\
\sigma & \sim \text{Uniform}(0.01, 100) \\
\beta_k & \sim \text{Normal}(0, 0.001), \quad k = 0, \ldots, 3.
\end{align*}
\]
In the WinBUGS code we modify the model section by commenting out the normal model and adding one line with the model based on the t-distribution and we run the MCMC again.

\[
#y[i] \sim \text{dnorm}(\mu[i], \tau) \\
y[i] \sim \text{dt}(\mu[i], \tau, 4)
\]

#DIC Normal
\[
\begin{array}{cccc}
Dbar & Dhat & pD & DIC \\
Y & 110.537 & 105.800 & 4.736 & 115.273 \\
total & 110.537 & 105.800 & 4.736 & 115.273
\end{array}
\]

#DIC t
\[
\begin{array}{cccc}
Dbar & Dhat & pD & DIC \\
Y & 109.043 & 104.103 & 4.940 & 113.983 \\
total & 109.043 & 104.103 & 4.940 & 113.983
\end{array}
\]

A very modest difference between the two models.

Variable Selection

We modify the structure of the distribution of the regression coefficients by adding a common distribution with unknown variance. This is called a ridge regression model, where the \( \beta \)'s are assumed exchangeable.

Model 3 specification:

\[
\begin{align*}
y_i & \sim \text{Normal}(\mu_i, \tau), \quad \tau = 1/\sigma^2, \quad i = 1, \ldots, 21 \\
\mu_i & = \beta_0 + \beta_1 z_{1,i} + \beta_2 z_{2,i} + \beta_3 z_{3,i} \\
\sigma & \sim \text{Uniform}(0.01, 100) \\
\beta_k & \sim \text{Normal}(0, \phi), \quad \phi = 1/\sigma_\beta^2 \quad k = 0, \ldots, 3 \\
\sigma_\beta & \sim \text{Uniform}(0.01, 100).
\end{align*}
\]
In WinBUGS

for (j in 1 : p) {
    # beta[j] ~ dnorm(0, 0.001)    # coefs independent
    beta[j] ~ dnorm(0, phi)       # coefs exchangeable (ridge regression)
}

phi <- 1/(sigmaB*sigmaB)
sigmaB ~ dunif(0.01, 100)     #Gelman’s prior
We see that $\beta_3$ is not a relevant variable in the model. Now, we try another variable selection procedure, by modifying the distribution of the regression coefficients.

**Model 5** specification:

$$
\begin{align*}
\gamma_i & \sim \text{Normal}(\mu_i, \sigma^2) \quad i = 1, \ldots, 21 \\
\mu_i & = \beta_0 + \beta_1 \pi_1 z_{1,i} + \beta_2 \pi_2 z_{2,i} + \beta_3 \pi_3 z_{3,i} \\
\sigma & \sim \text{Uniform}(0.01, 100) \\
\beta_k & \sim \text{Normal}(0, 100), \quad k = 0, \ldots, 3, \\
\pi_1 & \sim \text{Bernoulli}(0.5) \\
\pi_2 & \sim \text{Bernoulli}(0.5) \\
\pi_3 & \sim \text{Bernoulli}(0.5).
\end{align*}
$$

In WinBUGS we change the equation of $\mu_i$:

```r
#mean equation model

#priors
for (j in 1 : p) {
  beta[j] ~ dnorm(0, 0.001)
  pi[j] ~ dbern(0.5)
}
```

We run the model for 40,000 iterations and we discard the first 20,000. Results are:

- $\pi[1] = 0.9987 \pm 0.0367$ $\leftarrow$ X1 very important
- $\pi[2] = 0.8361 \pm 0.3702$ $\leftarrow$ X2 non meaningful
- $\pi[3] = 0.0425 \pm 0.2018$ $\leftarrow$ X1 definitively no important
Example: Speed of light measurements by Michelson

This is a classical data set available in R and corresponds to Measurements of the speed of light in air, made between 5th June and 2nd July, 1879. The data consists of five experiments, each consisting of 20 consecutive runs. The response is the speed of light in km/s, less 299000. The currently accepted value, on this scale of measurement, is 734.5.

We start by comparing the 5 experiments with boxplots:

```r
> library(MASS)
> data(michelson)
> attach(michelson)
> plot(Expt, Speed, main="Speed of Light Data",
        xlab="Experiment No.",ylab="Speed")
```
ANOVA model: Bayesian analysis in WinBUGS

The Bayesian approach to the ANOVA model is similar to the regression model, with mean equation according to the mean groups parametrization. So if we have $n_j$ observations in $J$ groups with $n = \sum_{j=1}^{J} n_j$.

Model 1

$$y_{i,j} \sim \text{Normal}(\mu_j, \tau), \quad \tau = 1/\sigma^2 \quad i = 1, \ldots, n_j,$$

$$\mu_j = \mu + \alpha_j, \quad j = 1, \ldots, J,$$

$$\alpha_j \sim \text{Normal}(0, 0.001), \quad j = 2, \ldots, J,$$

$$\mu \sim \text{Normal}(0, 0.001),$$

$$\sigma \sim \text{Uniform}(0.01, 100).$$
The WinBUGS implementation of Model 1 is:

```r
model{
  for(i in 1:n){
    y[i] ~ dnorm( mu[i], tau)
    mu[i] <- mu0 + alpha[ a[i] ]
  }

  # Corner constrains parametrization
  # alpha[1] <- 0
  # Sum to zero parametrization

  # group means:
  for( i in 1:J){
    m.g[i] <- mu0 + alpha[i]}

  # mean differences:
  d[1] <- (m.g[2] - m.g[1] )
  d[2]<- (m.g[3] - m.g[1] )
  ...
  # Priors
  mu0 ~ dnorm(0, 0.0001)
  for( j in 2:J){
    alpha[j] ~ dnorm(0, 0.0001)
  }
  tau <- 1/(sigma*sigma)
  sigma ~ dunif(0.01, 100) #Gelman’s prior
}
```
One serious problem of ANOVA modeling is the lack of variance homogeneity between groups. We can extend our Bayesian set up to include this data feature as follows:

**Model 2**

\[ y_{i,j} \sim \text{Normal}(\mu_j, \tau_j), \quad \tau_j = 1/\sigma^2_j \quad i = 1, \ldots, n_j, \]

\[ \mu_j = \mu + \alpha_j, \quad j = 1, \ldots, J, \]

\[ \alpha_j \sim \text{Normal}(0, 0.001), \quad j = 2, \ldots, J, \]

\[ \mu \sim \text{Normal}(0, 0.001), \]

\[ \sigma_j \sim \text{Uniform}(0.01, 100), \quad j = 1, \ldots, J. \]

This model includes a structural dispersion sub-model for each treatment group.

The WinBUGS implementation of Model 2 change to:

```r
{  
  for(i in 1:n){
  #y[i] ~ dnorm( mu[i], tau)
    y[i] ~ dnorm( mu[i], tau[i])
  
    mu[i] <- mu0 + alpha[ a[i] ]
    tau[i] <- gamma[ a[i] ]
  }
  # Priors for groups dispersion model
  for( j in 1:J){
      gamma[j] ~ dgamma(0.001, 0.001)
      sigma2[j] <- 1/ gamma[j]
      sigma[j] <- pow(sigma2[j], 0.5)
  }
}
```
For models with more than 3 groups the estimation based on simple means can be improved by adding exchangeability structure to the $\alpha_i$’s (Stein, 1956, Lindley 1962, Casella and Berger, pag.574). This assumed a sub-model for $\alpha_i$ in the following way:

**Model 3**

\[
y_{i,j} \sim \text{Normal}(\mu_j, \tau_j), \quad \tau_j = 1/\sigma_j^2 \quad i = 1, \ldots, n_j,
\]
\[
\mu_j = \mu + \alpha_j, \quad j = 1, \ldots, J,
\]
\[
\alpha_j \sim \text{Normal}(0, \phi), \quad \phi = 1/\sigma_\alpha \quad j = 2, \ldots, J,
\]
\[
\mu \sim \text{Normal}(0, 0.001),
\]
\[
\phi \sim \text{Uniform}(0.01, 100), \quad j = 1, \ldots, J,
\]
\[
\sigma_j \sim \text{Uniform}(0.01, 100), \quad j = 1, \ldots, J.
\]

The WinBUGS implementation of Model 3 change to:

```r
# Priors
mu0 ~ dnorm(0, 0.0001)
for( j in 2:J){
  alpha[j] ~ dnorm(0, xi)
}
xi <- 1/(sigma.alpha*sigma.alpha)
sigma.alpha ~ dunif(0.01, 100) #Gelman’s prior
```
One alternative to exchangeability between $\alpha_i$’s is to use a mixture model to investigate the structure of the data, for example:

**Model 4**

\[
\begin{align*}
  y_{i,j} & \sim \text{Normal}(\mu_j, \tau_j), \quad \tau_j = 1/\sigma_j^2 \quad i = 1, \ldots, n_j, \\
  \mu_j & = \mu + \alpha_j \pi_j, \quad j = 1, \ldots, J, \\
  \alpha_j & \sim \text{Normal}(0, 0.001), \quad j = 2, \ldots, J, \\
  \mu & \sim \text{Normal}(0, 0.001), \\
  \pi_j & \sim \text{Bernoulli}(0.5), \quad j = 2, \ldots, J, \\
  \sigma_j & \sim \text{Uniform}(0.01, 100), \quad j = 1, \ldots, J.
\end{align*}
\]

The WinBUGS implementation of Model 3 change to:

```r
# group means mixture model:
for( i in 1:J){
  m.g[i] <- mu0 + alpha[i]*pi[i]
  pi[i] ~ dbern(0.5)
}
```

The next slides present some graphical results of the main features of each model. The full WinBUGS script for this analysis is `anova.odc`, this includes some other calculations for residual analysis as well.
ANOVA: classical model

Posterior distributions for mean groups $\mu_j$, Model 1.

Posterior distributions for mean differences between all groups $\mu_k - \mu_l$ ($k \neq l$), Model 1
Posterior distributions for $\sigma_j$, Model 2.

Posterior distributions for mean differences between all groups $\mu_k - \mu_l \ (k \neq l)$, Model 2
ANOVA: exchangeability model

Posterior distributions for mean differences between all groups with exchangeability, Model 3.

Dr. Pablo E. Verde

ANOVA: Mixture models

Posterior distributions for the group means with mixture distributions, Model 4.

Dr. Pablo E. Verde
Logistic regression: combining multiple information in Risk analysis

**Example: The Challenger O-Ring Data: A Bayesian Risk Analysis**

**Historical background**

- The Space Shuttle Challenger’s final mission was on January 28th 1986, on an unusually cold morning (31F/-0.5C)
- It disintegrated 73 seconds into its flight after an **O-ring** seal in its right solid rocket booster failed
- The uncontrolled flame caused structural failure of the external tank, and the resulting aerodynamic forces broke up the orbiter
- All seven members of the crew were killed

**Technical background**
The Challenger’s O-Ring Thermal-Distress Data

**Example:** Regression modelling with change point

- On the night of January 27, 1986, the night before the space shuttle Challenger accident, there was a three-hour teleconference among people at Marton Thiokol (manufacturer of the solid rocket motor), Marshal Space Center and Kennedy Space Center.

- The discussion focused on the forecast of a 31 F temperature for lunch time the next morning, and the effect of low temperature on O-ring performance.

- The available data of previous shuttle flights consisted on occurrence of thermal distress (yes, no) and temperature at launch time. Let’s take a look at these data and fit a logistic regression in R:

```r
> # distress yes=1, no =0
> y = c(1,1,1, 1,0,0,0, 0,0,0,0, 0,1,1,0,
> 0,0,1,0, 0,0,0,0)
> # temperature at launch time
> x = c(53,57,58, 63,66, 67,67, 67,68, 69,70,
> 70,70, 70,72, 73,75, 75,76, 76,78, 79,81)
> # number of previous flights
> N = 23
> summary(f.b1 <- glm(y ~ x, family=binomial))
> ...
> AIC: 24.315
```

```r
> summary(f.b2 <- update(f.b1, family=binomial(link=cloglog)))
> ...
> AIC: 23.531
```
These data have been analyzed several times in the literature. I found that fitting a change point model makes an improvement on previous published analysis. The model is:

\[
\Pr(y_i = 1) = \logit^{-1}(\beta_0 + \beta_1 z_i)
\]

where

\[
z_i = \begin{cases} 
1 & \text{for } x_i \geq K, \\
0 & \text{otherwise}.
\end{cases}
\]

In this model \(K\) is unknown and represents the temperature from which the probability of distress is the lowest.

The parameter \(\beta_1\) represents the reduction of risk under temperatures greater than \(K\).
This model is implemented in WinBUGS as following:

```r
model {
  for(i in 1 : N) {
    y[i] ~ dbern(p[i])
    logit(p[i]) <- beta0 + beta1 * z[i] 
  }

  for(i in 1:N){z[i] <- step(x[i] - K) } # step = 0 until K

  #priors
  K ~ dunif(53, 81)
  beta0 ~ dnorm(0.0, 0.01)
  beta1 ~ dnorm(0.0, 0.01)
}
```

We run the model with R2WinBUGS:

```r
data.b <- c("x", "y", "N")
par.b <- c("beta0", "beta1", "K")

> chall.1 <- bugs(data.b, inits=NULL, par.b, "challenger-1.txt",
  n.chains=1, n.iter=20000, n.thin=1, bugs.directory = bugsdir,
  working.directory = getwd(), clearWD=TRUE, debug=TRUE)

> print(chall.1)

      mean    sd  2.5%  25%  50%  75% 97.5%
beta0   6.2  3.9  -0.2  3.3  5.8  8.4 15.3
beta1  -8.0  3.9 -17.2 -10.2 -7.6  5.1 -2.1
   K    63.8  2.9  58.2  63.1 64.1 65.1 67.0
deviance 19.1  2.8  16.6  16.9 18.0 20.4 26.9

pD = 2.4 and DIC = 21.5
```
Example: Probabilistic Risk Assessment

- **Event a**: It erodes
- **Event b**: It suffers blow-by | a
- **Event c**: It erodes | a, b
- **Event d**: It suffers blow-by | a, b, c
A catastrophic failure of a field joint is expected when all four events occur during the operation of the solid rocket boosters:

\[ P_{\text{field}} = p_a \times p_b \times p_c \times p_d \]

Since there are 6 field joints per launch, assuming the all 6 joint failures are independent, the probability of at least one failure is

\[ \text{Risk} = 1 - (1 - P_{\text{field}})^6 \]

\( p_a \) is calculated from the logistic regression model as:

\[ p_a = \Pr(\text{O-Ring Thermal-Distress at 31F}) \]

The available data for the other events was very sparse:

- Event b: 2 in 7 flights
- Event c: 1 in 2 flights
- Event d: 0 in 1 flight

We model the probabilities of events b, c and d with a beta-binomial model with uninformative priors Beta(0.5, 0.5).

In WinBUGS we modify the model file "challenger-1.txt" by adding these risk calculations. We add, also, the calculation of risk at temperature \( K \) or greater. To run the model in R by adding the date of events b, c, and d:

```r
# Risk analysis
y.b <- 2; y.c <- 1; y.d <- 0
data.r <- c("x", "y", "N", "y.b", "y.c", "y.d")
par.r <- c("beta0", "beta1", "K", "p.cat", "p.catK")
chall.2<- bugs(data.r, inits=NULL, par.r, "challenger-1.txt", n.chains = 1, ...)
> print(chall.2, 3)
    mean  sd   2.5%   25%   50%   75%  97.5%
K   63.726 2.653 58.190 63.090 64.120 65.120 66.010
p.cat 0.173 0.204 0.000 0.019 0.088 0.258 0.736
p.catK 0.038 0.061 0.000 0.014 0.047 0.213
```

...
Summary results of our analysis:

- The risk of a catastrophic failure with launching temperature of 31 F is 17%
- The risk of a catastrophic failure with temperatures greater than 63 F is 3.8%
- The odds ratio of the risk between these temperatures is 9.8

One interesting historical note:

The Roger Commission, appointed by president Reagan to investigate the causes of the accident, pointed out:

... a mistake in the analysis of the thermal distress data was that the flights with zero incidents were left off because it was felt that these flights did not contribute any information about the temperature effect. (p. 145)

Practical Exercise: a nonconjugate nonlinear model

Volume 2 in WinBUGS help: Dugongs

Originally, Carlin and Gelfand (1991) consider data on length $y_i$ and age $x_i$ measurements for 27 dugongs (sea cows) and use the following nonlinear growth curve with no inflection point and an asymptote as $x_i$ tends to infinity:

$$y_i \sim \text{Normal}(\mu_i, \sigma^2)$$

$$\mu_i = \alpha - \beta \gamma^{x_i},$$

where $\alpha, \beta > 0$ and $\gamma \in (0, 1)$. 
Practical

▷ Open the file in WinBUGS and run the model

▷ Change the last observation 2.57 to 2.17 and run the model. Did you see different results?

▷ Modify the WinBUGS code as:

```r
# y[i] ~ dnorm(mu[i], tau)
# y[i] ~ dt(mu[i], tau, df) # fit robust t distribution
...
df <- 5
```

▷ Run the model with this change and compare results
Learning from the information of the others ...

- During the previous lectures we have seen several examples, where we performed a single statistical analysis.

- Now, suppose that instead of having a single analysis, you have several ones. Each one giving independent results from each other.

One might ask:

**Should we combine these independent results in a single global analysis?**

The general answer is:

**YES!!**

- Hierarchical models give us the statistical framework to combine multiple sources of information in a single analysis.

- Informally, by combining several individual results, each individual analysis is improve by the information we have from the others. This information is summarized in an *Empirical Prior distribution*.

- From the classical point of view, Charles Stein demonstrated in the 50s a fundamental theoretical result, which shows the benefit of combining individual results in a single analysis.

  *Charles Stein (22nd of March 1920) ... and he still working everyday!*
Hierarchical Models

It becomes common practice to construct statistical models which reflects the underline complexity of the problem under study. Such us different patterns of heterogeneity, dependence, miss-measurements, missing data, etc.

Statistical models which reflect complexity of the data involve multiple parameters. Examples are:

- "Study effect" in meta-analysis
- "Subject effect" in growth curves models
- "Identification of hidden process" in sequence of observations
- "Relative risks of disease outcome in different areas/time periods
- "Frailty effects" in correlated survival data
- ...

Statistical Inference for Multiple Parameters

How to make inference on multiple parameters \{\theta_1, \ldots, \theta_N\} measured in \(N\) units (person, centers, areas, ...) which are related or connected by the structure of the problem?

We can identify three different scenarios

1. **Identical parameters**: All the \(\theta\)'s are identical, i.e. all the data can be pooled and the individual units ignored.

2. **Independent parameters**: All the \(\theta\)'s are entirely unrelated, i.e. the results from each unit can be analyzed independently.

3. **Exchangeable parameters**: The \(\theta\)'s are assumed to be 'similar' in the sense that the "labels" convey no information.
Exchangeability

- The assumption of exchangeable units is mathematically equivalent to assuming that the $\theta$’s are drawn at random from some population distribution.

- "Exchangeability" express formally the idea that we find no systematic reason to distinguish the individual random variables $X_1, \ldots, X_n$.

- We assume that $X_1, \ldots, X_n$ are exchangeable if the probability that we assign to any set of potential outcomes, $p(x_1, \ldots, x_n)$, is unaffected by permutations of the labels attached to the variables.

Example:

Suppose that $X_1, X_2, X_3$ are the outcomes of the three patients enrolled in a clinical trial. Were $X_i = 1$ indicates positive reaction to a treatment and $X_i = 0$ no reaction.

We may judge

$p(X_1 = 1, X_2 = 0, X_3 = 1) = p(X_2 = 1, X_1 = 0, X_3 = 1) = p(X_1 = 1, X_3 = 0, X_2 = 1)$

- i.e. the probability of getting 2 positive outcomes is NOT affected by the particular patient on which the positive outcome comes.

- Note that this is a very strong assumption. In reality we may expect that patients may behave in different way. For example they may fail to comply a treatment.

- Note that "exchangeability" does not mean we believe that $X_1, X_2, \ldots X_n$ are independent!
Exchangeability and Hierarchical Models

Suppose $y_{ij}$ is outcome for individual $j$, unit $i$, with unit-specific parameter $\theta_i$

- Assumption of partial exchangeability of individuals within units is represented by

$$y_{ij} \sim p(y_{ij} | \theta_i)$$

$$\theta_i \sim p(\theta_i | \phi)$$

- Assumption of exchangeability of units can be represented by

$$\theta_i \sim p(\theta_i | \phi)$$

$$\phi \sim p(\phi)$$

where, $p(\phi)$ can be considered as a common prior for all units, but with unknown parameters.

- Assuming that $\theta_1, \ldots, \theta_N$ are drawn from some common prior distribution whose parameters are unknown is known as a hierarchical or multilevel model.

- Bayesian statistical inference is based on:

$$p(\theta_1, \ldots, \theta_N, \phi | y) \propto p(\phi) p(\theta_1, \ldots, \theta_N | \phi) p(y | \theta_1, \ldots, \theta_N, \phi)$$

- The dimension of $(\theta_1, \ldots, \theta_N)$ could be very large in practice.

- Empirical Bayes techniques omit $p(\phi)$. They are useful in practice, but they may biased variability estimates be reusing $y$ to estimate $\phi$. 
Exchangeability some further comments

- Note that there does not need to be any actual sampling - perhaps these $N$ units are the only ones that exists - this is very common in meta-analysis.

- The probability structure is a consequence of the belief in exchangeability rather than a physical randomization mechanism.

- We emphasis that an assumption of exchangeability is a judgement based on our knowledge of the context.

Hierarchical models and shrinkage

Suppose in each unit we observe a response $y_i$ assumed to have a Normal likelihood

$$ y_i \sim N(\theta_i, s_i^2) $$

Unit means $\theta_i$ are assumed to be exchangeable, and to have a Normal distribution

$$ \theta_i \sim N(\mu, \sigma^2) $$

where $\mu$ and $\sigma^2$ are "hyper-parameters" for the moment assumed known.

After observing $y_i$, Bayes theorem gives

$$ \theta_i | y_i \sim N(w_i \mu + (1 - w_i) y_i, (1 - w_i) s_i^2) $$

where $w_i = s_i^2 / (s_i^2 + \sigma^2)$ is the weight given to the prior mean.
Hierarchical models and shrinkage

- An exchangeable model therefore leads to the inferences for each unit having narrowed intervals that if they are assumed independent, but shrunk towards the prior mean response.

- $w_i$ controls the "shrinkage" of the estimate towards $\mu$, and the reduction in the width of the interval for $\theta_i$.

- Shrinkage ($w_i$) depends on precision of the individual unit $i$ relative to the variability between units.

---

Example: Toxoplasmosis data

- These data present the relation between rainfall and the proportions of people with toxoplasmosis for 34 cities in El Salvador (Efron 1986).

- The question is how to combine results of 34 different cities in a single model?

- The data have been used to illustrate non-linear relationship between the amount of rain and toxoplasmosis prevalence.

- We illustrate a series of hierarchical models.

...we take some preliminary visualization.
Pooled approach:

To start we ignore possible (complex) relation between rainfall and proportion and we fit same beta-binomial model to all the cities

\[
\prod_{i=1}^{34} p(r_i | \pi, n_i) = \prod_{i=1}^{34} \text{Binomial}(n_i, \pi) \\
p(\pi) = \text{Beta}(a, b) \\
p(\pi | r, n) \propto \prod_{i=1}^{34} p(r_i | \pi, n_i)p(\pi) \\
= \text{Beta} \left( a + \sum_i r_i, b + \sum_i (n_i - r_i) \right)
\]

Some comments:

▶ Now, is it reasonable to assume **common probability** \( \pi \) of Toxoplasmosis for each city?

▶ The beta-binomial model assumes that each outcome is independent and identically distributed according to the binomial probability distribution with parameter \( \pi \)

▶ Does this model adequately describe the random variation in outcomes for each city?

▶ Are the cities rates more variable that our model assumes?

**Question:** How to model the excess of variation in the data?
Modeling the excess of variation

**Model 1:**

Combining information with a Generalized Linear Mixed Model (GLMM)

\[ r_i \sim \text{Binomial}(n_i, \pi_i) \]
\[ \text{logit}(\pi_i) \sim N(\mu, \sigma^2) \]
\[ \mu \sim N(0, 100) \]
\[ \sigma \sim \text{Uniform}(0.01, 10) \]

This model combines information between cities in a single model.

**Model 2:**

Modeling each city rate independently

\[ r_i \sim \text{Binomial}(n_i, \pi_i) \]
\[ \text{logit}(\pi_i) \sim N(0, 100). \]

This model does NOT use information between cities. Each rate \( \pi_i \) is estimated independently.
In WinBUGS we run both models simultaneously as follows:

model{
  for( i in 1 : I ) {
    r[i] ~ dbin(p[i,1],n[i])
    logit(p[i,1]) <- a[i]
    a[i] ~ dnorm(alpha1, tau1) # Exchangeable
    r2[i] ~ dbin(p[i,2],n[i]) # Copy of r[i]
    logit(p[i,2]) <- b[i]
    b[i] ~ dnorm(0, 0.01) # Independent
  }
  tau1 <- 1/(sigma1*sigma1) # Priors
  sigma1 ~ dunif(0.01, 5)
  alpha1 ~ dnorm(0,0.01)
}

#data
list(I=34,
r=c(2,3,1,3,2,3,2,7,3,8,7,0,15,4 ,0,6 ,0,33,4,5 ,2 ,0,8, 41,24,7, 46,9,23,53,8,3,1,23),

r2=c(2,3,1,3,2,3,2,7,3,8,7,0,15,4 ,0,6 ,0,33,4,5 ,2 ,0,8,41,24,7, 46, 9,23,53,8,3,1,23),

n=c(4,20,5,10,2,5,8,19,6,10,24,1,30,22,1,11,1,54,9,18,12,1,11,77,51, 16,82,13,43,75,13,10,6,37) )
Results:

DIC for Model 1 (GLMM) = 145.670

DIC for Model 2 (independent) = 176.504

- Clearly Model 1 which combines information between cities is the winner.
- The use of Model 2 has the effect of reduce the variability between cities
- The use of Model 2 gives better results at the level of the city.

Clear conclusion: We should take advantage of modeling simultaneously multiple results!

Example: Toxoplasmosis data continue ...

Two important questions are:

- Which is the influence of the amount of rain in toxoplasmosis prevalence?
- Which is the influence of the number of participants in each town?

Model 3:

\[ r_i \sim \text{Binomial}(n_i, \pi_i) \]

\[ \logit(\pi_i) = a_i + \beta_1 \times (x_{i,1} - \bar{x}_1) + \beta_2 \times (x_{i,1} - \bar{x}_1) \]

\[ a_i \sim N(\alpha, \sigma^2) \]

\[ \sigma \sim \text{Uniform}(0.01, 10) \]

\[ \alpha, \beta_1, \beta_2 \sim N(0,100), \]
In WinBUGS:

```r
model
{
  for(i in 1:N)
  {
    log.n[i] <- log(n[i])
  }
  for( i in 1 : N ) {
    r[i] ~ dbin(p[i], n[i])
    a[i] ~ dnorm(alpha,tau)
    logit(p[i]) <- a[i] + beta1 * (rain[i]-mean(rain[])) +
    beta2 * (log.n[i] - mean(log.n[]))
  }
}
# Priors
tau <- 1/(sigma*sigma)
sigma ~ dunif(0.01, 5)
alpha ~ dnorm(0,0.01)
beta1 ~ dnorm(0, 0.01)
beta2 ~ dnorm(0, 0.01)
```

Posterior of $\beta_1$ clearly indicates no linear influence of the amount of rain. Posterior of $\beta_2$ shows a clear trend.
**Example:** Ranking of the eighteen baseball players (Efron and Morris, 1977)

How can we rank the players ability? Who was the best player of the season 1970?

We use the ranking function in WinBUGS to answer this question.

<table>
<thead>
<tr>
<th>Name</th>
<th>hit/AB</th>
<th>Observed Avg (ML)</th>
<th>&quot;TRUTH&quot;</th>
<th>James-Stein</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clemente</td>
<td>18/45</td>
<td>.400</td>
<td>.346</td>
<td>.290</td>
</tr>
<tr>
<td>Robinson</td>
<td>17/45</td>
<td>.378</td>
<td>.298</td>
<td>.286</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>Total Squared error</td>
<td>.077</td>
<td>0.022</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

![Graph showing batting average for ML and Bayes methods](image.png)
model {
  for (i in 1 : N) {
    r[i] ~ dbin(p[i], n[i])
    logit(p[i]) <- b[i]
    b[i] ~ dnorm(mu, tau)
    p.rank[i] <- rank(p[], i)
  }
}

# hyper-priors
mu ~ dnorm(0.0, 1.0E-6)
sigma ~ dunif(0, 100)
tau <- 1/(sigma * sigma)

# Data
list(r = c(145, 144, 160, 76, 128, 140, 167, 41, 148, 57, 83, 79, 142, 152, 52, 168, 137, 21),
n = c(412, 471, 566, 320, 463, 511, 631, 183, 555, 245, 322, 315, 480, 583, 231, 603, 453, 115), N=18)
Rank distributions for Robinson, Howard and Clemente.

Left panel: posterior distributions of ranks. Right panel: posterior distributions of performances.
Summary on hierarchical models

- Hierarchical models allows to "borrow strength" across units
- Posteriors distribution of $\theta_i$ for each unit borrows information from the likelihood contributions for all other units. Estimation is more efficient.
- MCMC allows considerable flexibility over choice of random effects distribution (not restricted to normal random errors)
- MCMC allows to make inference on difficult questions, e.g. ranking estimation of random effects
- Easy to extend to more complicated models (e.g. non-linear repeated measurements, etc.)

Summary of the course

Bayesian statistics:

- A new interpretation of probability as a subjective mental construct
- Relationship with classical statistics
- Uses of prior distribution as: sensitivity analysis, prior predictions, model building, etc.
- Making inference using MCMC
- Thinking different about regression models
- Different modeling tools: DAGs, DIC and WinBUGS
- Introduction to hierarchical modeling
Finally

Nice to see that most people attended and survived the course!!

Hope that everybody will be now enthusiastic modern Bayesians ;-) 

Thank you very much ... Muchas gracias !!!