Bayesian methods
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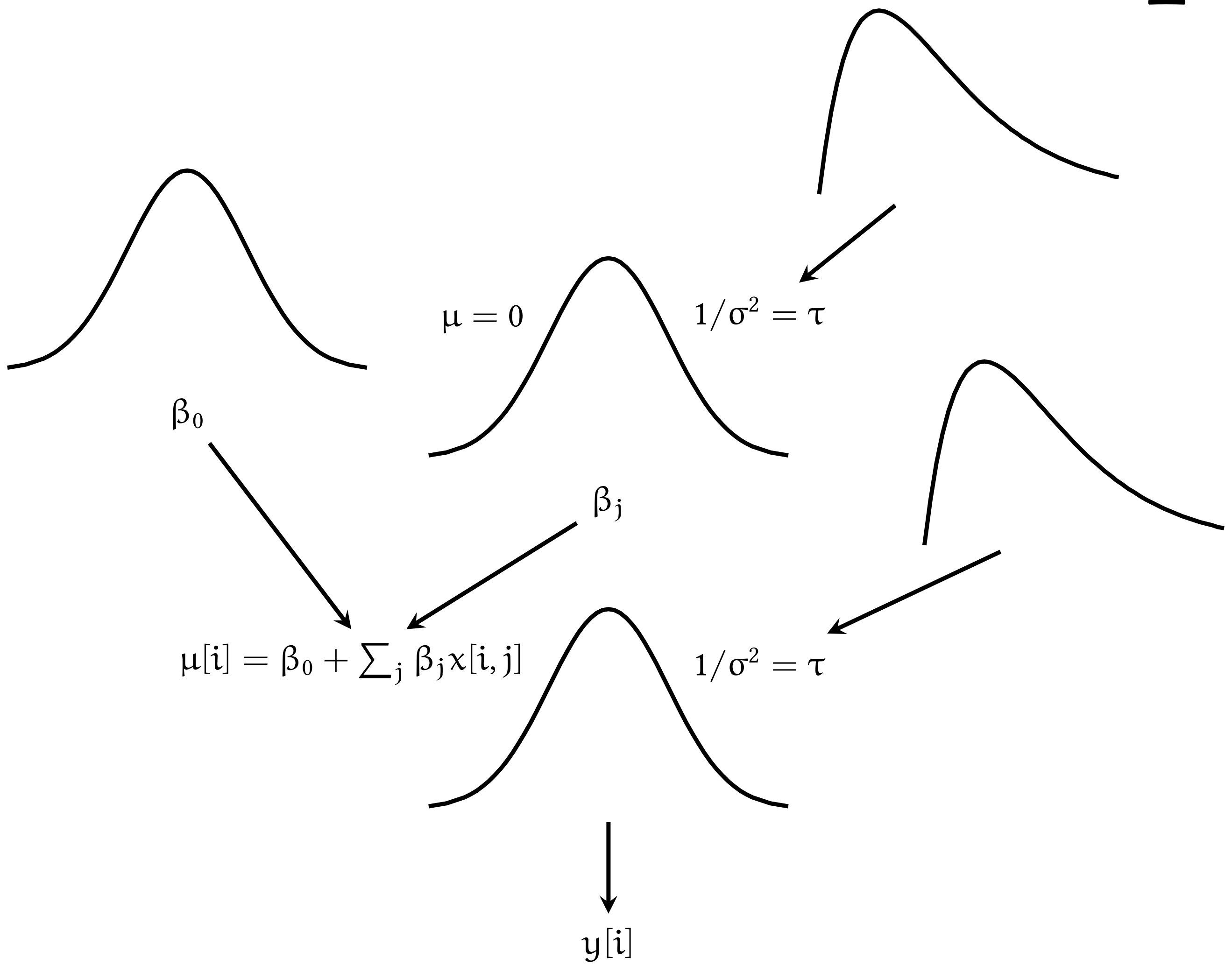


Contents

1 Introduction

1.1 Preliminaries

Purpose of this handout In this handout you find the content of the slides I am using in the lecture. The handout is not supposed to replace a book. I recommend some books on the webpage and in the course.

Homepage: http://www.kirchkamp.de/

Literature:

- Kruschke, Doing Bayesian Data Analysis
- Hoff, A First Course in Bayesian Statistical Methods.

To learn more about MCMC sampling you can also read C. Andrieu, de Freitas, N., Doucet, A, Jordan, M. "An Introduction to MCMC for Machine Learning." Machine Learning. 2003, 50(1-2), pp 5-43.

Aim of the course

- Compare Bayesian with frequentist methods.

  Two schools of statistical inference: Bayesian / Frequentist
  - Frequentist: Standard hypothesis testing, p-values, confidence intervals. Well known.
  - Bayesian: beliefs conditional on data.
- Learn to apply Bayesian methods.
  - What is the equivalent of frequentist method X in the Bayesian world?
  - How to put Bayesian methods into practice?

1.2 Motivation

1.3 Using Bayesian inference

Pros:

- Prior knowledge
- Model identification is less strict
- Small-sample size
- Non-standard models

  - Non-normal distributions
  - Categorical data
  - Multi-level models
  - Missing values
  - Latent variables
- Interpretation

Cons:

- Prior knowledge
- Computationally expensive
- Model-fit diagnostic

Comparison Frequentist: Null Hypothesis Significance Testing (Ronald A. Fisher, Statistical Methods for Research Workers, 1925, p. 43)

- $X \leftarrow \theta$, X is random, θ is fixed.
- Confidence intervals and p-values are easy to calculate.
- Interpretation of confidence intervals and p-values is awkward.
- p-values depend on the intention of the researcher.
- We can test "Null-hypotheses" (but where do these Null-hypotheses come from).
- Not good at accumulating knowledge.
- More restrictive modelling.

Bayesian: (Thomas Bayes, 1702-1761; Metropolis et al., "Equations of State Calculations by Fast Computing Machines". Journal of Chemical Physics, 1953.)

- $X \rightarrow \theta$, X is fixed, θ is random.
- Requires more computational effort.
- "Credible intervals" are easier to interpret.
- Can work with "uninformed priors" (similar results as with frequentist statistics)

- Efficient at accumulating knowledge.
- Flexible modelling.

Most people are still used to the frequentist approach. Although the Bayesian approach might have clear advantages it is important that we are able to understand research that is done in the context of the frequentist approach.

$$\Pr(A \wedge B) = \Pr(A) \cdot \Pr(B|A) = \Pr(B) \cdot \Pr(A|B)$$

$$\text{rewrite:} \qquad \Pr(A) \cdot \Pr(B|A) \frac{1}{\Pr(B)} = \Pr(A|B)$$

$$\text{with } A = \underbrace{\theta}_{\text{parameter}} \text{ and } B = \underbrace{X}_{\text{data}} :$$

$$\underbrace{\Pr(\theta)}_{\text{prior}} \cdot \underbrace{\Pr(X|\theta)}_{\text{likelihood}} \cdot \frac{1}{\underbrace{\Pr(X)}_{\int \Pr(\theta)\Pr(X|\theta)\,d\theta}} = \underbrace{\Pr(\theta|X)}_{\text{posterior}}$$

Before we come to a more formal comparison, let us compare the two approaches, frequentist versus Bayesian, with the help of an example.

I will use an example from the legal profession. Courts have to decide whether a defendant is guilty or innocent. Scientists have to decide whether a hypothesis is correct or not correct. Statistically, in both cases we are talking about the value of a parameter. $\theta =$ guilty or $\theta =$ not guilty. Alternatively, $\beta = 0$ or $\beta \neq 0$.

My hope is that the legal context makes it more obvious how the decision process fails or succeeds.

The prosecutors' fallacy
Assuming that the prior probability of a random match is equal to the probability that the defendant is innocent.

Two problems:

- p-values depend on the researcher's intention. E.g. multiple testing (several suspects, perhaps the entire population, is "tested", only one suspect is brought to trial)
- Conditional probability (neglecting prior probabilities of the crime)
- Lucia de Berk:
  - $\Pr(\text{evidence}|\text{not guilty}) = 1/342$ million
  - $\Pr(\text{evidence}|\text{not guilty}) = 1/25$

- Sally Clark
  - Pr(evidence|not guilty) = 1/73 million
  - Pr(not guilty|evidence) = 78%

The Sally Clark case

- 1996: First child dies from SIDS (sudden infant death syndrome): $P = 1/8543$
- 1998: Second child dies from SIDS: $P = 1/8543$
- $\to$: $\Pr(\text{evidence}|\text{not guilty}) = (1/8543)^2 \approx 1/73$ million
- 1999: life imprisonment, upheld at appeal in 2000.

Problems:

- Correlation of SIDS within a family. $\Pr(\text{2nd child}) = (1/8543) \times 5 \ldots 10$
- SIDS is actually more likely in this case: $P = 1/8543 \to P = 1/1300$

  $\Pr(\text{evidence}|\text{1 not guilty mother}) = 1/(1300 \cdot 130) = 0.000592\ \%$
- Intention of the researcher/multiple testing: $\approx$ 750 000 births in England and Wales / year. How likely is it to find two successive SIDS or more among 750 000 mothers.

  $\Pr(\text{evidence}|\text{750 000 not guilty mothers}) = 98.8\ \%$.

But what is the (posterior) probability of *guilt*? Here we need prior information.

- What is the prior probability of a mother murdering her child?

$$\underbrace{\Pr(\theta)}_{\text{prior}} \cdot \underbrace{\Pr(X|\theta)}_{\text{likelihood}} \cdot \frac{1}{\Pr(X)} = \underbrace{\Pr(\theta|X)}_{\text{posterior}}$$

$$\underbrace{\Pr(g)}_{\text{prior}} \cdot \underbrace{\Pr(X|g)}_{\text{likelihood}} \cdot \frac{1}{\underbrace{\Pr(g) \cdot \Pr(X|g) + (1-\Pr(g)) \cdot \Pr(X|\text{not } g)}_{\Pr(X)}} = \underbrace{\Pr(g|X)}_{\text{posterior}}$$

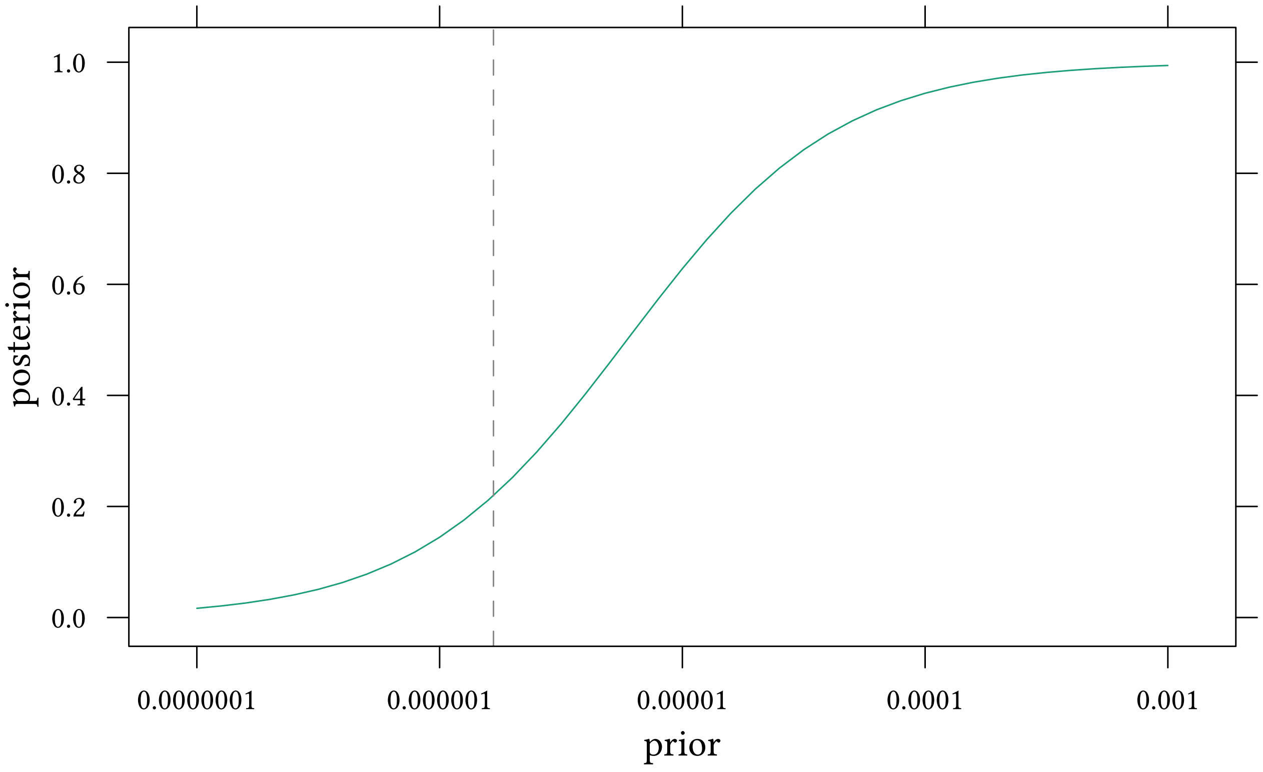
Data from the U.S.A. (Miller, Oberman, 2004): per 600 000 mothers 1 killed child, $\Pr(g) = 1/600\,000$.

$\Pr(X|g) = 1$, $\Pr(X) = \underbrace{\frac{1}{600\,000}}_{\text{guilty}} + \underbrace{\frac{599\,999}{600\,000} \cdot \frac{1}{1300 \cdot 130}}_{\text{not guilty}}$

$$\Pr(g|\text{evidence}) = 22\%$$

If $\Pr(g) = 1/18800$ then $\Pr(g|\text{evidence}) = 90\%$

If $\Pr(g) = 1/1710$ then $\Pr(g|\text{evidence}) = 99\%$



$$\Pr(X|\theta) \quad \neq \quad \Pr(\theta|X)$$

- The interpretation of $\Pr(X|\theta)$ as a p-value is affected by multiple testing (the intention of the researcher)
- $\Pr(\theta|X)$ is not affected by multiple testing (the intention of the researcher)
- $\Pr(\theta|X)$ forces us to think about a (subjective) *prior.*

Lessons

- Since p-values in Null-hypothesis significance testing are derived under the assumption that the Null-hypothesis is true:

$\rightarrow$ When the Null-hypothesis is rejected, we can't make any statement about the effect, except that the Null-hypothesis is not likely.

- Since the Null-hypothesis is a point-hypothesis, the statement might be trivial.

1.4 The intention of the researcher — p-hacking

X data

ϕ_j test procedure

- choice of control variables
- data exclusion
- coding
- analysis
- interactions
- predictors
- $\vdots$

$T(X, \phi_j)$ test result

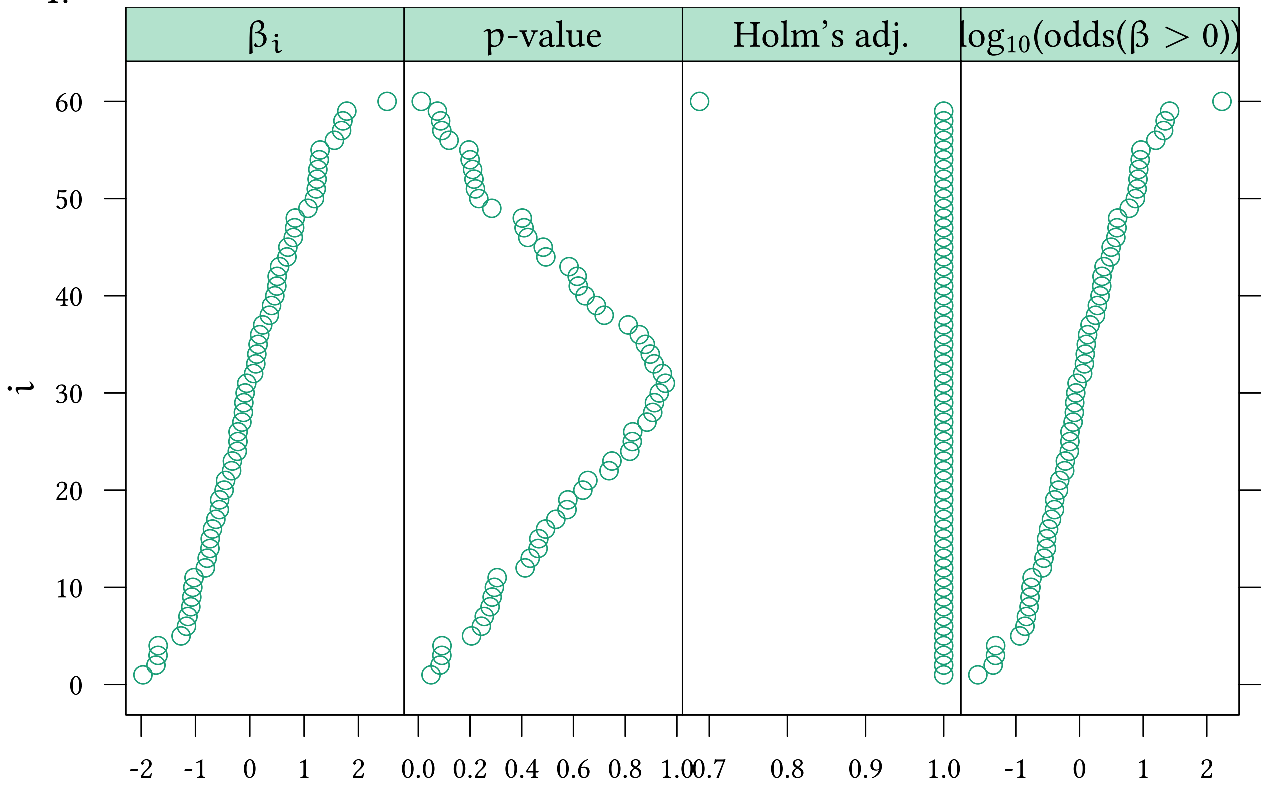
p-hacking

- perform J tests: $\{\ldots, T(X, \phi_j), \ldots\}$
- report the best result, given the data: $T(X, \phi_{\text{best}})$

$\rightarrow$ to correct for multiple testing we need to know $J \downarrow$

$\rightarrow$ robustness checks (for all $J \downarrow$)

An example: A researcher uses 60 explanatory variables to explain one dependent variable. Here we assume (for simplicity) that they all have the same standard error $\sigma = 1$.



smallest p-value:	no correction	$p = 0.011$
	Holm's adjustment	$p = 0.69$

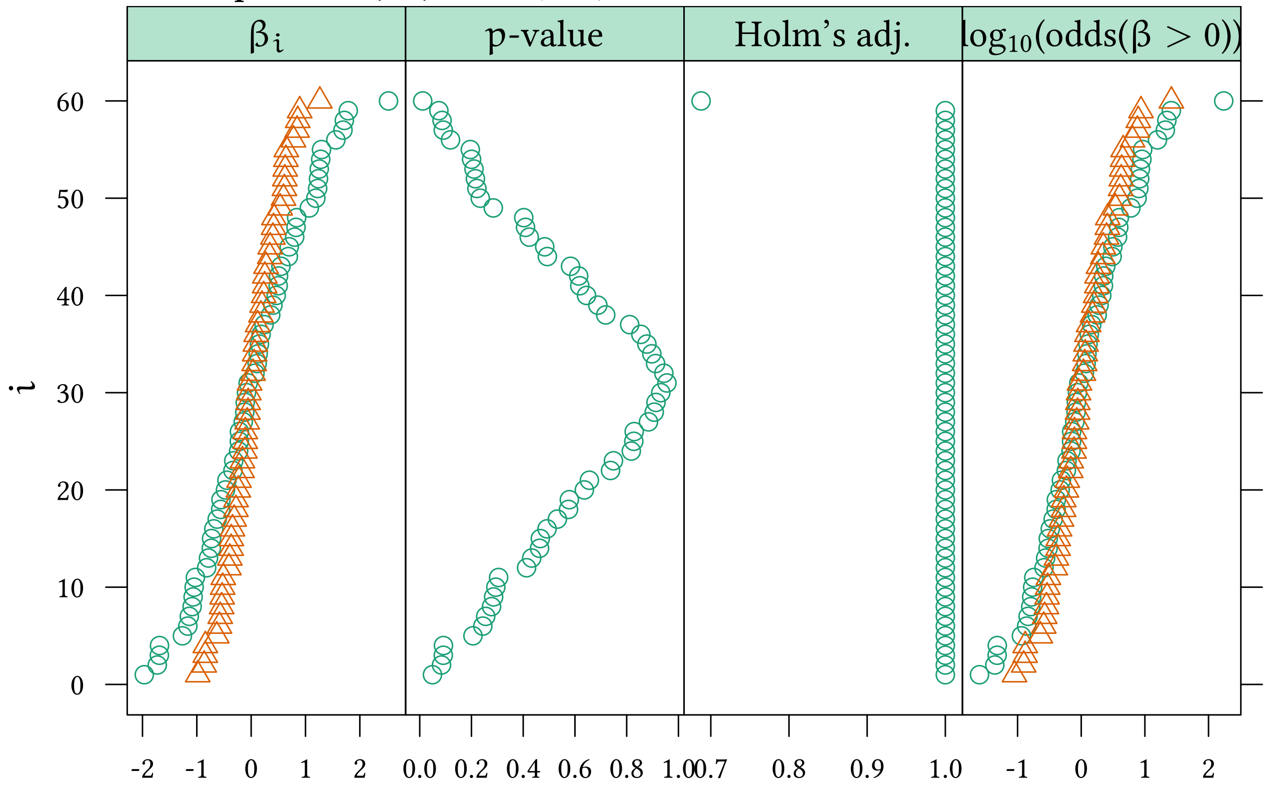
A statement about the p-value depends on the intention of the researcher. It is affected by multiple testing.

A statement about the posterior odds does not depend on the intention of the researcher. It does, though, depend, on a prior.

Above we assumed a flat prior. Is this reasonable? Perhaps, if we have already studied dozens of these variables, and they all seem to be drawn from a distribution with $\mu = 0$ and $\sigma = 1$, it is no longer reasonable to have a flat prior.

Above we pretended to be ignorant. We used a flat prior in each study.

Now we use a prior for β: $\beta_i \sim N(0, 1)$



largest odds:	flat prior	$\beta_i > 0 / \beta_i < 0$	odds=170 : 1
	informed prior	$\beta_i > 0 / \beta_i < 0$	odds=26 : 1

Pretending to be ignorant and assuming a flat prior can be misleading.

- Flat prior in the Sally Clark case:

  $\Pr(\text{guilt}) : \Pr(\text{innocence}) = \frac{1}{2} : \frac{1}{2}$.

  This is absurd.

- Also $H_0 : \forall_i \beta_i = 0$ could be absurd.

1.5 Compare: The Maximum Likelihood estimator

Maximum likelihood has very nice asymptotic properties.

But what if the assumptions for these properties are not fulfilled?

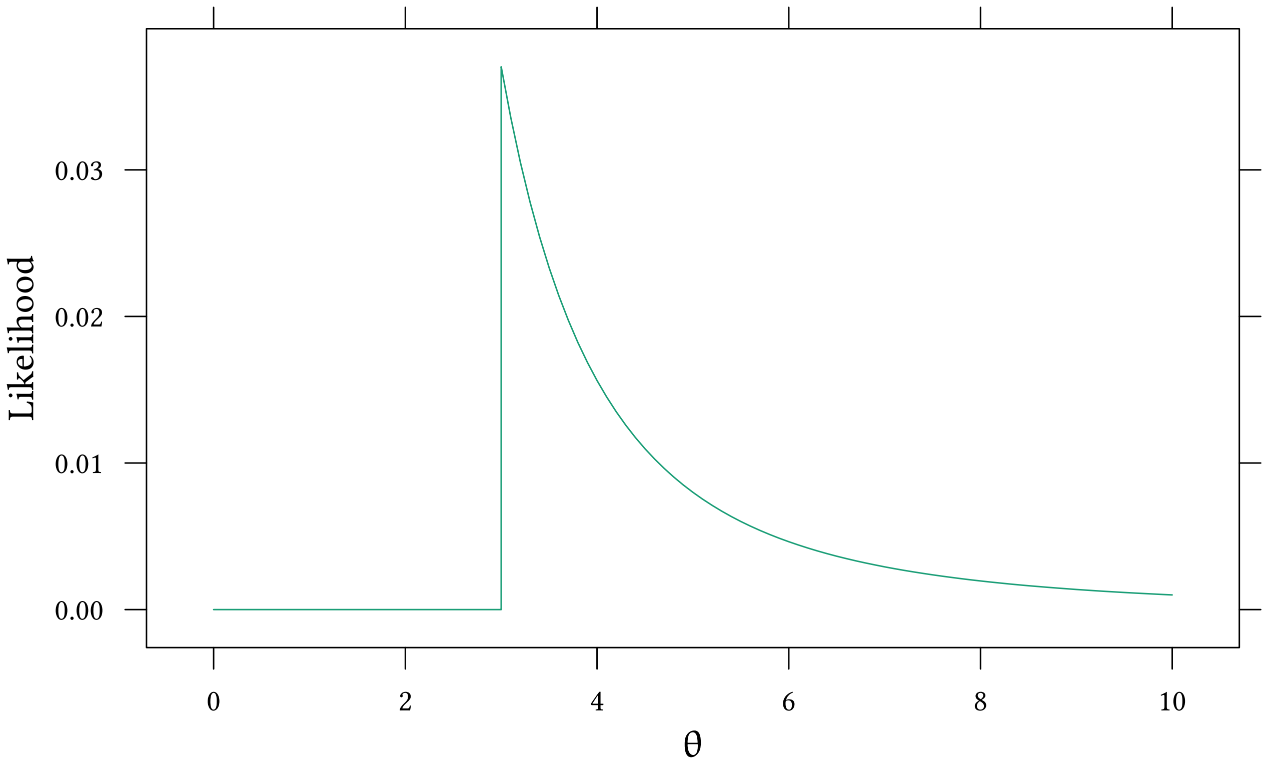
- Consistency
- Asymptotic normality
  - θ_0 must be away from the boundary (not trivial with panel data).
  - the number of nuisance parameters must not increase with the sample size (not trivial with panel data).
  - $\vdots$
- Efficiency when the sample size tends to infinity

Example *A* wants to estimate the capacity of B's firm (German tank problem):

- *A* samples the daily output of the firm.
- The output of the firm follows a uniform distribution over $[0, \theta]$.
- The sample contains the numbers $\{1, 2, 3\}$.

The Maximum Likelihood estimator:

$$L = \begin{cases} 1/\theta^3 & \text{if } \theta \geqslant 3 \\ 0 & \text{otherwise} \end{cases} \quad \Rightarrow \quad \theta^*_{ML} = 3$$



The ML estimator yields a biased estimate.

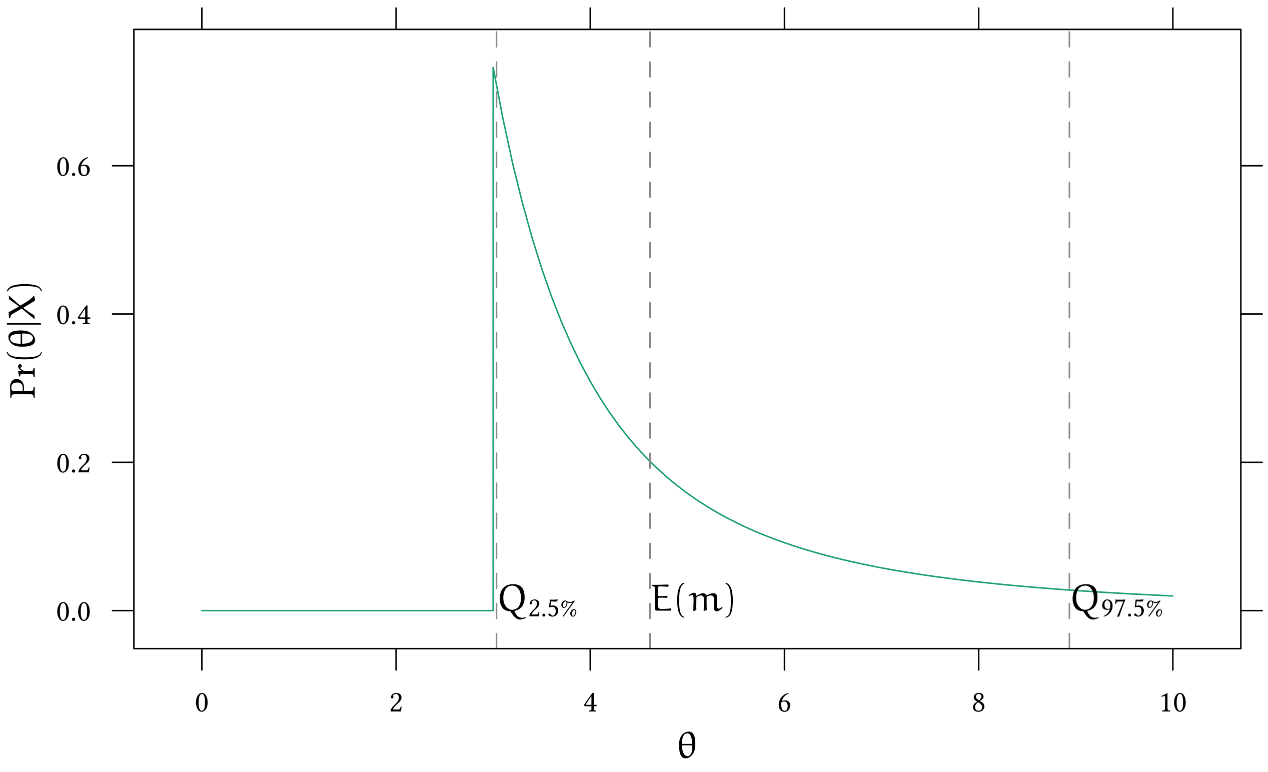
For a Bayesian estimate we need a prior. Let us assume that A assumes all capacities between 0 and M to be equally likely. Then (for $\theta \geqslant 3$):

$$\Pr(\theta|X) = \frac{\Pr(\theta)\cdot\Pr(X|\theta)}{\int \Pr(\theta)\Pr(X|\theta)\,d\theta} = \frac{\frac{1}{M}\frac{1}{\theta^3}}{\int_3^M \frac{1}{M}\frac{1}{\theta^3}\,d\theta} = \frac{18M^2}{(M^2-9)\theta^3}$$

Hence

$$E(\theta) = \int \theta\cdot f(\theta)\,d\theta = \int_3^M \theta\cdot\Pr(\theta|x)d\theta = \frac{6M}{M+3}$$

E.g. if $M = 10$, then $E(\theta) = 60/13 = 4.615$. If $M = 100$, then $E(\theta) = 600/103 = 5.825$.



Remember: density function:

$$\Pr(\theta|X) = \frac{18M^2}{(M^2-9)\theta^3}$$

Distribution function:

$$F(q) = \int_3^q \Pr(\theta|x)d\theta = \frac{M^2(q^2-9)}{(M^2-9)q^2}$$

Quantile function:

$$\text{Solve } F(q) = p \quad\Rightarrow\quad Q(p) = \frac{3M}{\sqrt{(1-p)M^2+9p}}$$

For $M = 10$ we have $CI_{[2.5\%,97.5\%]} = \left[\frac{20\cdot\sqrt{30}}{\sqrt{1303}}, \frac{6\cdot 10^{3/2}}{\sqrt{451}}\right] = [3.035, 8.743]$

1.6 Terminology

1.6.1 Probabilities

Consider the following statements:

Frequentist probability

- The probability to throw two times a six is 1/36.
- The probability to win the state lottery is about 1:175 000 000.
- The probability of rainfall on a given day in August is 1/3.
- The probability for a male human to develop lung or bronchus cancer is 7.43%.

Subjective probability

- The probability of rainfall tomorrow is 1/3.
- The probability that a Mr. Smith develops lung or bronchus cancer is 7.43%.
- The probability that Ms. X commited a crime is 20%.

Frequentist

- P = objective probability (sampling of the data X is infinite).

$\rightarrow$ but what if the event occurs only once (rainfall tomorrow, Mr. Smith's health,...)?
  - $\rightarrow$ von Mises: event has no probability
  - $\rightarrow$ Popper: invent a fictitious population from which the even is a random sample (propensity probability).

- Parameters θ are unknown but fixed during repeated sampling.

Bayesian

- P = subjective probability of an event (de Finetti/Ramsey/Savage)

  $\approx$ betting quotients
- Parameters θ follow a (subjective) distribution.

Fixed quantities:

Frequentist

- Parameters θ are fixed (but unknown).

Bayesian

- Data X are fixed.

Probabilistic statements:

Frequentist

- …about the frequency of errors p.
- Data X are a random sample and could potentially be resampled infinitely often.

Bayesian

- …about the distribution of parameters θ.

1.6.2 Prior information

- Prior research (published / unpublished)
- Intuition (of researcher / audience)
- Convenience (conjugate priors, vague priors).

Prior information is *not* the statistician's personal opinion. Prior information is the result of and subject to scientific debate.

1.6.3 Objectivity and subjectivity

- Bayesian decision making requires assumptions about…
  - $\Pr(\theta)$ (prior information)
  - g_0, g_0 (cost and benefits)

  Scientists might disagree about this information.

$\rightarrow$ Bayesian decision making is therefore accused of being "subjective".

Bayesian's might "choose" priors, cost and benefits, to subjectively determine the result. E.g. in the Sally Clark case, the researcher might "choose" the prior probability of a mother to kill her child to be $1/1710$ to conclude guilt with $\Pr(g|\text{evidence}) = 99\%$.

The Bayesian's answer:

- Prior information, cost and benefits are relevant information. Disregarding them (as the frequentists do) is a strange concept of "objectivity".
- Priors, cost and benefits are subject to scientific debate, like any other assumption. We have to talk about priors, not assume them away.
- Subjectivity exists in both worlds:
  - B.+F. make assumptions about the model $\rightarrow$ more dangerous than priors.
  - In F. the intention of the researcher has a major influence on p-values and confidence intervals.

1.6.4 Issues

- Probability: frequentist vs. subjective.
- Prior information, how to obtain?
- Results, objective / subjective.
- Flexible modelling: F. has only a limited number of models.

  F: precise method, using a tool which is sometimes not such a good representation of the problem.

  B: approximate method, using a tool which can give a more precise representation of the problem.
- Interpretation: p-values versus posteriors.

  B. predicts (posterior) probability of a hypothesis.

  F. writes carefully worded statements which are wrong 5% of the time (or any other probability) provided H_0 is true.
- Quality of decisions: p-values are only a heuristic for a decision rule.

  B.'s decisions are better in expectation.

1.7 Decision making

Which decision rule, Bayesian or frequentist, uses information more efficiently?

$$\Pr(\theta) \cdot \Pr(X|\theta) \cdot \frac{1}{\Pr(X)} = \Pr(\theta|X)$$

Assume $\theta \in \{0, 1\}$. Implement an action $a \in \{0, 1\}$. Payoffs are $\pi_{a\theta}$.

We have $\pi_{11} > \pi_{01}$ and $\pi_{00} > \pi_{10}$, i.e. it is better to choose $a = \theta$. Expected payoffs:

$$E(\pi|a) = \pi_{a1} \cdot \Pr(\theta = 1) + \pi_{a0} \cdot \Pr(\theta = 0)$$

Optimal decision: choose $a = 1$ iff

$$\underbrace{\pi_{11} \cdot \Pr(\theta = 1) + \pi_{10} \cdot \Pr(\theta = 0)}_{E(\pi|a=1)} > \underbrace{\pi_{01} \cdot \Pr(\theta = 1) + \pi_{00} \cdot \Pr(\theta = 0)}_{E(\pi|a=0)} .$$

Rearrange: choose $a = 1$ iff

$$\Pr(\theta = 1) \underbrace{(\pi_{11} - \pi_{01})}_{g_1} > \Pr(\theta = 0) \underbrace{(\pi_{00} - \pi_{10})}_{g_0} .$$

Here g_a can be seen as the gain from choosing the correct action (or the loss from choosing the wrong action) if $\theta = a$.

If we have some data X:

$$\Pr(\theta = 1|X) g_1 > \Pr(\theta = 0|X) g_0.$$

Bayes' rule:

$$\Pr(\theta) \cdot \Pr(X|\theta) \cdot \frac{1}{\Pr(X)} = \Pr(\theta|X)$$

$$\text{choose } a = 1 \text{ iff } \frac{g_1}{g_0} > \frac{\Pr(\theta = 0|X)}{\Pr(\theta = 1|X)} = \frac{\frac{\Pr(\theta=0)\cdot\Pr(X|\theta=0)}{\Pr(X)}}{\frac{\Pr(\theta=1)\cdot\Pr(X|\theta=1)}{\Pr(X)}}$$

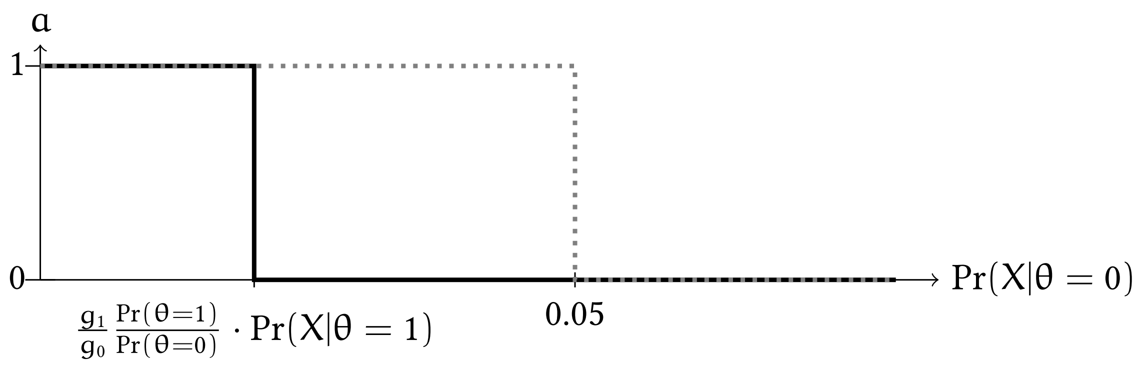
$$\text{choose } a = 1 \text{ iff } \frac{g_1}{g_0} \frac{\Pr(\theta = 1)}{\Pr(\theta = 0)} \cdot \Pr(X|\theta = 1) > \Pr(X|\theta = 0)$$

$$\text{Bayesian chooses } a = 1 \text{ iff } \Pr(X|\theta = 0) < \frac{g_1}{g_0} \frac{\Pr(\theta = 1)}{\Pr(\theta = 0)} \cdot \Pr(X|\theta = 1)$$

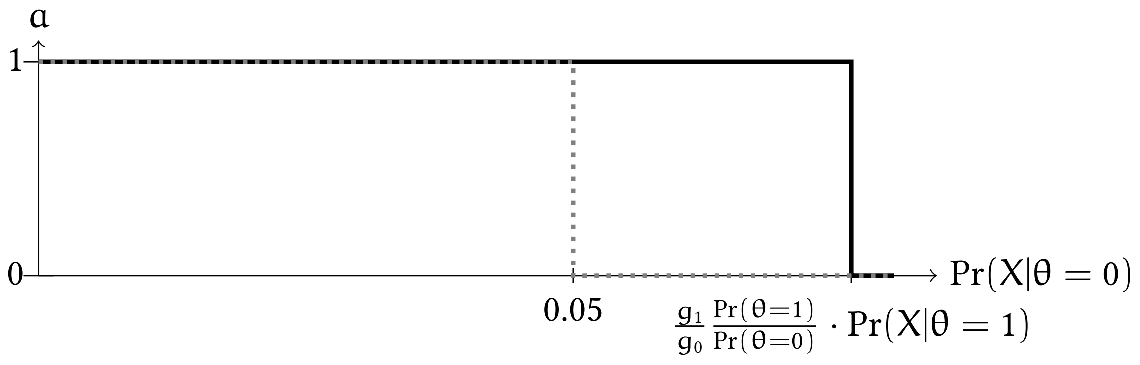
$$\text{Frequentist chooses } a = 1 \text{ iff } \Pr(X|\theta = 0) < 0.05 .$$

(Here we assume that H_0 is $\theta = 0$.)

When do Bayesians and Frequentists disagree?



a
1
0
$\Pr(X|\theta = 0)$
$\frac{g_1}{g_0}\frac{\Pr(\theta=1)}{\Pr(\theta=0)} \cdot \Pr(X|\theta = 1)$
0.05



For very small and for very large values of $\Pr(X|\theta = 0)$ both Bayesians and frequentists make the same choice. Only in the range between $\frac{g_1}{g_0}\frac{\Pr(\theta=1)}{\Pr(\theta=0)} \cdot \Pr(X|\theta = 1)$ and 0.05 choices differ. In that range the Bayesian choice maximises expected payoffs while the frequentist does not.

1.8 Technical Background

$(\Omega, \mathcal{F}, P)$ is a probability space:

- Ω, a sample space (set of possible outcomes)
- $\mathcal{F}$, a set of events ($\mathcal{F}$ is a collection of subsets of Ω that is closed under countable-fold set operations. $\mathcal{F}$ is a σ-algebra, $(\mathcal{F}, \Omega)$ is a measurable space).
- P, a probability measure function.
- Axiom 1: $\forall A \in \Omega : \Pr(A) \geqslant 0$
- Axiom 2: $\Pr(\Omega) = 1$
- Axiom 3: For pairwise disjoint $A_i \in \mathcal{F} : \Pr(\sum_i A_i) = \sum_i \Pr(A_i)$
- $\Pr(\neg A) = 1 - \Pr(A)$
- $\Pr(A \cup B) = \Pr(A) + \Pr(B) - \Pr(A \cap B)$

Definition: $\Pr(A|B) := \Pr(A \cap B)/\Pr(B)$
$\rightarrow \Pr(\theta) \cdot \frac{\Pr(X|\theta)}{\int \Pr(\theta)\cdot\Pr(X|\theta)d\theta} = \Pr(\theta|X)$

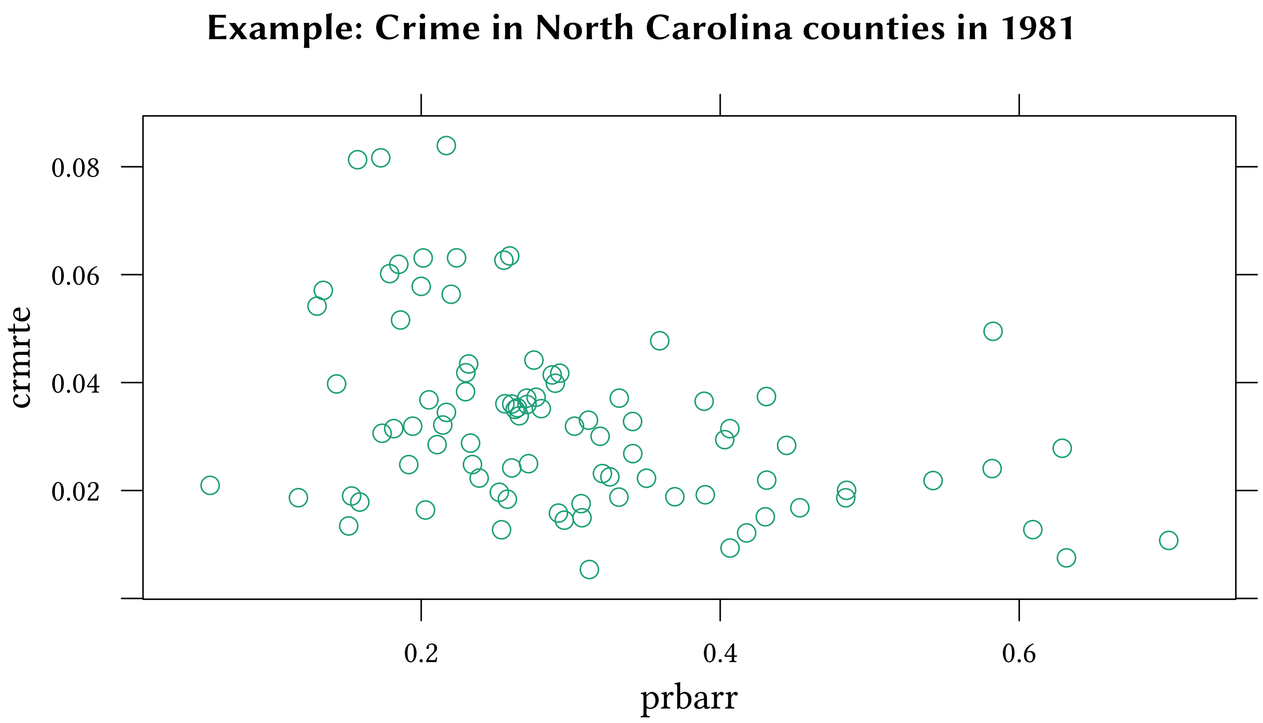
$X \sim \text{Exp}(\lambda)$	$E(X) = 1/\lambda$	$\text{var}(X) = 1/\lambda^2$
$X \sim \text{Gamma}(\alpha, \beta)$	$E(X) = \alpha/\beta$	$\text{var}(X) = \alpha/\beta^2$
$X \sim \text{Poisson}(\lambda)$	$E(X) = \lambda$	$\text{var}(X) = \lambda$
$X \sim \text{Beta}(\alpha, \beta)$	$E(X) = \alpha/(\alpha + \beta)$	$\text{var}(X) = \frac{\alpha\beta}{(\alpha+\beta)^2(\alpha+\beta+1)}$
$X \sim N(\mu, \tau)$	$E(X) = \mu$	$\text{var}(X) = 1/\tau$
$X \sim \chi^2(k)$	$E(X) = k$	$\text{var}(X) = 2k$
$X \sim t(k)$	$E(X) = 0$	$\text{var}(X) = k/(k-2)$
$X \sim F(k_1, k_2)$	$E(X) = k_2/(k_2 - 2)$	$\text{var}(X) = \frac{2k_2^2(k_1+k_2-2)}{k_1(k_2-2)^2(k_2-4)}$

2 A practical example

2.1 The distribution of the population mean

Here we ask the question: “What is the probability to be arrested in North Carolina in 1981 (conditional on a crime committed)?”

```
library(Ecdat)
data(Crime)
xyplot(crmrte ~ prbarr,data=Crime,subset=year==81)
```



```
y <- subset(Crime,year==81)[["prbarr"]]
```

We can have a look at a part of the data with *head*:

```
head(y)

[1] 0.289696 0.202899 0.406593 0.431095 0.631579 0.369650
```

If we suspect that average rate to be arrested to be 0.3, we use a *t.test*:

```
t.test(y,mu=.3)


One Sample t-test

data:  y
```

```
t = -0.070496, df = 89, p-value = 0.944
alternative hypothesis: true mean is not equal to 0.3
95 percent confidence interval:
 0.2724894 0.3256254
sample estimates:
mean of x
0.2990574
```

An alternative: The Bayesian Approach Required:

- Priors for μ and τ.
- Likelihood: $y \sim N(\mu, \tau)$ with $\tau = 1/\sigma^2$

$\rightarrow$ Posterior distribution of μ and τ.

We will here just "use" our software got get a result. Below we will explain what the software actually does.

```
library(runjags)
X.model <- 'model {
 for (i in 1:length(y)) {
        y[i] ~ dnorm(mu,tau)
    }
    mu    ~ dnorm (0,.0001)
    tau   ~ dgamma(.01,.01)
    sd   <- sqrt(1/tau)
}'
X.jags<-run.jags(model=X.model,data=list(y=y),monitor=c("mu","sd"))
```

Notation for nodes

- Stochastic nodes (discrete/continuous univariate/multivariate distributed):

```
y[i] ~ dnorm(mu,tau)
...
mu   ~ dnorm (0,.0001)
```

  - …can be specified by *data* (have always this value)
  - …can be specified by *inits* (have this value before the first sample)
  - …can be unspecified

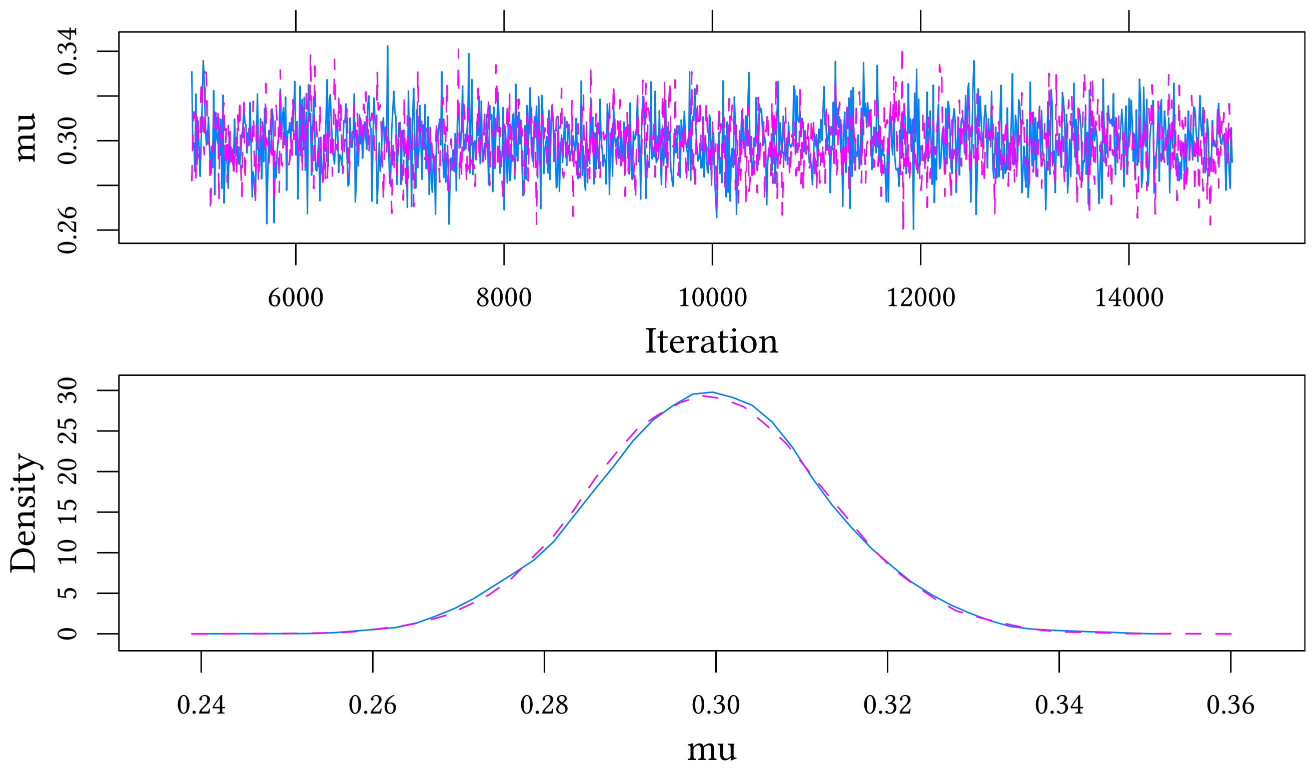
  Note: if *data* or *inits* sets a value to NA, this means "unspecified".

- Deterministic nodes:

```
        sd  <- sqrt(1/tau)
```

JAGS samples from the posterior of μ and τ. Here is a distribution for μ:

```
plot(X.jags,var="mu",plot.type=c("trace","density"))
```



Here is a *summary* of our estimation results:

```
summary(X.jags)

    Lower95   Median  Upper95      Mean          SD       Mode         MCerr
mu 0.272034 0.298984 0.325091 0.2990328 0.013468671 0.2986450 0.00009523789
sd 0.110458 0.128171 0.148288 0.1288285 0.009782551 0.1278104 0.00006969668
   MC%ofSD SSeff         AC.10      psrf
mu     0.7 20000  0.002831988 1.0000202
sd     0.7 19701 -0.003087232 0.9999656
```

Testing a point prediction in the `t.test`, as in $\mu = 0.3$, is a bit strange, at least from the Bayesian perspective. It might be more interesting to make a statement about the probability of an interval.

First, we convert our jags-object into a dataframe: How probable is $\mu \in (0.29, 0.31)$?

```
X.df<-data.frame(as.mcmc(X.jags))
str(X.df)

'data.frame': 20000 obs. of  2 variables:
 $ mu: num  0.331 0.289 0.316 0.317 0.303 ...
 $ sd: num  0.126 0.119 0.116 0.122 0.118 ...
```

We can now say, how probable it is, ex post, that $\mu \in [0.29, .31]$:

```
100*mean(with(X.df,mu > 0.29 & mu < 0.31))

[1] 54.755
```

…or in a more narrow interval:

```
100*mean(with(X.df,mu > 0.299 & mu < 0.301))

[1] 5.825

100*mean(with(X.df,mu > 0.2999 & mu < 0.3001))

[1] 0.645
```

If, say, a government target is to have an average arrest rate of at least 0.25, we can now calculate the probability that $\mu > 0.25$.

How probable is $\mu > 0.25$?

```
100*mean(with(X.df,mu > 0.25))

[1] 99.98
```

Odds for $\mu > 0.25$

```
p<-mean(with(X.df,mu > 0.25))
p/(1-p)

[1] 4999
```

In the following section we will explain how all this works:

2.2 Gibbs sampling

The *model* that we specified above, contained two parts, a likelihood and a prior. Here is a model with only a prior:

We use JAGS notation:

$$\mathtt{dnorm}(\mu, \tau)$$

with μ=mean and $\tau = 1/\sigma^2$=precision.

```
modelPri <- 'model {
    mu   ~ dnorm (0,.0001)
}'
```

Now we use this model to draw a sample of size 100, so far only given the prior.

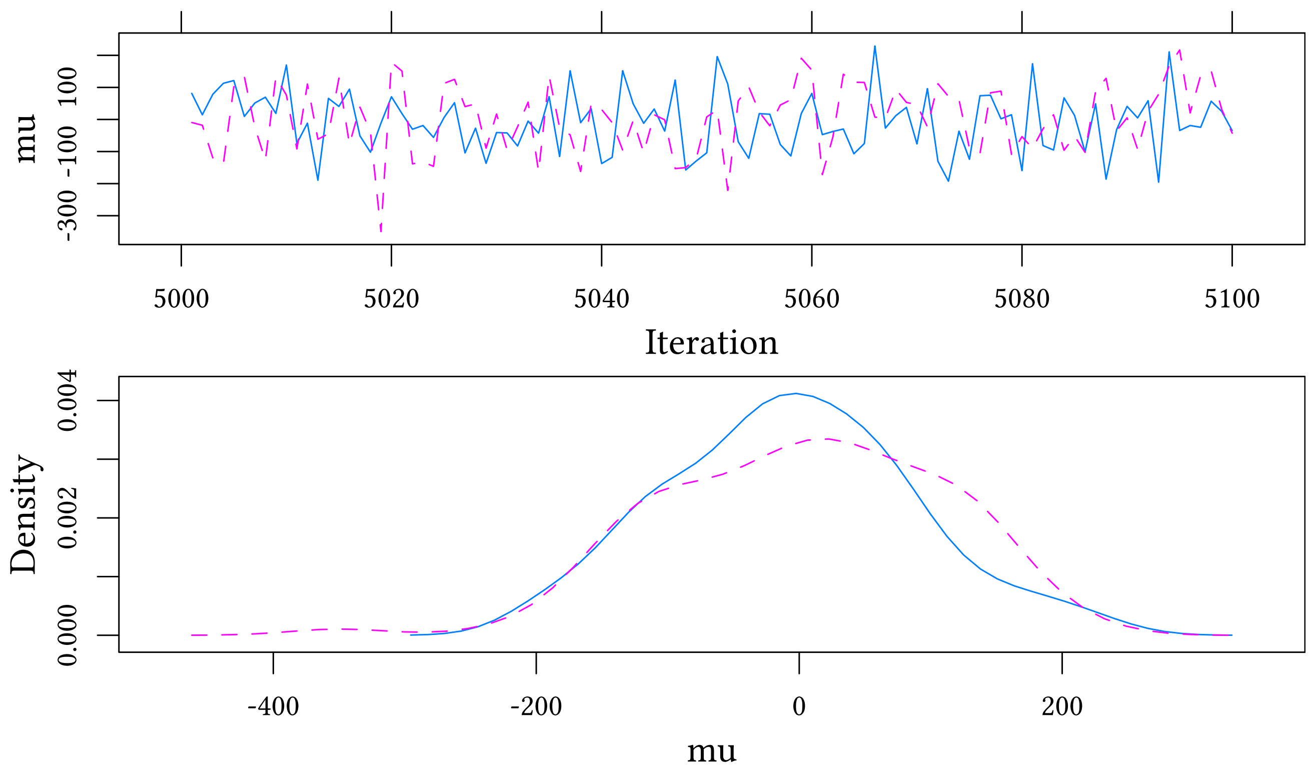
```
pri.jags<-run.jags(model=modelPri,monitor=c("mu"),sample=100)
```

Here are the properties of our sample:

```
summary(pri.jags)

    Lower95   Median Upper95      Mean       SD      Mode     MCerr MC%ofSD SSeff
mu -195.466 3.00919 169.874 -2.227341 98.9364 14.38885 8.278946     8.4   143
       AC.10      psrf
mu 0.1140479 1.005316
```

And here is a plot of the distribution. Since we did not include a likelihood, it is at the same time the distribution of the prior and of the posterior.

```
plot(pri.jags,var="mu",plot.type=c("trace","density"))
```



2.3 Convergence

In the sample above we saw only observations after round 5000, i.e. we skipped 5000 samples of adaptation and burnin. This was not necessary, since we had only a prior, i.e. the sampler would only sample from the prior.

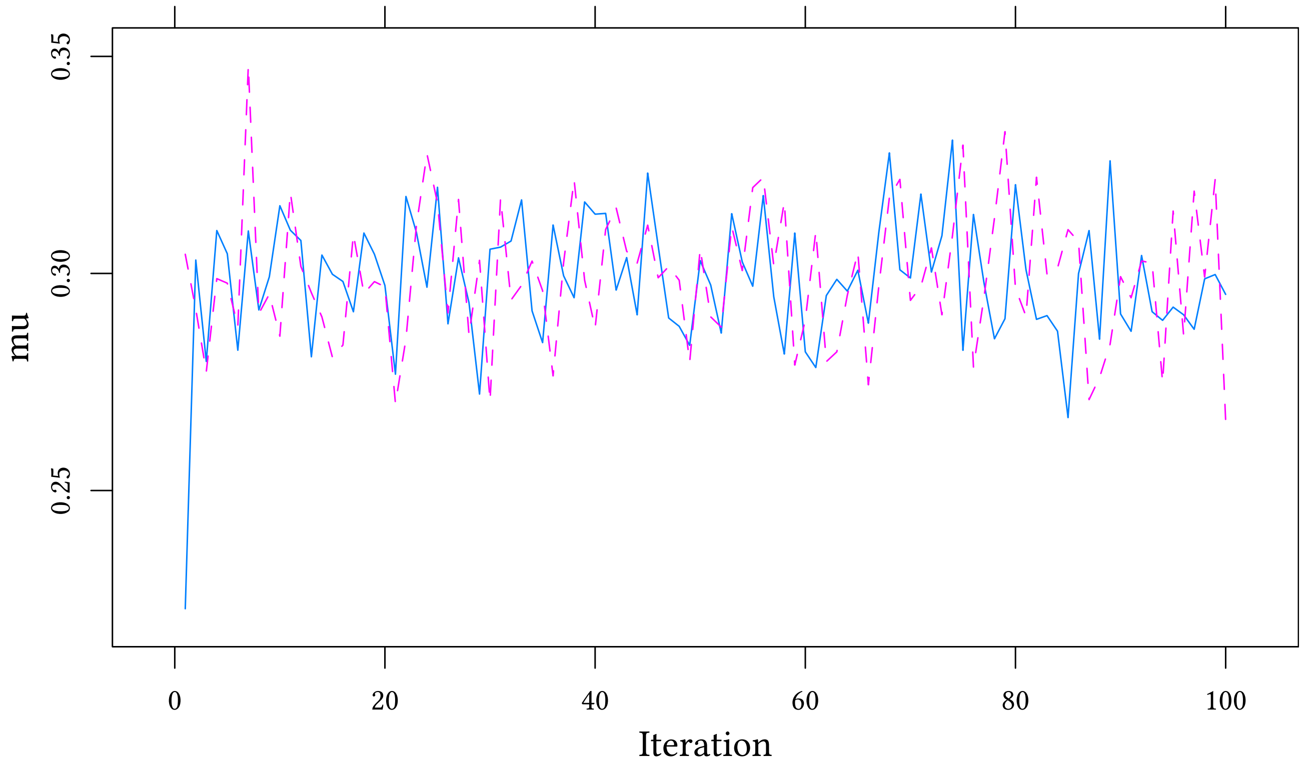
Things become more interesting when we add a likelihood (which we will do next). Then it is not clear that the sampler will directly start sampling from the posterior distribution. It takes some time. The hope is that after 5000 samples of adaptation and burnin the sampler has converged, that it samples from an almost stationary distribution (which is described by our prior and our likelihood).

In the following we add the likelihood to the model. We drop adaptation and burnin and see what happens at the start.

```
ini<-genInit(2,function(i) list(mu=c(100,-100)[i]))
X2.model <- 'model {
 for (i in 1:length(y)) {
       y[i] ~ dnorm(mu,tau)
    }
    mu   ~ dnorm (200,.0001)
    tau  ~ dgamma(.01,.01)
    sd  <- sqrt(1/tau)
}'
X100.jags<-run.jags(model=X2.model,data=list(y=y),
    monitor=c("mu","sd"),adapt=0,burnin=0,sample=100,inits=ini)
```

(To obtain reproducible results, I use a custom *genInit* function in this handout. You find this function in the attachment to this document. You also find a definition in Section 16. For you own calculations you can also drop the *inits=ini* part.)

```
plot(X100.jags,var="mu",plot.type=c("trace"))
```



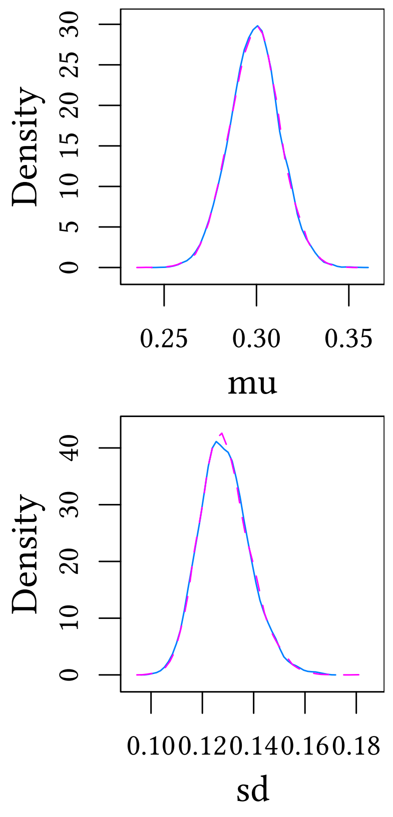
At least here the sampler seems to converge fast. Nevertheless, including a safe number of adaptation and burnin is good practice. Let us look at the posterior with adaptation and burnin:

```
X1001.jags<-run.jags(model=X2.model,data=list(y=y),monitor=c("mu","sd"),
                     inits=ini)
```

2.4 Distribution of the posterior

We have now a posterior distribution for `mu` and one for (the nuisance parameter) `sd`.

```
plot(X1001.jags,var=c("mu","sd"),plot.type=c("density"))
```



Since we sampled from two separate “chains”, we actually have two such distributions. Luckily they are quite similar. This enhances our trust in the estimate of the posterior.

2.5 Accumulating evidence

↑ Above we used non-informative priors. ($\mu \sim N(0, 0.0001)$)

- Assume that we know something about μ (or that we talk to somebody who knows).
  - E.g. we ran a similar study in a different state.

    We found $\mu = 0.4$ and $\sigma_\mu = 0.014$ (i.e. the same σ_μ from our data, but a different μ).

    ($\sigma_\mu = 0.014$ is equivalent to $\tau_\mu = 1/\sigma^2_\mu = 5102$)
  - Now we combine the data, i.e. we use a prior $\mu \sim N(0.4, 5102)$

```
XA.model <- 'model {
 for (i in 1:length(y)) {
        y[i] ~ dnorm(mu,tau)
    }
    mu   ~ dnorm (0.4,1/0.014^2)
    tau  ~ dgamma(.01,.01)
    sd  <- sqrt(1/tau)
}'
XA.jags<-run.jags(model=XA.model,data=list(y=y),monitor=c("mu","sd"))
```

```
summary(XA.jags)

    Lower95    Median  Upper95      Mean          SD      Mode          MCerr
mu 0.329932 0.3514325 0.372681 0.3516260 0.01084617 0.3515811 0.00008563219
sd 0.117564 0.1381880 0.161305 0.1390088 0.01128897 0.1372491 0.00008957363
   MC%ofSD SSeff       AC.10      psrf
mu     0.8 16043 0.002953220 0.9999910
sd     0.8 15884 0.006200908 0.9999954
```

- Prior mean: 0.4
- Sample mean: 0.3
- Posterior mean: 0.35

"A Bayesian is one who, vaguely expecting a horse, and catching a glimpse of a donkey, strongly believes he has seen a mule."

2.6 Priors

- noninformative, flat, vague, diffuse
- weakly informative: intentionally weaker than the available prior knowledge, to keep the parameter within "reasonable bounds".
- informative: available prior knowledge.

3 Conjugate Priors

3.1 Accumulating evidence, continued

Exchangability
When we accumulate data X_1 and X_2 it should not matter, whether we first observe X_1 and then add X_2 or vice versa.

Call $\mathcal{D}$ the distribution of parameter θ.

$$\begin{tikzcd}\mathcal{D}_0 \arrow[r, "X_1"] & \mathcal{D}_1 \arrow[r, "X_2"] & \mathcal{D}_{12}\end{tikzcd}$$
$$\begin{tikzcd}\mathcal{D}_0 \arrow[r, "X_2"] & \mathcal{D}_2 \arrow[r, "X_1"] & \mathcal{D}_{12}\end{tikzcd}$$

This is easier if $\mathcal{D}_0, \mathcal{D}_1, \mathcal{D}_2, \mathcal{D}_{12}$ belong to one family.

For a some combinations of prior distributions and likelihoods we can actually calculate analytically the posterior distribution.

Conjugate priors for a likelihood function

Likelihood	known	model parameter
$X \sim N(\mu, \sigma^2)$	$\tau = 1/\sigma^2.$	$\mu \sim N(\mu_0, \sigma_0^2)$
$X \sim N(\mu, \tau)$	μ	$\tau \sim \Gamma(\alpha_0, \beta_0)$
$X \sim \text{bern}(p)$		$p \sim \text{Beta}(\alpha_0, \beta_0)$
$\vdots$		

If the prior model parameter follows the conjugate prior, then the posterior model parameter is in the same family.

3.2 Normal Likelihood

Conjugate Priors, example: Normal Likelihood μ

- Likelihood: $X \sim N(\mu, \sigma^2)$ with known $\tau = 1/\sigma^2$.
- Model parameter: μ
- Conjugate prior distribution: $\mu \sim N(\mu_0, \sigma_0^2)$
- Prior hyperparameter: μ_0, σ_0^2 i.e. prior $\mu \sim N(\mu_0, \sigma_0^2)$.
- Posterior hyperparameter:

$$\mu_{\text{post}} = \left(\frac{\mu_0}{\sigma_0^2} + \frac{n \cdot \bar{x}}{\sigma^2}\right) \Big/ \left(\frac{1}{\sigma_0^2} + \frac{n}{\sigma^2}\right) = \frac{\tau_0 \mu_0 + n\tau\bar{x}}{\tau_0 + n\tau}$$
$$\tau_{\text{post}} = 1/\sigma^2_{\text{post}} = \left(\frac{1}{\sigma_0^2} + \frac{n}{\sigma^2}\right) = \tau_0 + n\tau$$

i.e. posterior $\mu \sim N(\mu_{\text{post}}, \sigma^2_{\text{post}})$.

In other words:

- Prior parameter: $\mu \sim N(\mu_0, \tau_0)$
- Likelihood: $X \sim N(\mu, \tau)$

- Posterior parameter: $\mu \sim N(\mu_{\text{post}}, \tau_{\text{post}})$.

Terminology:

- Hyperparameters: μ_0, τ_0 (they determine the distribution of μ)
- Parameters: μ, τ
- Posterior hyperparameters: $\mu_{\text{post}}, \tau_{\text{post}}$

Conjugate Priors, example: Normal Likelihood τ

- Likelihood: $X \sim N(\mu, \tau)$ with known μ.
- Model parameter: $\tau = 1/\sigma^2$
- Conjugate prior distribution: $\tau \sim \Gamma(\alpha_0, \beta_0)$
- Prior hyperparameter: α_0, β_0
- Posterior hyperparameter:

$$\begin{aligned} \text{shape} \quad \alpha_{\text{post}} &= \alpha_0 + \frac{n}{2} \\ \text{rate} \quad \beta_{\text{post}} &= \beta_0 + \frac{n}{2}\text{var}(x) \end{aligned}$$

In other words:

- Prior parameter: $\tau \sim \Gamma(\alpha_0, \beta_0)$
- Likelihood: $X \sim N(\mu, \tau)$
- Posterior parameter: $\tau \sim \Gamma(\alpha_{\text{post}}, \beta_{\text{post}})$.

Terminology:

- Hyperparameters: α_0, β_0 (they determine the distribution of μ)
- Parameters: μ, τ
- Posterior hyperparameters: $\alpha_{\text{post}}, \beta_{\text{post}}$

3.3 Bernoulli Likelihood

Conjugate Priors, example: Bernoulli Likelihood

- Likelihood: $X \sim \text{bern}(p)$.
- Model parameter: p
- Conjugate prior distribution: $p \sim \text{Beta}(\alpha_0, \beta_0)$
- Prior hyperparameter: α_0, β_0
- Posterior hyperparameter:

$$\begin{aligned}\alpha_{\text{post}} &= \alpha_0 + \sum x_i \\ \beta_{\text{post}} &= \beta_0 + n - \sum x_i\end{aligned}$$

In other words:

- Prior parameter: $p \sim \text{Beta}(\alpha_0, \beta_0)$
- Likelihood: $X \sim \text{bern}(p)$
- Posterior parameter: $p \sim \text{Beta}(\alpha_{\text{post}}, \beta_{\text{post}})$

Terminology:

- Hyperparameters: α_0, β_0 (they determine the distribution of μ)
- Parameters: μ, τ
- Posterior hyperparameters: α_{post}, β_{post}

3.4 Problems with the analytical approach

- Restrictive for…
  - priors
  - likelihood (“the model” in the frequentist world)
- For many relevant cases we have no analytical solution.
- $\rightarrow$ numerical methods, Markov Chain Monte Carlo (MCMC) methods, Metropolis-Hastings sampling, Gibbs sampling,…

Construct a Markov Chain that has the posterior distribution as its equilibrium distribution.

3.5 Exercises

1. An event can have two possible outcomes, 0 or 1. You are interested in the probability p of obtaining a 1. You assume that p follows a Beta distribution. Your prior is that the parameters of the Beta distribution are $\alpha = \beta = 0$. You observe three times a 1 and no 0. What is your posterior for α and β?

2. Later you observe three more times a 1 and four times 0. Given all your observations, what is now your posterior for α and β?

3. A random variable X follows a normal distribution with mean μ and precision τ. You want to infer the posterior distribution of μ. Your prior for μ also follows a normal distribution $\mu \sim N(\mu_0, \tau_0)$ with hyperparameters $\mu_0 = 10$ and $\tau_0 = 2$. Now you observe a sample of size $n = 10$, mean $\mu = 20$ and precision $\tau = 1/5$. What is your posterior μ_{post}?

4. What is your posterior τ_{post}

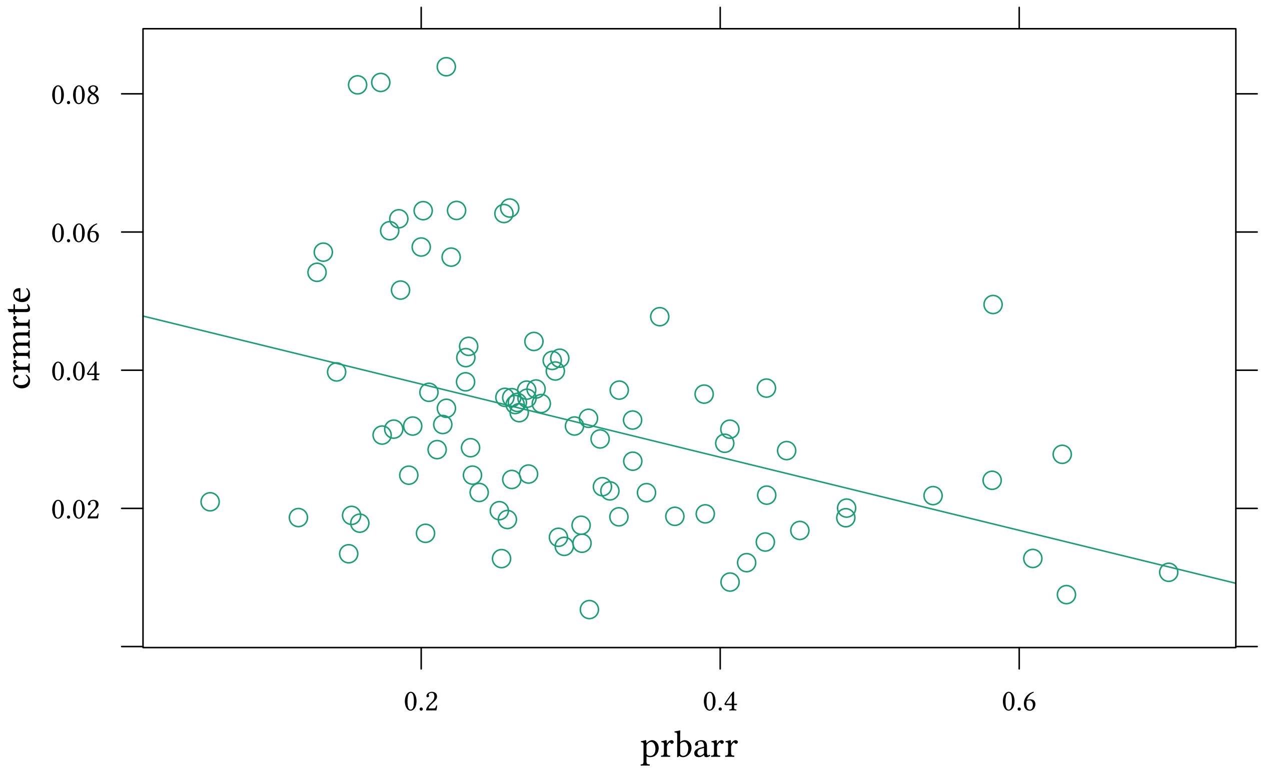
4 Linear Regression

We use linear regression as an example to illustrate some issues of the mechanics behind the MCMC sampling mentioned in the previous section.

4.1 Introduction

Example: Crime in North Carolina in 1981 Let us have another look at the crime rate and the arrest rate in North Carolina.

```
library(Ecdat)
data(Crime)
xyplot(crmrte ~ prbarr,data=Crime,subset=year==81,type=c("p","r"))
```



We suspect that the crime rate is a linear function of the arrest rate. The standard tool would be OLS:

```
est<-lm(crmrte ~ prbarr,data=Crime,subset=year==81)
summary(est)



Call:
lm(formula = crmrte ~ prbarr, data = Crime, subset = year ==
    81)

Residuals:
      Min        1Q    Median        3Q       Max
-0.027125 -0.009932 -0.000848  0.007013  0.046819

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.048577   0.004261  11.400  < 2e-16 ***
prbarr      -0.052924   0.013129  -4.031 0.000118 ***
---
Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1

Residual standard error: 0.01571 on 88 degrees of freedom
Multiple R-squared:  0.1559,Adjusted R-squared:  0.1463
F-statistic: 16.25 on 1 and 88 DF,  p-value: 0.0001177
```

OLS

$$
\begin{aligned}
&Y = \beta_0 + \beta_1 X + u \text{ where } u \sim N(0, \sigma^2)\\
&Y \sim N(\beta_0 + \beta_1 X, \sigma^2)\\
&Y \sim N(\beta_0 + \beta_1 X, \tau)
\end{aligned}
$$

Both notations are equivalent. The former is more common in the frequentist context, the latter more common in the Bayesian context.

Now we do the same exercise in JAGS:

```
data<-with(subset(Crime,year==81),list(y=crmrte,x=prbarr))
reg.model<-'model {
 for (i in 1:length(y)) {
        y[i] ~ dnorm(beta0 + beta1*x[i],tau)
    }
    beta0 ~ dnorm (0,.0001)
    beta1 ~ dnorm (0,.0001)
    tau   ~ dgamma(.01,.01)
}'
reg.jags<-run.jags(model=reg.model,data=data,monitor=c("beta0","beta1"))
```

```
reg.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

        Lower95    Median   Upper95      Mean        SD      Mode      MCerr
beta0   0.03718  0.048729  0.060465  0.048809 0.0059047  0.048566 0.00014557
beta1 -0.089838 -0.053553 -0.018249 -0.053655  0.018233 -0.053532 0.00045766

      MC%ofSD SSeff   AC.10   psrf
beta0     2.5  1645 0.20733 1.0007
beta1     2.5  1587 0.20768 1.0006

Total time taken: 0.4 seconds

summary(est)[["coefficients"]]

               Estimate  Std. Error   t value     Pr(>|t|)
(Intercept)  0.04857749 0.004261233 11.399865 5.087079e-19
prbarr      -0.05292384 0.013128767 -4.031136 1.177237e-04
```

The distribution we get here is very similar to the distribution parameters from the simple OLS.

4.2 Demeaning

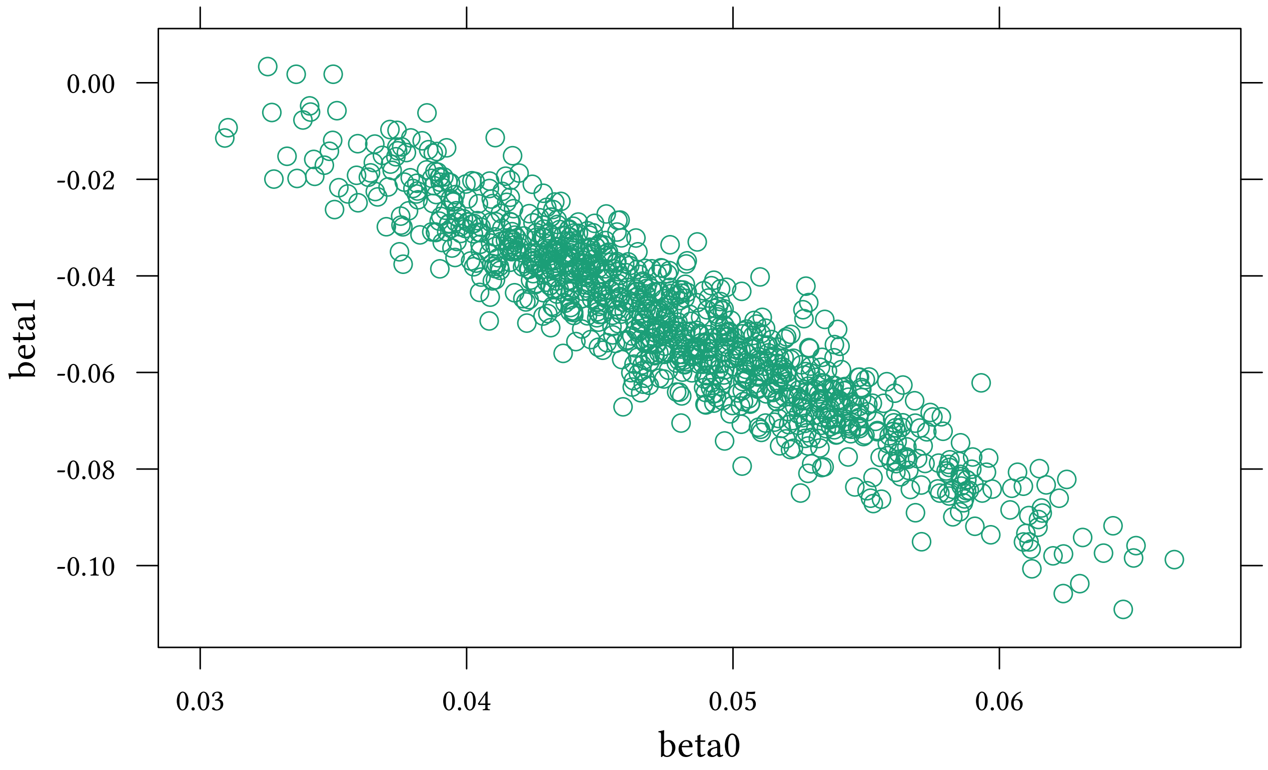
This is a technical issue. Demeaning might help improving the performance of our sampler.

Demeaning does not change the estimate of the coefficient of X, it does change the constant, though.

$$Y = \beta_0 + \beta_1 X \tag{1}$$
$$Y - \bar{Y} = \underbrace{\beta_0 - \bar{Y} + \beta_1 \bar{X}}_{\beta_0'} + \beta_1 (X - \bar{X}) \tag{2}$$

Let us look more closely at the distribution of the sampled posterior:

```
reg.df<-data.frame(combine.mcmc(reg.jags))
xyplot(beta1~beta0,data=head(reg.df,1000))
```



We see that *beta0* and *beta1* are correlated. As we will see below, this correlation makes the Gibbs sampler slower.

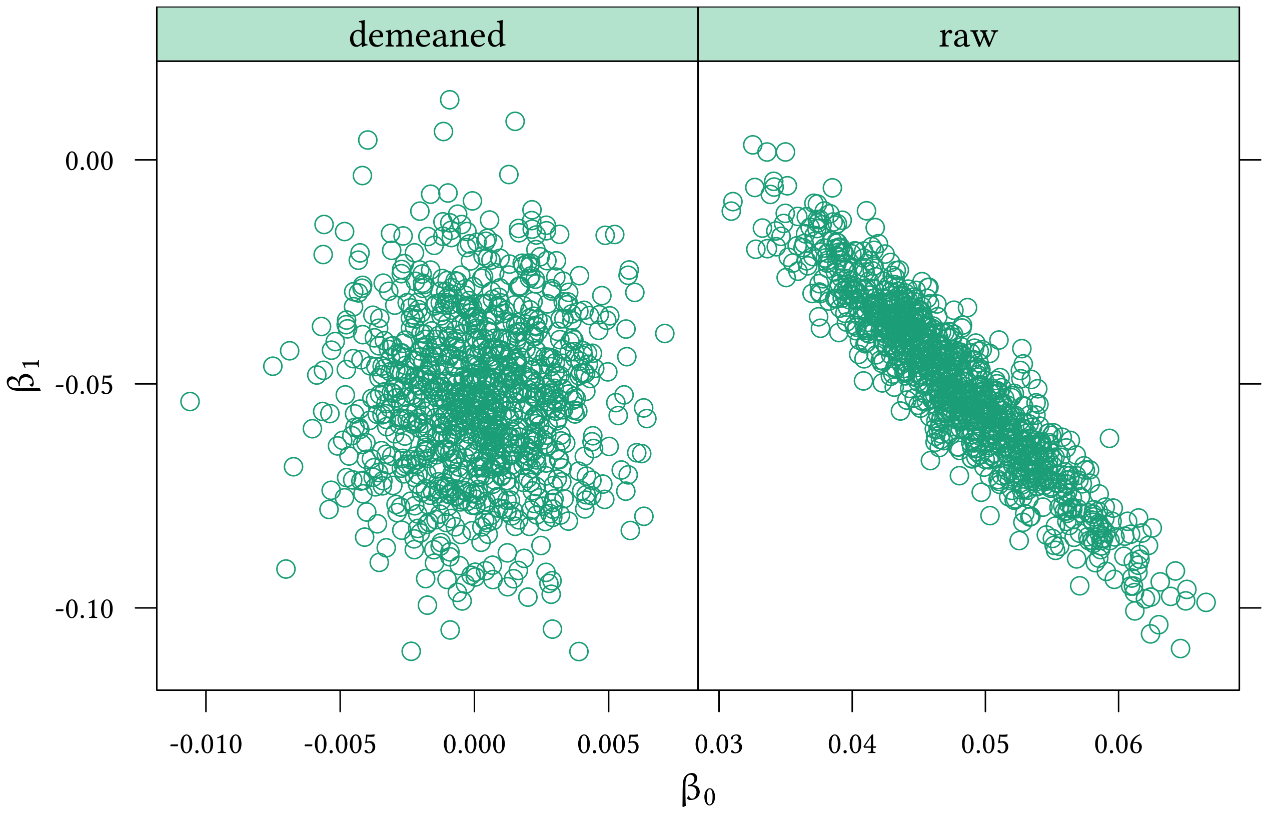
Now we demean the data:

```
data2<-with(data,list(y=y-mean(y),x=x-mean(x)))
reg2.jags<-run.jags(model=reg.model,data=data2,monitor=c("beta0","beta1"))
```

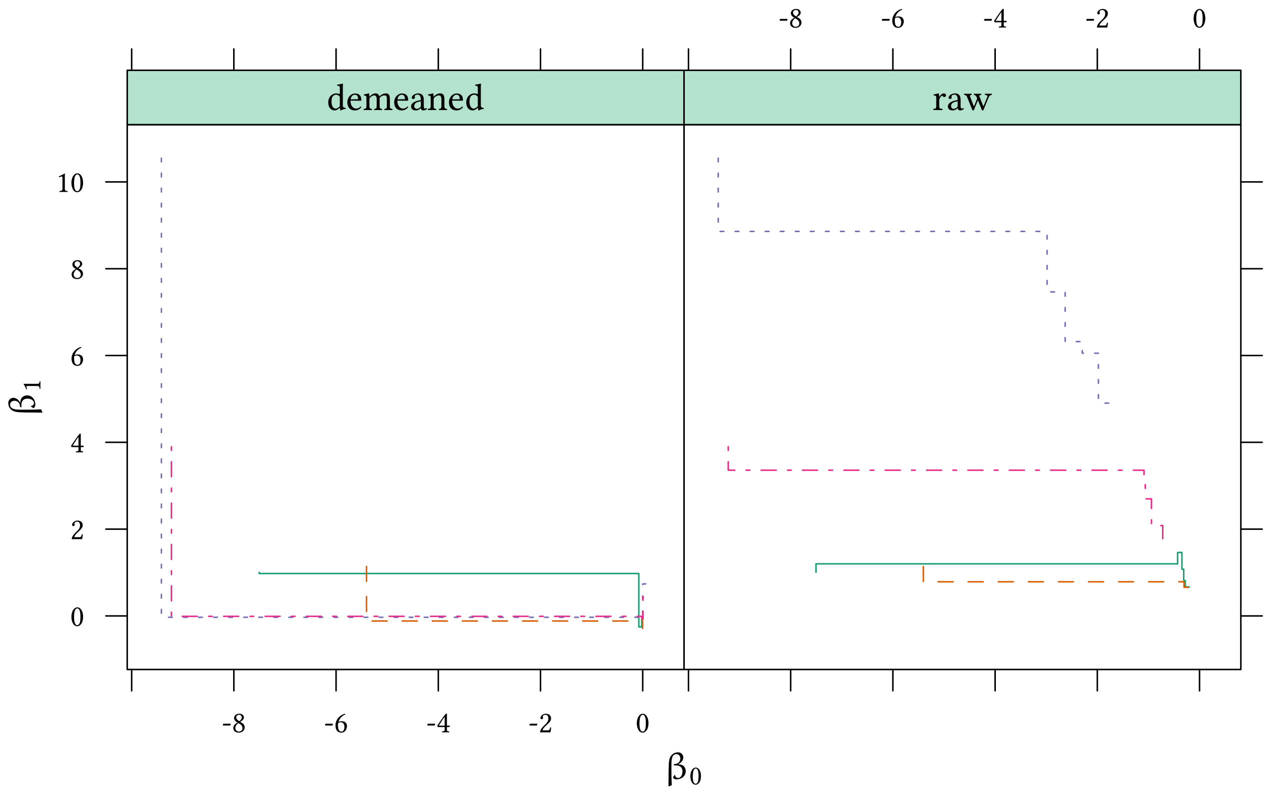
```
reg2.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

         Lower95      Median   Upper95         Mean         SD          Mode
beta0 -0.0045531 -6.5843e-06 0.0045534 -3.5199e-06 0.0023276 -0.000015878
beta1  -0.089072    -0.05303 -0.016717    -0.053151  0.018546    -0.052681

            MCerr MC%ofSD SSeff      AC.10   psrf
beta0 0.000016459     0.7 20000 -0.0079691 1.0003
beta1   0.0001271     0.7 21291  0.0066523 1.0001

Total time taken: 0.4 seconds
```

The estimate for *beta1* does not change (here we assume that we are mainly interested in the marginal effect, i.e. in *beta1*).

Now *beta0* and *beta1* are no longer correlated:

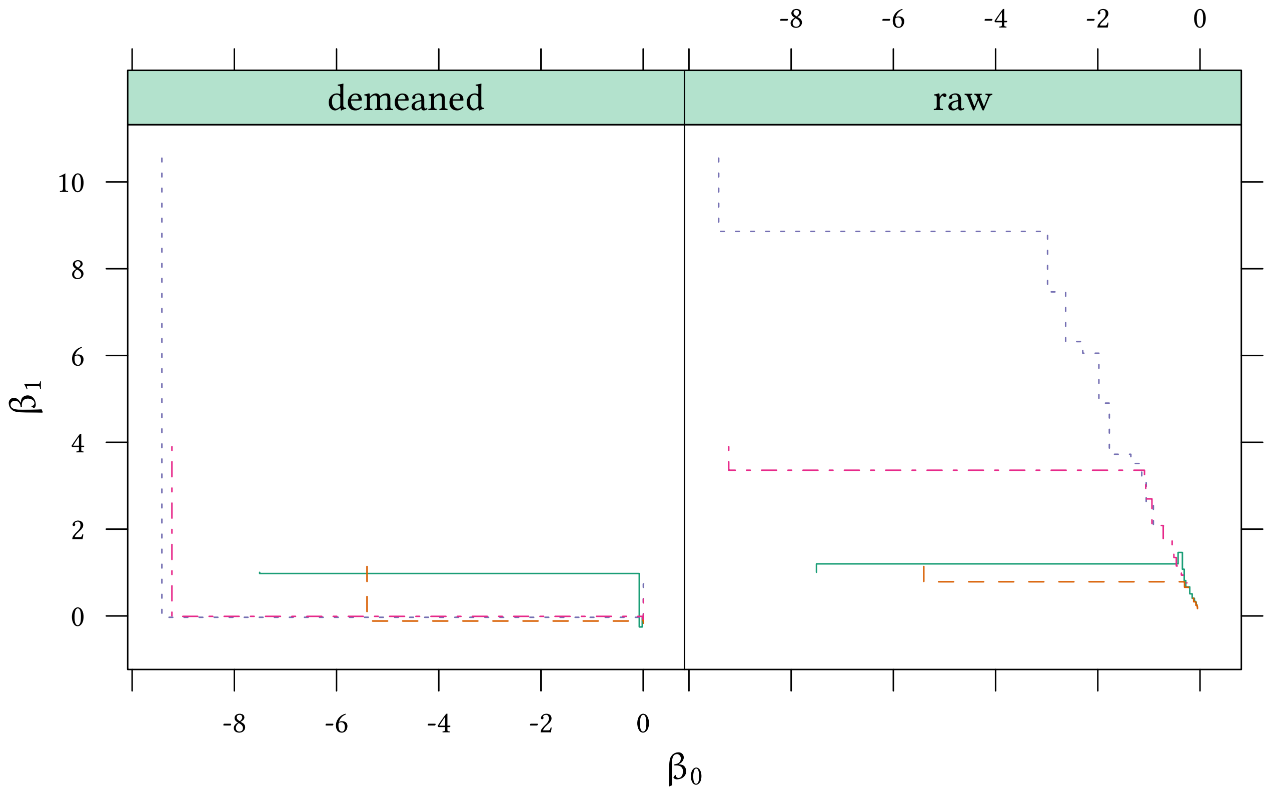


Convergence with raw and demeaned data To better understand convergence, we look at the first few samples in each case. Let us look at 5 chains with 5 samples each:

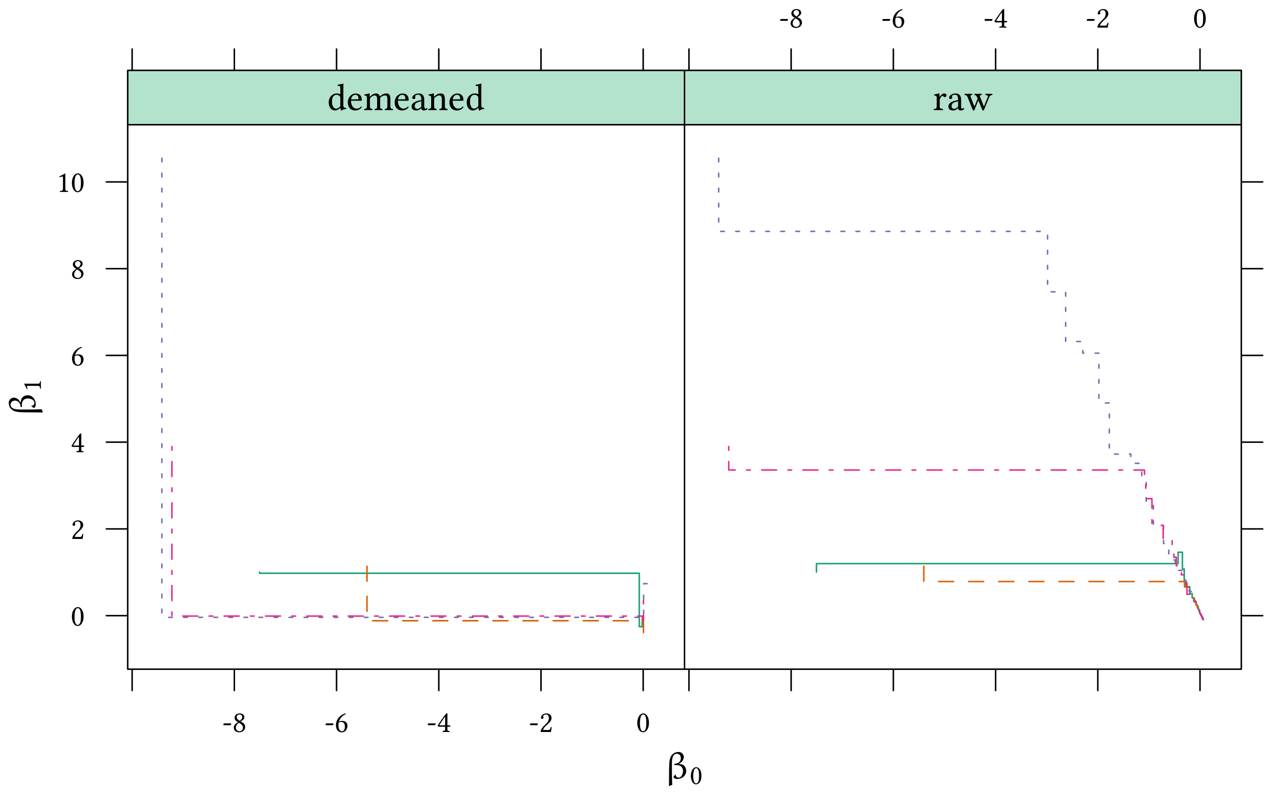


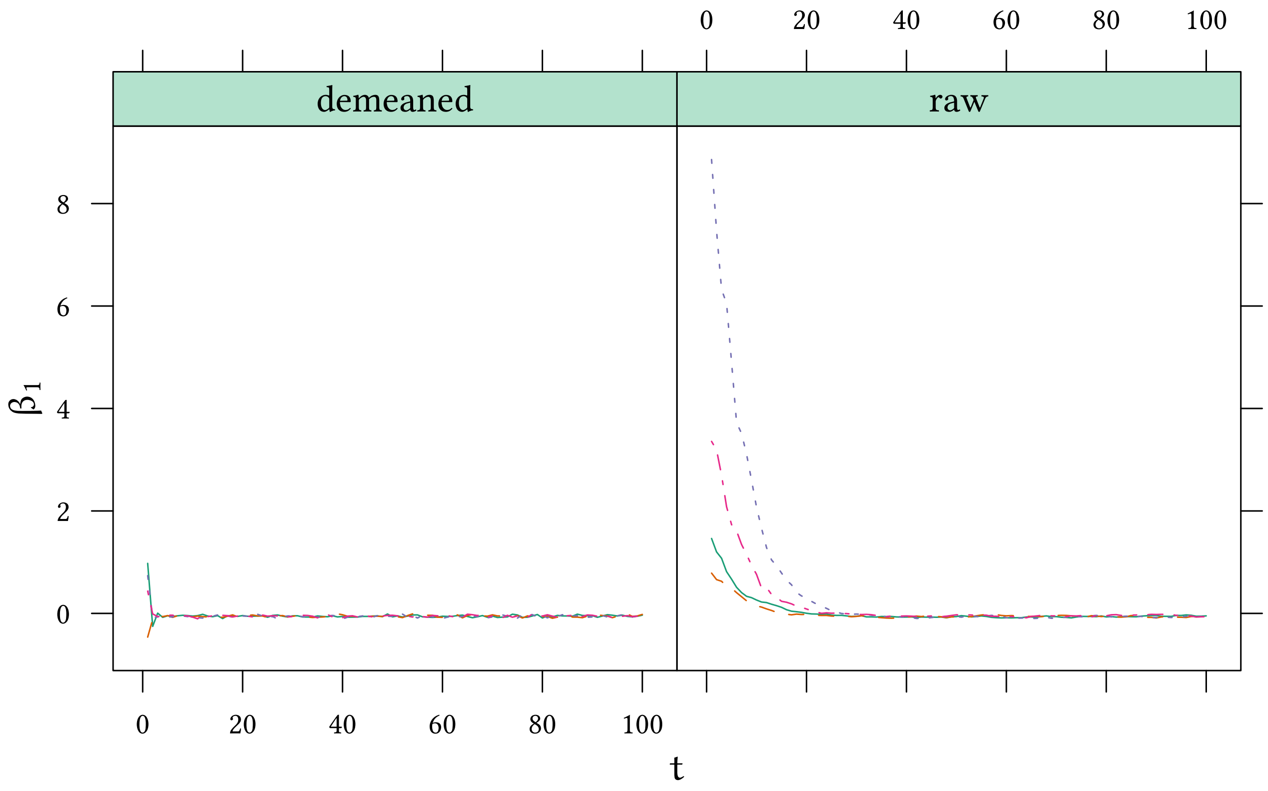
In the demeaned case, the Gibbs sampler jumps almost immediately to the center of the distribution. Convergence is reached within a small number of steps. In the not-demeaned case the Gibbs sampler walks slowly along the joint distribution of `beta0` and `beta1`. It takes a longer number of steps to reach the center of the distribution and to converge.

Here are 10 samples:



Here are 100 samples:



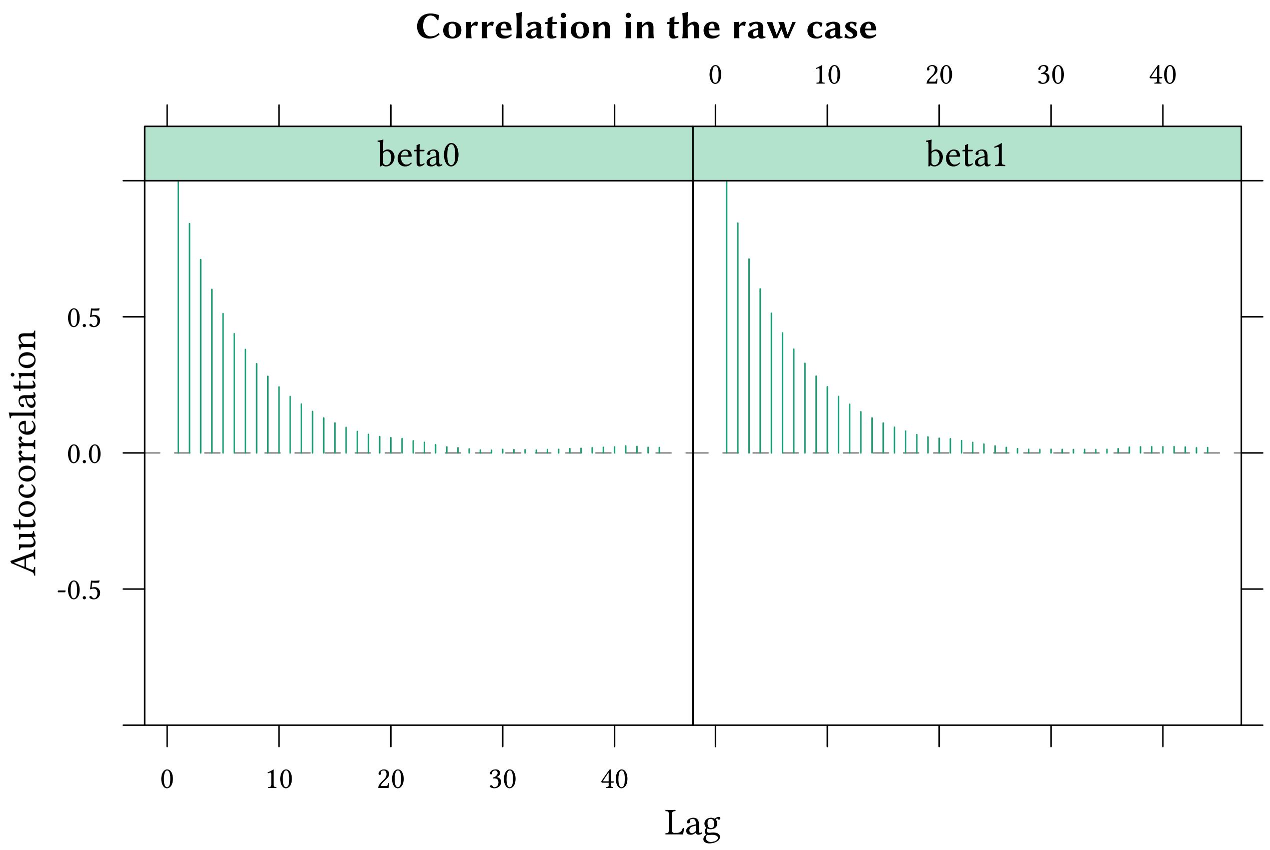


The Gibbs sampler can only increase the probability of *one* single posterior parameter in one step. In the posterior distribution the sampler, therefore, can only move parallel to one of the axes. If the posterior distribution is asymmetric (as in the raw data) convergence is slow.

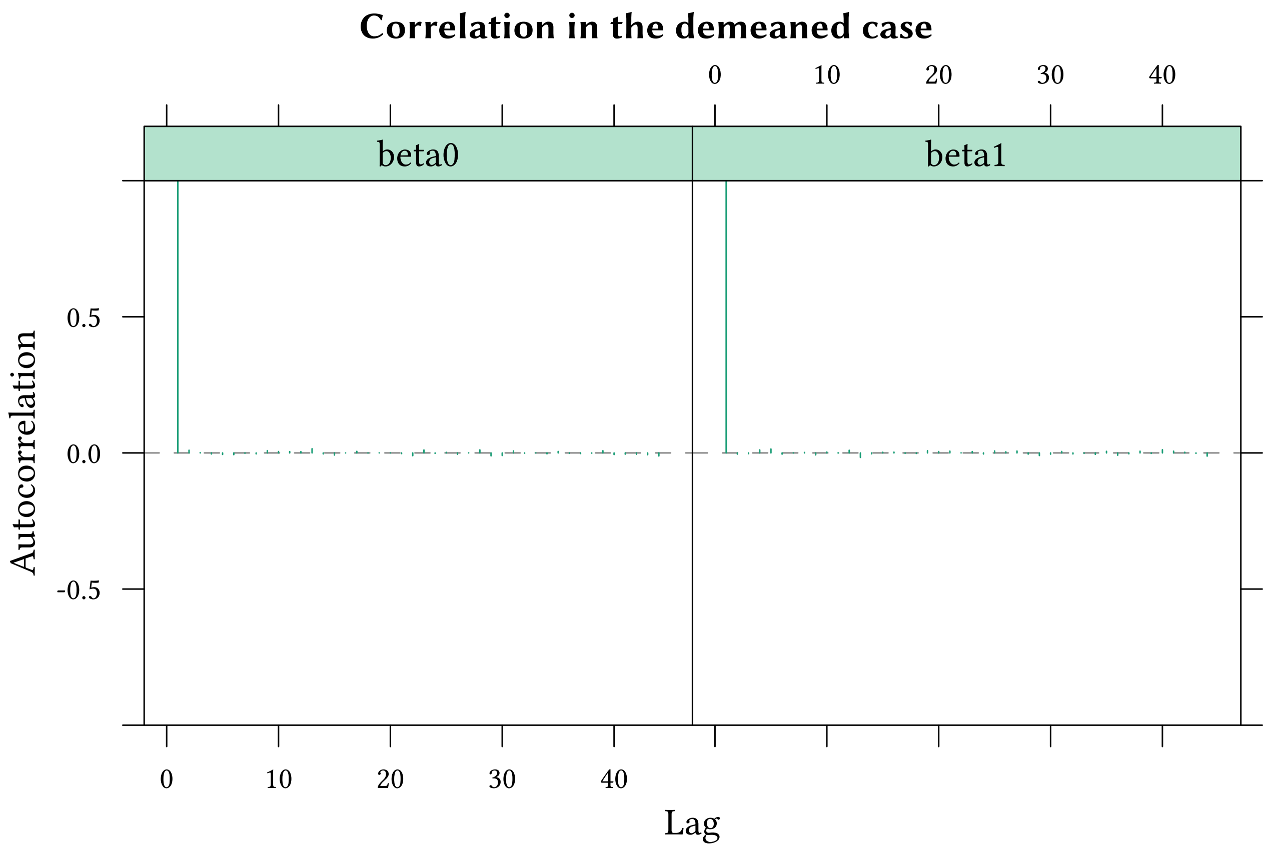
4.3 Correlation

A related problem of the Gibbs sampler is that two successive samples may be correlated.

```
acfplot(as.mcmc(reg.jags),ylim=c(-1,1),aspect="fill",layout=c(2,1))
```



```
acfplot(as.mcmc(reg2.jags),ylim=c(-1,1),aspect="fill",layout=c(2,1))
```



- A sample of 10 000 can, thus, not be treated as 10 000 independent observations.
- Thinning (take only every nth sample) does not lose much information.

4.4 The three steps of the Gibbs sampler

The three steps of the Gibbs sampler

adaptation: optimise the algorithm

burnin: converge to the approximate shape of the distribution

sample: use a fixed algorithm to sample from posterior

Our problem:

- make sure that the sampler has converged

Solution:

- Demeaning (converge quickly to posterior)
- Good init values (start already from within the posterior)

4.5 Exercises

Consider the year 1979 from the data set `LaborSupply` from `Ecdat`.

1. Which variables could explain labor supply?
2. Estimate your model for the year 1979 only.
3. Compare your results with and without demeaning.

5 Finding posteriors

5.1 Overview

$$\underbrace{\Pr(\theta)}_{\text{prior}} \cdot \underbrace{\Pr(X|\theta)}_{\text{likelihood}} \cdot \frac{1}{\underbrace{\Pr(X)}_{\int \Pr(\theta)\cdot\Pr(X|\theta)\,d\theta}} = \underbrace{\Pr(\theta|X)}_{\text{posterior}}$$

Find $\Pr(\theta|X)$:

- Exact: but $\int \Pr(\theta) \cdot \Pr(X|\theta)\,d\theta$ can be hard (except for specific priors and likelihoods).
- MCMC Sampling
  - Rejection sampling: can be very slow (for a high-dimensional problem, and our problems are high-dimensional).
  - Metropolis–Hastings: quicker, samples are correlated, requires sampling of θ from joint distribution $\Pr(X|\theta)$.
  - Gibbs sampling: quicker, samples are correlated, requires sampling of θ_i from conditional (on θ_{-i}) distribution $\Pr(X|\{\theta_i, \theta_{-i}\})$.

    $\rightarrow$ this is easy! (at least much easier than $\Pr(X|\theta)$)

5.2 Example for the exact way:

Above we talked about conjugate priors. Consider the case of Normal Likelihood:

- Likelihood: $N(\mu, \sigma^2)$ with known $\tau = 1/\sigma^2$.
- Model parameter: μ
- Conjugate prior distribution: $\mu \sim N()$
- Prior hyperparameter: μ_0, σ_0^2

- Posterior hyperparameter:

$$\mu_{\text{post}} = \left(\frac{\mu_0}{\sigma_0^2} + \frac{n\cdot\bar{x}}{\sigma^2}\right) \Big/ \left(\frac{1}{\sigma_0^2} + \frac{n}{\sigma^2}\right) = \frac{\tau_0\mu_0 + n\tau\bar{x}}{\tau_0 + n\tau}$$

$$\tau_{\text{post}} = 1/\sigma^2_{\text{post}} = \left(\frac{1}{\sigma_0^2} + \frac{n}{\sigma^2}\right) = \tau_0 + n\tau$$

5.3 Rejection sampling

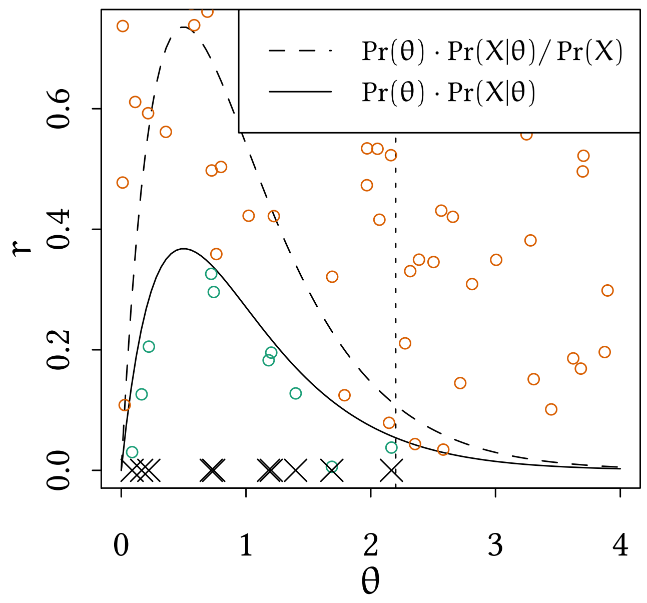
$$\underbrace{\Pr(\theta)}_{\text{prior}} \cdot \underbrace{\Pr(X|\theta)}_{\text{likelihood}} \cdot \frac{1}{\underbrace{\Pr(X)}_{\int \Pr(\theta)\cdot\Pr(X|\theta)\,d\theta}} = \underbrace{\Pr(\theta|X)}_{\text{posterior}}$$

How it works: Iterate the following:

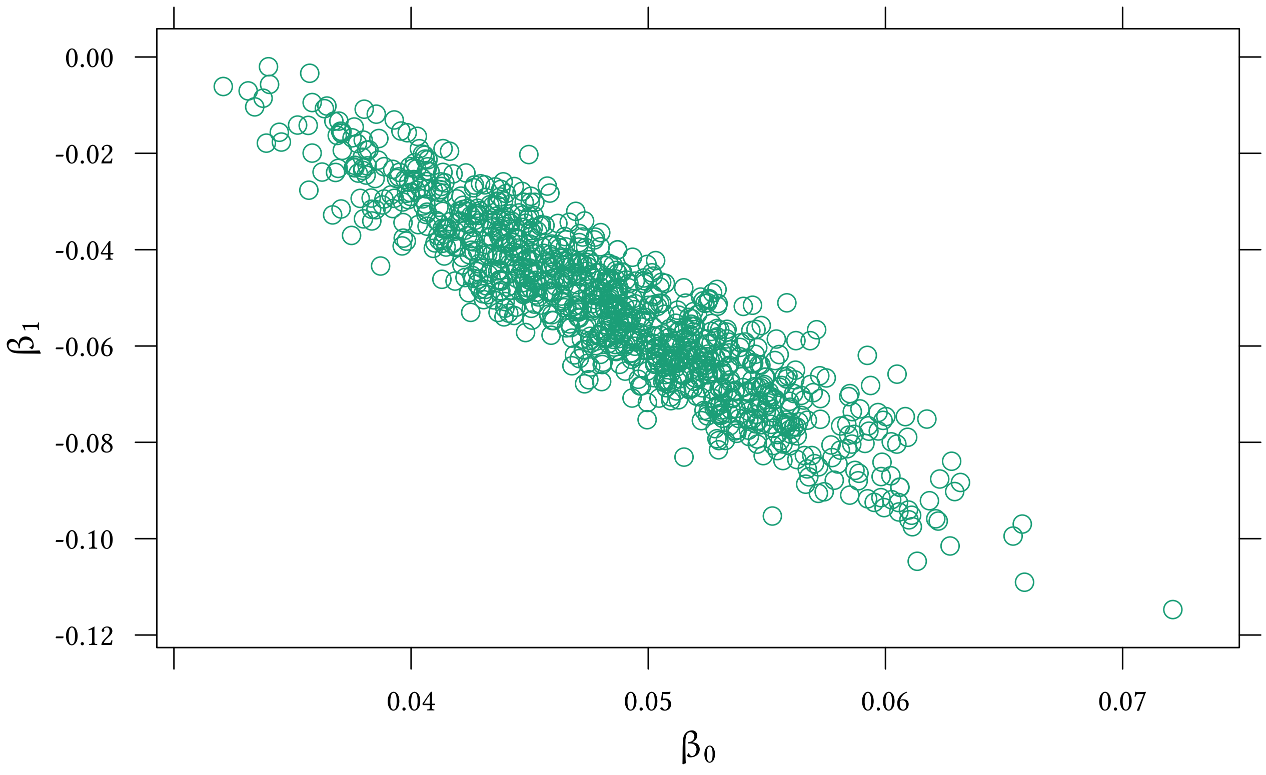
- Sample a candidate θ and a uniformly distributed random number r.
- If $\Pr(\theta)\cdot\Pr(X|\theta) > r$ then θ goes into the sample.

Problems:

- Slow (reject most of the time)
- $\max(r) > \max(\Pr(\theta)\cdot\Pr(X|\theta))$



The more dimensions we have, the more rejections. It would be nice to sample mainly in the posterior.



5.4 Metropolis-Hastings

$$\underbrace{\Pr(\theta)}_{\text{prior}} \cdot \underbrace{\Pr(X|\theta)}_{\text{likelihood}} \cdot \frac{1}{\underbrace{\Pr(X)}_{\int \Pr(\theta)\cdot\Pr(X|\theta)\,d\theta}} = \underbrace{\Pr(\theta|X)}_{\text{posterior}}$$

Generates a sample of $\Pr(\theta|X)$, needs only $f(\theta) = \Pr(\theta) \cdot \Pr(X|\theta)$ (more generally, MH requires only a function which is *proportional* to the density function desired).

How it works:

- Starting point $\eta = \theta_0$, arbitrary symmetric PDF $Q(\theta|\eta)$, e.g. $Q = N$.
- Iterate:
  - Sample a candidate $\theta' \sim Q(\theta'|\theta_t)$.
  - Acceptance ratio is $\alpha = f(\theta')/f(\theta_t)$.
  - If $\alpha \geqslant 1$: $\underbrace{\theta_{t+1} = \theta'}_{\text{jump}}$
  - If $\alpha < 1$: with probability α we have $\underbrace{\theta_{t+1} = \theta'}_{\text{jump}}$, otherwise $\underbrace{\theta_{t+1} = \theta_t}_{\text{stay}}$.

Advantages:

- Faster than rejection sampling (in particular if θ is from a higher dimension).

Disadvantages:

- Samples are correlated (depending on Q).
  - If Q makes wide jumps: more rejections but less correlation.
  - If Q makes small jumps: fewer rejections but more correlation.
- Initial samples are from a different distribution. “burn-in” required.
- Finding a “good” jumping distribution $Q(x|y)$ can be tricky.

5.5 Gibbs sampling

Essentially as in Metropolis-Hastings, except that sampling is performed for each component of θ sequentially.

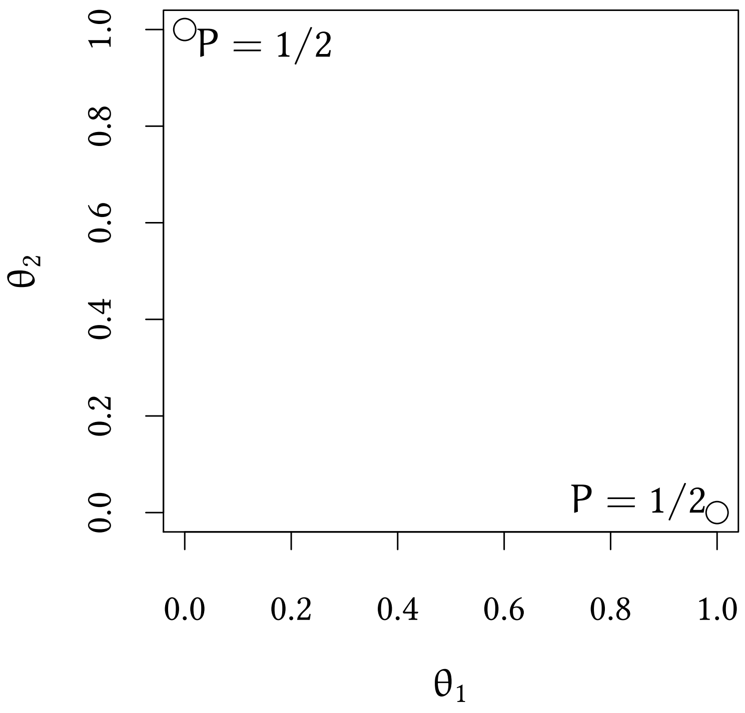
- determine θ_1^{t+1} with $f(\theta_1|\theta_2^t, \theta_3^t, \theta_4^t, \ldots, \theta_n^t)$
- determine θ_2^{t+1} with $f(\theta_2|\theta_1^{t+1}, \theta_3^t, \theta_4^t, \ldots, \theta_n^t)$
- determine θ_3^{t+1} with $f(\theta_3|\theta_1^{t+1}, \theta_2^{t+1}, \theta_4^t, \ldots, \theta_n^t)$
- $\vdots$
- determine θ_n^{t+1} with $f(\theta_n|\theta_1^{t+1}, \theta_2^{t+1}, \ldots, \theta_{n-1}^{t+1})$

Advantages:

- Requires only conditional distributions. $f(\theta_i|\theta_{-1})$, not joint distributions.
- Finding a “good” jumping distribution $Q(x|y)$ is easier.

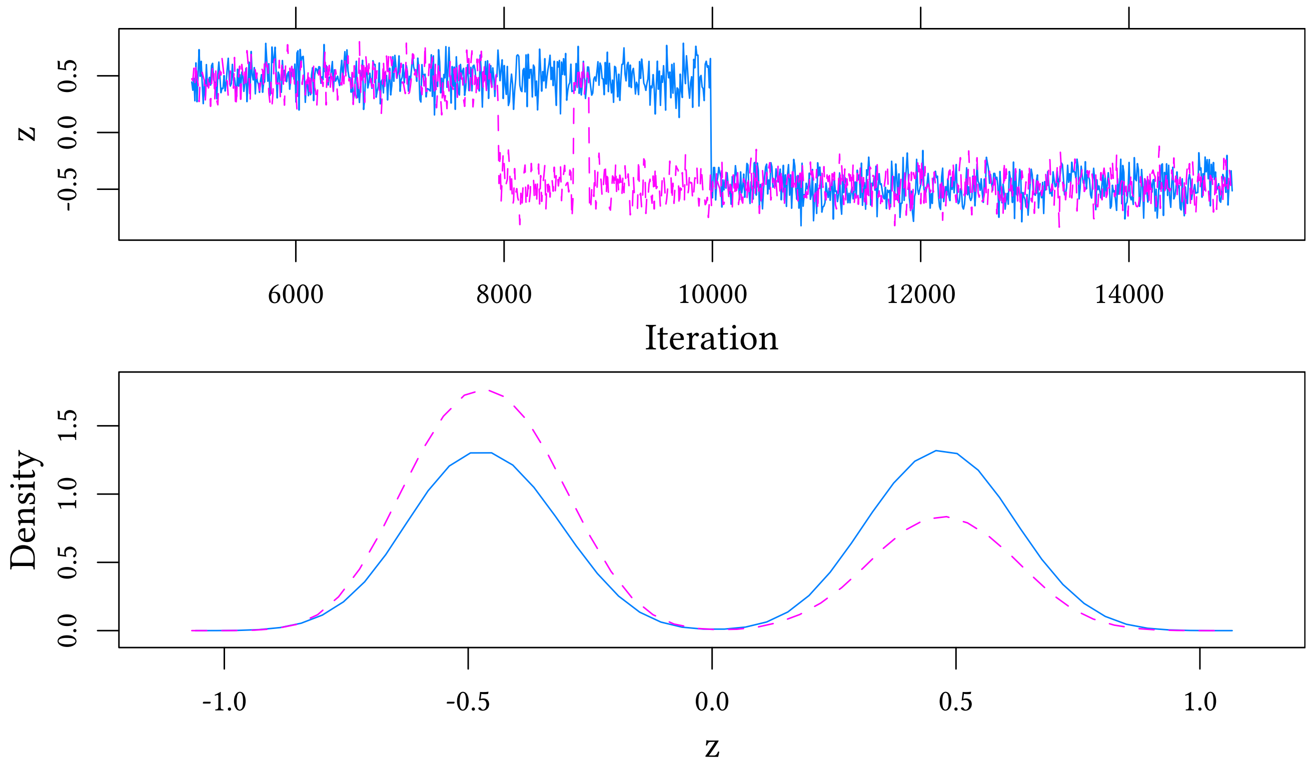
Disadvantages:

- Samples are correlated (potentially more than in MH if the number of dimensions is large).
- Initial samples are from a different distribution. “burn-in” required.
- Can get stuck on “unconnected islands”.



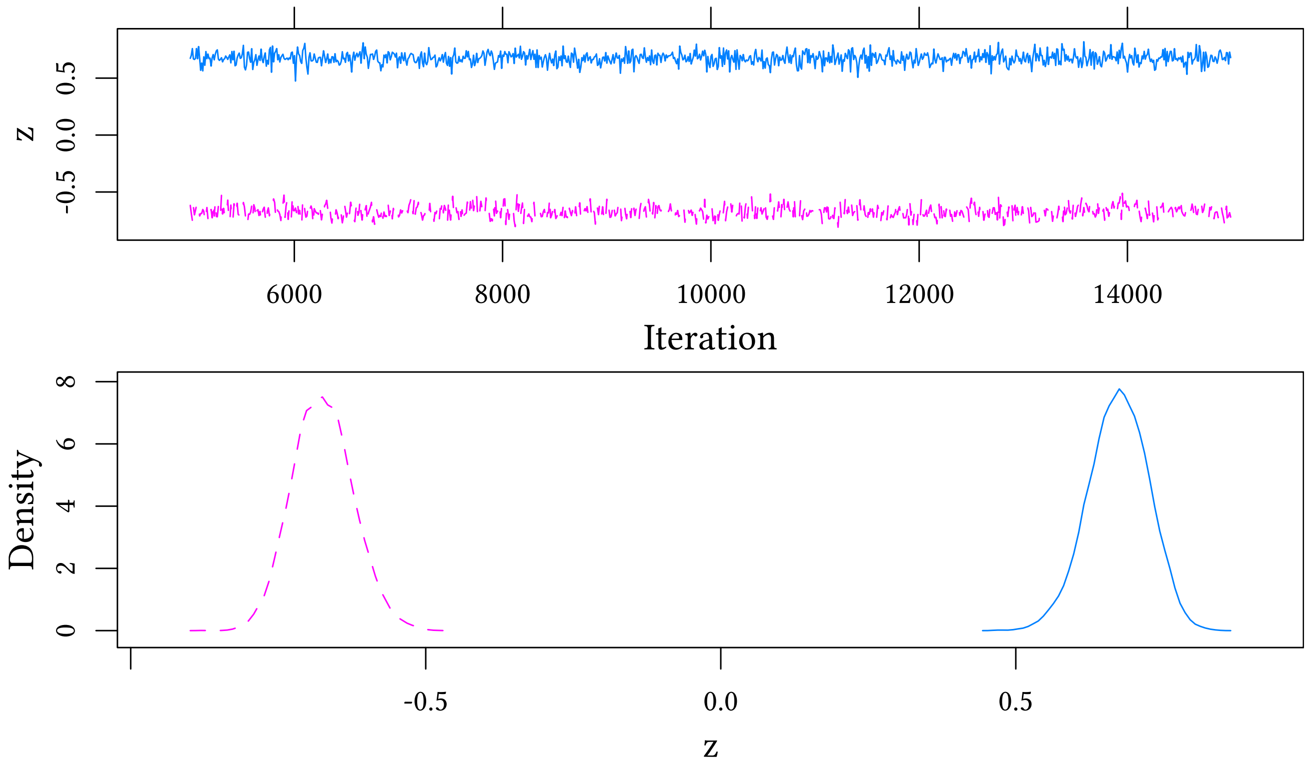
In the following example we create on purpose a situation with two (almost) unconnected islands:

```
x<-rbinom(9,1,.5)
x

[1] 0 0 0 1 0 1 0 0 0

island.mod<-'model {
 for (i in 1:length(x)) {
        x[i] ~ dbern(z^2)
    }
  z ~ dunif(-1,1)
}'
island.jags<-run.jags(model=island.mod,data=list(x=x),monitor=c("z"),
                      inits=ini)
```



Now we create more evidence (of the same type). This makes the Gibbs sampler more persistent.

```
x<-rbinom(50,1,.5)
x

 [1] 0 0 0 1 0 1 0 0 0 0 1 0 0 0 1 0 1 0 1 0 1 1 1 0 1 0 1 0 1 0 0 0 0 1 0 1 1 0
[39] 1 0 1 0 1 0 0 1 1 1 1 1

island2.jags<-run.jags(model=island.mod,data=list(x=x),monitor=c("z"),
                       inits=ini)
```



5.6 Check convergence

5.6.1 Gelman, Rubin (1992): potential scale reduction factor

Idea: take k chains, discard "warm-up", split remaining chains, so that we have $2k$ sequences $\{\psi\}$, each of length n.

$$\begin{aligned} B &= \text{between sequence variance} \\ W &= \text{within sequence variance} \end{aligned}$$

Variance of all chains combined:

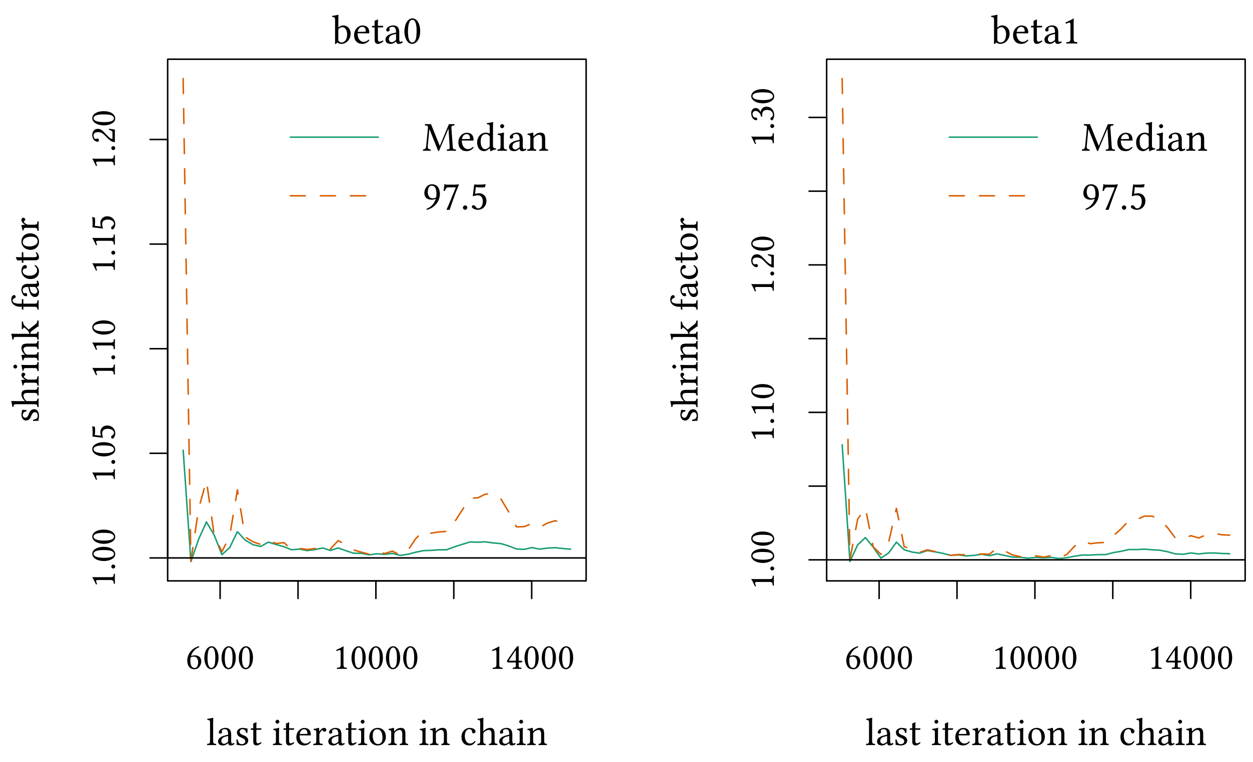
$$\hat{\sigma}^2 = \frac{n-1}{n}W + \frac{B}{n}$$

Potential scale reduction:

$$\hat{R} = \sqrt{\frac{\hat{\sigma}^2}{W}}$$

Let us first look at the *psrf* for a "nice" case:

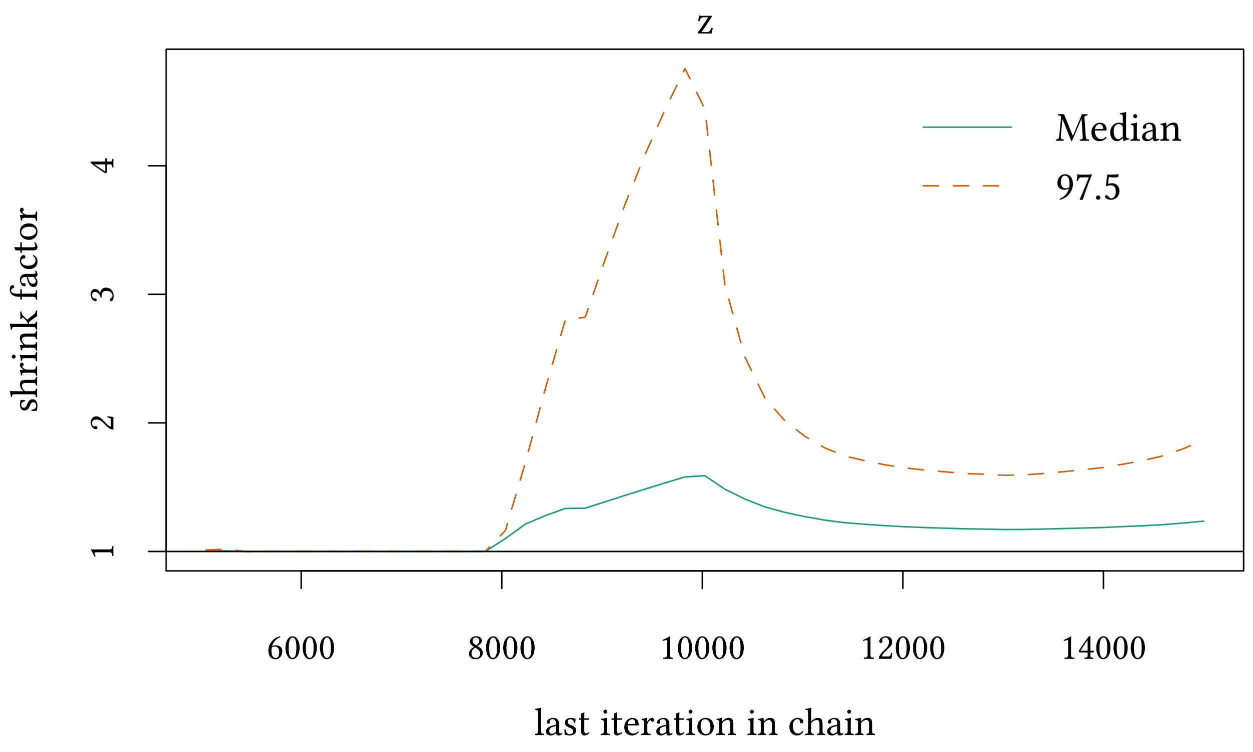
```
gelman.plot(reg.jags)
```



```
gelman.diag(reg.jags)

Potential scale reduction factors:

      Point est. Upper C.I.
beta0          1       1.02
beta1          1       1.02

Multivariate psrf

1

summary(reg.jags)[,c("Mean","SD","SSeff","psrf")]

             Mean          SD SSeff     psrf
beta0  0.04852363 0.006013956  1790 1.004317
beta1 -0.05281219 0.018536459  1625 1.003977
```

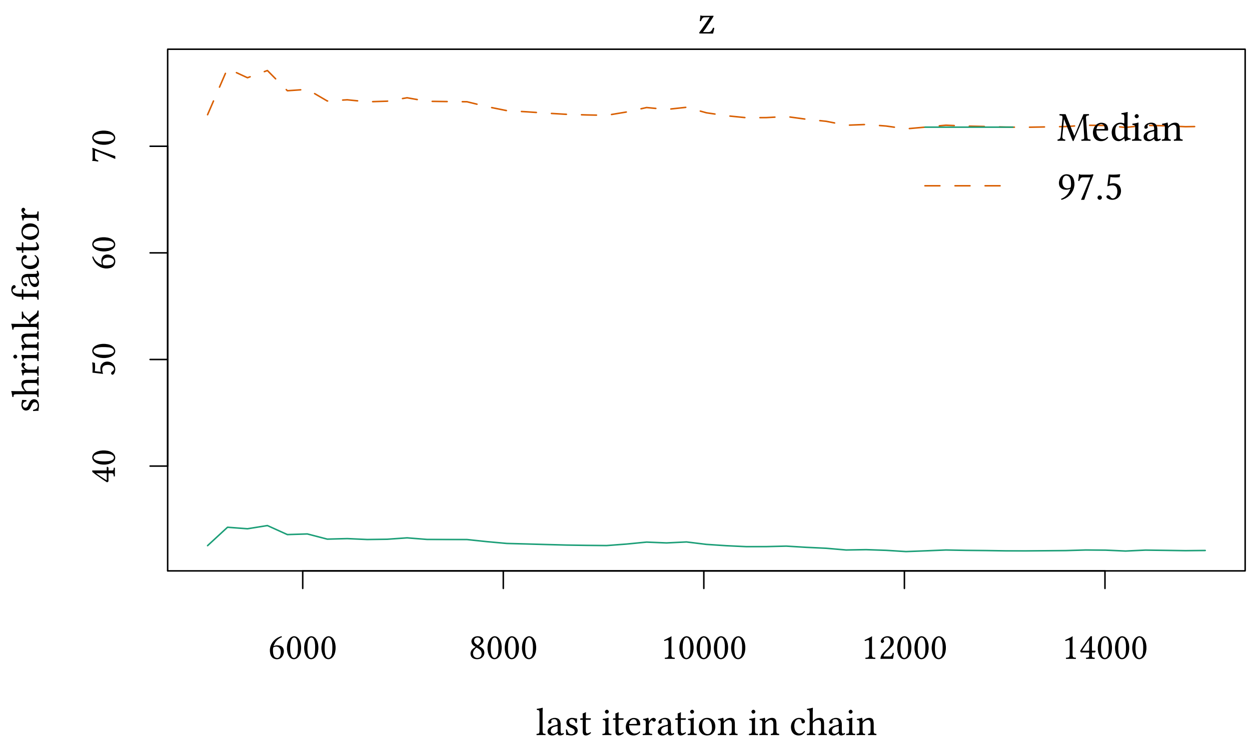
And now the island case:

```
gelman.plot(island.jags)
```



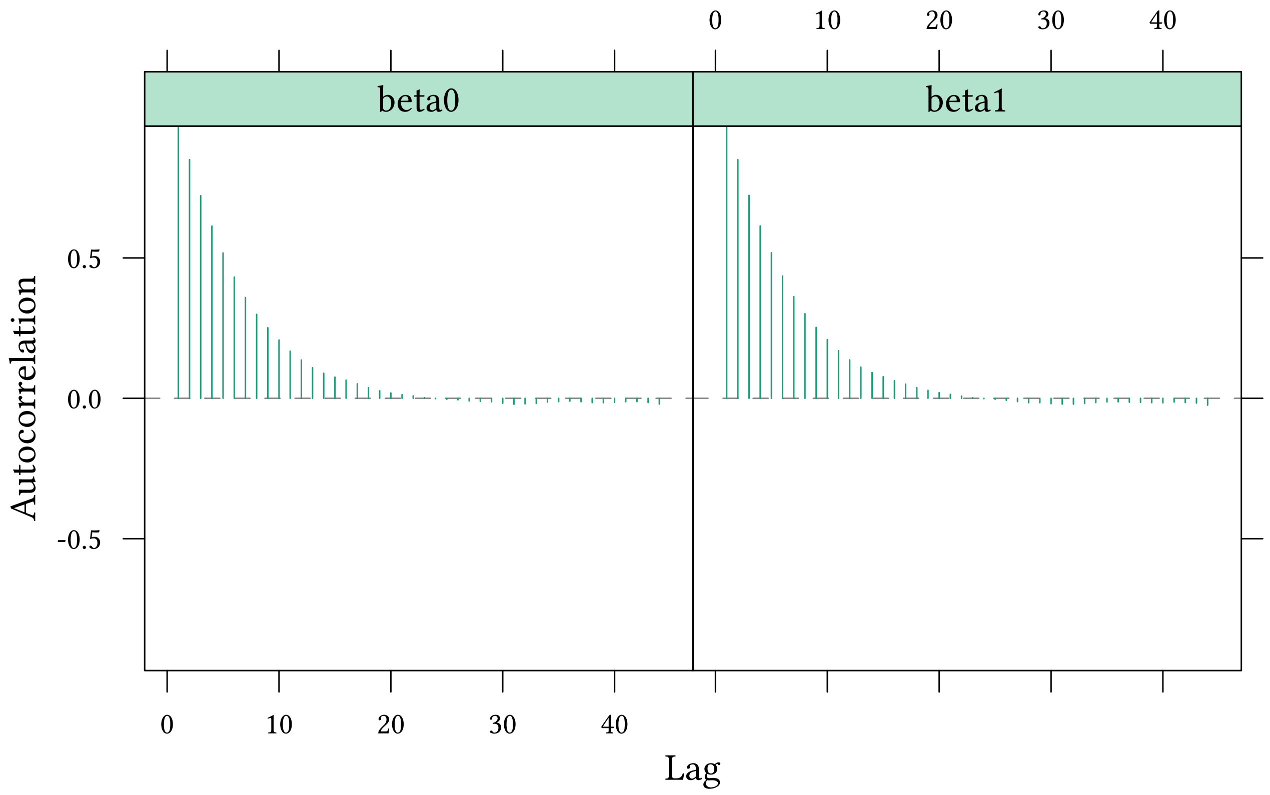
```
gelman.diag(island.jags)

Potential scale reduction factors:

  Point est. Upper C.I.
z       1.24       1.87

summary(island.jags)[,c("Mean","SD","SSeff","psrf")]

       Mean           SD        SSeff         psrf
-0.08831173   0.47855963   7.00000000   1.06201321
```

```
gelman.plot(island2.jags)
```



```
gelman.diag(island2.jags)

Potential scale reduction factors:

  Point est. Upper C.I.
z       32.1       71.9

summary(island2.jags)[,c("Mean","SD","SSeff","psrf")]

            Mean                SD             SSeff              psrf
   -0.0003617406      0.6761477054 11651.0000000000     32.3159757818
```

```
acfplot(as.mcmc(reg.jags),aspect="fill",layout=c(2,1))
```



As a result of autocorrelation, the "effective size" is smaller than the sample size.

```
effectiveSize(as.mcmc.list(reg.jags))

   beta0    beta1
1789.540 1624.828

effectiveSize(as.mcmc.list(reg2.jags))

   beta0    beta1
20451.02 19314.84

effectiveSize(as.mcmc.list(island.jags))

       z
7.127945

effectiveSize(as.mcmc.list(island2.jags))

      z
11650.9
```

The effective sample size is also shown in the standard summary:
As a result of autocorrelation, the "effective size" is smaller than the sample size.

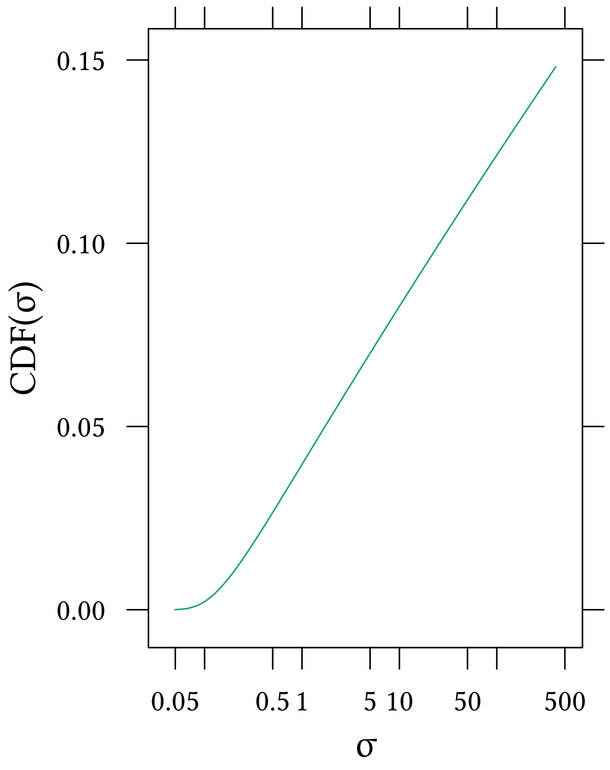
```
summary(reg.jags)[,c("Mean","SD","SSeff","psrf")]

             Mean          SD SSeff     psrf
beta0  0.04852363 0.006013956  1790 1.004317
beta1 -0.05281219 0.018536459  1625 1.003977
```

```
summary(reg2.jags)[,c("Mean","SD","SSeff","psrf")]

                  Mean          SD  SSeff     psrf
beta0  0.000002490592 0.002313587 20451 1.000003
beta1 -0.052811075786 0.018378246 19315 1.000053

summary(island.jags)[,c("Mean","SD","SSeff","psrf")]

       Mean          SD       SSeff        psrf
-0.08831173  0.47855963  7.00000000  1.06201321

summary(island2.jags)[,c("Mean","SD","SSeff","psrf")]

            Mean                 SD            SSeff              psrf
   -0.0003617406     0.6761477054 11651.0000000000    32.3159757818
```

5.7 A better vague prior for τ

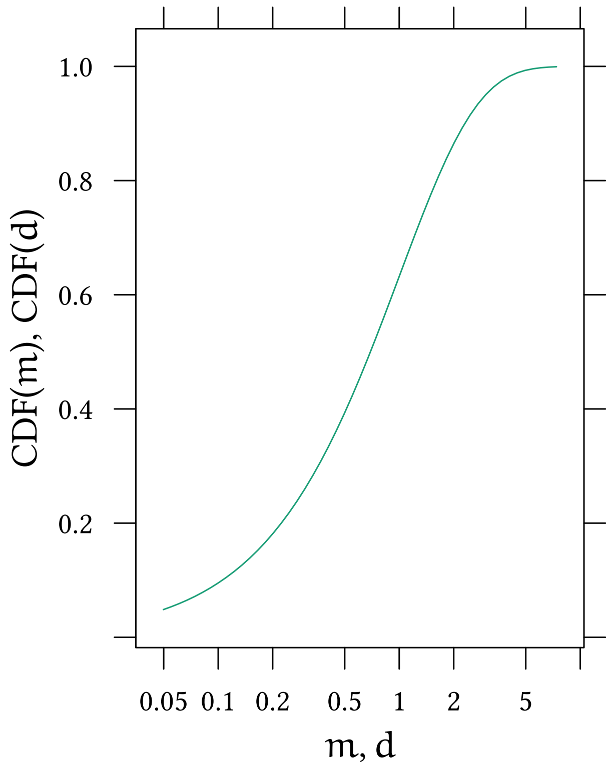
When we specify a regression model we need a precision parameter τ. So far we did this:

```
reg.model<-'model {
 for (i in 1:length(y)) {
        y[i] ~ dnorm(beta0 + beta1*x[i],tau)
    }
    beta0 ~ dnorm (0,.0001)
    beta1 ~ dnorm (0,.0001)
    tau   ~ dgamma(.01,.01)
}'
```



Here is an alternative specification:

```
reg2.model<-'model {
 for (i in 1:length(y)) {
        y[i] ~ dnorm(beta0 + beta1*x[i],tau)
    }
    beta0 ~ dnorm (0,.0001)
    beta1 ~ dnorm (0,.0001)
    tau   ~ dgamma(m^2/d^2,m/d^2)
    m     ~ dgamma(1,1)
    d     ~ dgamma(1,1)
}'
```



- $\tau \sim \Gamma(0.01, 0.01)$

Remember:

- If $\tau \sim \Gamma(\alpha, \beta)$ then $E(\tau) = \alpha/\beta$ and $\text{var}(\tau) = \alpha/\beta^2$.
- $\alpha = 0.01$, $\beta = 0.01$ works well if $E(\tau) \approx 1$ and $\text{var}(\tau) \approx 100$.

Alternative:

- $\tau \sim \Gamma\left(\frac{m^2}{d^2}, \frac{m}{d^2}\right)$
- $m \sim \Gamma(1, 1)$
- $d \sim \Gamma(1, 1)$

$\rightarrow E(\tau) = m, \text{var}(\tau) = d^2$

- Speed: no substantial loss
- Convergence: often faster

5.8 More on History

To learn more about the development of the field, have a look at the following text:

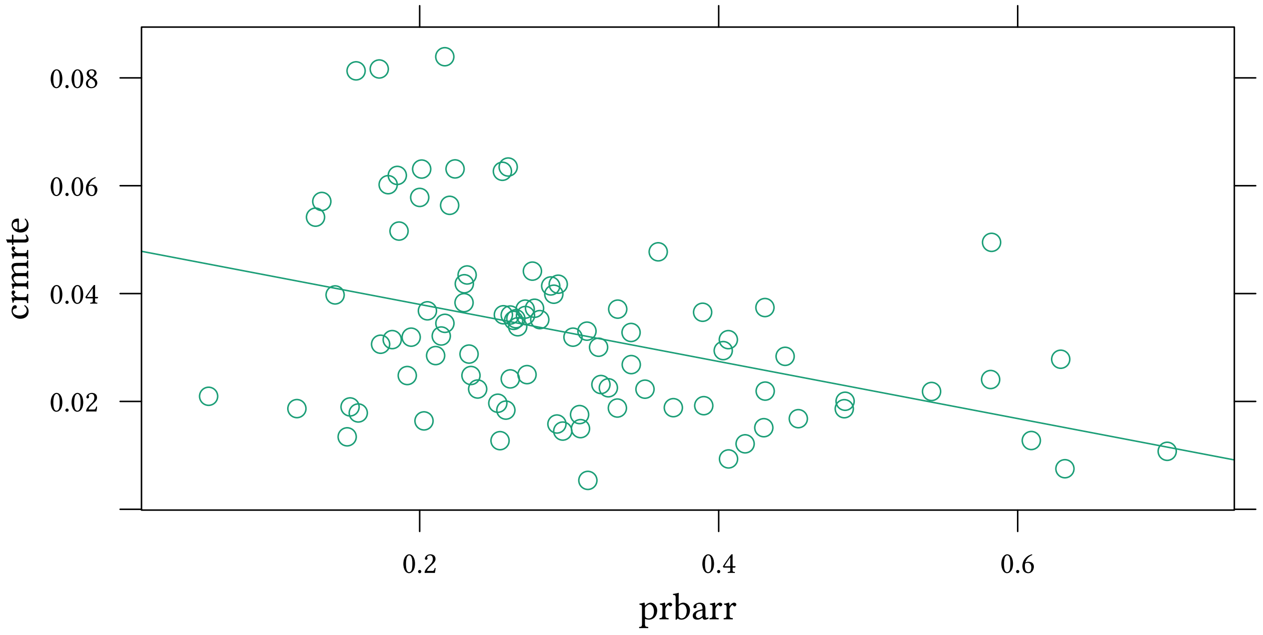
Christian Robert and George Casella (2011). A Short History of Markov Chain Monte Carlo: Subjective Recollections from Incomplete Data. *Statistical Science.* 26(1), 102–115.

6 Robust regression

6.1 Robust regression with the Crime data

Crime rate and probability of arrest:

```
xyplot(crmrte~prbarr,data=subset(Crime,year==81),type=c("p","r"))
```



Is the linear regression estimate driven by outliers?

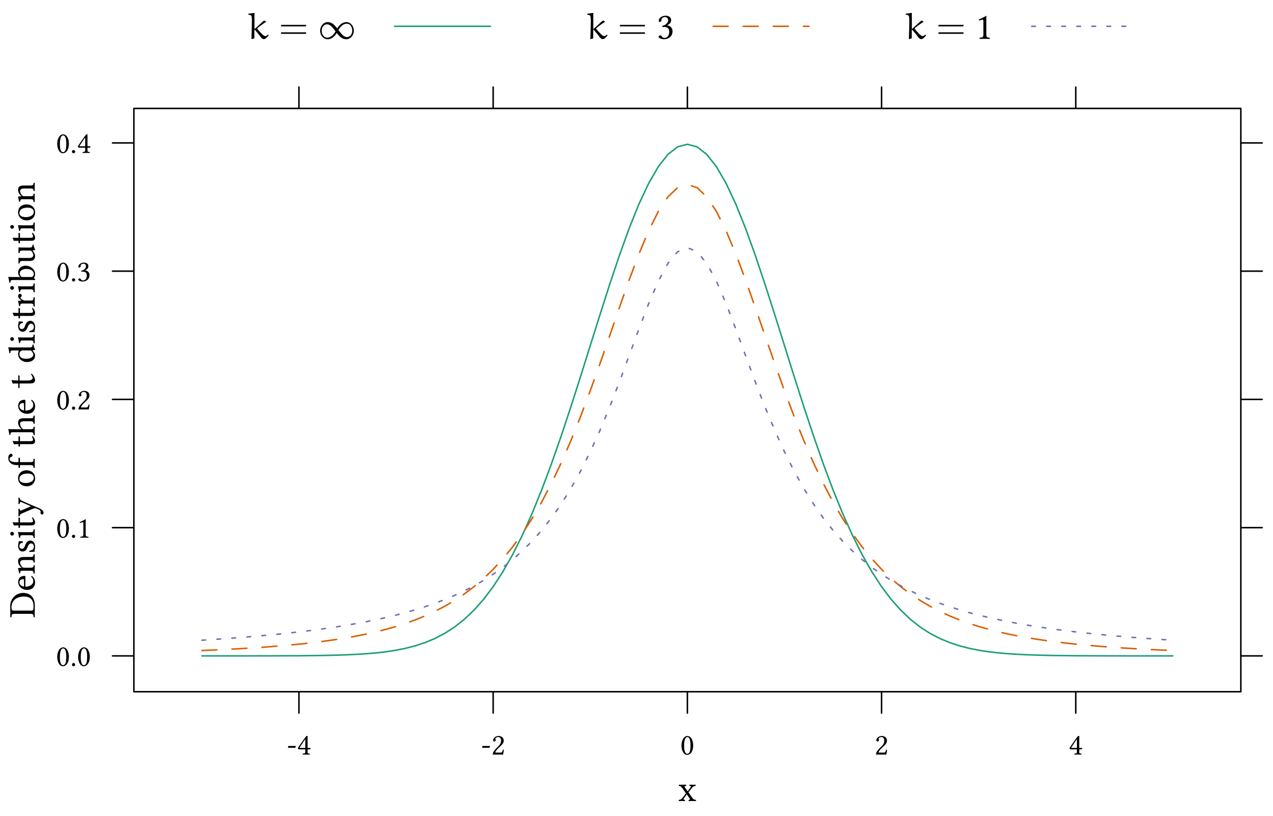
Residuals follow a normal distribution

$$\texttt{crmrte} \sim N(\beta_0 + \beta_1 \texttt{prbarr}, \tau)$$

```
reg.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

         Lower95     Median  Upper95       Mean         SD       Mode       MCerr
beta0   0.039913   0.048647  0.05738   0.048602  0.0045036   0.048399  0.00011053
beta1  -0.080205  -0.053137  -0.0261  -0.053014   0.013874  -0.053153  0.00033847

       MC%ofSD  SSeff    AC.10     psrf
beta0      2.5   1660  0.19674  0.99996
beta1      2.4   1680  0.19726  0.99995

Total time taken: 0.6 seconds
```

Allow fat tails

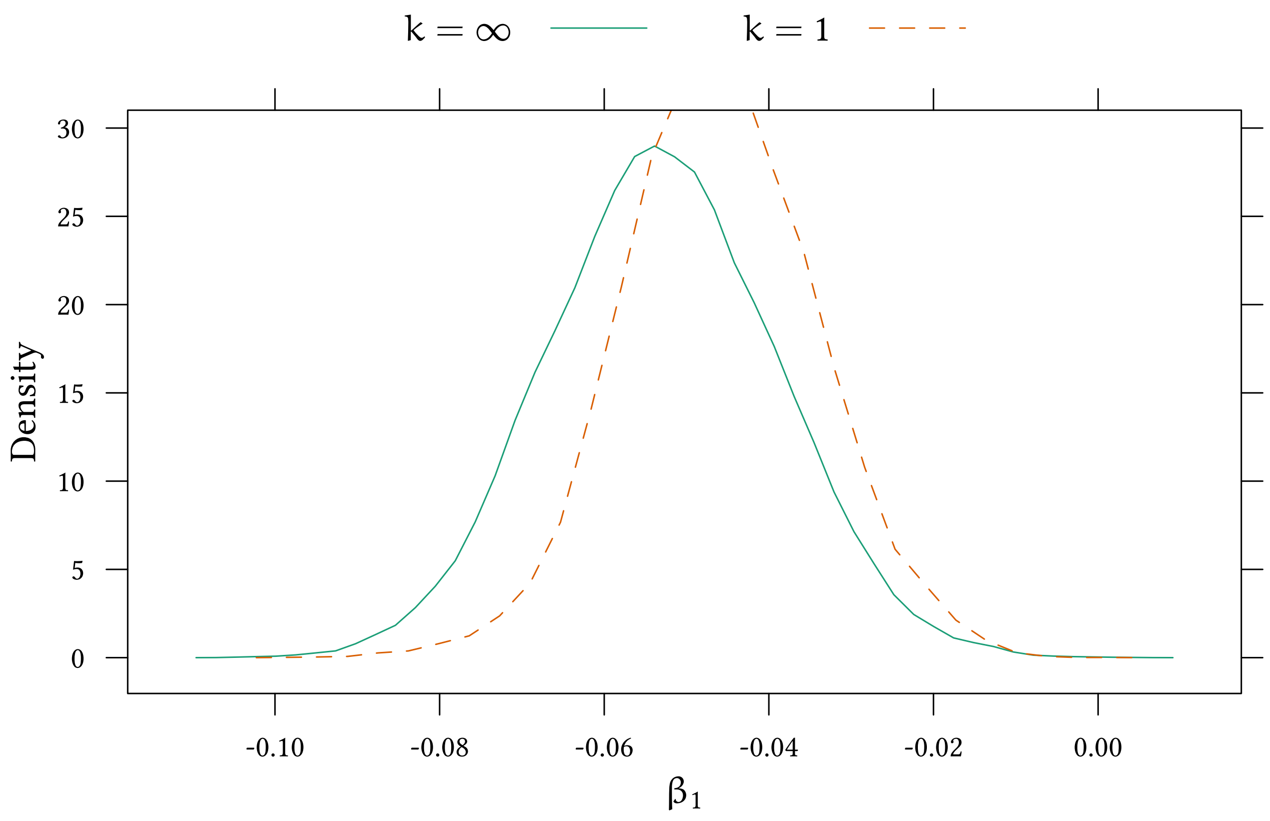
$$\texttt{crmrte} \sim t(\beta_0 + \beta_1 \texttt{prbarr}, \tau, k)$$



```
t1.model<-'model {
 for (i in 1:length(y)) {
        y[i] ~ dt(beta0 + beta1*x[i],tau,1)
    }
    beta0 ~ dnorm (0,.0001)
    beta1 ~ dnorm (0,.0001)
    tau ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
}'
```

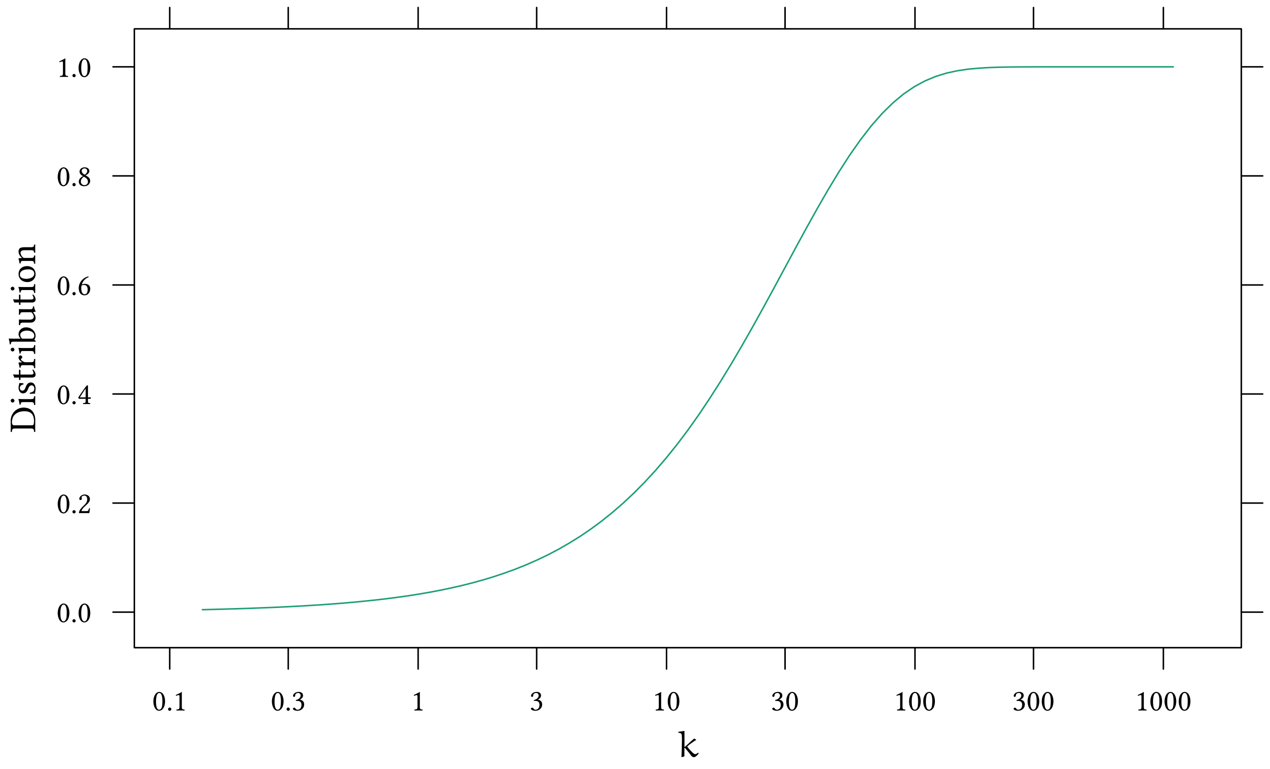
```
data<-with(subset(Crime,year==81),list(y=crmrte,x=prbarr))
t1.jags<-run.jags(model=t1.model,data=data,monitor=c("beta0","beta1"))
t1.df<-data.frame(as.mcmc(t1.jags))
```

```
densityplot(reg.df[["beta1"]],plot.points=FALSE,
            auto.key=list(text=c("$k=\\infty$","$k=1$"),columns=2),
            xlab="$\\beta_1$")+
                layer(panel.densityplot(t1.df[["beta1"]],plot.points=FALSE),style=2)
```



Now make k endogeneous. We need a prior for k:

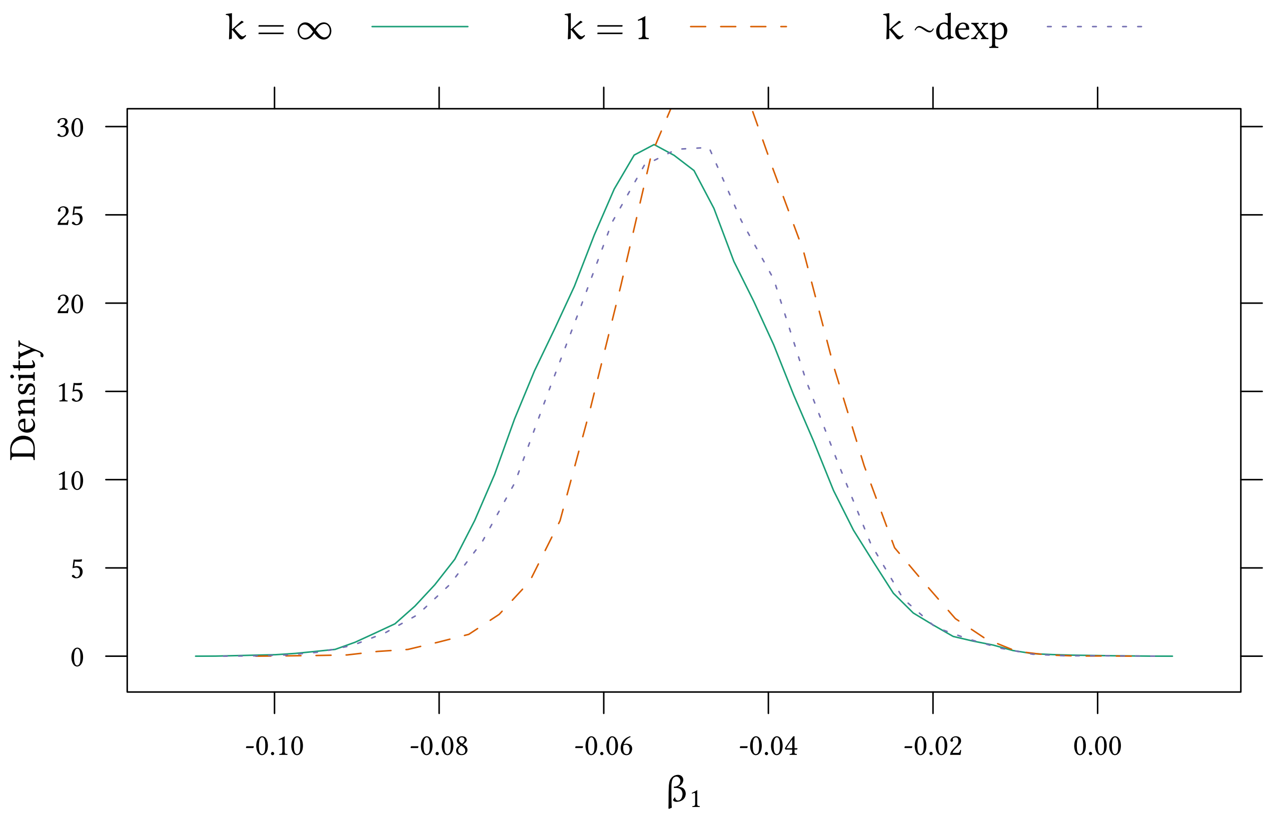
```
xxExp<-within(data.frame(list(x=exp(seq(-2,7,.1)))),{y=pexp(x,1/30)})
xyplot(y ~ x,data=xxExp,scales=list(x=list(log=10)),xscale.components = xscale.components.l
```



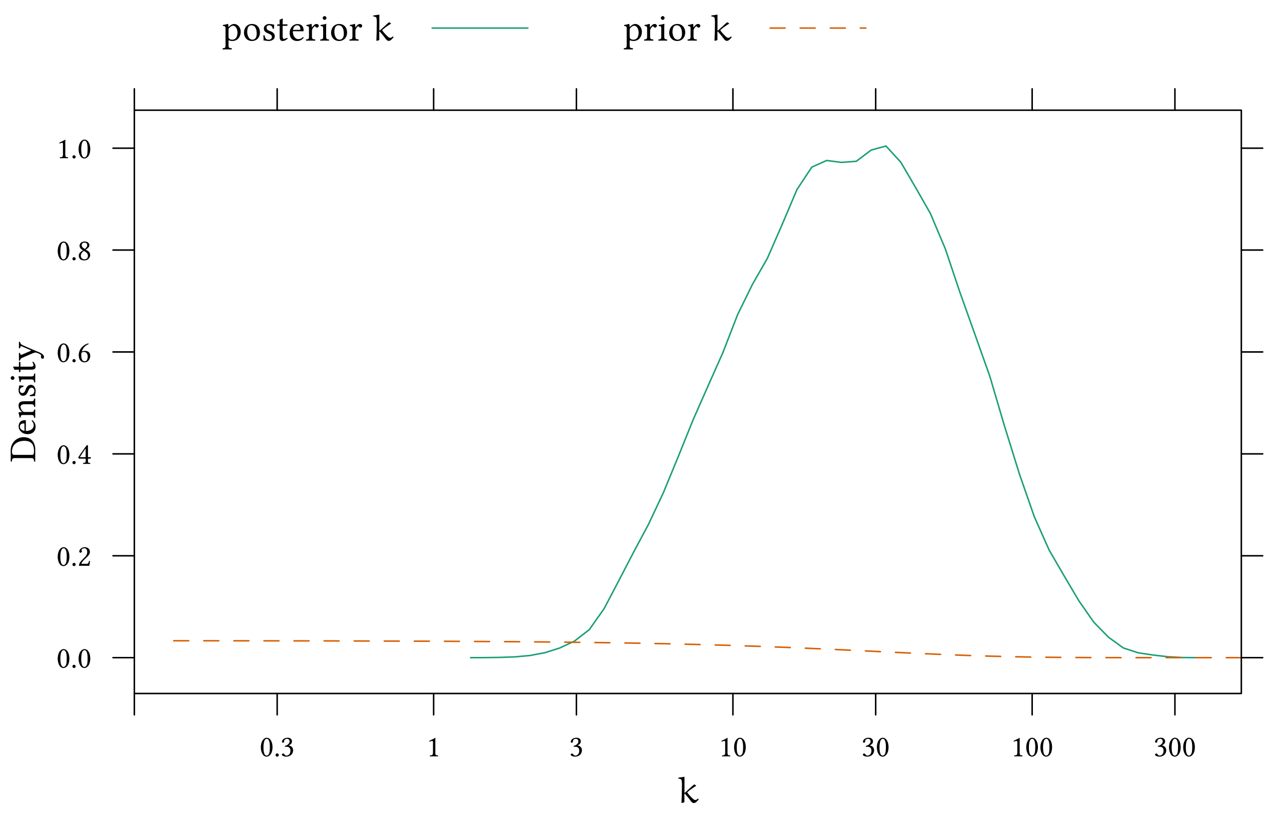
```
t.model<-'model {
 for (i in 1:length(y)) {
        y[i] ~ dt(beta0 + beta1*x[i],tau,k)
    }
    beta0 ~ dnorm (0,.0001)
    beta1 ~ dnorm (0,.0001)
    tau ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
    k     ~ dexp(1/30)
}'
```

```
t.jags<-run.jags(model=t.model,data=data,monitor=c("beta0","beta1","k"))
t.df<-data.frame(as.mcmc(t.jags))
```

```
densityplot(reg.df[["beta1"]],plot.points=FALSE,
            auto.key=list(text=c("$k=\\infty$","$k=1$","$k\\sim$dexp"),columns=3),
            xlab="$\\beta_1$")+
                layer(panel.densityplot(t1.df[["beta1"]],plot.points=FALSE),style=2)+
                    layer(panel.densityplot(t.df[["beta1"]],plot.points=FALSE),style=3)
```



```
xxExp<-within(data.frame(list(x=exp(seq(-2,7,.1)))),{y=dexp(x,1/30)})
densityplot(t.df[["k"]],xlab="$k$",scales=list(x=list(log=10)),xscale.components = xscale.comp
```



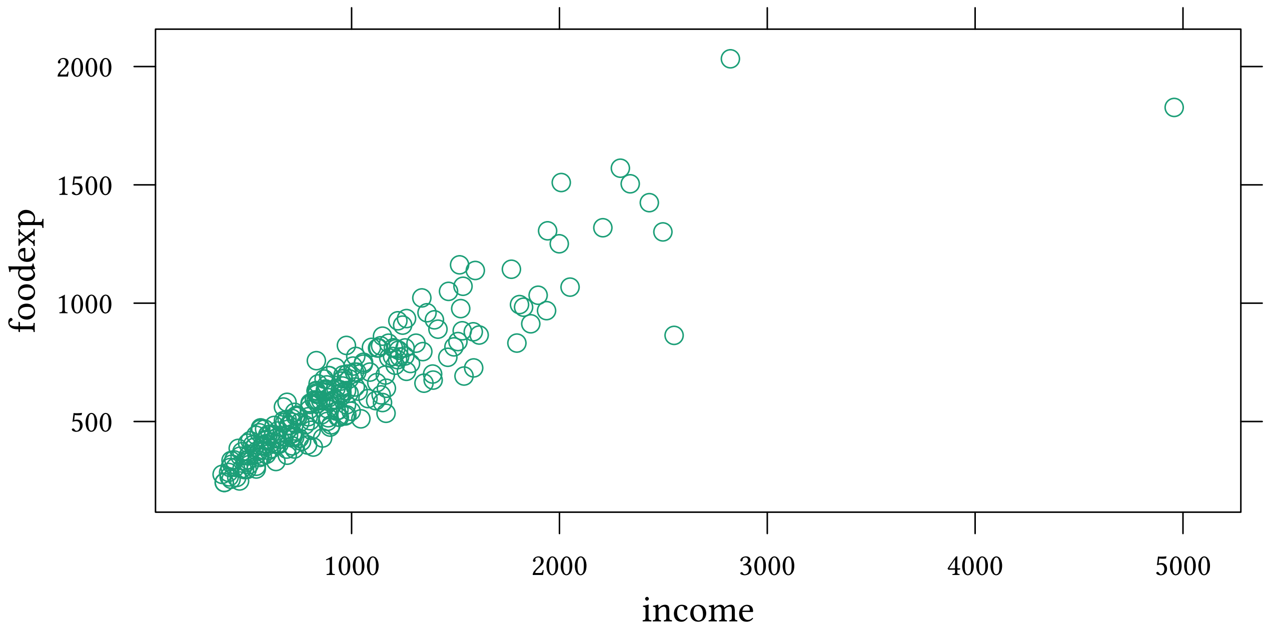
```
reg.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

        Lower95    Median Upper95      Mean        SD      Mode       MCerr
beta0  0.039913  0.048647 0.05738  0.048602 0.0045036  0.048399 0.00011053
beta1 -0.080205 -0.053137 -0.0261 -0.053014  0.013874 -0.053153 0.00033847

      MC%ofSD SSeff   AC.10    psrf
beta0     2.5  1660 0.19674 0.99996
beta1     2.4  1680 0.19726 0.99995

Total time taken: 0.6 seconds
```

```
t.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

        Lower95    Median   Upper95      Mean        SD      Mode       MCerr
beta0  0.038775  0.047485  0.056528  0.047574 0.0045245  0.047272 0.00014157
beta1 -0.078285 -0.050903 -0.025615 -0.051205  0.013533 -0.051473 0.00041669
k        2.8615    24.643    92.466    33.591    29.017    14.079     0.50232

      MC%ofSD SSeff    AC.10   psrf
beta0     3.1  1021  0.36906 1.0007
beta1     3.1  1055  0.36185 1.0007
```

```
k          1.7  3337 0.053228 1.0004

Total time taken: 7.7 seconds
```

6.2 Robust regression with the Engel data

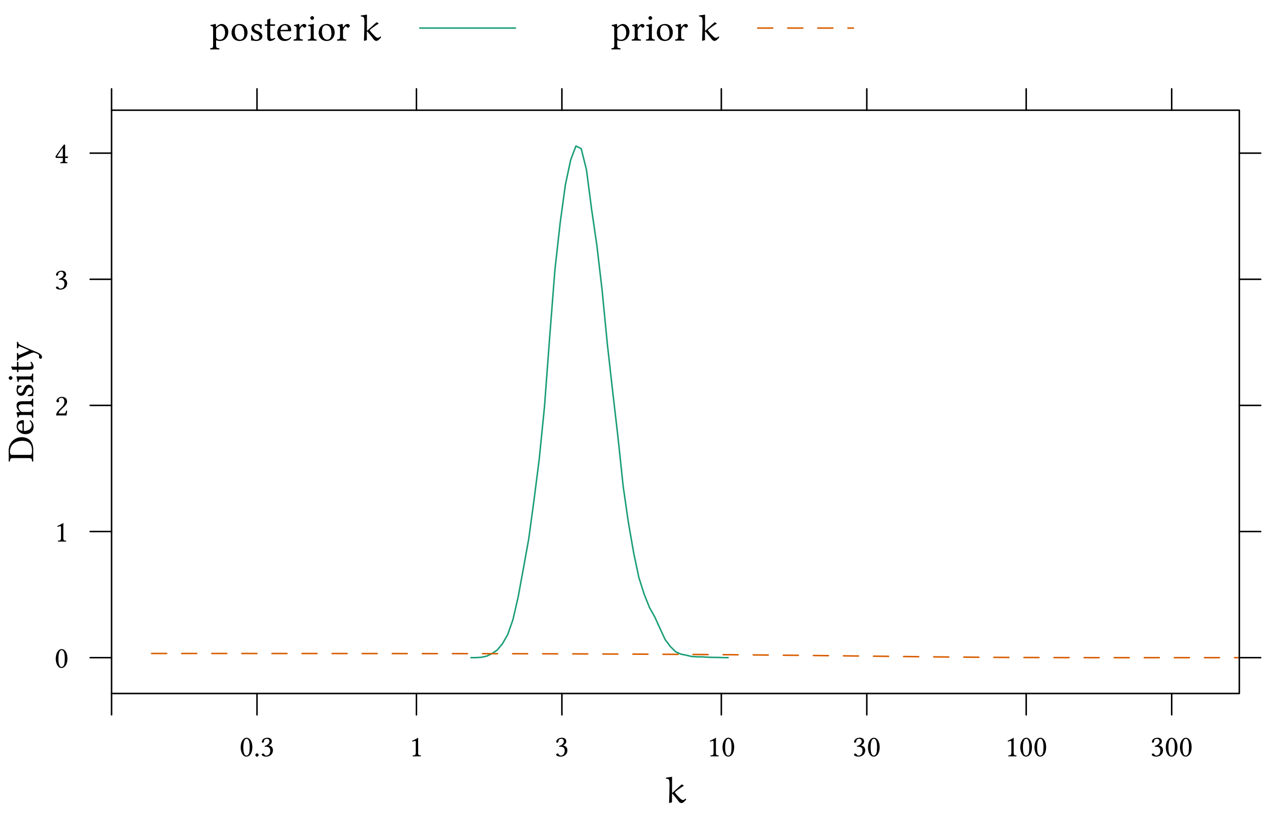
```
library(quantreg)
data(engel)
xyplot(foodexp ~ income, data=engel)
```



```
data<-with(engel,list(y=foodexp,x=income))
engel.reg.jags<-run.jags(model=reg.model,data=data,
                         monitor=c("beta0","beta1"),inits=ini)
engel.t.jags<-run.jags(model=t.model,data=data,
                       monitor=c("beta0","beta1","k"),inits=ini)
```

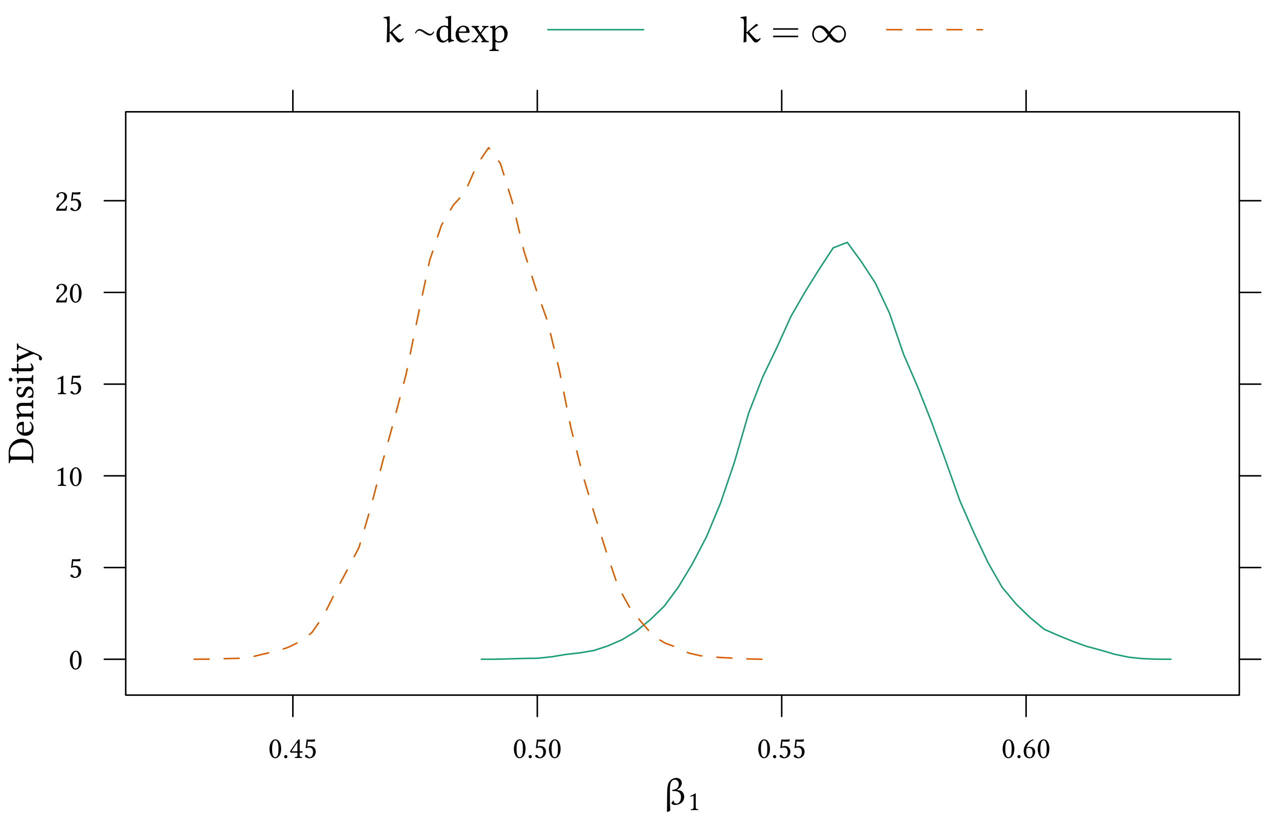
Here we find a much smaller k. We see that fat tails matter.

```
engel.t.df<-data.frame(as.mcmc(engel.t.jags))
densityplot(engel.t.df[["k"]],xlab="$k$",scales=list(x=list(log=10)),
            xscale.components = xscale.components.log10.3,plot.points=FALSE,
            auto.key=list(text=c("posterior $k$","prior $k$"),columns=3),xlim=c(.1,500))+
    layer(panel.xyplot(log10(xxExp$x),xxExp$y,t="l"),scales=list(x=list(log=10)),style=2)
```



```
engel.reg.df<-data.frame(as.mcmc(engel.reg.jags))
all.df<-rbind.fill(within(engel.reg.df,type<-"$k=\\infty$"),within(engel.t.df,type<-"$k\\si
```

```
densityplot(~beta1,group=type,data=all.df,plot.points=FALSE,xlab="$\\beta_1$",auto.key=list
```



```
engel.reg.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

      Lower95  Median Upper95    Mean       SD    Mode      MCerr MC%ofSD SSeff
beta0   112.5  143.34  174.37  143.37   15.917  143.64    0.32063       2  2465
beta1 0.45943 0.48864 0.51525 0.48848 0.014371 0.48796 0.00028645       2  2517

         AC.10   psrf
beta0 0.072199 1.0003
beta1 0.069264 1.0004

Total time taken: 0.7 seconds
```

```
engel.t.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

      Lower95  Median Upper95   Mean       SD   Mode      MCerr MC%ofSD SSeff
beta0  49.531  79.555  110.84 79.526   15.465 80.325    0.52445     3.4   869
beta1 0.52548 0.56206 0.59697 0.5621 0.018052 0.5613 0.00060312     3.3   896
k      2.0817  3.4211  5.2599 3.5472  0.84881 3.2658   0.013462     1.6  3976

         AC.10   psrf
beta0  0.41396 1.0005
beta1  0.41633 1.0006
k     0.053926 1.0001

Total time taken: 33.3 seconds
```

6.3 Exercises

Consider the data set `Wages` from `Ecdat`. The data set contains seven observations for each worker. Consider for each worker the first of these observations. You want to study the impact of education on wage.

1. Could there be outliers in `lwage`?
2. How can you take outliers into account?
3. Estimate your model.

7 Nonparametric

7.1 Preliminaries

- Is the “nonparametric” idea essentially frequentist?
- After all, with “nonparametrics” we avoid a discussion about distributions.
- Perhaps it would be more honest to model what we know about the distribution.

Still…

- Equivalent for “binomial test”: $X \sim \mathrm{dbern}()$.
- Equivalent for “χ^2 test”: $X \sim \mathrm{dpois}()$.

Furthermore…

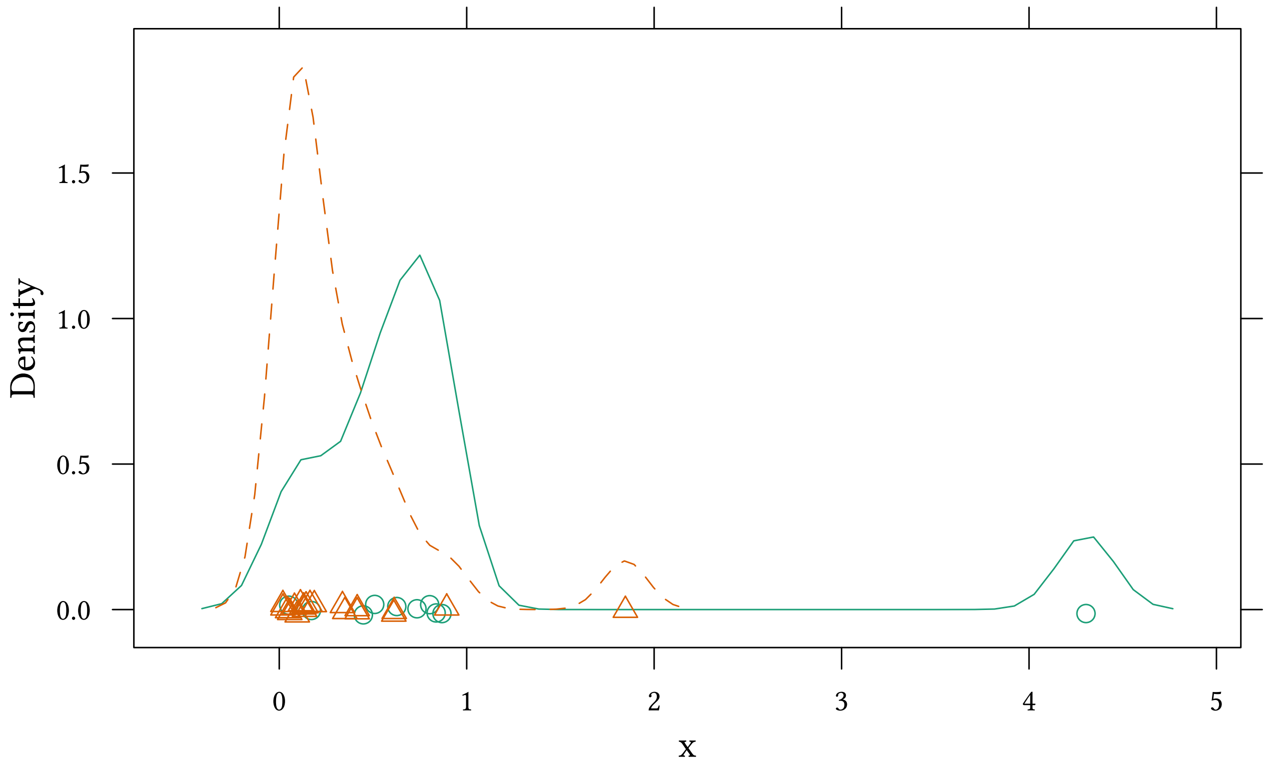
- As in the frequentist world we can translate one (less known) distribution to another by using ranks.

7.2 Example: Rank sum based comparison

Here we create two variables who both follow an exponential distribution. We might forget this information and use ranks to compare.

```
set.seed(4)
xx<-rbind(data.frame(list(x=rexp(10,1),t=1)),
          data.frame(list(x=rexp(20,3),t=2)))
wilcox.test(x~t,data=xx)


Wilcoxon rank sum test

data:  x by t
W = 156, p-value = 0.01273
alternative hypothesis: true location shift is not equal to 0
```

```
densityplot(~x,group=t,data=xx)
```



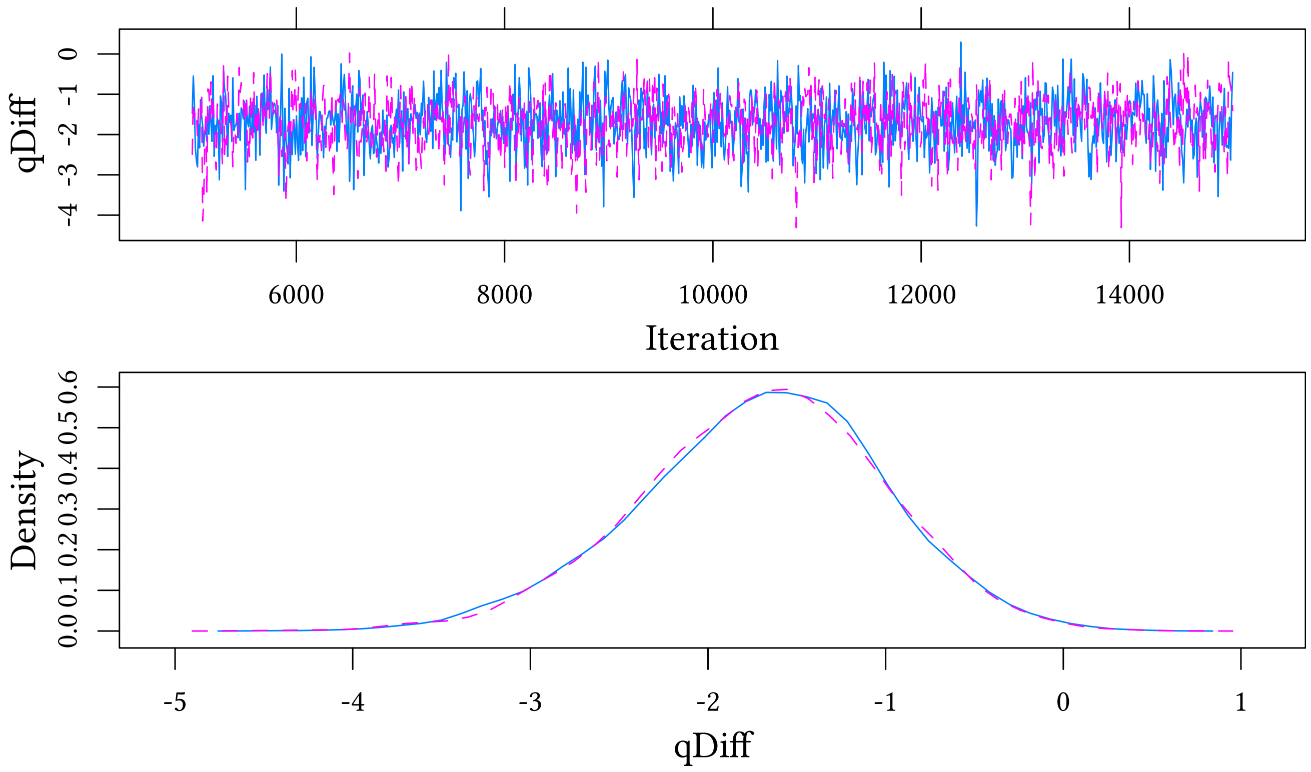
The parametric approach Here we know that x follows an exponential distribution:

```
EXP.model<-'model {
 for (i in 1:length(y)) {
        y[i] ~ dexp(beta[t[i]])
    }
 for(i in 1:2) {
    beta[i] ~ dgamma(m[i]^2/d[i]^2,m[i]/d[i]^2); m[i] ~ dexp(1); d[i] ~ dexp(1);
  }
  qDiff<-beta[1]-beta[2]
}'
data<-with(xx,list(y=x,t=t))
EXP.jags<-run.jags(model=EXP.model,data=data,monitor=c("beta","qDiff"))
```

```
EXP.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

        Lower95 Median  Upper95   Mean      SD     Mode     MCerr MC%ofSD SSeff
beta[1] 0.52638 1.0664   1.7872 1.0989 0.32894   1.0186 0.0046557     1.4  4992
beta[2]  1.7014 2.7485   4.0375  2.802 0.60491     2.65 0.0086881     1.4  4848
qDiff    -3.083 -1.666 -0.39739 -1.703 0.68659  -1.5829 0.0097705     1.4  4938

           AC.10    psrf
beta[1] 0.036854  1.0002
beta[2] 0.042479  1.0004
```

```
qDiff   0.042407 0.99998

Total time taken: 0.7 seconds
```

```
plot(EXP.jags,var="qDiff",plot.type=c("trace","density"))
```



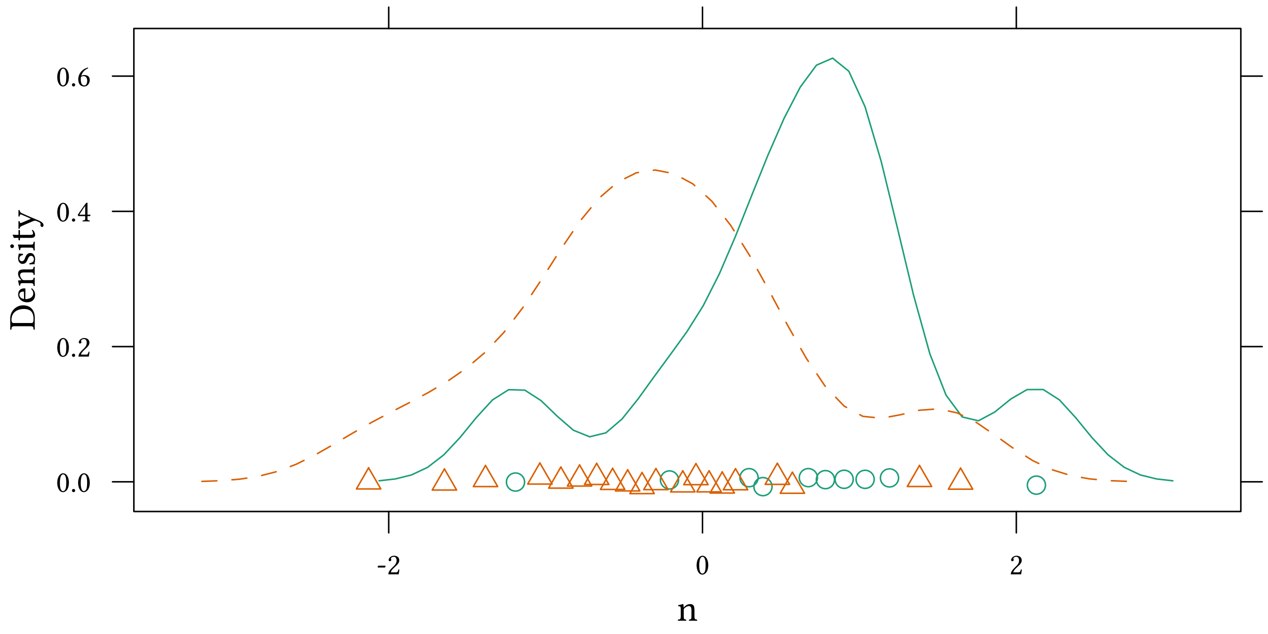
```
EXP.df<-data.frame(as.mcmc(EXP.jags))
(p<-mean(EXP.df[["qDiff"]]<0))

[1] 0.99655
```

The odds are, hence

```
p/(1-p)

[1] 288.8551
```

The non-parametric approach As with the rank sum test, we normalise the data, using ranks. Regardless what the initial distribution was, if the two samples come from the same distribution, we now have a uniform distribution. Using `qnorm` we obtain a normal distribution.

```
xx<-within(xx,{r<-rank(x);n<-qnorm((r-.5)/max(r))})
densityplot(~n,group=t,data=xx)
```

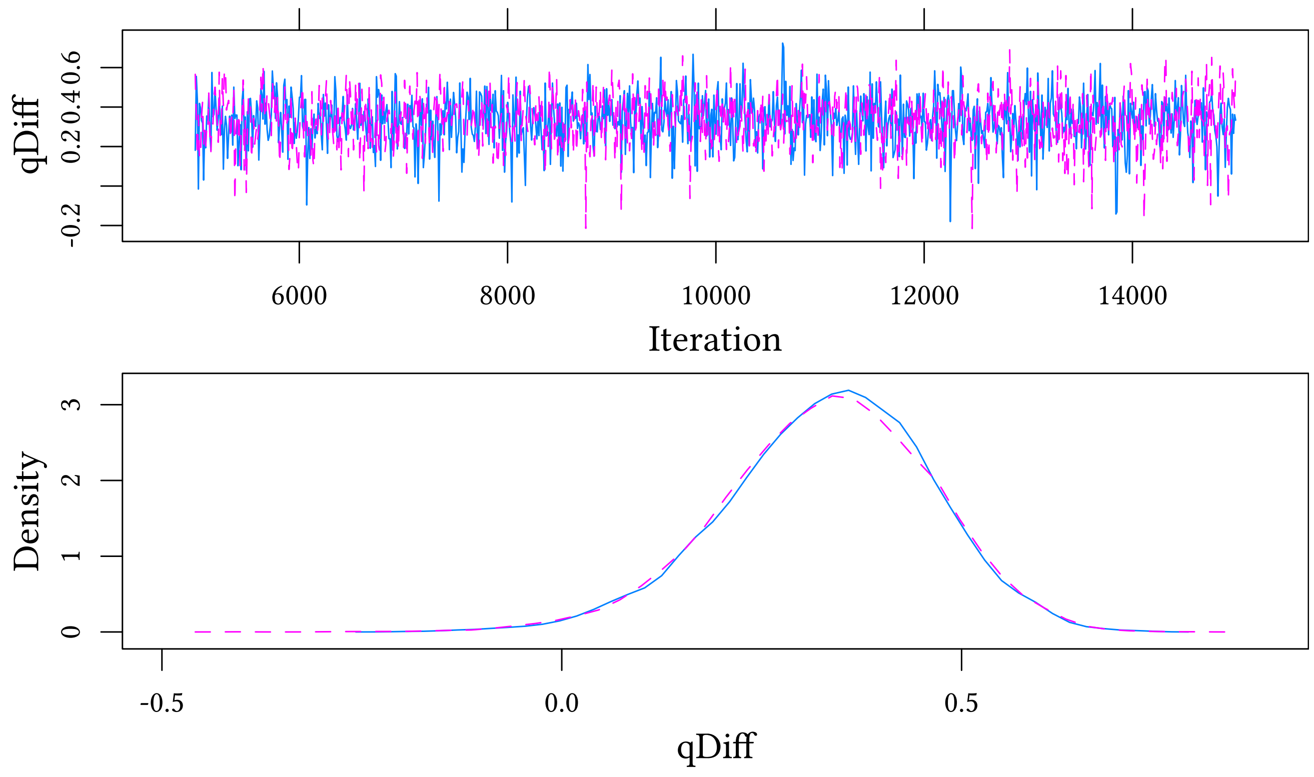


```
NP.model<-'model {
 for (i in 1:length(y)) {
        y[i] ~ dnorm(beta[t[i]],tau[t[i]])
    }
 for(i in 1:2) {
    beta[i] ~ dnorm (0,.0001)
    tau[i] ~ dgamma(m[i]^2/d[i]^2,m[i]/d[i]^2); m[i] ~ dexp(1); d[i] ~ dexp(1);
    qBet[i]<-pnorm(beta[i],0,1)
  }
  qDiff<-qBet[1]-qBet[2]
}'
data<-with(xx,list(y=n,t=t))
NP.jags<-run.jags(model=NP.model,data=data,monitor=c("qBet","qDiff","tau"))
```

```
NP.jags


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

         Lower95  Median Upper95    Mean       SD    Mode      MCerr MC%ofSD
qBet[1]  0.51498 0.72528 0.90258 0.71713  0.10052 0.73647 0.00071828     0.7
qBet[2]  0.22149 0.38143  0.5428 0.38479 0.081606 0.37161 0.00057704     0.7
qDiff   0.071169 0.33926 0.57884 0.33234  0.12943 0.33946 0.00092595     0.7
tau[1]   0.37563  1.2102  2.3619  1.2842  0.53886  1.0736  0.0093625     1.7
tau[2]   0.51239  1.1427  1.9118  1.1828  0.36586  1.0728  0.0055136     1.5

        SSeff      AC.10   psrf
qBet[1] 19587  0.0059906 1.0002
```

```
qBet[2] 20000 -0.0088586 1.0002
qDiff   19539 -0.0039439 1.0002
tau[1]   3313   0.083678 1.0006
tau[2]   4403   0.045728 1.0006

Total time taken: 0.7 seconds
```

```
plot(NP.jags,var="qDiff",plot.type=c("trace","density"))
```



```
NP.df<-data.frame(as.mcmc(NP.jags))
(p<-mean(NP.df[["qDiff"]]>0))

[1] 0.98975
```

The odds are, hence

```
p/(1-p)

[1] 96.56098
```

8 Identification

Collinearity Regressors which are collinear are (in the linear model) not simultaneously identifiable. Here we create two such regressors.

```
library(Ecdat)
data(Crime)
dataC<-within(subset(Crime,year==81)[,c("crmrte","prbarr")],
             prbarr100<-100*prbarr)
est<-lm(crmrte ~ prbarr + prbarr100,data=dataC)
summary(est)


Call:
lm(formula = crmrte ~ prbarr + prbarr100, data = dataC)

Residuals:
      Min        1Q    Median        3Q       Max
-0.027125 -0.009932 -0.000848  0.007013  0.046819

Coefficients: (1 not defined because of singularities)
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.048577   0.004261  11.400  < 2e-16 ***
prbarr      -0.052924   0.013129  -4.031 0.000118 ***
prbarr100          NA         NA      NA       NA
---
Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1

Residual standard error: 0.01571 on 88 degrees of freedom
Multiple R-squared:  0.1559,Adjusted R-squared:  0.1463
F-statistic: 16.25 on 1 and 88 DF,  p-value: 0.0001177
```

As we see, OLS makes an identifying assumption and sets the coefficient of *prbarr100* to zero.

Now we do the same with JAGS:

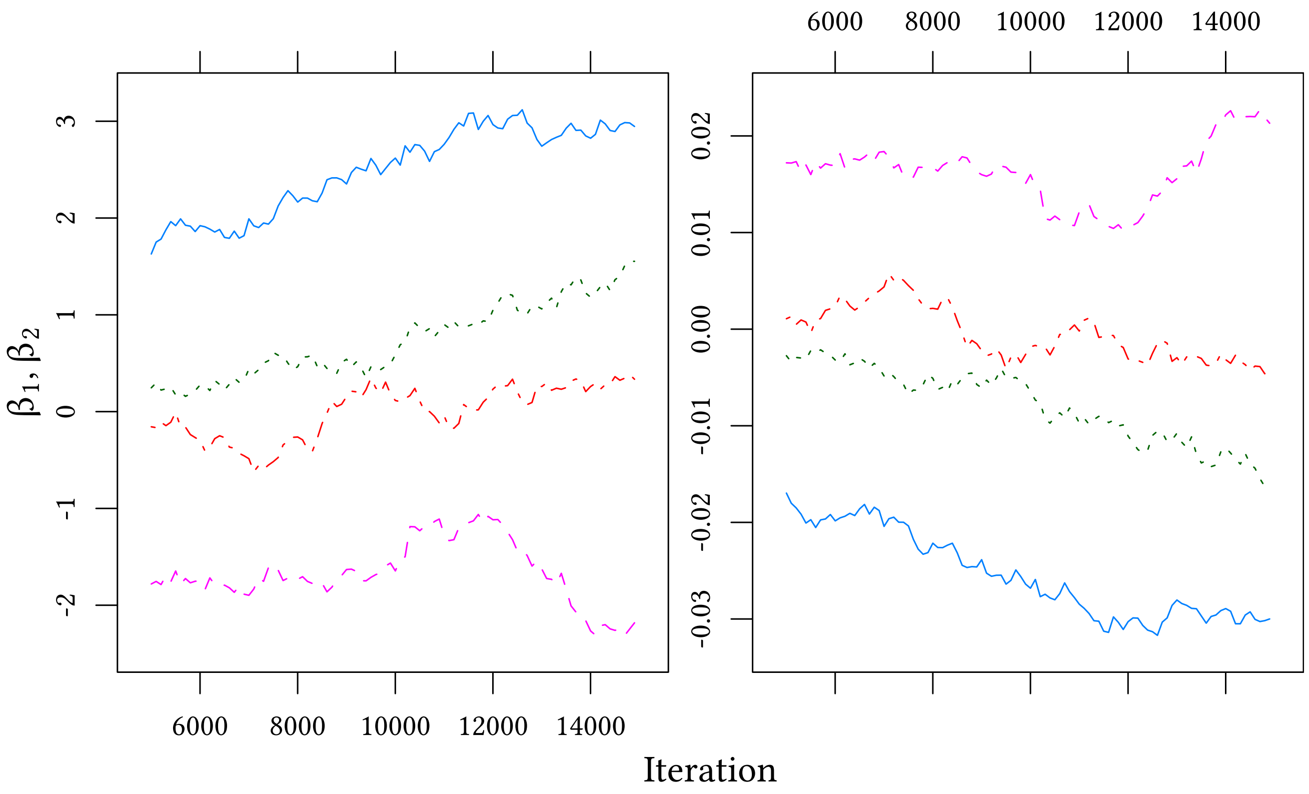
```
regM.model<-’model {
 for (i in 1:length(y)) {
        y[i] ~ dnorm(inprod(beta,X[i,]),tau)
    }
  for (k in 1:K) {
    beta[k] ~ dnorm (0,.0001)
  }
    tau ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
}’
ini <- genInit(4,function(i) list(beta1=rnorm(1,0,0.0001),
                                   beta2=rnorm(1,0,0.0001)))
regM.jags<-run.jags(model=regM.model,
                    data=with(dataC,list(y=crmrte,X=cbind(1,prbarr,prbarr100),K=3)),
                    monitor=c("beta"),
                    inits=ini,sample=100,thin=100)
```

```
summary(regM.jags)[,c("Mean","SD","SSeff","psrf")]

                Mean           SD SSeff     psrf
```

```
beta[1]  0.048510672 0.004424766   463 1.003878
beta[2]  0.390078051 1.539589057     9 6.558625
beta[3] -0.004426064 0.015395795     9 6.564672
```

- Standard errors for coefficients are much larger.
- The potential scale reduction factor is larger than 1.1.

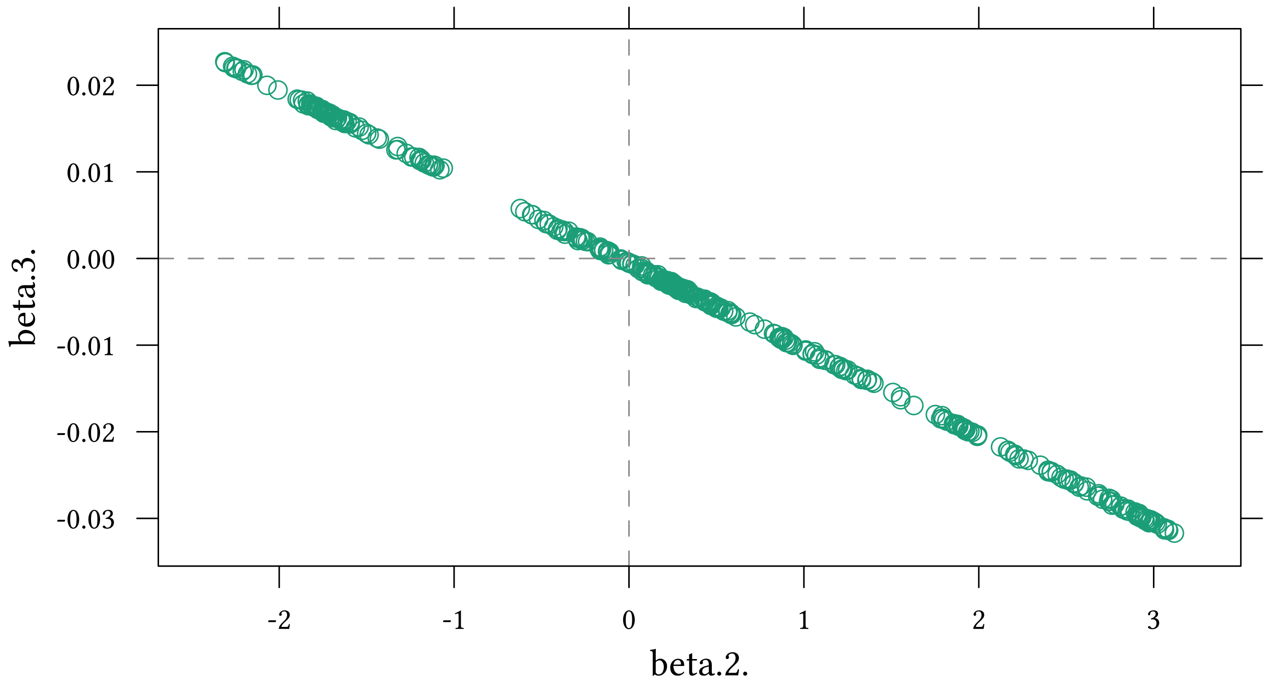
```
c(update(plot(regM.jags,vars="beta[2]",plot.type="trace",file="null.pdf")[[1]],ylab="$\\bet
  plot(regM.jags,vars="beta[3]",plot.type="trace",file="null.pdf")[[1]])
```



The different chains do not converge.

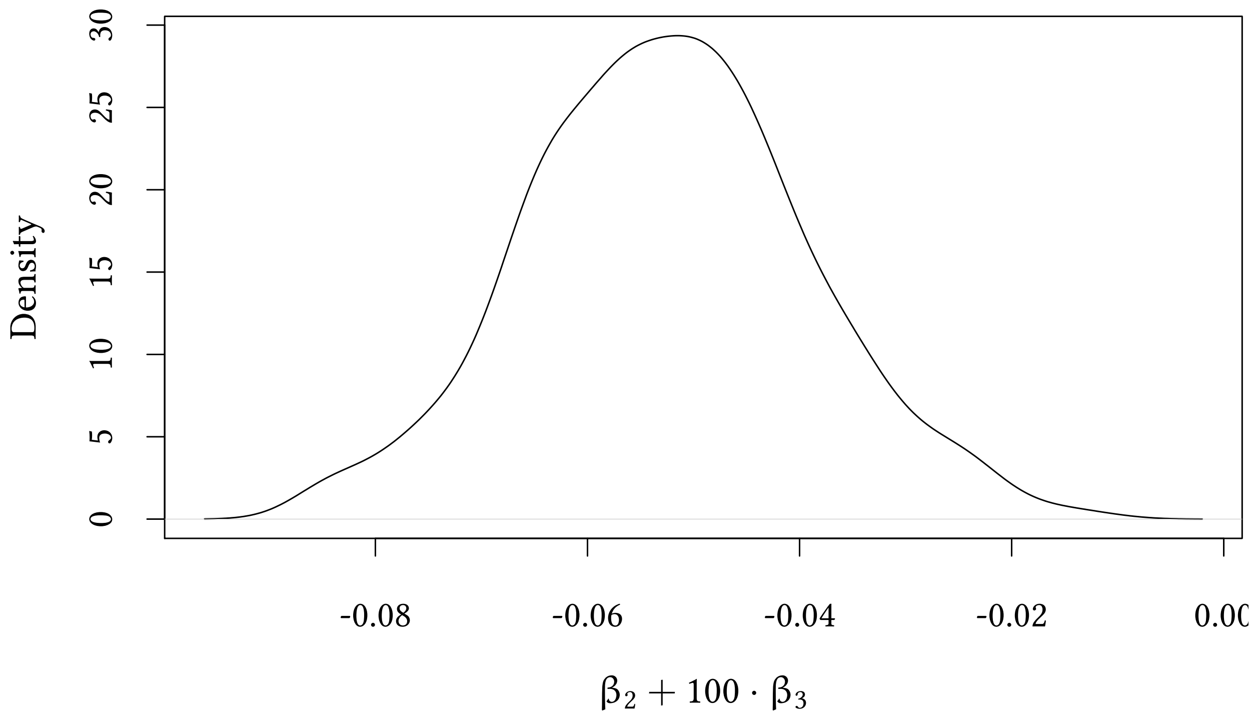
$$y \sim N(\beta_0 + \beta_1 X + \beta_2 \cdot 100 \cdot X, \tau)$$

```
regM.df<-data.frame(as.mcmc(regM.jags),optional=TRUE)
xyplot(beta.3.~beta.2.,data=regM.df)+layer(panel.refline(h=0,v=0))
```



- The joint distribution of β_1 and β_2 shows the dependence of the two regressors.
- But – perhaps we are only interested in $\beta_2 + 100 \cdot \beta_3$?

```
with(regM.df,plot(density(beta.2.+beta.3.*100),main="",xlab="$\\beta_2 + 100\\cdot \\beta_3$")
```



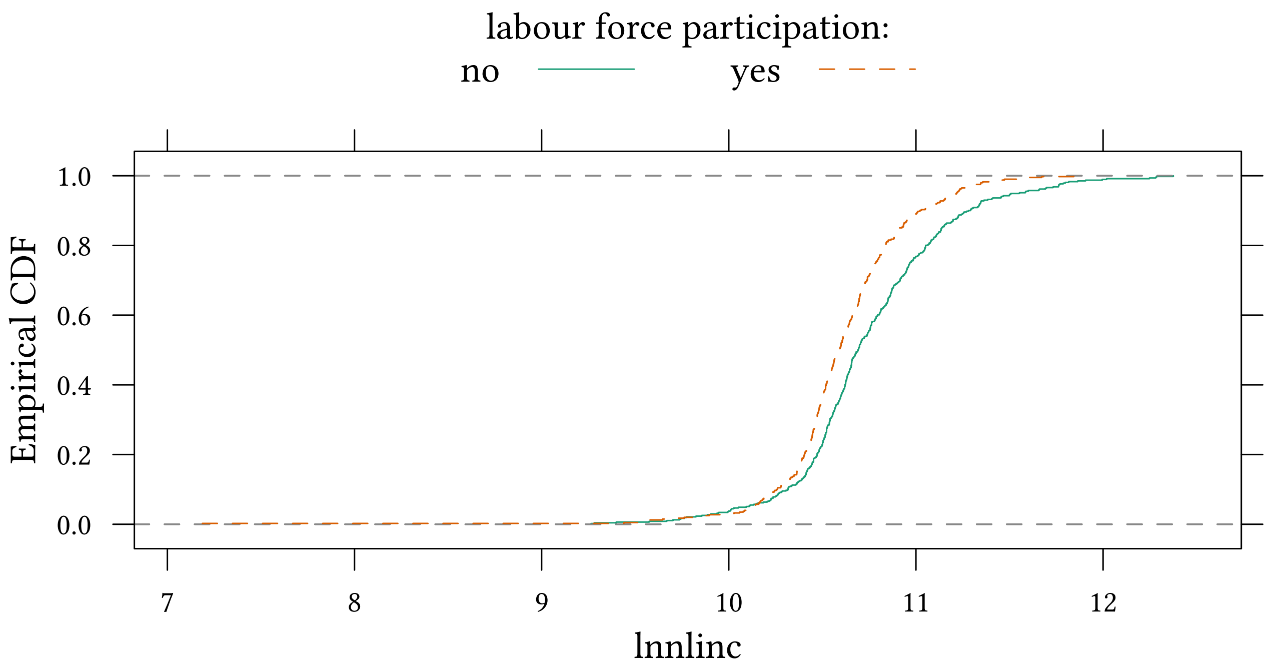
Identification Summary

- Many frequentist tools try to obtain point estimates. Hence, they must detect under-identification. Often they make identifying assumptions on their own.
- In the Bayesian world we estimate a joint distribution. Under-identification need not be a problem. It shows up as large standard deviation, lack of convergence, a large *gelman.diag*, etc.

9 Discrete Choice

9.1 Labor force participation

```
library(Ecdat)
data(Participation)
ecdfplot(~lnnlinc,group=lfp,data=Participation,auto.key=list(title="labour force participat
```



9.2 A generalised linear model

$$P(Y = 1|X) = \Phi(\beta_0 + \beta_1 X)$$

$$\text{alternative:} \qquad \Phi^{-1}\left(P(Y = 1|X)\right) = \beta_0 + \beta_1 X$$

```
probit.glm<-glm(lfp=="yes" ~ lnnlinc,data=Participation,family=binomial(link=probit))
summary(probit.glm)[["coefficients"]]
```

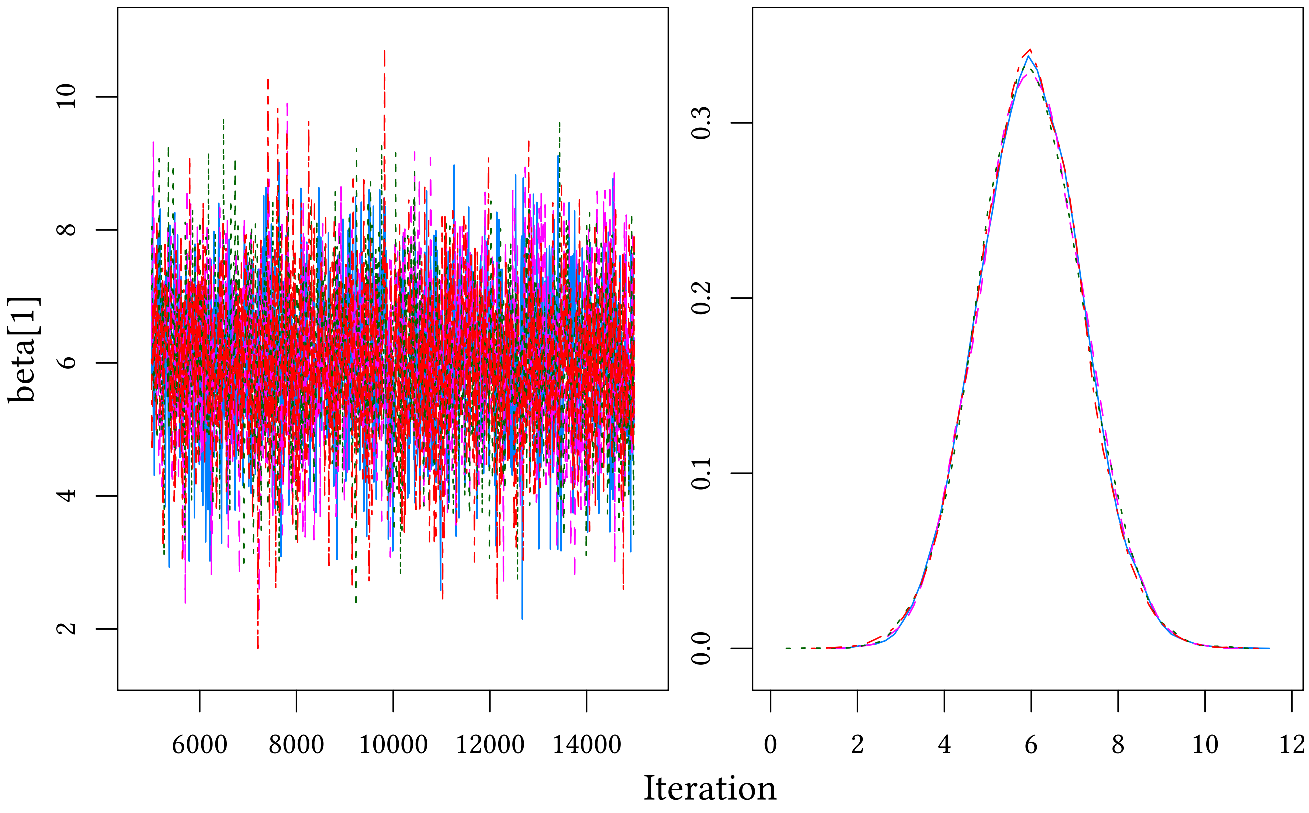
```
              Estimate Std. Error   z value        Pr(>|z|)
(Intercept)  5.9705580  1.1943613  4.998955 0.0000005764194
lnnlinc     -0.5685645  0.1117688 -5.086972 0.0000003638259
```

9.3 Bayesian discrete choice

```
probit.model <- 'model {
 for (i in 1:length(y)) {
        y[i] ~ dbern(p[i])
        p[i] <- phi(inprod(X[i,],beta))
    }
 for (k in 1:K) {
    beta[k]  ~ dnorm (0,.0001)
 }
}'
Part.data<-with(Participation,list(y=as.numeric(lfp=="yes"),X=cbind(1,lnnlinc),K=2))
probit.jags<-run.jags(model=probit.model,modules="glm",
       data=Part.data,inits=ini,monitor=c("beta"))
summary(probit.jags)[,c("Mean","SD","SSeff","psrf")]

              Mean        SD SSeff     psrf
beta[1]  5.9838734 1.1902539 29769 1.000072
beta[2] -0.5698306 0.1114429 29693 1.000070
```

(We should use *phi(...)* and not *pnorm(...,0,1)*. The latter is slower to converge.)
The following specification is equivalent:

```
probit.model <- 'model {
 for (i in 1:length(y)) {
        y[i] ~ dbern(p[i])
        probit(p[i]) <- inprod(X[i,],beta)
    }
 for (k in 1:K) {
    beta[k]  ~ dnorm (0,.0001)
 }
}'
Part.data<-with(Participation,list(y=as.numeric(lfp=="yes"),X=cbind(1,lnnlinc),K=2))
probit.jags<-run.jags(model=probit.model,modules="glm",
       data=Part.data,inits=ini,monitor=c("beta"))
summary(probit.jags)[,c("Mean","SD","SSeff","psrf")]

              Mean        SD SSeff     psrf
beta[1]  5.9838734 1.1902539 29769 1.000072
beta[2] -0.5698306 0.1114429 29693 1.000070
```



9.4 Exercise

Consider the dataset *Mroz* from *Ecdat*.

- Which variables could explain work participation?
- Estimate your model.

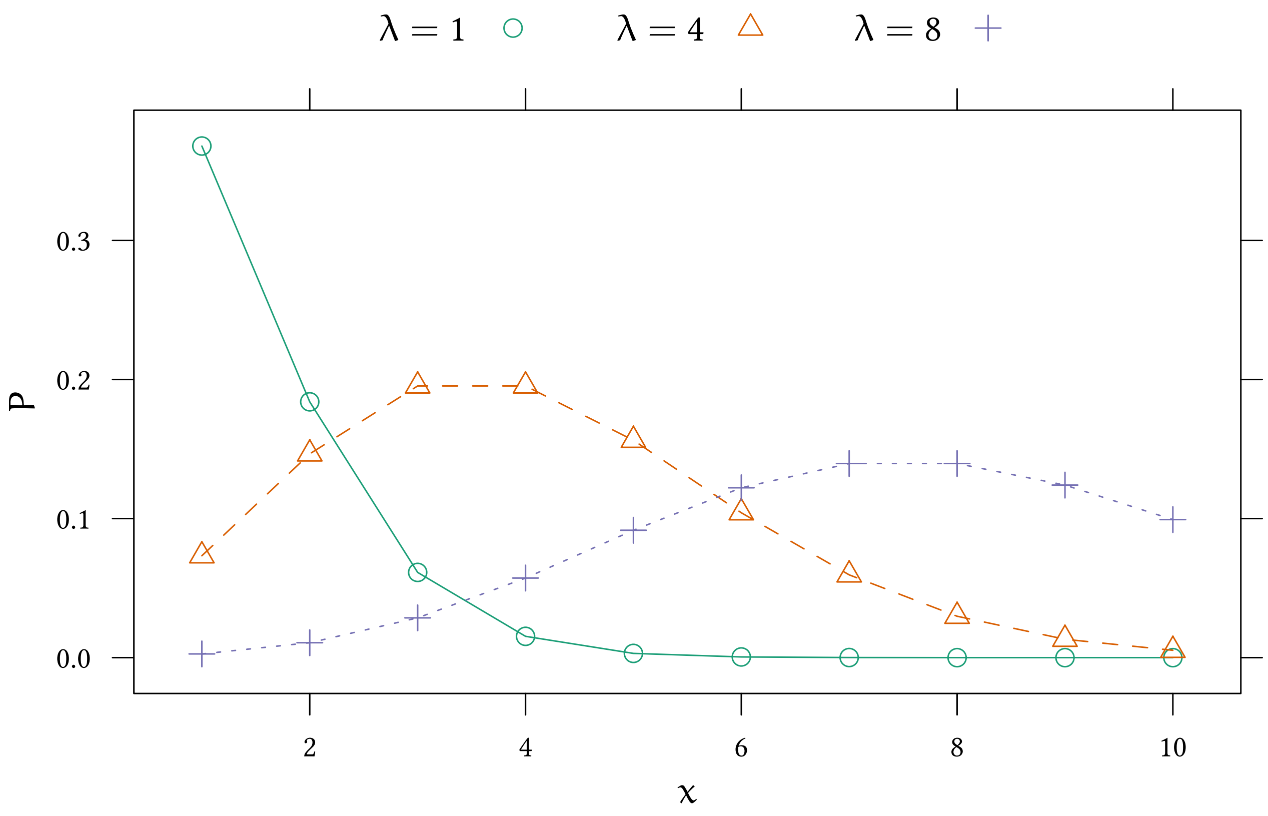
10 Count data

10.1 Poisson model

The Poisson process:

- During one unit of time you expect λ many events.
- During 1/10 unit of time you expect $\lambda/10$ many events.
- During 1/100 unit of time you expect $\lambda/100$ many events.
- $\vdots$

Events are stochastically independent of each other (no interaction among events). (Purely random process)
The Poisson distribution for different values of λ:



$$Y \sim \text{Pois}(\lambda)$$
$$Y \sim \text{Pois}(\exp(\beta_0 + \beta_1 X))$$
$$Y \sim \text{Pois}(\exp(1 + 2X))$$

Generate some data:

```
set.seed(123)
N<-100
x<-rnorm(N)
y<-rpois(N,exp(1+2*x))
pois.glm<-glm(y~x,family=poisson(link=log))
summary(pois.glm)[["coefficients"]]

             Estimate Std. Error  z value     Pr(>|z|)
(Intercept) 0.9611632 0.06330281 15.18358 4.542996e-52
x           2.0389185 0.03799288 53.66581 0.000000e+00
```

We could specify the model like this…

```
count.model <- 'model {
 for (i in 1:length(y)) {
        y[i] ~ dpois(lambda[i])
        lambda[i] <- exp(inprod(X[i,],beta))
    }
 for (k in 1:K) {
    beta[k] ~ dnorm (0,.0001)
 }
}'
count.jags<-run.jags(model=count.model,modules="glm",
       data=list(y=y,X=cbind(1,x),K=2),inits=ini,monitor=c("beta"))
summary(count.jags)[,c("Mean","SD","SSeff","psrf")]
```

…or like this…

```
count.model <- 'model {
 for (i in 1:length(y)) {
        y[i] ~ dpois(lambda[i])
        log(lambda[i]) <- inprod(X[i,],beta)
    }
 for (k in 1:K) {
    beta[k] ~ dnorm (0,.0001)
 }
}'
count.jags<-run.jags(model=count.model,modules="glm",
       data=list(y=y,X=cbind(1,x),K=2),inits=ini,monitor=c("beta"))
summary(count.jags)[,c("Mean","SD","SSeff","psrf")]

             Mean         SD SSeff     psrf
beta[1] 0.9583643 0.06270963  3032 1.000460
beta[2] 2.0400627 0.03769276  3648 1.000473
```

10.2 Negative binomial

Count data and the negative binomial distribution

Poisson distribution: $\text{Pois}(\lambda)$

Mean: λ

Variance: λ

Negative binomial distribution: $\text{NB}(\mu, r)$

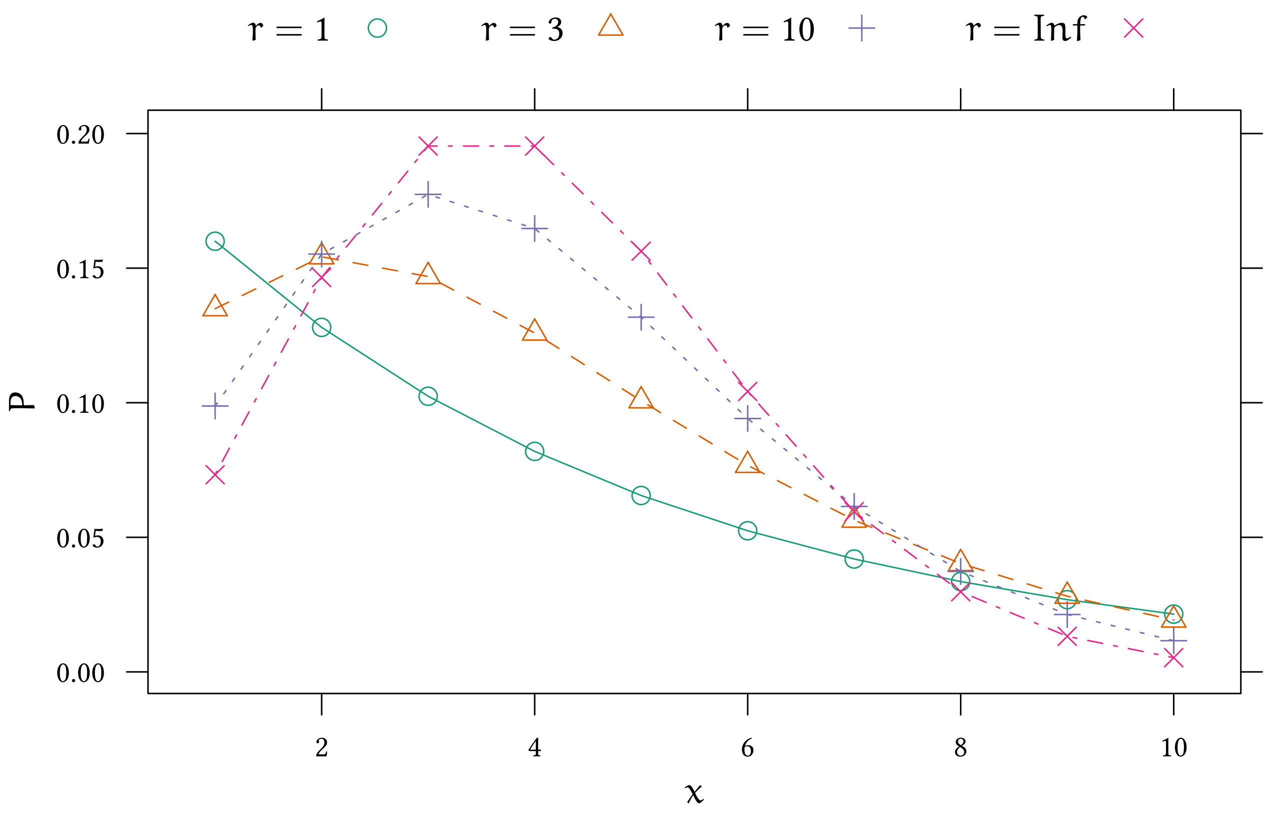
Mean: μ

Variance: $\mu + \mu^2/r$

Poisson is a special case of NB:

$$\lim_{r\to\infty} \text{NB}(\mu, r) = \text{Pois}(\mu)$$

The NB distribution for $\mu = 4$ and for different values of r:



Two notations:

$$\begin{array}{ll} NB(p,r) & \text{(used by JAGS as } \texttt{dnegbin(p,r)}) \\ NB(\mu,r) & \text{(perhaps easier to interpret)} \end{array}$$

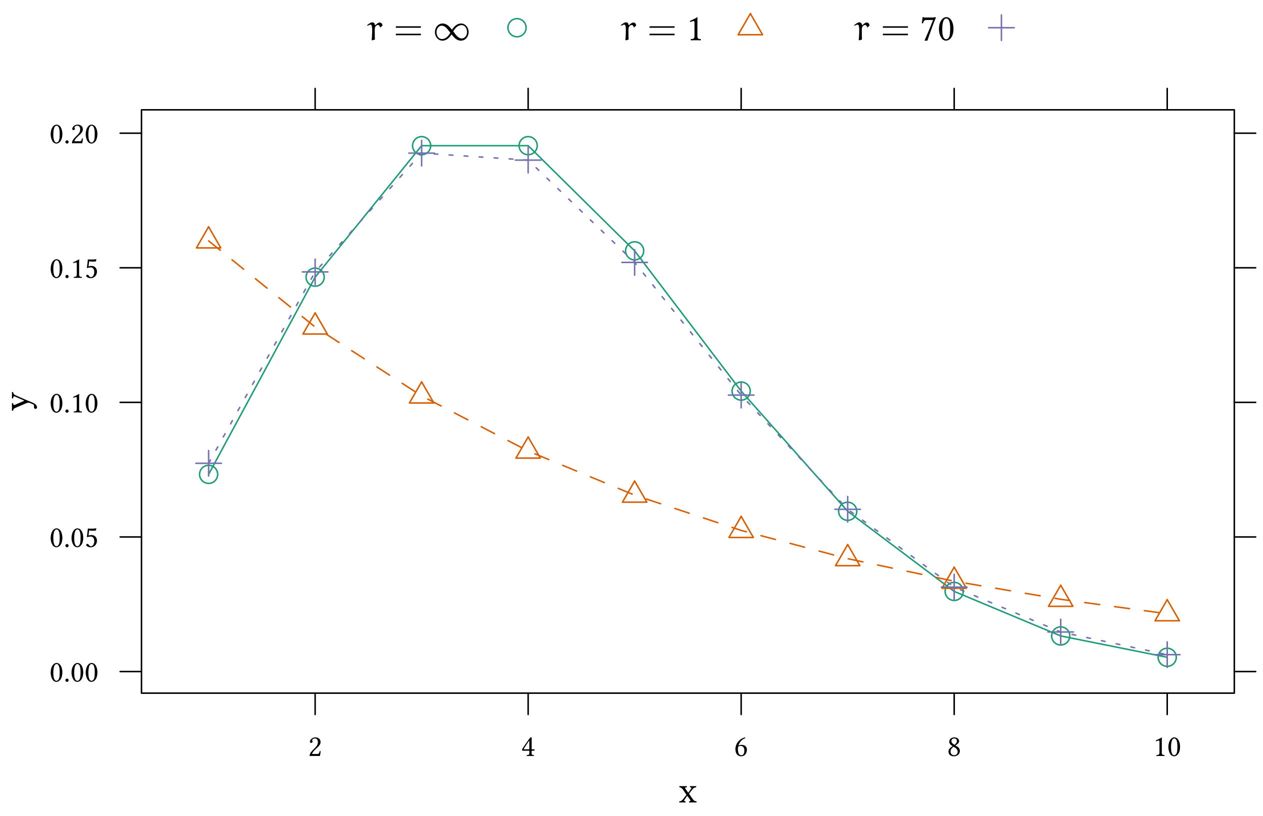
where $p = \frac{r}{r+\mu}$ or $\mu = \frac{r}{p} - r$

$$\lim_{r\to\infty} NB(\mu,r) = Pois(\mu)$$

(r is sometimes called θ)
Let us use the NB model with our Poisson data:

```
countNB.model <- 'model {
 for (i in 1:length(y)) {
        y[i] ~ dnegbin(p[i],r)
        p[i] <- r/(r+mu[i])
        log(mu[i]) <- inprod(X[i,],beta)
 }
 r ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
 for (k in 1:K) {
    beta[k] ~ dnorm (0,.0001)
 }
}'
countNB.jags<-run.jags(model=countNB.model,modules=c("glm"),
       data=list(y=y,X=cbind(1,x),K=2),inits=ini,monitor=c("beta","r"))
summary(countNB.jags)[,c("Mean","SD","SSeff","psrf")]
```

```
              Mean          SD  SSeff     psrf
beta[1]  0.9452762  0.07232891   3930 1.000826
beta[2]  2.0548921  0.05386288   3822 1.000954
r       69.9999621 55.61963601   3537 1.001263
```



10.3 Exercise

Consider the dataset *Doctor* from *Ecdat*. Explain the number of doctor visits as a function of children in the household.

- Use a Possion model.
- Use a negative binomial model.

11 Multinomial (polytomous) logit

11.1 Motivation and background

Multinomial logit

- choices are mutually exclusive
- choices are exhaustive
- choices are finite

Problems

- one can map problems that do not look mutually exclusive or not exhaustive into a problem that is

  E.g.: heating modes: gas / oil / wood / electricity

  What about households which use, e.g., gas + electricity $\to$

  - introduce an additional category
  - ask for 'primary source of heating'

  Some households do not use any of the above:

  - introduce an additional category

- Using discrete choice models for metric variables
  - E.g.: consumption of goods which follow a non-linear tariff (telephone, electricity)

Random utility models

Can we tell a story like in the logit/probit case?
A latent variable model (random utility model):

$$\begin{aligned}\eta_1 &= x'\beta_1 + \xi_1 \\ \eta_2 &= x'\beta_2 + \xi_2 \\ \eta_3 &= x'\beta_3 + \xi_3 \\ &\vdots\end{aligned}$$

The decision maker chooses alternative k if $\eta_k \geqslant \eta_j$ for all j
Note: these models are equivalent to their affine transformations.

Normalisations

- We often normalise the constant part of one of the equations to zero.
- If ξ_j are i.i.d. we often normalise their variance to a convenient value.

  (this implies that different distributions for ξ will lead to different scales for coefficients — logit coefficients will be $\pi/\sqrt{6}$ times larger than probit.)

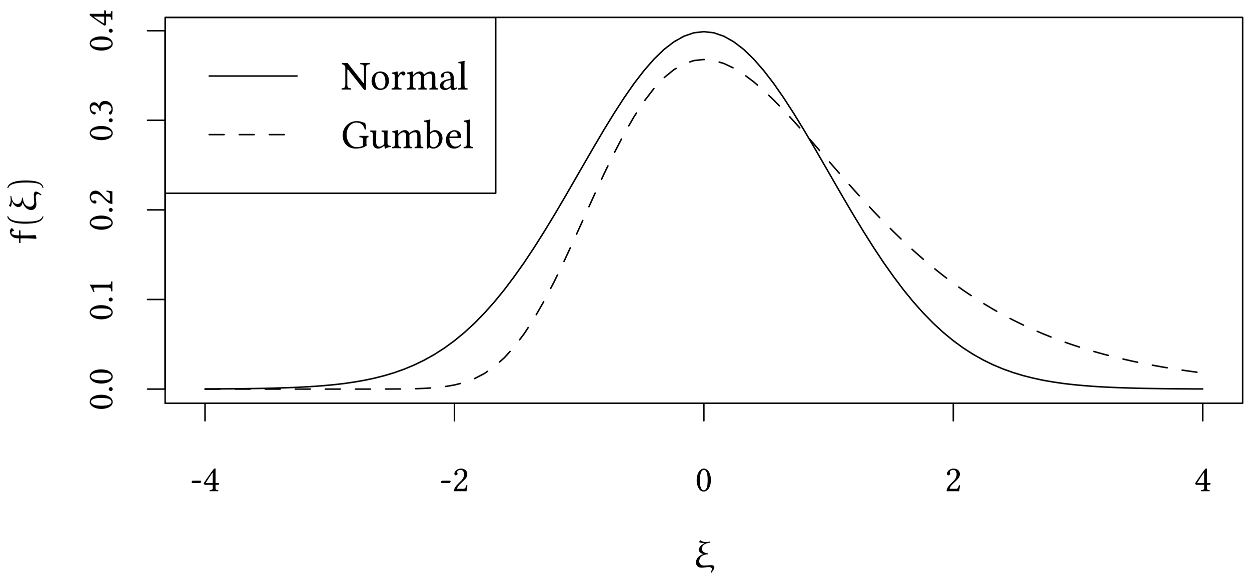
Differences

Let us look at the differences between two alternatives:

$$\nu_{kj} = \eta_k - \eta_j = x'(\beta_k - \beta_j) + \xi_k - \xi_j$$

- $\xi \sim N(0,1)$: $\xi_k - \xi_j$ has variance 2 and covariance 1 (for $k \neq j$)

```
dgumbel<-function(x) exp(-exp(-x)-x)
plot(dnorm,-4,4,ylab="$f(\\xi)$",xlab="$\\xi$")
curve(dgumbel,add=TRUE,lty=2)
legend("topleft",c("Normal","Gumbel"),lty=1:2)
```



- $\xi \sim$ Gumbel $\left(F_{\text{Gumbel}}(\xi) = e^{-e^{-\xi}}\right)$ then
  - the difference ν_{ki} follows a logistic distribution

$$\Pr(y = k|\xi_k) = \prod_{j\neq k} \underbrace{F_{\text{Gumbel}}(x'(\beta_k - \beta_j) + \xi_k)}_{\Pr(\eta_j < \eta_k)}$$

average over ξ_k

$$\Pr(y = k) = \int f_{\text{Gumbel}}(\xi_k) \prod_{j\neq k} F_{\text{Gumbel}}(x'(\beta_k - \beta_j) + \xi_k)\, d\xi_k$$

$$\Pr(y = k) = \frac{e^{x'\beta_k}}{\sum_{i=1}^{m} e^{x'\beta_i}}$$

$\rightarrow$ we get the following multinomial logit (McFadden)

$$\begin{aligned}
\Pr(y=1) &= \frac{e^{x'\beta_1}}{\sum_{k=1}^{m} e^{x'\beta_k}} \\
\Pr(y=2) &= \frac{e^{x'\beta_2}}{\sum_{k=1}^{m} e^{x'\beta_k}} \\
\Pr(y=3) &= \frac{e^{x'\beta_3}}{\sum_{k=1}^{m} e^{x'\beta_k}} \\
&\vdots
\end{aligned}$$

- $0 < \Pr(y=k) < 1$
- $\sum_k \Pr(y=k) = 1$

$\uparrow$ β_k are not identified

Normalise:

$$\begin{aligned}
\Pr(y=1) &= \frac{1}{1+\sum_{k=2}^{m} e^{x'\beta_k}} \\
\Pr(y=2) &= \frac{e^{x'\beta_2}}{1+\sum_{k=2}^{m} e^{x'\beta_k}} \\
\Pr(y=3) &= \frac{e^{x'\beta_3}}{1+\sum_{k=2}^{m} e^{x'\beta_k}} \\
&\vdots
\end{aligned}$$

the odds ratios are:

$$\frac{\Pr(y=k)}{\Pr(y=1)} = e^{x'\beta_k}$$

This is a strong assumption on the error terms.

Indenpendence from irrelevant alternatives — IIA

Example:

- Dependent = choice of travel mode
- unobservable = personal preference for/against means of mass transportation (tube/train).

$\frac{\Pr(y=\text{tube})}{\Pr(y=1)} = e^{x'\beta_{\text{tube}}}$ $\frac{\Pr(y=\text{train})}{\Pr(y=1)} = e^{x'\beta_{\text{train}}}$

- $\to$ choices/error terms are correlated.

$\to$ multinomial logit can represent systematic variation of choices (explained by observed characteristics) but *not* systematic individual (unobserved) variation of choices.

The log-likelihood:

With $I_k(y_i) = \begin{cases} 1 & \text{if } y_i = i \\ 0 & \text{otherwise} \end{cases}$

$$\begin{aligned} \log L &= \sum_i \sum_{k=1}^{m} I_k(y_i) \log \Pr(y_i = k) \\ &= \sum_i \sum_{k=1}^{m} I_k(y_i) \log \frac{e^{x_i' \beta_k}}{1 + \sum_{k=2}^{m} e^{x_i' \beta_k}} \end{aligned}$$

this function $\log L$ is globally concave in β (McFadden, 1974)

11.2 Example

The purpose of this example is to illustrate an identification problem in the context of multinomial logit. There are different ways to describe the same choices. In the example we see that we use one set of parameters (`mat`) to generate the choices but the estimator gives us a different set of parameters back (`coef(est)`). We also see how these two sets of parameters are related.

Let us first create individual explanatory variables, `x1`, `x2`.

```
N<-100
sd<-10
ex <- cbind(x1=runif(N),x2=runif(N))
head(ex)

            x1        x2
[1,] 0.2875775 0.5999890
[2,] 0.7883051 0.3328235
[3,] 0.4089769 0.4886130
[4,] 0.8830174 0.9544738
[5,] 0.9404673 0.4829024
[6,] 0.0455565 0.8903502
```

The following matrix determines how individual characteristics translate into preferences for three choices:

```
mat<-rbind(c(400,0),
          c(250,200),
          c(100,300))
mat
```

```
     [,1] [,2]
[1,]  400    0
[2,]  250  200
[3,]  100  300
```

```
latent<-(ex %*% t(mat)) + sd * cbind(rnorm(N),rnorm(N),rnorm(N))
head(latent)

          [,1]     [,2]     [,3]
[1,] 107.92694 213.8803 201.6020
[2,] 317.89089 276.7651 171.1507
[3,] 161.12385 197.3154 178.0962
[4,] 349.73154 417.0811 364.1188
[5,] 366.67073 327.5539 234.5459
[6,]  17.77232 184.6967 274.9725

max.col(latent)

 [1] 2 1 2 2 1 3 2 1 2 1 2 1 1 3 3 1 3 3 3 1 1 1 1 1 1 2 1 1 2 3 1 2 2 2 3 2 2 3
[39] 3 3 3 2 1 1 3 2 2 1 1 2 3 2 1 3 1 3 3 1 1 1 1 3 3 2 1 2 2 1 1 1 2 1 2 3 2 3
[77] 2 2 3 3
 [ reached getOption("max.print") -- omitted 20 entries ]
```

```
choice <- max.col(latent)
library(nnet)
est<-multinom(choice ~ x1 + x2,data.frame(ex))

# weights:  12 (6 variable)
initial  value 109.861229
iter  10 value 18.323213
iter  20 value 16.923568
iter  30 value 16.881715
iter  40 value 16.880637
iter  50 value 16.880332
iter  60 value 16.880044
iter  70 value 16.879931
final  value 16.879896
converged
```

```
est

Call:
multinom(formula = choice ~ x1 + x2, data = data.frame(ex))

Coefficients:
  (Intercept)        x1       x2
2   0.9444688 -25.80588 31.72050
3   0.1557040 -58.59718 52.66552
```

```
Residual Deviance: 33.75979
AIC: 45.75979
```

Note that the estimated coefficients are not the matrix of coefficients *mat* that we employed above. However, they are a projection. We are expecting this:

```
mat

     [,1] [,2]
[1,]  400    0
[2,]  250  200
[3,]  100  300
```

but we got that:

```
coef(est)

  (Intercept)        x1       x2
2   0.9444688 -25.80588 31.72050
3   0.1557040 -58.59718 52.66552
```

The estimator normalises the first category to zero

```
mat

     [,1] [,2]
[1,]  400    0
[2,]  250  200
[3,]  100  300

mat - cbind(c(1,1,1)) %*% mat[1,]

     [,1] [,2]
[1,]    0    0
[2,] -150  200
[3,] -300  300
```

and sets the variance to one:

```
(mat -  cbind(c(1,1,1)) %*% mat[1,])*pi / sqrt(6) / 10

          [,1]     [,2]
[1,]   0.00000  0.00000
[2,] -19.23825 25.65100
[3,] -38.47649 38.47649
```

To access estimation results we have the usual extractor functions:

```
coef(est)
```

```
  (Intercept)        x1       x2
2   0.9444688 -25.80588 31.72050
3   0.1557040 -58.59718 52.66552

confint(est)

, , 2

                  2.5 %    97.5 %
(Intercept)  -3.098834  4.987771
x1          -43.459195 -8.152558
x2           11.420190 52.020819

, , 3

                 2.5 %     97.5 %
(Intercept)  -4.74507   5.056478
x1          -89.59278 -27.601578
x2           26.23746  79.093575
```

11.3 Bayesian multinomial

```
modelM <- 'model {
 for (i in 1:length(y)) {
        for (j in 1:3) { # three different choices
          exb[i,j] <- exp(inprod(beta[,j],ex[i,]))
        }
        y[i] ~ dcat(exb[i,1:3])
    }
    for (k in 1:K) {
        beta[k,1] <- 0 # identifying restriction
    }
    for (j in 2:3) {
      for (k in 1:K) {
         beta[k,j] ~ dnorm(0,.0001)
      }
    }
}'
dataList<-list(y=choice,ex=cbind(1,ex),K=dim(ex)[2]+1)
bayesM <-run.jags(model=modelM,data=dataList,monitor=c("beta"))
```

```
bayesM$summary$quantiles[-c(1,2,3),c("2.5%","50%","97.5%")]

                2.5%          50%      97.5%
beta[1,2]    -2.93526   1.05255000   6.407701
beta[2,2]   -57.90451 -30.54820000 -15.823597
beta[3,2]    20.81504  37.89850000  67.242305
beta[1,3]    -5.02241   0.07058615   6.171032
```

```
beta[2,3] -109.86352 -71.58410000 -44.914368
beta[3,3]   41.19685  64.41970000  95.933505

confint(est)

, , 2

                 2.5 %    97.5 %
(Intercept)  -3.098834  4.987771
x1          -43.459195 -8.152558
x2           11.420190 52.020819

, , 3

                2.5 %     97.5 %
(Intercept)  -4.74507   5.056478
x1          -89.59278 -27.601578
x2           26.23746  79.093575
```

11.4 Exercise

Consider the data set *ModeChoice* from *Ecdat*.

- Which variables could explain the transport mode?
- Estimate your model.

12 Ordered probit

12.1 Model

We observe whether latent variables $x'\beta$ are in an interval

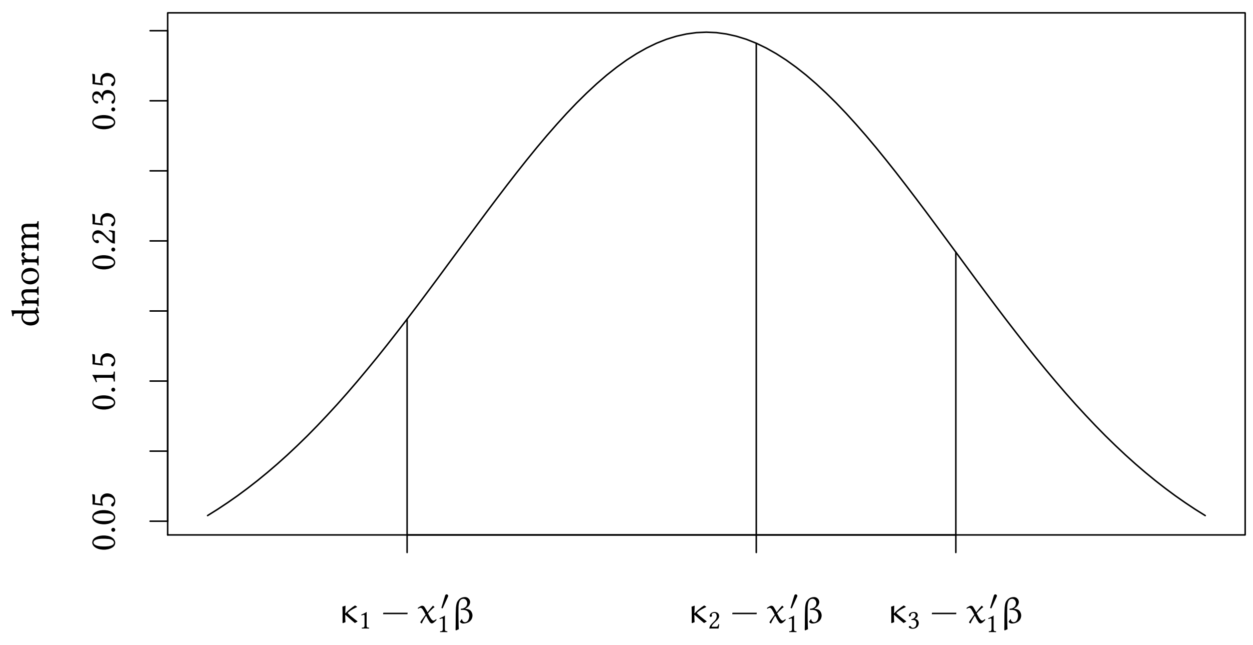
$$\begin{aligned}
\Pr(y_i = 1) &= \Pr(\kappa_0 < x_i'\beta + u \leqslant \kappa_1) \\
\Pr(y_i = 2) &= \Pr(\kappa_1 < x_i'\beta + u \leqslant \kappa_2) \\
\Pr(y_i = 3) &= \Pr(\kappa_2 < x_i'\beta + u \leqslant \kappa_3) \\
&\vdots
\end{aligned}$$

or (solving for u)

$$\begin{aligned}
\Pr(y_i = 1) &= \Pr(\kappa_0 - x_i'\beta < u \leqslant \kappa_1 - x_i'\beta) \\
\Pr(y_i = 2) &= \Pr(\kappa_1 - x_i'\beta < u \leqslant \kappa_2 - x_i'\beta) \\
\Pr(y_i = 3) &= \Pr(\kappa_2 - x_i'\beta < u \leqslant \kappa_3 - x_i'\beta) \\
&\vdots
\end{aligned}$$

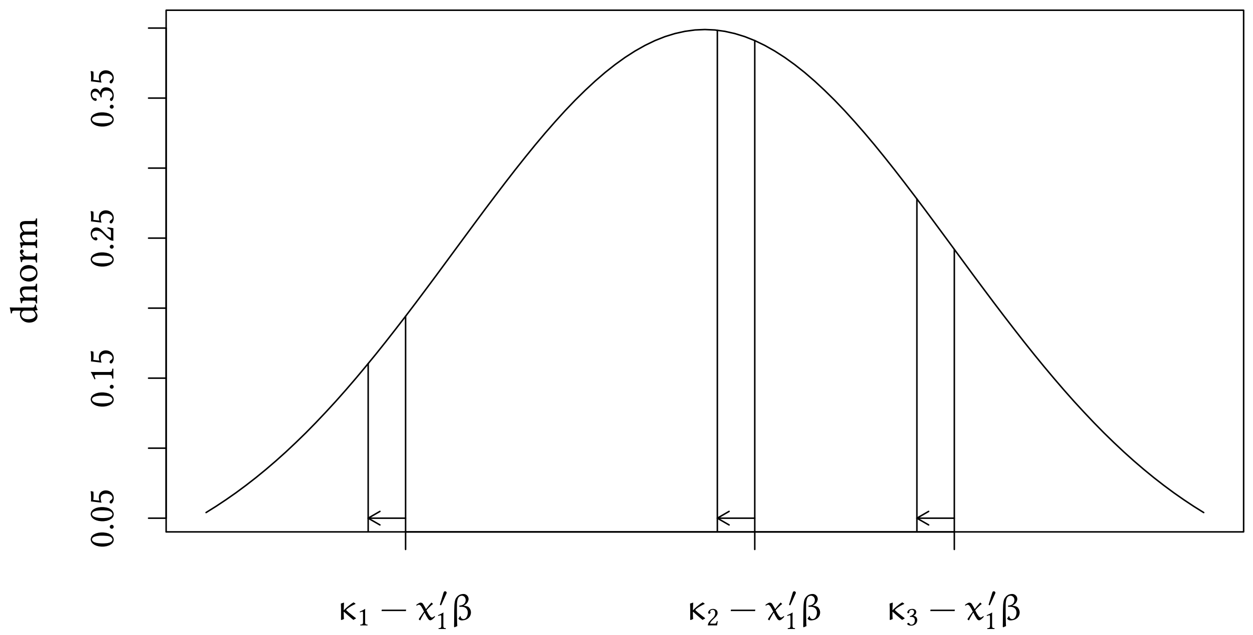
The u can follow any (standard) distribution (logistic, normal, …)

```
plot(dnorm,-2,2,xaxt="n",xlab=NA)
kappas<-c(-1.2,.2,1)
for(i in 1:length(kappas)) {x<-kappas[i];lines(c(x,x),c(0,dnorm(x)))}
axis(1,kappas,sapply(1:length(kappas),function(d) sprintf("$\\kappa_%d - x_1'\\beta$",d)))
```



Marginal effects:

```
plot(dnorm,-2,2,xaxt="n",xlab=NA)
kappas<-c(-1.2,.2,1)
for(i in 1:length(kappas)) {
    x<-kappas[i];lines(c(x,x),c(0,dnorm(x)))
    y<-kappas[i]-.15;lines(c(y,y),c(0,dnorm(y)))
    arrows(x,.05,y,.05,length=.05)
}
axis(1,kappas,sapply(1:length(kappas),function(d) sprintf("$\\kappa_%d - x_1'\\beta$",d)))
```



The maximum likelihood problem

$$\begin{aligned}
\Pr(y_i = 1) &= \Pr(\kappa_0 - x_i'\beta < u \leqslant \kappa_1 - x_i'\beta) \\
\Pr(y_i = 2) &= \Pr(\kappa_1 - x_i'\beta < u \leqslant \kappa_2 - x_i'\beta) \\
\Pr(y_i = 3) &= \Pr(\kappa_2 - x_i'\beta < u \leqslant \kappa_3 - x_i'\beta) \\
&\vdots
\end{aligned}$$

$$\log L = \sum_i \sum_{k=1}^{m} I_k(y_i) \log \Pr(y_i = k)$$

with $I_k(y_i) = \begin{cases} 1 & \text{if } y_i = i \\ 0 & \text{otherwise} \end{cases}$

12.2 Illustration — the Fair data

As an illustration, let us look at a dataset on extramarital affairs, collected by Ray Fair. Two variables from the dataset are

- *ym* number of years married
- *rate* self rating of mariage (unhappy=1…5=happy)

Does the rating of marriage change over time? A naïve approach would be to use OLS and to explain `rate` as a linear function of *ym*.

```
library(MASS)
library(Ecdat)
data(Fair)
lm(rate ~ ym,data=Fair)


Call:
lm(formula = rate ~ ym, data = Fair)

Coefficients:
(Intercept)           ym
    4.32546     -0.04814
```

This approach would assume that all ratings are equidistant. More appropriate is, perhaps, an ordered logistic model…

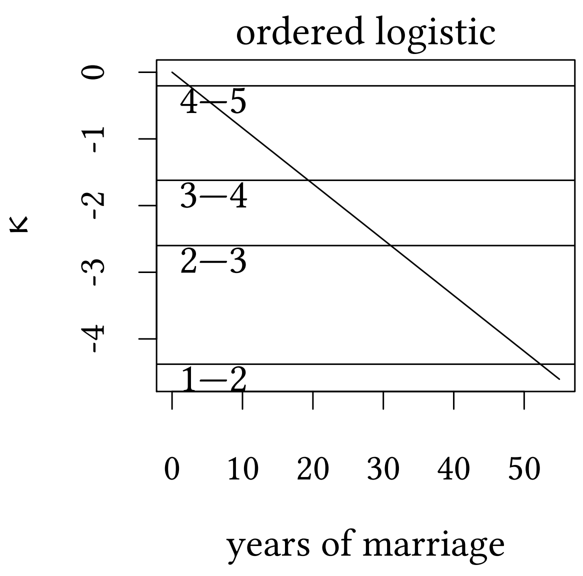
```
(estL<-polr(factor(rate) ~ ym,data=Fair))

Call:
polr(formula = factor(rate) ~ ym, data = Fair)

Coefficients:
         ym
-0.08371391

Intercepts:
       1|2        2|3        3|4        4|5
-4.3786529 -2.5996956 -1.6207810 -0.2043441

Residual Deviance: 1597.27
AIC: 1607.27
```

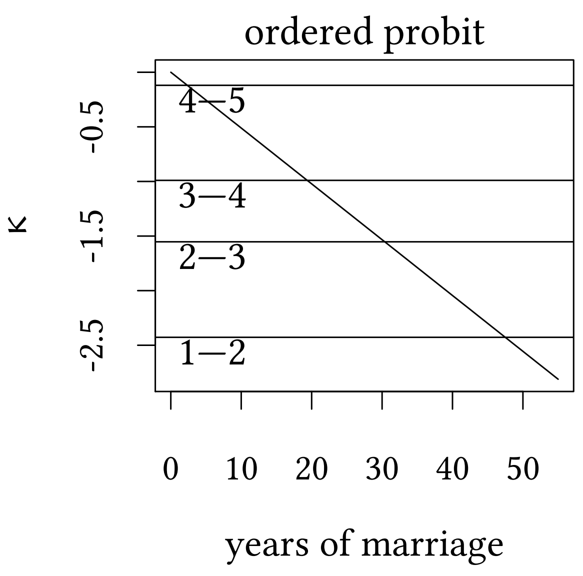
…or an ordered probit:

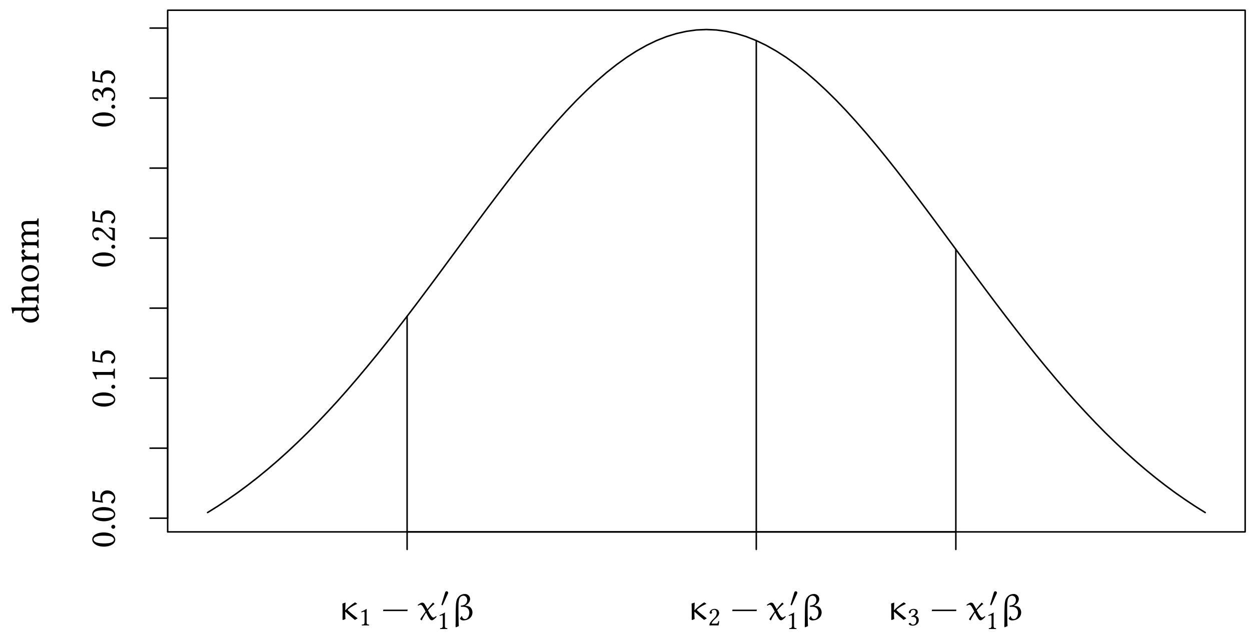
```
(estP<-polr(factor(rate) ~ ym,data=Fair,method="probit"))

Call:
polr(formula = factor(rate) ~ ym, data = Fair, method = "probit")

Coefficients:
         ym
-0.05110974

Intercepts:
      1|2       2|3       3|4       4|5
-2.427247 -1.552900 -0.990142 -0.119791

Residual Deviance: 1594.99
AIC: 1604.99
```

The following graph illustrates the estimated thresholds κ_i:

```
probFig <- function (est,main) {
  plot(function(x) {x * est$coef},0,55,ylab="$\\kappa$",xlab="years of marriage",main=main
  for (a in est$zeta) {
    abline(h=a)
    lab=names(est$zeta)[which(est$zeta==a)]
    text(1,a,labels=lab,adj=c(0,1))
  }
}
probFig(estL,main="ordered logistic")
probFig(estP,main="ordered probit")
```







- Dependent variable *y[i]*
- Latent variable *t[i]*
- Independent variable *x[i]*
- Parameters *beta, kappa[j]*

JAGS notation for intervals

```
y[i] ~ dinterval(t[i],kappa)
```

where

t[i]	realisation of latent variable
y[i]	observable rating
kappa	thresholds

If $Y \sim \texttt{dinterval}(t, \kappa)$ then

$$\begin{array}{lll} Y = 0 & \text{if } t \leqslant \kappa[1] & \\ Y = m & \text{if } \kappa[m] < t \leqslant \kappa[m+1] & \text{for } 1 \leqslant m < M \\ Y = M & \text{if } \kappa[M] < t & \end{array}$$

Note: We have to give JAGS possible initial values:

```
dataList<-list(y=Fair$rate-1,x=Fair$ym,K=max(Fair$rate)-1)
initList<-with(dataList,list(t=y+1/2,kappa0=1:K))
```

```
model0 <- 'model {
 for (i in 1:length(y)) {
    y[i] ~ dinterval(t[i],kappa)
    t[i] ~ dnorm(beta*x[i],1)
 }
 for (j in 1:K) {
    kappa0[j] ~ dnorm(0,.0001)
 }
 kappa[1:4] <- sort(kappa0)
 beta ~ dnorm(0,.0001)
}'
dataList<-list(y=Fair$rate-1,x=Fair$ym,K=max(Fair$rate)-1)
initList<-with(dataList,list(t=y+1/2,kappa0=1:K))
bayes0 <-run.jags(model=model0,data=dataList,inits=list(initList,initList),
                  monitor=c("beta","kappa"))
```

```
bayes0$summary$quantiles[,c("2.5%","50%","97.5%")]

                2.5%         50%        97.5%
beta     -0.05883133 -0.04208000  0.005145038
kappa[1] -2.61775050 -2.31008000 -1.701987250
kappa[2] -1.66015100 -1.45323000 -0.821465625
kappa[3] -1.04795200 -0.87123050 -0.271165975
kappa[4] -0.18787128 -0.01349525  0.521559200

estP

Call:
polr(formula = factor(rate) ~ ym, data = Fair, method = "probit")

Coefficients:
         ym
-0.05110974

Intercepts:
      1|2       2|3       3|4       4|5
-2.427247 -1.552900 -0.990142 -0.119791

Residual Deviance: 1594.99
AIC: 1604.99
```

Convergence is not too exciting

```
bayesO


JAGS model summary statistics from 20000 samples (chains = 2; adapt+burnin = 5000):

           Lower95    Median    Upper95      Mean        SD      Mode     MCerr
beta     -0.061539  -0.04208 -0.0005693 -0.038078 0.016126 -0.047019 0.0057683
kappa[1]   -2.6603   -2.3101    -1.7527   -2.2751   0.2228   -2.3448   0.03129
kappa[2]   -1.6862   -1.4532    -0.8756   -1.3938  0.21054   -1.5099  0.066847
kappa[3]   -1.0938  -0.87123   -0.38771  -0.82444   0.2017  -0.96236  0.077131
kappa[4]  -0.24793 -0.013495    0.40045  0.031712  0.17487 -0.060974  0.069547

         MC%ofSD SSeff   AC.10   psrf
beta        35.8     8 0.90535 1.2393
kappa[1]      14    51 0.94751 1.1735
kappa[2]    31.8    10 0.99001 1.2485
kappa[3]    38.2     7 0.99305 1.2836
kappa[4]    39.8     6 0.99375 1.2465

Total time taken: 6.8 seconds
```

12.3 Exercise

Consider the data set *Mathlevel* from *Ecdat*.

- Which variables could explain the attained math level.
- Estimate your model.

13 Instrumental variables

The problem:

$$Y = X\beta + \epsilon \qquad \text{but } X \not\vdash \boldsymbol{\epsilon}$$

Solution, use instrument $Z \vdash \epsilon$

$$\begin{aligned} \text{1st stage: } X &= Z\gamma + \nu \\ \hat{X} &= Z\gamma \\ \text{2nd stage: } Y &= \hat{X}\beta + \epsilon \end{aligned}$$

```
set.seed(123)
N<-100
eps<-rnorm(N)
Z<-rnorm(N)
X<- -eps+Z+.5*rnorm(N)
Y<-X + eps
summary(lm(Y~X))


Call:
lm(formula = Y ~ X)

Residuals:
     Min       1Q   Median       3Q      Max
-1.59416 -0.42295 -0.00768  0.45972  1.88043

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.03257    0.06706   0.486    0.628
X            0.58001    0.04503  12.881   <2e-16 ***
---
Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1

Residual standard error: 0.6678 on 98 degrees of freedom
Multiple R-squared:  0.6287,Adjusted R-squared:  0.6249
F-statistic: 165.9 on 1 and 98 DF,  p-value: < 2.2e-16
```

Naïve model: ignore that $X \not\perp \epsilon$

```
instNaive.model<-’model {
  for(i in 1:length(y)) {
    y[i]~dnorm(beta[1]+beta[2]*x[i],tau)
  }
    beta[1]~dnorm(0,.0001)
    beta[2]~dnorm(0,.0001)
    tau ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
}’
ini <- genInit(4)
instNaive.jags<-run.jags(model=instNaive.model,data=list(y=Y,x=X,z=Z),
                    monitor=c("beta","tau"),inits=ini)
```

```
summary(instNaive.jags)[,c("Mean","SD","SSeff","psrf")]

              Mean         SD SSeff      psrf
beta[1] 0.03274741 0.06846955 39339 1.0000189
beta[2] 0.57971640 0.04581343 38130 0.9999869
tau     2.20708778 0.30908647 12778 1.0001239
```

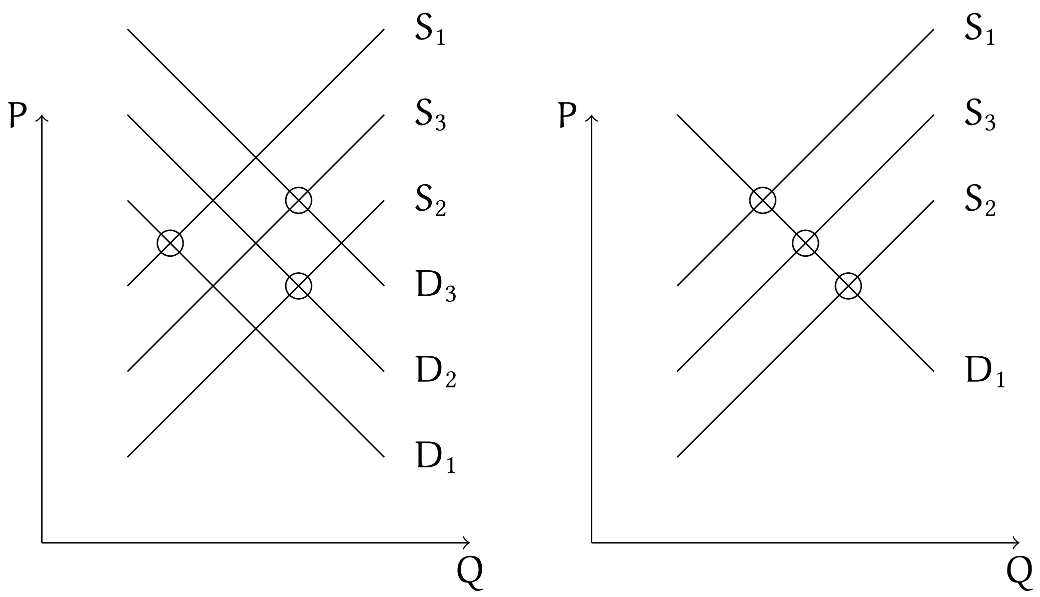
Instrument $Z \vdash \epsilon$

```
inst.model<-'model {
  for(i in 1:length(y)) {
    x[i]    ~  dnorm(xHat[i],tau[2])                 # 1st stage
    xHat[i]<- gamma[1]+gamma[2]*z[i]
    y[i]    ~  dnorm(beta[1]+beta[2]*xHat[i],tau[1]) # 2nd stage
  }
  for(k in 1:2) {
    beta[k] ~ dnorm(0,.0001)
    gamma[k]~ dnorm(0,.0001)
    tau[k] ~ dgamma(m[k]^2/d[k]^2,m[k]/d[k]^2); m[k] ~ dexp(1); d[k] ~ dexp(1);
    }
}'
```

```
inst.jags<-run.jags(model=inst.model,data=list(y=Y,x=X,z=Z),
                    monitor=c("beta","tau"),inits=ini)
```

```
summary(inst.jags)[,c("Mean","SD","SSeff","psrf")]

              Mean        SD SSeff     psrf
beta[1] 0.08822246 0.1224222  3465 1.001245
beta[2] 0.97934413 0.1204707  3588 1.000527
tau[1]  4.19849540 0.5962644 11327 1.000033
tau[2]  0.85500640 0.1194926 18651 1.000030
```

13.1 Example: Demand and Supply



How can we estimate the slope of D, if D and S are moving simultaneously?

The Demand for Cigarettes

The dataset

- `state`: Factor indicating state.
- `year`: Factor indicating year.
- `cpi`: Consumer price index.
- `population`: State population.
- `packs`: Number of packs per capita.
- `income`: State personal income (total, nominal).
- `tax`: Average state, federal and average local excise taxes for fiscal year.
- `price`: Average price during fiscal year, including sales tax.
- `taxs`: Average excise taxes for fiscal year, including sales tax.

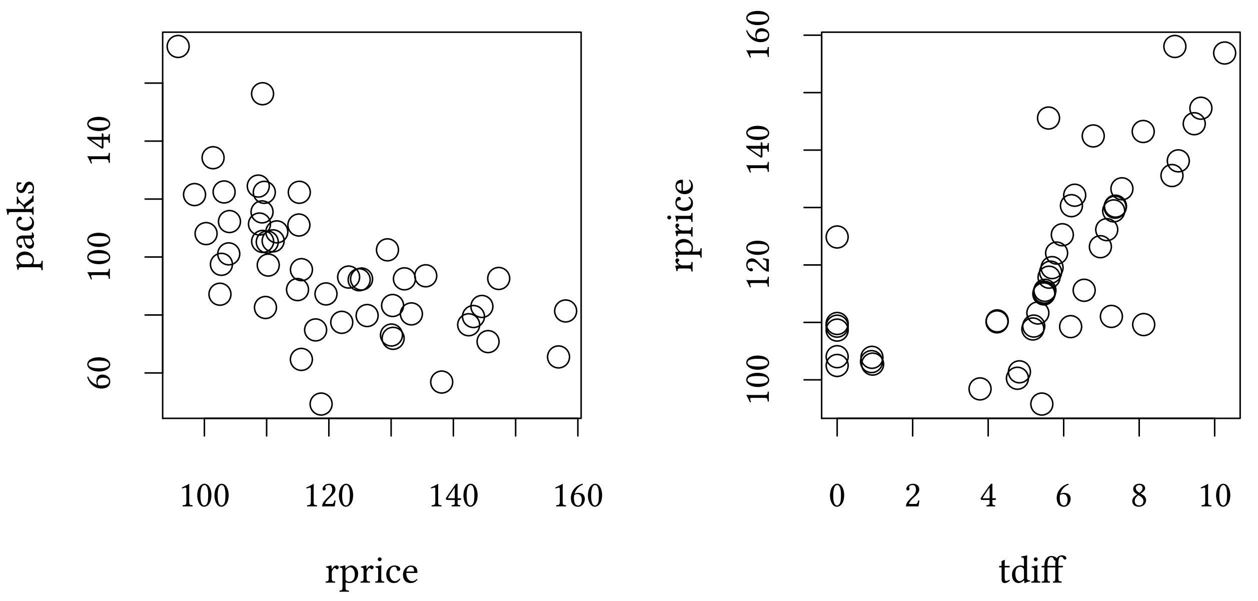
```
library(AER)
data("CigarettesSW", package = "AER")
head(CigarettesSW)

  state year   cpi population    packs    income  tax     price     taxs
1    AL 1985 1.076    3973000 116.4863  46014968 32.5 102.18167 33.34834
2    AR 1985 1.076    2327000 128.5346  26210736 37.0 101.47500 37.00000
3    AZ 1985 1.076    3184000 104.5226  43956936 31.0 108.57875 36.17042
4    CA 1985 1.076   26444000 100.3630 447102816 26.0 107.83734 32.10400
5    CO 1985 1.076    3209000 112.9635  49466672 31.0  94.26666 31.00000
6    CT 1985 1.076    3201000 109.2784  60063368 42.0 128.02499 51.48333
```

We have to construct some variables:
Clean the data:

```
Cig <- within(subset(CigarettesSW,year=="1995"),{
    rprice <- price/cpi
    rincome <- income/population/cpi
    tdiff <- (taxs - tax)/cpi
    rtax  <- tax/cpi
})
```

$\log(\texttt{packs}) = Y$
$\log(\texttt{rprice}) = X$
$\texttt{tdiff} = Z$

```
with(Cig,{plot(packs ~ rprice); plot(tdiff, rprice)})
```



We are interested in

$$\log(\texttt{packs}) = \beta_0 + \beta_1 \log(\texttt{rprice}) + u$$

However, `rprice` is endogeneous, correlated with u.
We can use `tdiff`, the sales tax on cigarettes, as an instrument for $\log(\texttt{rprice})$.

$$\begin{aligned}\text{1st stage:}\ \log(\texttt{rprice}) &= \gamma_0 + \gamma_1 \texttt{tdiff} + \nu \\ \log(\widehat{\texttt{rprice}}) &= \gamma_0 + \gamma_1 \texttt{tdiff} \\ \text{2nd stage:}\ \log(\texttt{packs}) &= \beta_0 + \beta_1 \log(\widehat{\texttt{rprice}}) + \epsilon\end{aligned}$$

The naïve approach

```
est0.model <- 'model {
  for(i in 1:length(y)) {
    y[i]    ~  dnorm(beta[1]+beta[2]*x[i],tau)
  }
  for(k in 1:2) {
    beta[k] ~ dnorm(0,.0001)
    }
    tau ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
}'
ini <- genInit(4)
est0.jags<-run.jags(model=est0.model,
                    data=with(Cig,list(y=log(packs),x=log(rprice))),
                    monitor=c("beta","tau"),inits=ini)
```

```
est0.jags


JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

        Lower95 Median  Upper95    Mean      SD    Mode    MCerr MC%ofSD SSeff
beta[1]  8.2997 10.166   11.923  10.082 0.95021  10.304  0.17318    18.2    30
beta[2] -1.5448 -1.177 -0.78779 -1.1595 0.19867 -1.2082 0.036321    18.3    30
tau      14.916 24.752   36.272  25.131  5.5338  24.523 0.039646     0.7 19483

           AC.10   psrf
beta[1]    0.985 1.2297
beta[2]    0.985 1.2248
tau     0.018035  1.001

Total time taken: 1.1 seconds
```

2 Stage Least Squares (2SLS)

We use the same model as before:

```
inst.model<-'model {
  for(i in 1:length(y)) {
    x[i]    ~  dnorm(xHat[i],tau[2])                 # 1st stage
    xHat[i]<- gamma[1]+gamma[2]*z[i]
    y[i]    ~  dnorm(beta[1]+beta[2]*xHat[i],tau[1]) # 2nd stage
  }
  for(k in 1:2) {
    beta[k] ~ dnorm(0,.0001)
    gamma[k]~ dnorm(0,.0001)
    tau[k] ~ dgamma(m[k]^2/d[k]^2,m[k]/d[k]^2); m[k] ~ dexp(1); d[k] ~ dexp(1);
    }
}'
```

```
cig.data <- with(Cig,list(y=log(packs)-mean(log(packs)),
                          x=log(rprice)-mean(log(rprice)),
                          z=tdiff-mean(tdiff)))
cig.jags <- run.jags(model=inst.model,
                     data=cig.data,
                     monitor=c("beta","sd"),
                     inits=ini)
```

```
cig.jags


JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

          Lower95      Median   Upper95        Mean       SD        Mode      MCerr
beta[1] -0.074083 0.00047877 0.075199 0.00033328 0.037873 -0.0013349 0.00023624
```

```
beta[2]   -2.1209    -1.1158 -0.29165    -1.1538  0.47205    -1.0608  0.0030556

        MC%ofSD SSeff      AC.10   psrf
beta[1]     0.6 25700 0.00035278 1.0003
beta[2]     0.6 23866  0.0058074 1.0001

Total time taken: 0.7 seconds
```

Extending the 2nd stage

Could there be an ommitted variable bias in our second stage equation. Perhaps demand is not only affected by price, but also by income?

$\rightarrow$ include log(`rincome`) in the second stage:

```
inst2.model<-'model {
  for(i in 1:length(y)) {
    x[i]    ~  dnorm(xHat[i],tau[2])                 # 1st stage
    xHat[i]<- gamma[1]+gamma[2]*z[i]
    y[i]    ~  dnorm(beta[1]+beta[2]*xHat[i]+beta[3]*x2[i],tau[1]) # 2nd stage
  }
  for(k in 1:3) {
    beta[k] ~ dnorm(0,.0001)
    gamma[k]~ dnorm(0,.0001)
    tau[k] ~ dgamma(m[k]^2/d[k]^2,m[k]/d[k]^2); m[k] ~ dexp(1); d[k] ~ dexp(1);
    }
}'
ini <- genInit(4)
cig2.data <- with(Cig,list(y=log(packs)-mean(log(packs)),
                           x=log(rprice)-mean(log(rprice)),
                           z=tdiff-mean(tdiff),
                           x2=log(rincome)))
cig2.jags <- run.jags(model=inst2.model,
                      data=cig2.data,
                      monitor=c("beta","sd"),
                      inits=ini)
```

```
cig2.jags


JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

         Lower95   Median  Upper95     Mean      SD     Mode      MCerr MC%ofSD
beta[1] -0.71018  0.60736   2.1043  0.65172 0.73187  0.62976    0.10195    13.9
beta[2]  -2.1018  -1.0514 -0.15304  -1.0869 0.49951 -0.99786  0.0041852     0.8
beta[3] -0.78136 -0.22658  0.26685 -0.24305 0.27274 -0.23149   0.037999    13.9

        SSeff    AC.10   psrf
beta[1]    52  0.97441 1.0345
beta[2] 14245 0.023295 1.0005
```

```
beta[3]    52  0.97447 1.0345

Total time taken: 1.2 seconds
```

Alternative: *ivreg*

```
est2.iv <- ivreg(log(packs) ~ log(rprice) + log(rincome) | log(rincome) + tdiff ,data = Cig
summary(est2.iv)


Call:
ivreg(formula = log(packs) ~ log(rprice) + log(rincome) | log(rincome) +
    tdiff, data = Cig)

Residuals:
      Min        1Q    Median        3Q       Max
-0.611000 -0.086072  0.009423  0.106912  0.393159

Coefficients:
             Estimate Std. Error t value     Pr(>|t|)
(Intercept)    9.4307     1.3584   6.943 0.0000000124 ***
log(rprice)   -1.1434     0.3595  -3.181      0.00266 **
log(rincome)   0.2145     0.2686   0.799      0.42867
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.1896 on 45 degrees of freedom
Multiple R-Squared: 0.4189,Adjusted R-squared: 0.3931
Wald test: 6.534 on 2 and 45 DF,  p-value: 0.003227
```

Note that the *ivreg* notation includes *log(rincome)* as an instrument for itself. Technically this means, that *log(rincome)* will be perfectly predicted, i.e. not instrumented.

```
lm(log(rincome) ~ I(log(rincome)) + tdiff,data=Cig)


Call:
lm(formula = log(rincome) ~ I(log(rincome)) + tdiff, data = Cig)

Coefficients:
    (Intercept)  I(log(rincome))            tdiff
      0.000e+00        1.000e+00        3.043e-19
```

13.2 Discrete endogeneous variables

```
set.seed(123)
N <- 1000
eps <- rnorm(N)
nu  <- rnorm(N)
Z  <- rnorm(N)
X <- as.numeric(( Z + eps + nu )>0)
Y <- X + eps
```

```
summary(lm( Y ~ X ))


Call:
lm(formula = Y ~ X)

Residuals:
     Min       1Q   Median       3Q      Max
-2.45873 -0.59440  0.00077  0.56316  2.74402

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.46093    0.03877  -11.89   <2e-16 ***
X            1.95795    0.05494   35.64   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8687 on 998 degrees of freedom
Multiple R-squared:   0.56,Adjusted R-squared:  0.5595
F-statistic:  1270 on 1 and 998 DF,  p-value: < 2.2e-16
```

Bayesian inference

```
discrete.model <- 'model {
  for(i in 1:length(y)) {
    x[i]   ~  dbern(xHat[i])              # 1st stage
    probit(xHat[i]) <- gamma[1]+gamma[2]*z[i]
    y[i]   ~  dnorm(beta[1]+beta[2]*xHat[i],tau[1])  # 2nd stage
  }
  for (k in 1:2) {
    beta[k]~dnorm(0,.0001)
    gamma[k]~dnorm(0,.0001)
  }
  tau ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
}'
disc.jags <- run.jags(model=discrete.model,data=list(y=Y,x=X,z=Z),
                    monitor=c("beta"),modules="glm",inits=ini)
```

```
disc.jags


JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

         Lower95   Median Upper95     Mean      SD     Mode      MCerr MC%ofSD
beta[1] -0.14957 0.055905 0.26195 0.05475 0.10514 0.060166 0.00057677     0.5
beta[2]  0.55179  0.91778  1.3055 0.92081 0.19287  0.91839  0.0010584     0.5

        SSeff     AC.10    psrf
beta[1] 33230 0.0091252       1
beta[2] 33209 0.0080993 0.99997

Total time taken: 2 minutes
```

2SLS applied to the non-linear case Without Bayes we could also use the 2SLS: Caution! We estimate a non-linear process with a linear model.

```
summary(ivreg(Y ~ X |Z))


Call:
ivreg(formula = Y ~ X | Z)

Residuals:
     Min       1Q   Median       3Q      Max
-2.86937 -0.66214 -0.02271  0.66499  3.26873

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.0596     0.0795   0.750    0.454
X             0.9127     0.1461   6.248 6.15e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.014 on 998 degrees of freedom
Multiple R-Squared: 0.4004,Adjusted R-squared: 0.3998
Wald test: 39.04 on 1 and 998 DF,  p-value: 6.15e-10
```

(see Chesher and Rosen, 2015, for a discussion)

Two stage non-linear estimation (biased standard errors)

```
step1 <- glm(X ~ Z, family=binomial(link=logit))
Xhat  <- plogis(predict(step1))
summary(lm (Y ~ Xhat))
```

```
Call:
lm(formula = Y ~ Xhat)

Residuals:
    Min      1Q  Median      3Q     Max
-3.3240 -0.9231 -0.0019  0.9277  3.7916

Coefficients:
            Estimate Std. Error t value   Pr(>|t|)
(Intercept)  0.05804    0.10057   0.577      0.564
Xhat         0.91584    0.18448   4.964 0.00000081 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.294 on 998 degrees of freedom
Multiple R-squared:  0.0241,Adjusted R-squared:  0.02312
F-statistic: 24.65 on 1 and 998 DF,  p-value: 0.00000081
```

13.3 Exercises

Consider the data set *`RetSchool`* from *`Ecdat`*. You want to study the impact of education on wage.

1. Why could education be endogeneous and why could this be problem?
2. Which variables could be used as instruments?
3. Compare a model with and without instruments.

14 Measurement errors

14.1 Single measures, known error

In OLS we assume that Y is measured only with precision τ, however, X is infinitely precise:

$$Y \sim N(\beta_0 + \beta_1 X, \tau_Y)$$

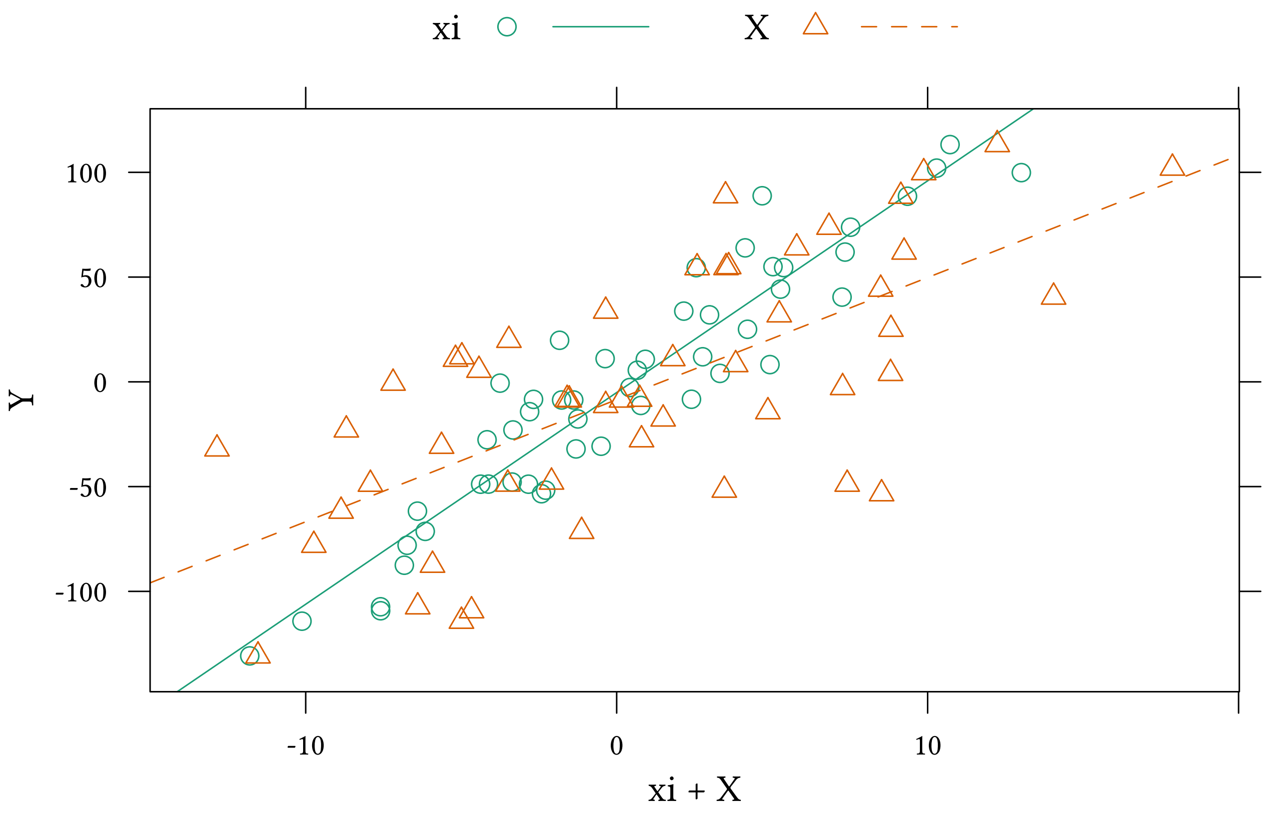
Assume that $X \sim N(\xi, \tau_\eta)$
We are interested in

$$Y \sim N(\beta_0 + \beta_1 \xi, \tau_Y)$$

Pretending that X is an infinitely precise measure for ξ leads to a biased estimate of β_1.

```
set.seed(123)
N <- 50
xi <- rnorm(N, 0, sd=6)
X <- rnorm(N, mean=xi, sd=5)
Y <- rnorm(N, mean=10*xi, sd=20)
```

```
xyplot(Y ~ xi + X,type=c("p","r"),
       auto.key=list(columns=2,lines=TRUE))
```



If we knew ξ, we could do the following:

```
summary(lm(Y~xi))


Call:
lm(formula = Y ~ xi)

Residuals:
   Min     1Q Median     3Q    Max 
-36.48 -13.64  -1.35  10.29  46.62 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  -5.0994     2.8280  -1.803   0.0776 .  
xi           10.1037     0.5139  19.661   <2e-16 ***
---
Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
Residual standard error: 19.98 on 48 degrees of freedom
Multiple R-squared:  0.8895,Adjusted R-squared:  0.8872
F-statistic: 386.6 on 1 and 48 DF,  p-value: < 2.2e-16
```

If we only know X, OLS does not work too well:

```
summary(lm(Y~X))


Call:
lm(formula = Y ~ X)

Residuals:
   Min     1Q Median     3Q    Max
-94.58 -31.51   4.51  42.48  76.88

Coefficients:
            Estimate Std. Error t value     Pr(>|t|)
(Intercept)  -8.4834     6.2152  -1.365        0.179
X             5.8283     0.8839   6.594 0.0000000309 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 43.56 on 48 degrees of freedom
Multiple R-squared:  0.4753,Adjusted R-squared:  0.4643
F-statistic: 43.48 on 1 and 48 DF,  p-value: 0.00000003089
```

Possible correction:

$$\hat{\beta}_1 = \beta_{1,\mathrm{OLS}} \cdot (1 + \tau_\xi/\tau_\eta) = \beta_{1,\mathrm{OLS}} \cdot \left(1 + \frac{1}{36}\Big/\frac{1}{25}\right) = \beta_{1,\mathrm{OLS}} \cdot \frac{61}{36}$$

```
naive.model <- "model {
for (i in 1:length(y)) {
    y[i] ~ dnorm(beta[1] + beta[2] * x[i], tau[2])
}
for (i in 1:2) {
   beta[i] ~ dnorm(0, .0001)
   tau[i] ~ dgamma(m[i]^2/d[i]^2,m[i]/d[i]^2); m[i] ~ dexp(1); d[i] ~ dexp(1);
}
}"
ini <- genInit(4)

naive.jags <- run.jags(naive.model, data=list(x=X,y=Y),monitor=c("beta"),
                       inits=ini)
```

```
        Lower95    Median Upper95      Mean        SD      Mode        MCerr
beta[1] -21.197 -8.455845 3.80715 -8.476362 6.3407720 -8.314211 0.032715032
```

```
beta[2]   4.060  5.828210 7.59205  5.832346 0.8989696  5.825623 0.004552546
        MC%ofSD SSeff         AC.10     psrf
beta[1]     0.5 37566  0.007309543 1.000062
beta[2]     0.5 38993 -0.005758597 1.000010
```

The following models allows to specify the measurement error as *tau[1]*

```
measure.model <- "model {
  for (i in 1:length(y)) {
    xi[i] ~ dnorm(0, tau[3])
    x[i] ~ dnorm(xi[i], tau[1])
    y[i] ~ dnorm(beta[1] + beta[2] * xi[i], tau[2])
  }
for (i in 1:2) {
   beta[i] ~ dnorm(0, .0001)
   tau[i] ~ dgamma(m[i]^2/d[i]^2,m[i]/d[i]^2); m[i] ~ dexp(1); d[i] ~ dexp(1);
}
}"
```

We replicate the “naïve” model by setting *tau[1]=100*.

```
naive2.jags<-run.jags(measure.model,
                      data=list(x = X, y = Y, tau=c(100,NA,1/36)),
                      monitor=c("beta"),inits=ini)
```

Pretending (as in *naive2.jags*) that there is no measurement error (*tau[1]=100*) does not help.

```
          Lower95    Median Upper95       Mean       SD       Mode       MCerr
beta[1] -21.18160 -8.48736 3.82251 -8.463209 6.345481 -8.455162 0.032222314
beta[2]   4.09644  5.83252 7.65871  5.829194 0.905098  5.806014 0.004669013
        MC%ofSD SSeff          AC.10      psrf
beta[1]     0.5 38781  0.0004631007 1.0000624
beta[2]     0.5 37579 -0.0005470156 0.9999804
```

Here we set the measurement error to the correct value: *tau[1]=1/25*.

```
run.jags(measure.model,data=list(x = X, y = Y, tau=c(1/25,NA,1/36)),
                         monitor=c("beta"),inits=ini)


JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

        Lower95  Median Upper95    Mean     SD    Mode   MCerr MC%ofSD SSeff
beta[1] -22.867 -8.2852  1.8318 -9.2168 6.4911 -6.9215 0.82292    12.7    62
beta[2]  8.8216  10.764    12.9  10.899 1.0461  10.531 0.12198    11.7    74

          AC.10   psrf
beta[1]  0.9225 1.1708
beta[2] 0.92962 1.0342

Total time taken: 1.3 seconds
```

The following example shows that it is also important to set the right prior for the distribution of ξ (`tau[3]=1/36`).

If we misspecify ξ (`tau[3]=1/10000`) we get another bias:

```
run.jags(measure.model,data=list(x = X, y = Y, tau=c(1/25,NA,1/10000)),
                         monitor=c("beta"),inits=ini)



JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

        Lower95 Median Upper95    Mean      SD    Mode   MCerr MC%ofSD SSeff
beta[1] -22.324 -10.37  2.0408 -10.21 6.2505   -10.1 0.39518     6.3   250
beta[2]  4.7197 7.1481  8.5492 6.9548 1.0206 7.4023 0.08308     8.1   151

          AC.10   psrf
beta[1] 0.54753 1.0646
beta[2] 0.72566 1.0519

Total time taken: 1 seconds
```

14.2 Multiple measures

Multiple measures help us to find τ_η.

```
set.seed(123)
N <- 50
xi <- rnorm(N, 0, sd=6)
X1 <- rnorm(N, mean=xi, sd=5)
X2 <- rnorm(N, mean=xi, sd=5)
Y <- rnorm(N, mean=10*xi, sd=20)
```

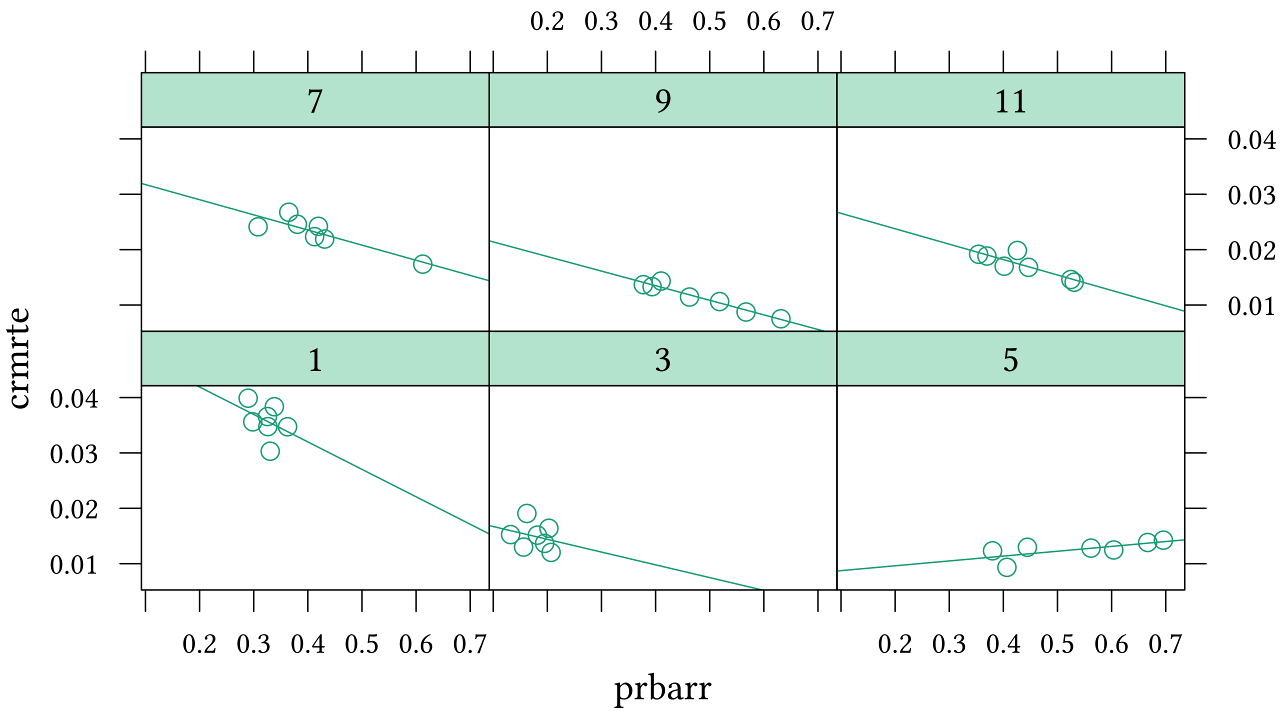
```
measure2.model <- 'model {
  for(i in 1:length(y)) {
     xi[i] ~ dnorm(0,1/36)
     x1[i] ~ dnorm(xi[i],tau[1])
     x2[i] ~ dnorm(xi[i],tau[1])
     y[i] ~ dnorm(beta[1]+beta[2]*xi[i],tau[2])
  }
  for(k in 1:2) {
     beta[k]~dnorm(0,.0001)
     tau[k] ~ dgamma(m[k]^2/d[k]^2,m[k]/d[k]^2); m[k] ~ dexp(1); d[k] ~ dexp(1);
     sd[k] <- 1/sqrt(tau[k])
  }
}'
ini <- genInit(4)
measure2.jags<-run.jags(model=measure2.model,
                       data=list(y=Y,x1=X1,x2=X2),
                       monitor=c("beta","sd"),inits=ini)
```

```
measure2.jags


JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

        Lower95 Median Upper95    Mean       SD    Mode     MCerr MC%ofSD SSeff
beta[1] -8.4686 2.3499  10.473 2.2222  4.8426  2.8516   0.49105    10.1    97
beta[2]  9.0339 10.146  11.662 10.206 0.71588  9.9559  0.070786     9.9   102
sd[1]    4.5768   5.28  6.0878 5.2982 0.38796  5.2429 0.0031453     0.8 15214
sd[2]   0.20604 1.0668  11.508 2.3694  3.9098 0.79647   0.30409     7.8   165

           AC.10   psrf
beta[1]  0.88184 1.2627
beta[2]  0.86929 1.0706
sd[1]   0.032975 1.0028
sd[2]    0.90334 1.0313

Total time taken: 1.3 seconds
```

14.3 Aggregating evidence

Let us have another look at the *Crime* dataset. Assume that we estimate a regression separately for each county. Here are the first six counties:

```
xyplot(crmrte ~ prbarr | factor(county),
       data=Crime,subset=as.numeric(factor(county))<7,type=c("p","r"))
```



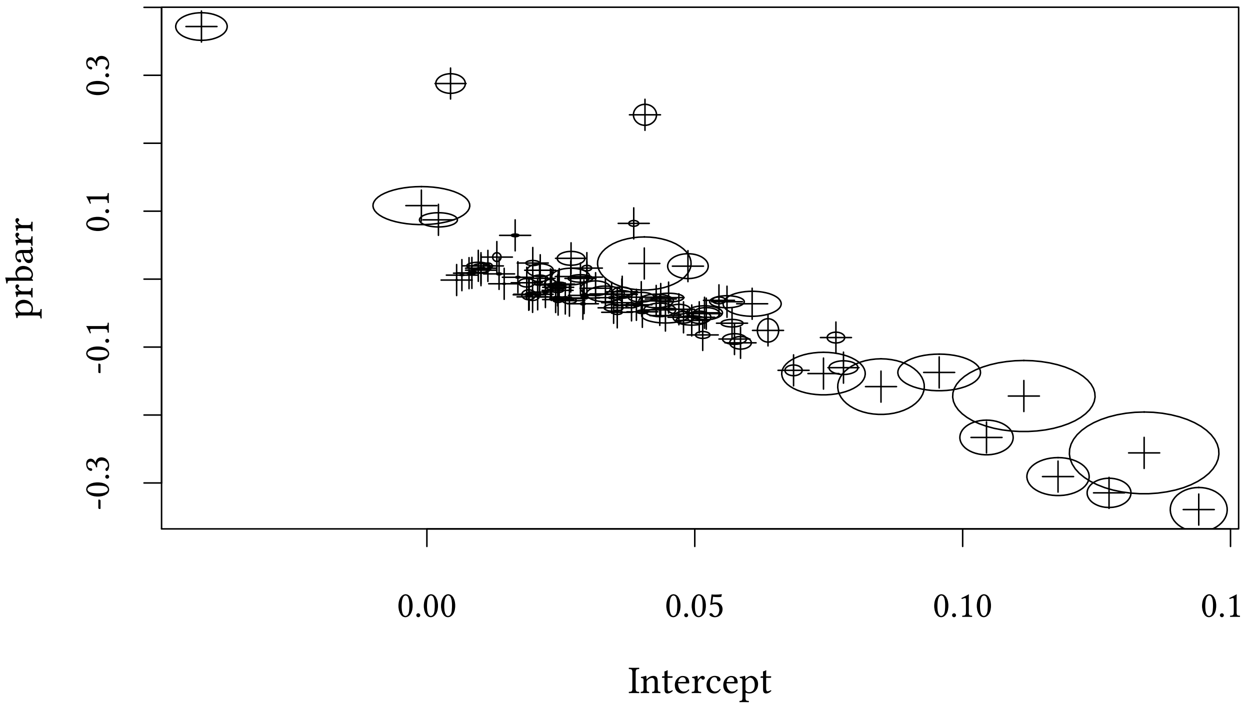
We use *ddply* to estimate the regressions for each county. Some renaming of variables is still necessary:

```
county.reg<-ddply(Crime,.(county),function(x) {
    est<-lm(crmrte~prbarr,data=x);
    c(coef(est),diag(vcov(est)))})
head(county.reg)

  county (Intercept)       prbarr    (Intercept)          prbarr
1      1 0.051820024 -0.049570699 0.000281127188 0.002659213984
2      3 0.019007347 -0.023043014 0.000042619822 0.001337414582
3      5 0.007865885  0.008754288 0.000004748707 0.000015708370
4      7 0.034483188 -0.027337535 0.000008038869 0.000043974025
5      9 0.024029389 -0.026352069 0.000001605456 0.000006734601
6     11 0.029341504 -0.027834640 0.000009683166 0.000049801482

names(county.reg) <- make.names(names(county.reg),unique=TRUE)
head(county.reg)

  county X.Intercept.       prbarr X.Intercept..1       prbarr.1
1      1  0.051820024 -0.049570699 0.000281127188 0.002659213984
2      3  0.019007347 -0.023043014 0.000042619822 0.001337414582
3      5  0.007865885  0.008754288 0.000004748707 0.000015708370
4      7  0.034483188 -0.027337535 0.000008038869 0.000043974025
5      9  0.024029389 -0.026352069 0.000001605456 0.000006734601
6     11  0.029341504 -0.027834640 0.000009683166 0.000049801482
```

```
county.reg<-rename(county.reg,c("X.Intercept."="Intercept",
                              "X.Intercept..1"="varX","prbarr.1"="varY"))
head(county.reg)

  county   Intercept       prbarr           varX           varY
1      1 0.051820024 -0.049570699 0.000281127188 0.002659213984
2      3 0.019007347 -0.023043014 0.000042619822 0.001337414582
3      5 0.007865885  0.008754288 0.000004748707 0.000015708370
4      7 0.034483188 -0.027337535 0.000008038869 0.000043974025
5      9 0.024029389 -0.026352069 0.000001605456 0.000006734601
6     11 0.029341504 -0.027834640 0.000009683166 0.000049801482
```

The following graph illustrates the difference in precision of the estimates:

```
with(county.reg,plot(prbarr ~ Intercept,pch=3))
library(car)
q<-apply(county.reg,1,function(x) ellipse(x[2:3],diag(x[4:5]),radius=.2,
                                          center.pch=0,col="black",lwd=1))
```



Besides: The purpose of this exercise is not necessarily economically meaningful. It is only supposed to illustrate what to do with noisy observations.

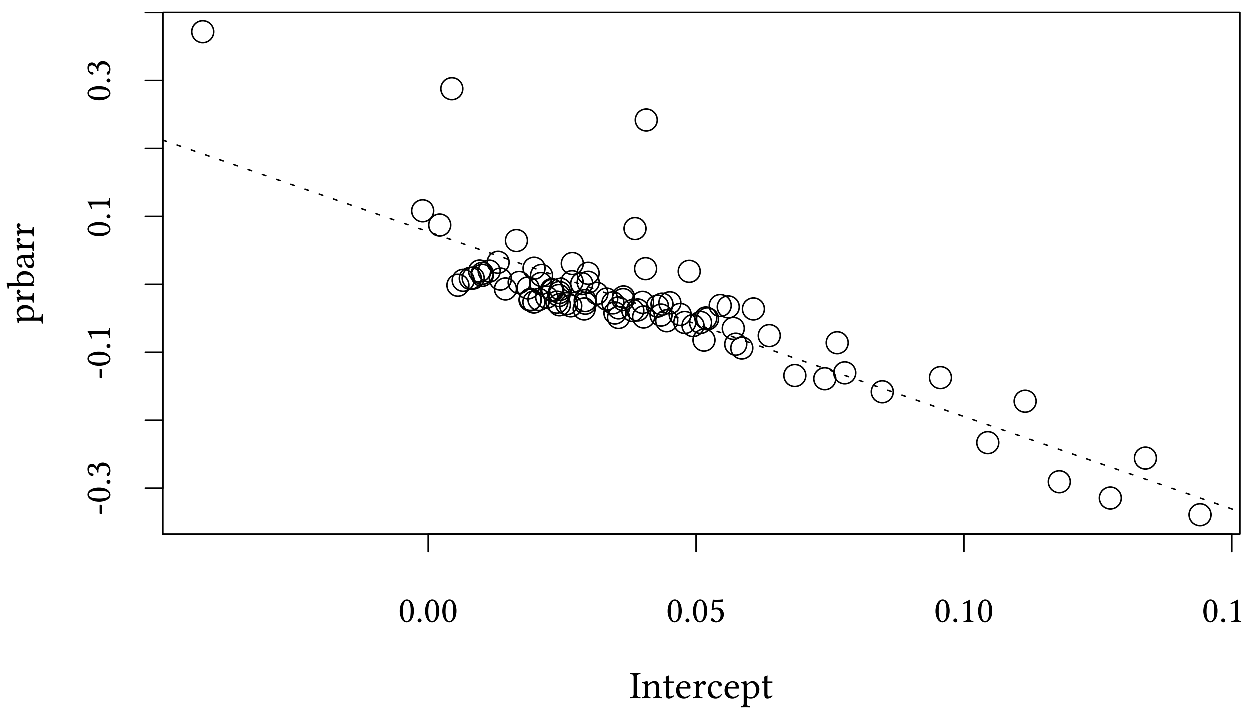
So, let us assume that all we have is the 90 observations for the different countries plus their precision.

Can we simply pretend that each observation is infinitely precise?

```
naiveMeta.model <- "model {
  for (i in 1:length(y)) {
    y[i] ~ dnorm(beta[1]+beta[2]*x[i],tau)
  }
  for (i in 1:2) {
    beta[i] ~ dnorm(0, .0001)
  }
  tau ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
}"
meta.data <- with(county.reg,list(y=prbarr,x=Intercept,
   tauX=1/varX,tauY=1/varY,meanXi=mean(Intercept),tauXi=1/var(Intercept)))
metaNaive.jags<-run.jags(naiveMeta.model,
               data=meta.data,monitor="beta",inits=ini)
```

```
           Lower95     Median    Upper95        Mean          SD         Mode
beta[1]  0.0588629  0.0774296  0.0964035  0.07741952 0.009567237  0.07779828
beta[2] -3.0952100 -2.7206050 -2.3456700 -2.71926333 0.191785409 -2.71790290
               MCerr MC%ofSD SSeff          AC.10     psrf
beta[1] 0.0001005751     1.1  9049 -0.0000987161 1.000101
beta[2] 0.0019988290     1.0  9206 -0.0003562718 1.000205
```

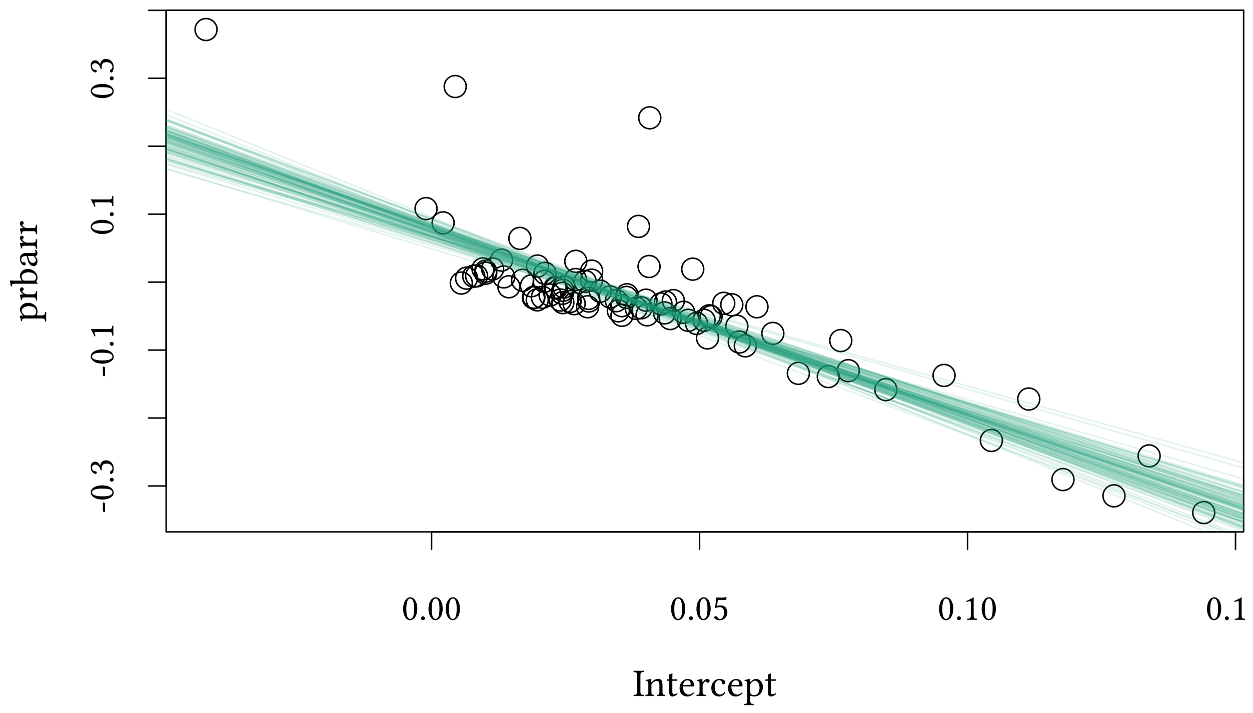
```
with(county.reg,plot(prbarr ~ Intercept))
abline(coef=summary(metaNaive.jags)[,"Median"],lty="dotted")
```



To illustrate the precision of the naïve estimate, we sample from the estimated coefficients and draw a regression line for each sample.

```
set.seed(123)
```

```
with(county.reg,plot(prbarr ~ Intercept))
metaNaive.df<-data.frame(as.mcmc(metaNaive.jags))
q<-apply(metaNaive.df[sample(1:nrow(metaNaive.df),100),],1,
      function(x) abline(coef=x,col=paste(palette()[1],"22",sep="")))
```



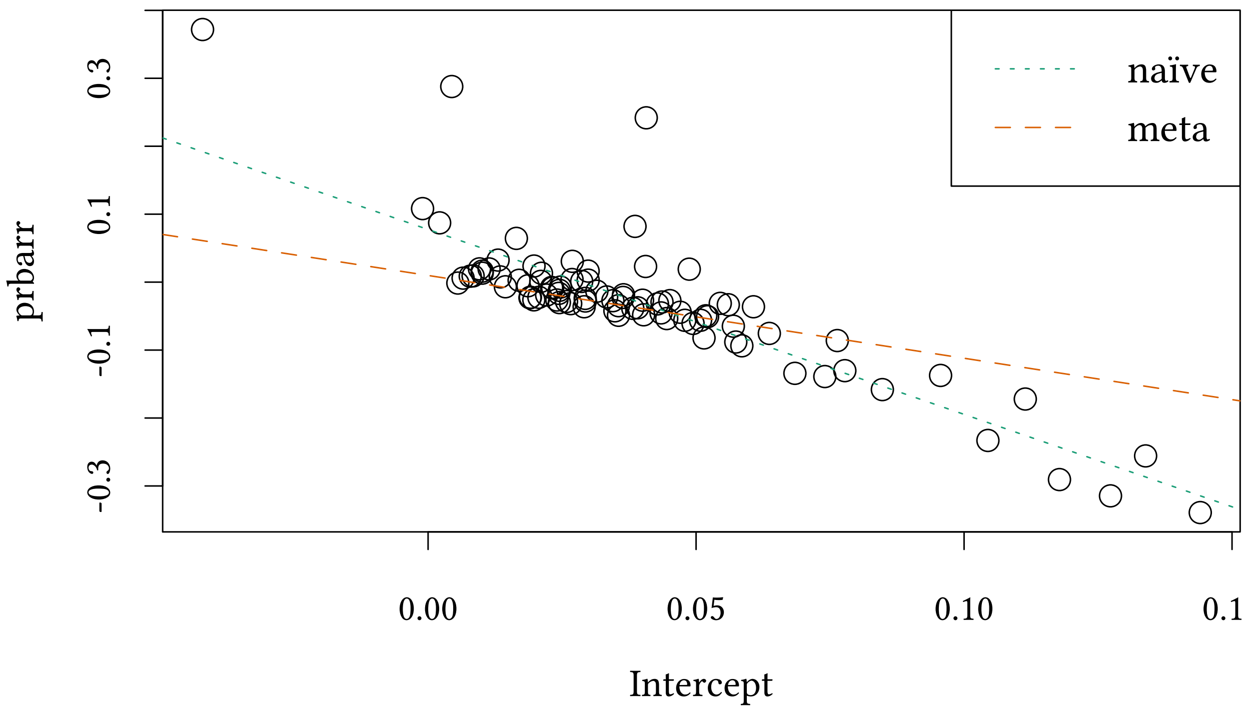
In the following model we descibe the precision of each observation explicitely:

```
meta.model <- "model {
  for (i in 1:length(y)) {
    xi[i] ~ dnorm(meanXi,tauXi)
    x[i] ~ dnorm(xi[i],tauX[i])
    y[i] ~ dnorm(beta[1]+beta[2]*xi[i], tauY[i])
  }
  for (i in 1:2) {
    beta[i] ~ dnorm(0, .0001)
  }
}"
meta.jags<-run.jags(meta.model,
                         data=meta.data,monitor=c("beta"),inits=ini)
```

```
             Lower95       Median     Upper95         Mean          SD
beta[1]  0.00644267  0.009803535  0.0136691  0.009875959 0.001839607
beta[2] -1.43539000 -1.218475000 -1.0192800 -1.221181582 0.106076059
                Mode        MCerr MC%ofSD SSeff      AC.10     psrf
beta[1]  0.009714675 0.00003809642     2.1  2332 0.3036751 1.000529
beta[2] -1.210261680 0.00197773858     1.9  2877 0.2537141 1.000557
```

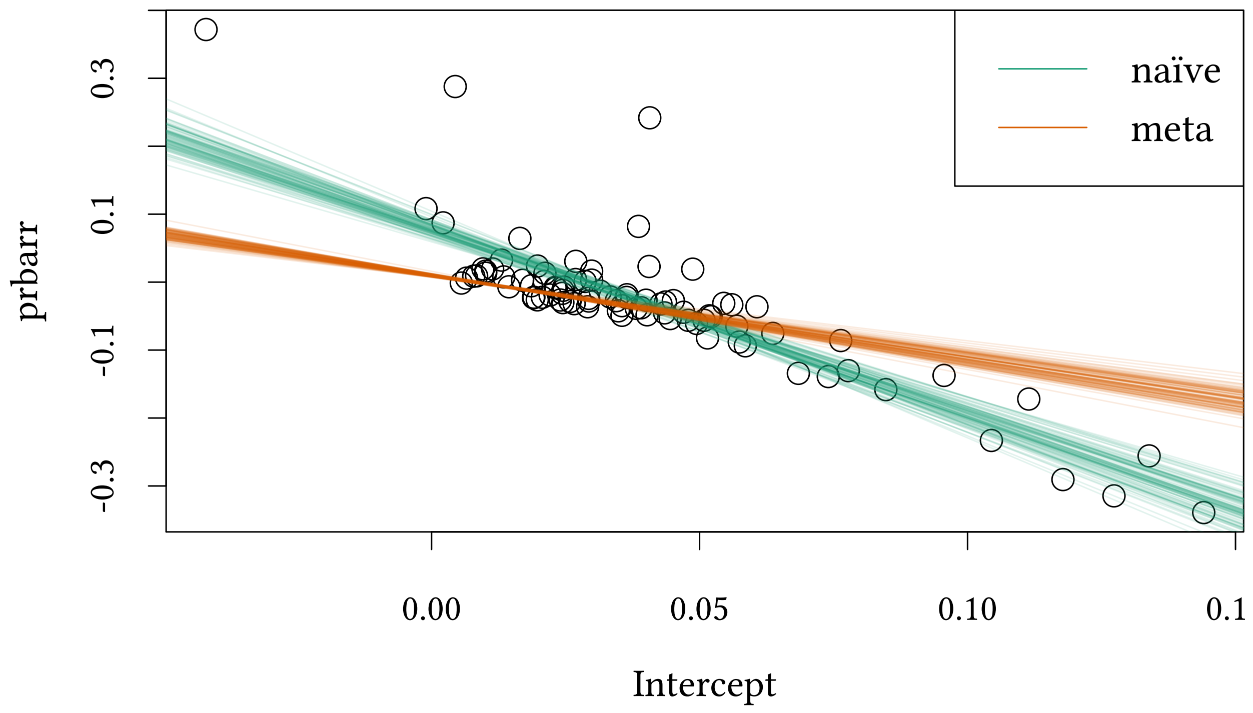
Here are the two regression lines:

```
with(county.reg,plot(prbarr ~ Intercept))
abline(coef=summary(metaNaive.jags)[,"Median"],lty=3,col=1)
abline(coef=summary(meta.jags)[,"Median"],lty=2,col=2)
legend("topright",c("naïve","meta"),col=1:2,lty=3:2)
```



And here is an illustration of the precision of both models:

```
meta.df<-data.frame(as.mcmc(meta.jags))
with(county.reg,plot(prbarr ~ Intercept))
legend("topright",c("naïve","meta"),col=1:2,lty=1)
q<-apply(metaNaive.df[sample(1:nrow(metaNaive.df),100),],1,
      function(x) abline(coef=x,col=paste(palette()[1],"22",sep="")))
q<-apply(meta.df[sample(1:nrow(meta.df),100),],1,
      function(x) abline(coef=x,col=paste(palette()[2],"22",sep="")))
```



15 Selection

15.1 Interval regression

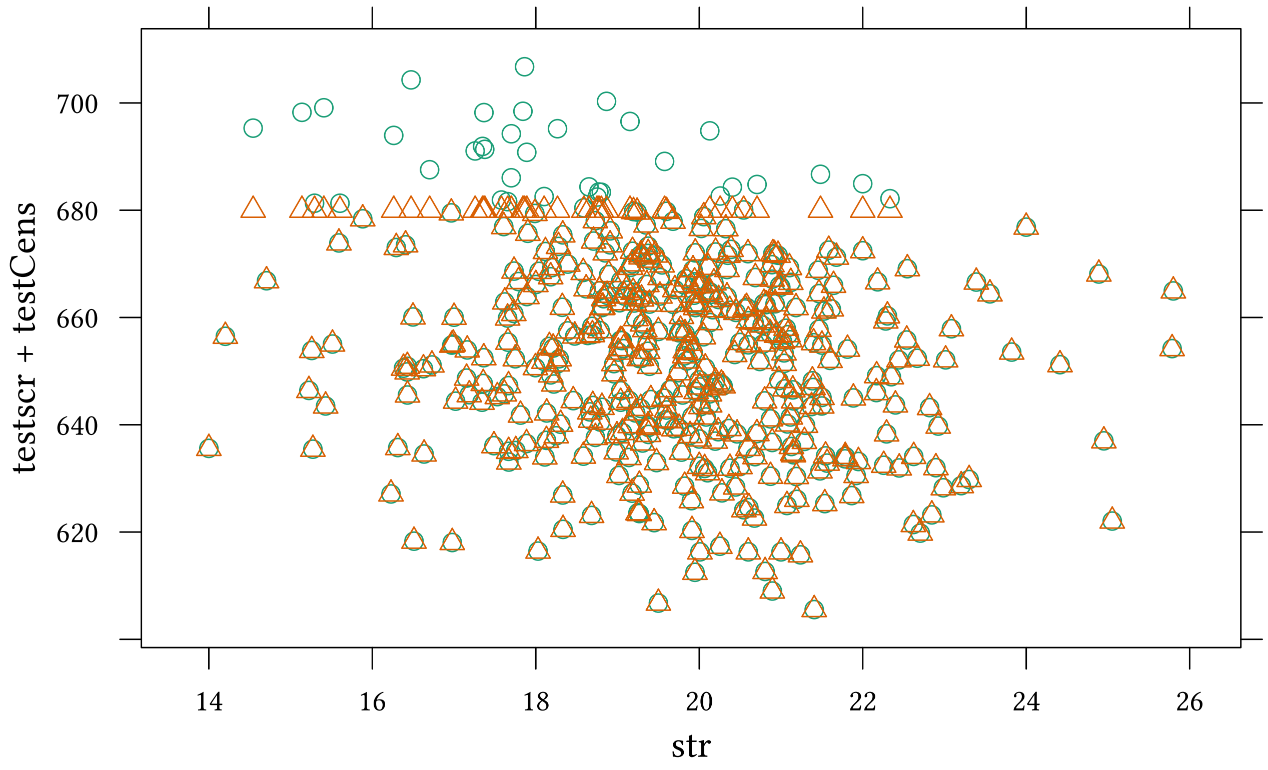
Assume the testscore data was censored:

```
library(Ecdat)
data(Caschool)
```

```
testCens<-with(Caschool,ifelse(testscr>680,680,testscr))
```

```
isCens<-testCens>=680
```

```
xyplot(testscr + testCens ~ str,data=Caschool)
```



The model with the uncensored data:

```
lm(testscr ~ str,data=Caschool)


Call:
lm(formula = testscr ~ str, data = Caschool)

Coefficients:
(Intercept)          str
     698.93        -2.28
```

Two naïve models:

```
lm(testCens ~ str,data=Caschool)


Call:
lm(formula = testCens ~ str, data = Caschool)

Coefficients:
(Intercept)          str
    689.193       -1.826

lm(testCens ~ str,data=Caschool,subset=!isCens)


Call:
lm(formula = testCens ~ str, data = Caschool, subset = !isCens)
```

```
Coefficients:
(Intercept)          str
   669.3012      -0.9384
```

Interval regression:

```
testMax<-testCens
testMax[isCens]<-NA
library(survival)
survreg(Surv(testCens,testMax,type="interval2") ~ str,dist='gaussian',
        data=Caschool)

Call:
survreg(formula = Surv(testCens, testMax, type = "interval2") ~
    str, data = Caschool, dist = "gaussian")

Coefficients:
(Intercept)         str
 696.767043   -2.171933

Scale= 18.51073

Loglik(model)= -1704.1   Loglik(intercept only)= -1714
Chisq= 19.8 on 1 degrees of freedom, p= 0.0000086
n= 420
```

15.2 Bayesian censored model

We need (JAGS) notation for interval-censored data:

Y ~ dinterval(t, c)

$$Y = \begin{cases} 0 & \text{if } t \leqslant c[1] \\ m & \text{if } c[m] < t \leqslant c[m+1] \quad \text{for } 1 \leqslant m < M \\ M & \text{if } c[M] < t \end{cases}$$

Here our data is censored from above, i.e.

$$Y = \begin{cases} 0 & \text{if } t \leqslant t_{\max} = c[1] \\ 1 & \text{if } c[1] = t_{\max} < t \end{cases}$$

	latent t (y)	observed c	Y (isCens)
not censored	testCens	testCens	0
censored	NA	testCens	1

One complication with the censored model is that the censored observations are unknown, so JAGS will fit random values. Unless we help JAGS a little, the *initial* values will be inconsistent, i.e. JAGS will randomise values for y which are not in the right interval.

We must avoid situations like the following:

- *y[1]=800, c[1]=600, isCens[1]=0*

  Problem: according to *isCens[1]* we have that *y[1]<c[1]* with certainty.

- *y[1]=400, c[1]=600, isCens[1]=1*

  Problem: according to *isCens[1]* we have that *y[1]>c[1]* with certainty.

Otherwise R would throw the following error:

```
Observed node inconsistent with unobserved parents at initialization.
Try setting appropriate initial values.
```

Solution: We set the initial y to "safe" values.

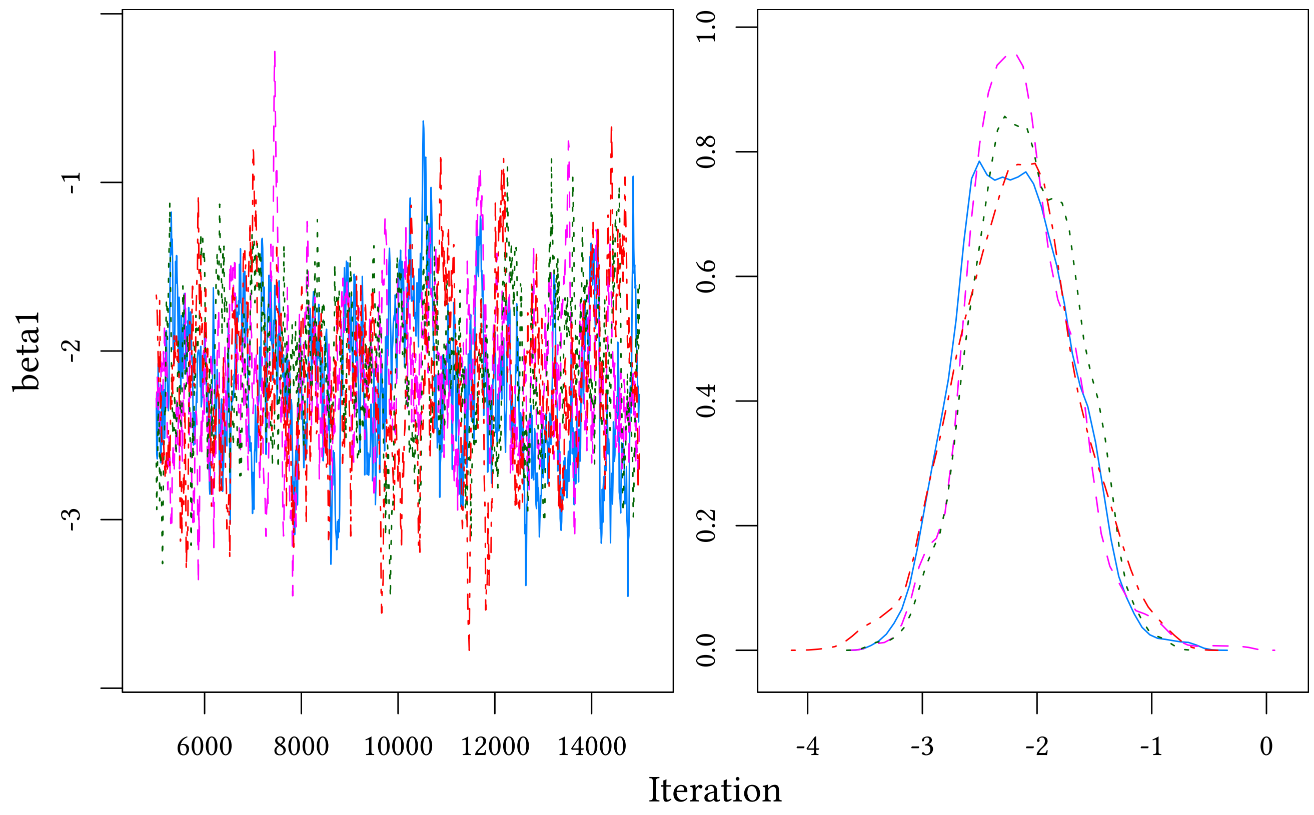
For the unobserved (censored) nodes, *y=testCens+99*.

For the observed (uncensored) nodes, we can not overwrite the observed nodes. Hence the init value is *y=NA*.

```
y       <- ifelse(isCens,NA,testCens)
yInit   <- ifelse(isCens,testCens+99,NA) #<- must resolve initial uncertainty about censored y
dataList<-list(y=y,c=testCens,x=Caschool$str,isCens=as.numeric(isCens))
ini <- genInit(4,function(i)
    list(beta0=rnorm(1,0,.001),beta1=rnorm(1,0,.001),y=yInit))
```

```
initJags<-list()
initJags[[1]]<-list(.RNG.seed=1,.RNG.name="base::Mersenne-Twister")
initJags[[2]]<-list(.RNG.seed=2,.RNG.name="base::Super-Duper")
initJags[[3]]<-list(.RNG.seed=3,.RNG.name="base::Wichmann-Hill")
initJags[[4]]<-list(.RNG.seed=4,.RNG.name="base::Marsaglia-Multicarry")

genInit <- function(nChains,fn=NULL) {
    x<-list()
    for (i in 1:nChains) {
        x[[i]]<-initJags[[i]]
        if(!is.null(fn)) {
            vals<-fn(i)
            lapply(1:length(vals),function(j)
                x[[i]][[names(vals)[j]]]<<-vals[[j]])
        }
    }
    x
}
```

```
intreg.model <- 'model {
 for (i in 1:length(y)) {
        y[i] ~ dnorm(beta0+beta1*x[i],tau)
        isCens[i] ~ dinterval(y[i],c[i])
    }
    beta0 ~ dnorm (600,.0001)
    beta1 ~ dnorm (-2,.0001)
    tau   ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
    sd <- 1/sqrt(tau)
}'
intreg.jags <- run.jags(model=intreg.model,data=dataList,
       inits=ini,monitor=c("beta0","beta1","sd"))
```



```
summary(intreg.jags)[,c("Mean","SD","SSeff","psrf")]

             Mean        SD SSeff      psrf
beta0 696.43012 9.1064378   204 1.0076618
beta1  -2.15479 0.4608198   217 1.0076879
sd     18.58396 0.6899363 30178 0.9999979
```

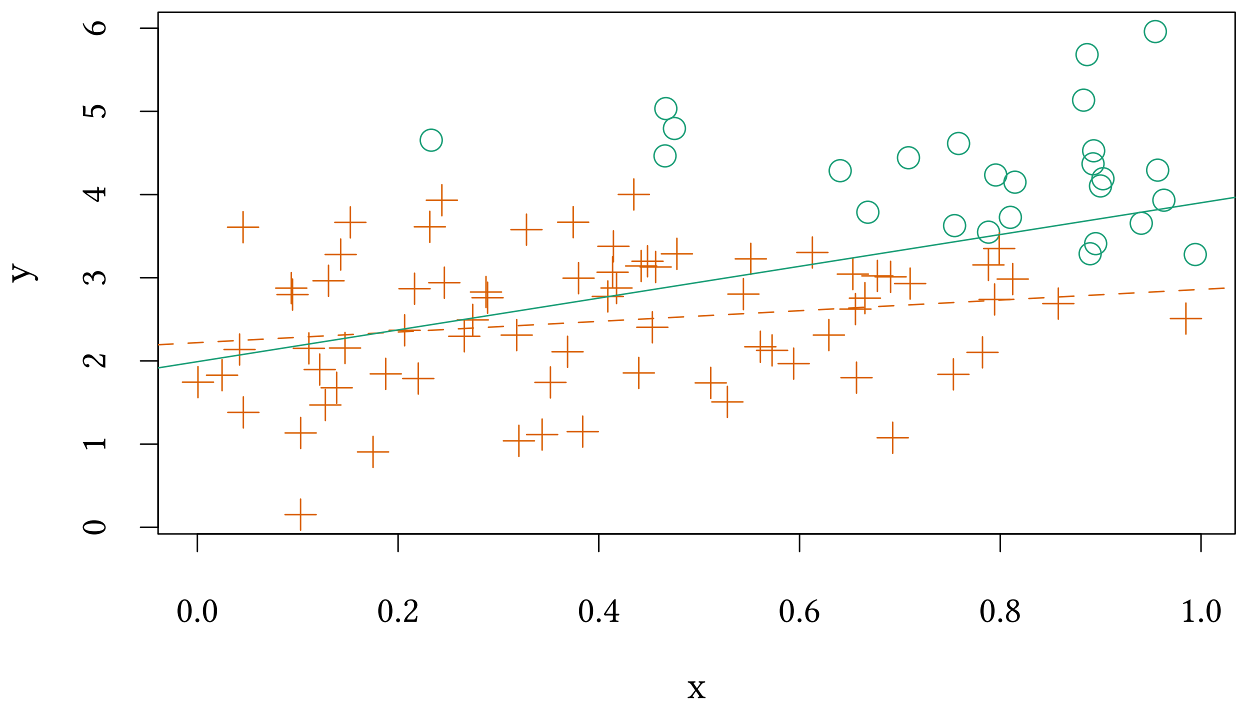
15.3 Heckman correction

What, if selection is determined by a different, but correlated process?

```
set.seed(123)
N <- 100
```

```
x <- runif(N)
u <- rnorm(N)
u2 <- u + .1*rnorm(N)
cor(u,u2)

[1] 0.9952951

y <- 2+2*x+u
S <- 4*x+u2<3
df <- within(data.frame(list(y=y,x=x,S=S)),y[!S]<-0)
```

```
plot(y ~ x,col=S+1,pch=2*S+1)
abline(lm(y ~ x,data=subset(df,y!=0)),col=2,lty=2)
abline(lm(y ~ x),col=1)
```



```
summary(lm(y ~ x,data=subset(df,y!=0)))


Call:
lm(formula = y ~ x, data = subset(df, y != 0))

Residuals:
     Min       1Q   Median       3Q      Max 
-2.13288 -0.55295  0.01347  0.57709  1.55626 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept)   2.2195     0.1787  12.420   <2e-16 ***
x             0.6406     0.3831   1.672   0.0989 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.7964 on 72 degrees of freedom
Multiple R-squared:  0.03738,Adjusted R-squared:  0.02401
F-statistic: 2.796 on 1 and 72 DF,  p-value: 0.09885
```

We want to explain

$$Y = X\beta + u$$

We observe Y only when $S = 1$:

$$\Pr(S = 1|Z) = \Phi(Z\gamma)$$

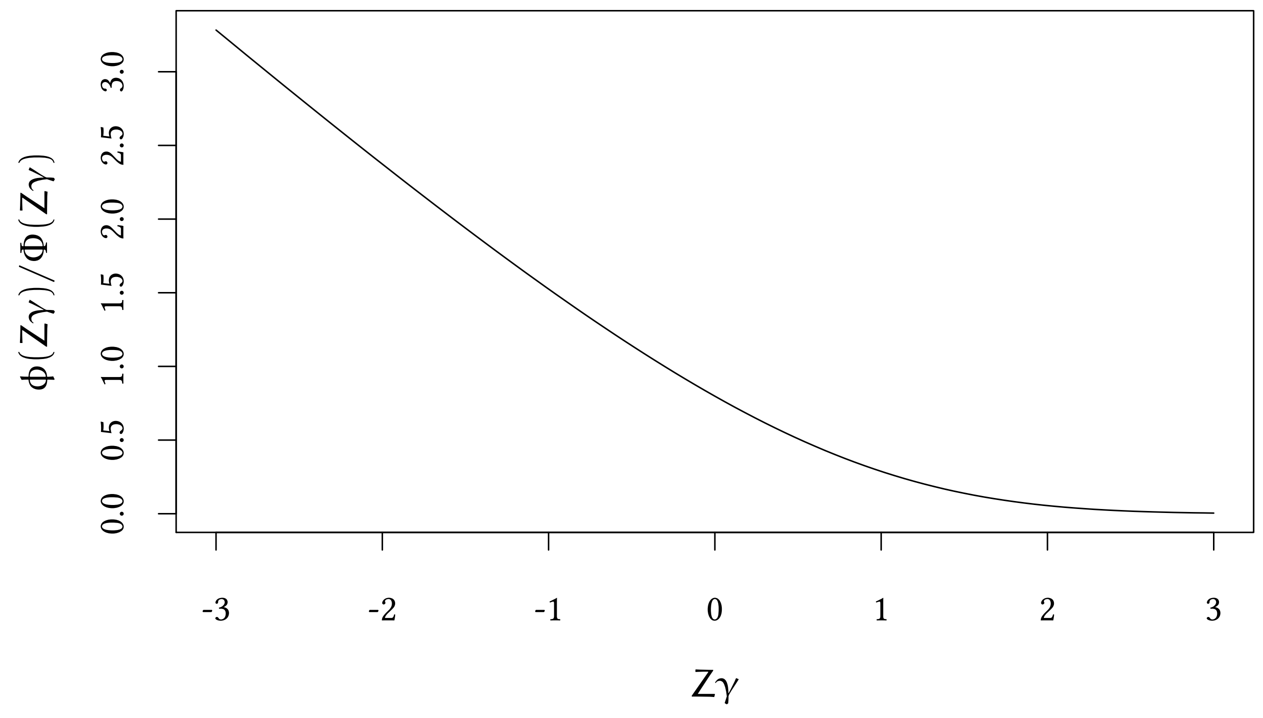
Hence, we are interested in

$$E[Y|X, S = 1] = X\beta + E[u|X, S = 1]$$

$$E[Y|X, S = 1] = X\beta + \rho\sigma_u\lambda(Z\gamma)$$

where

$$\lambda(Z\gamma) = \frac{\phi(Z\gamma)}{\Phi(Z\gamma)} \qquad \text{(inverse Mills ratio)}$$



This model can be estimated with ML:

```
  library(sampleSelection)
  summary(heckit(selection = S ~ x,outcome= y ~ x,data=df))

--------------------------------------------
Tobit 2 model (sample selection model)
2-step Heckman / heckit estimation
100 observations (26 censored and 74 observed)
7 free parameters (df = 94)
Probit selection equation:
            Estimate Std. Error t value    Pr(>|t|)
(Intercept)   3.0335     0.5356   5.664 0.000000161 ***
x            -4.0255     0.7795  -5.164 0.000001345 ***
Outcome equation:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.0274     0.2683   7.557 2.69e-11 ***
x             1.7366     1.0678   1.626    0.107
Multiple R-Squared:0.0545,Adjusted R-Squared:0.0278
   Error terms:
              Estimate Std. Error t value Pr(>|t|)
invMillsRatio  -0.8932     0.7570   -1.18    0.241
sigma           0.9110         NA      NA       NA
rho            -0.9804         NA      NA       NA
--------------------------------------------
```

15.4 Bayesian Heckman correction

```
s.model <- 'model {
   for (i in 1:length(y)) {
      y[i] ~ dnorm(ifelse(S[i],Xbeta[i]+rhoSigma*lambda[i],0),
                   ifelse(S[i],tau,0.0001))
      Xbeta[i] <- beta[1] + beta[2]*x[i]
      S[i] ~ dbern(p[i])
      p[i] <- phi(Zgamma[i])
      Zgamma[i] <- gamma[1]+gamma[2]*x[i]
      lambda[i] <- dnorm(Zgamma[i],0,1)/phi(Zgamma[i])
   }
   for (i in 1:2) {
      beta[i] ~ dnorm (0,.0001)
      gamma[i] ~ dnorm (0,.0001)
   }
   rhoSigma ~ dnorm (0,.0001)
   tau   ~ dgamma(m^2/d^2,m/d^2)
   m     ~ dgamma(1,1)
   d     ~ dgamma(1,1)
}'
```

```
data<-with(df,list(y=y,x=x,S=as.numeric(S)))
run.jags(s.model,data=data,monitor=c("beta","gamma","rhoSigma"),inits=genInit(4))
```

```
JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

           Lower95    Median Upper95     Mean       SD      Mode      MCerr MC%ofSD
beta[1]     1.5597    2.0398  2.5262   2.0415 0.24686    2.0216 0.0068395     2.8
beta[2]   -0.57032     1.829  4.4669   1.8987  1.2834    1.7863  0.053792     4.2
gamma[1]    1.9511     2.886  3.9597   2.9079 0.52496    2.8471  0.019446     3.7
gamma[2]   -5.2501   -3.7935 -2.2889  -3.8196 0.76987   -3.7706  0.028283     3.7
rhoSigma   -3.4739  -0.99067 0.99711  -1.1132  1.1601  -0.87304  0.048647     4.2

          SSeff   AC.10   psrf
beta[1]    1303 0.48573 1.0019
beta[2]     569 0.75123 1.0123
gamma[1]    729 0.68522 1.0032
gamma[2]    741  0.6909 1.0022
rhoSigma    569 0.74052 1.0186

Total time taken: 8.8 seconds
```

15.5 Exercise

1. Consider the data set *Workinghours* from *Ecdat*.
   - Which variables could explain the labour supply of the wife?
   - In which way could the labour supply be censored?
   - Estimate your model.
2. Consider the data set *Mroz87* from *sampleSelection*.
   - Explain *wage* as a function of experience and education.

     Assume that selection into the labour force is determinded by age, family income and education.

16 More on initialisation

We use different random number generators to make sure that each chain will take a different turn.

```
str(initJags)

List of 4
 $ :List of 2
  ..$ .RNG.seed: num 1
  ..$ .RNG.name: chr "base::Mersenne-Twister"
 $ :List of 2
  ..$ .RNG.seed: num 2
  ..$ .RNG.name: chr "base::Super-Duper"
 $ :List of 2
  ..$ .RNG.seed: num 3
  ..$ .RNG.name: chr "base::Wichmann-Hill"
 $ :List of 2
  ..$ .RNG.seed: num 4
  ..$ .RNG.name: chr "base::Marsaglia-Multicarry"
```

The *genInit()* function helps adding more variables to the init.

```
genInit <- function(nChains,fn=NULL) {
    x<-list()
    for (i in 1:nChains) {
        x[[i]]<-initJags[[i]]
        if(!is.null(fn)) {
            vals<-fn(i)
            lapply(1:length(vals),function(j)
                x[[i]][[names(vals)[j]]]<<-vals[[j]])
        }
    }
    x
}
```

now *genInit()* can be called like this:

```
ini <- genInit(4,function(i) list(beta0=rnorm(1,0,0.0001),
                                   beta1=rnorm(1,0,0.0001)))
run.jags(...,inits=ini,...)
```

17 Hierarchical Models

17.1 Mixed effects

OLS:

$$Y_i = X_i\beta + \epsilon_i \text{ with } \epsilon \sim N(0,\sigma)$$

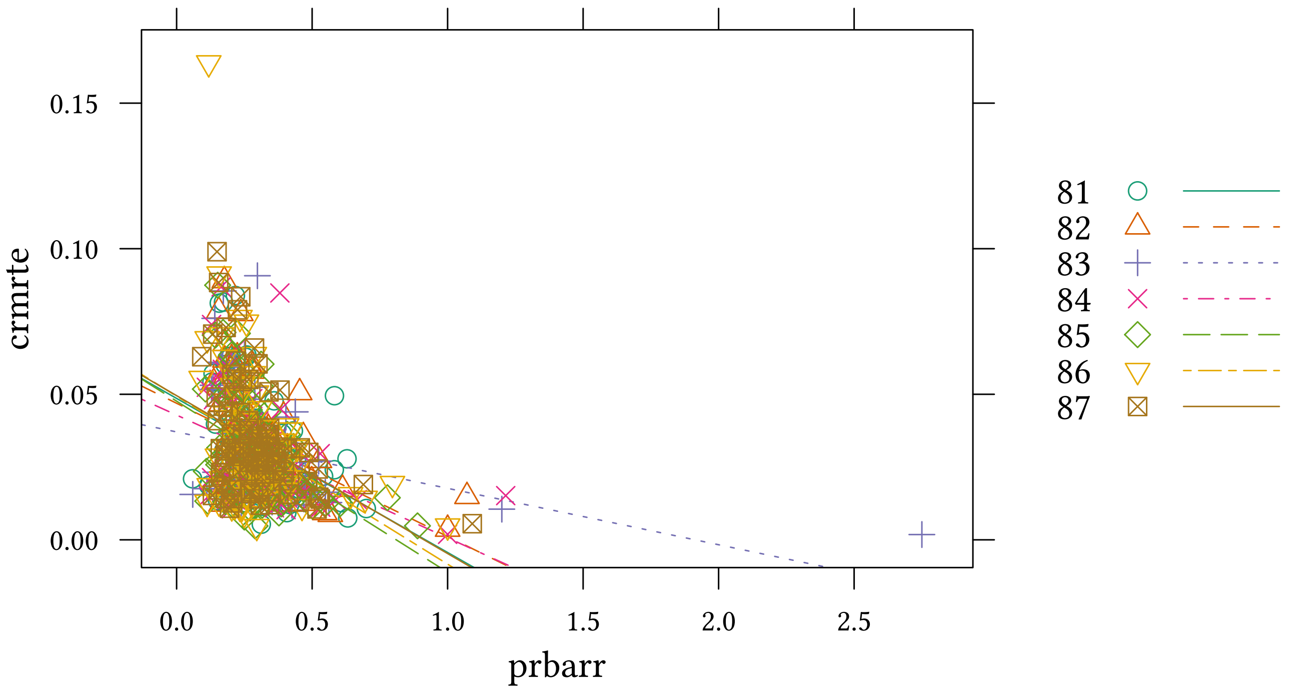
Mixed effects (with groups k):

$$Y_{ik} = \underbrace{X_{ik}\beta}_{\text{fixed}} + \underbrace{Z_{ik}\nu}_{\text{random}} + \epsilon_{ik} \text{ with } \nu \sim N(0,\Sigma), \epsilon \sim N(0,\sigma)$$

17.2 Example: Crime in North Carolina

The dataset *Crime* contains information about several years. Perhaps the relationship between *crmrte* and *prbarr* is not the same in each year?

```
xyplot(crmrte ~ prbarr,data=Crime,group=year,type=c("p","r"),auto.key=list(space="right",li
```



We are estimating the following equation:

$$\texttt{crmrte}_{ik} = (\beta_1 + \nu_{1,k}) + (\beta_2 + \nu_{2,k})\texttt{prbarr} + \epsilon_{ik} \text{ or, equivalently,}$$
$$\texttt{crmrte}_{ik} \sim N\big((\beta_1 + \nu_{1,k}) + (\beta_2 + \nu_{2,k})\texttt{prbarr}, \tau_3\big)$$

First we use Maximum Likelihood (and the *lmer* function).

```
summary(lmer(crmrte ~ prbarr  + (prbarr+1|year),data=Crime))

Linear mixed model fit by REML ['lmerMod']
Formula: crmrte ~ prbarr + (prbarr + 1 | year)
   Data: Crime

REML criterion at convergence: -3339

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.7122 -0.6575 -0.1795  0.4460  7.3139

Random effects:
 Groups   Name        Variance   Std.Dev. Corr
 year     (Intercept) 0.00001702 0.004125
          prbarr      0.00016957 0.013022 -1.00
 Residual             0.00028084 0.016758
Number of obs: 630, groups:  year, 7
```

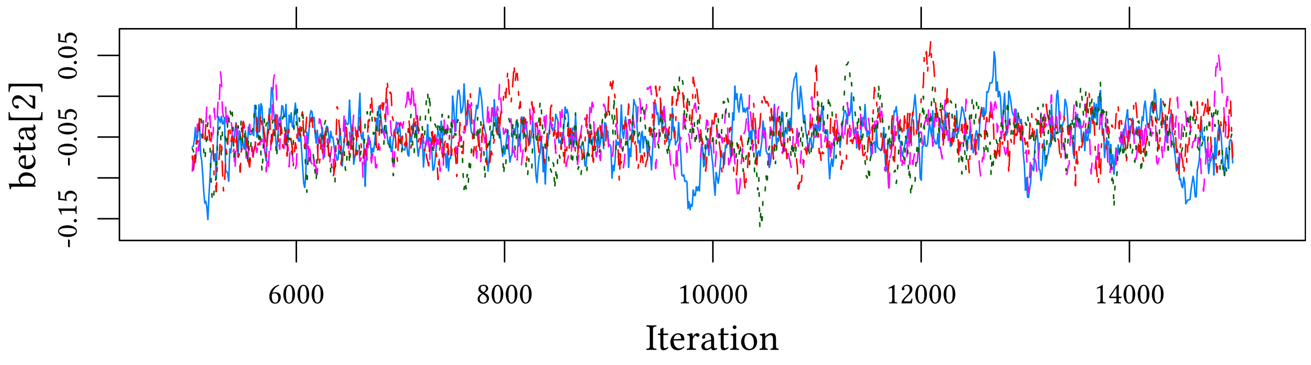
```
Fixed effects:
             Estimate Std. Error t value
(Intercept)  0.045302   0.002156  21.012
prbarr      -0.044918   0.006579  -6.827

Correlation of Fixed Effects:
       (Intr)
prbarr -0.951
```

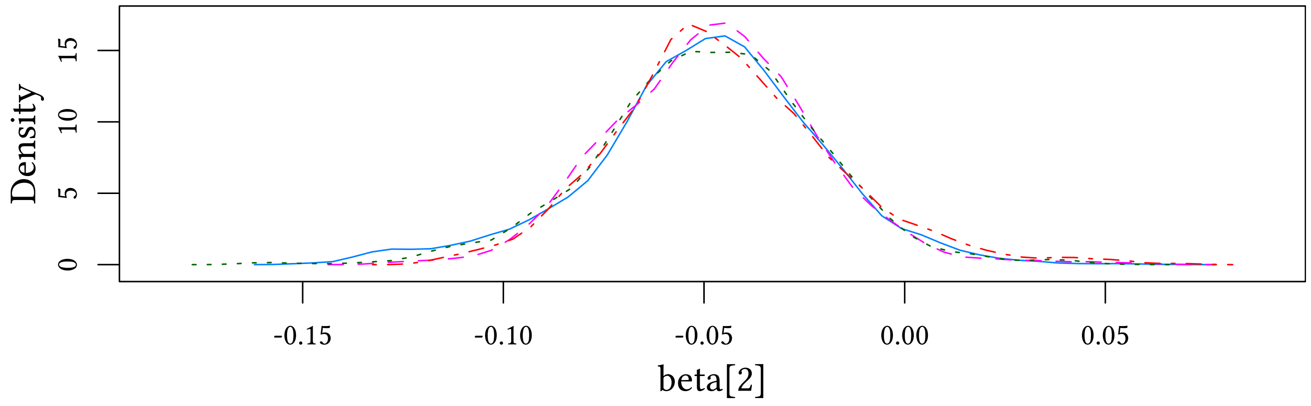
17.3 Bayes and mixed effects

Next we specify the mixed model as a JAGS model (since we are mainly interested in the marginal effect, we de-mean *crmrte* and *prbarr*).

```
mer.model <- 'model {
 for (i in 1:length(y)) {
    y[i] ~ dnorm(mu[i],tau[3])
    mu[i]<-beta[1]+nu[1,group[i]]+(beta[2]+nu[2,group[i]])*x[i]
 }
 for (k in 1:2) {
    beta[k] ~ dnorm (0,.0001)
    for (j in 1:max(group)) {
       nu[k,j] ~ dnorm(0,tau[k])
    }
 }
 for (k in 1:3) {
    tau[k] ~ dgamma(.01,.01)
    sd[k] <- sqrt(1/tau[k])
 }
}'
dataList<-with(Crime,list(y=crmrte-mean(crmrte),x=prbarr-mean(prbarr),
                          group=as.numeric(year)))
mer.jags<-run.jags(model=mer.model,data=dataList,inits=ini,
                 monitor=c("beta","sd"))
```

```
plot(mer.jags,vars="beta[2]",plot.type=c("trace","density"))
```





```
summary(mer.jags)

           Lower95      Median     Upper95         Mean           SD
beta[1] -0.0462595 -0.00514395 0.05187930 -0.003347422 0.0241357489
beta[2] -0.1018100 -0.04774460 0.00766026 -0.047687166 0.0272752288
sd[1]    0.0327307  0.06092845 0.10912800  0.065766763 0.0226257983
sd[2]    0.0344519  0.06396180 0.11685600  0.069254872 0.0244287265
sd[3]    0.0167867  0.01775840 0.01875400  0.017767788 0.0005034746
                Mode          MCerr MC%ofSD SSeff        AC.10     psrf
beta[1] -0.006693705 0.004800954408    19.9    25  0.987742660 1.185623
beta[2] -0.046329427 0.001272228093     4.7   460  0.797183583 1.004203
sd[1]    0.055648617 0.000342035187     1.5  4376  0.089509358 1.003326
sd[2]    0.057399691 0.000343445832     1.4  5059  0.104591527 1.001137
sd[3]    0.017747729 0.000002527245     0.5 39688 -0.009773427 1.000303
```

17.4 Robust mixed effects

Looking at the graph we might find that some observations look like outliers. As in section 6 we can use the t-distribution with endogenous degrees of freedom to allow for more robustness. In the model we replace *dnorm* with *dt* and add a prior for the degrees of freedom.

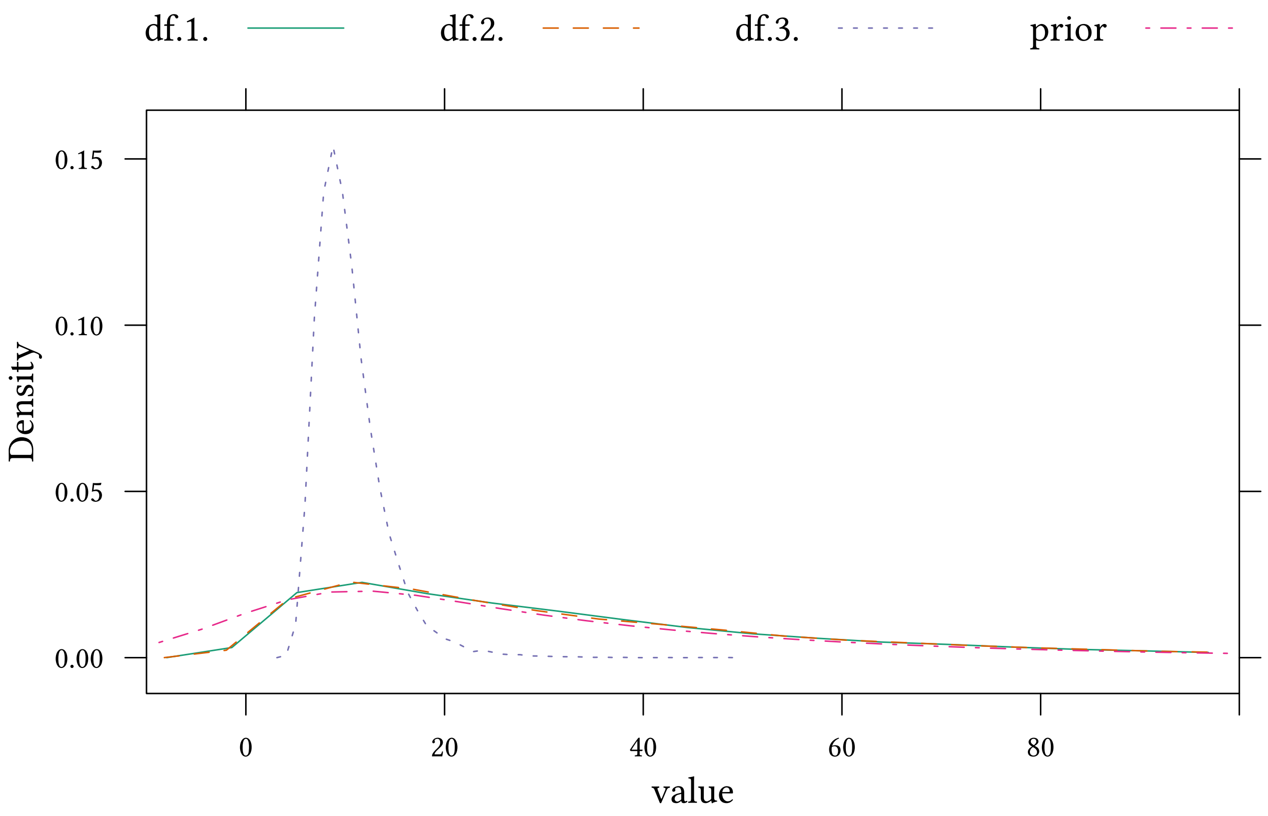
We are conservative here and make all random effects follow a t-distribution.

```
merT.model <- 'model {
 for (i in 1:length(y)) {
    y[i] ~ dt(mu[i],tau[3],df[3])
    mu[i]<-beta[1]+nu[1,group[i]]+(beta[2]+nu[2,group[i]])*x[i]
 }
 for (k in 1:2) {
    beta[k] ~ dnorm (0,.0001)
    for (j in 1:max(group)) {
       nu[k,j] ~ dt(0,tau[k],df[k])
    }
 }
 for (k in 1:3) {
    tau[k] ~ dgamma(.01,.01)
    sd[k] <- sqrt(1/tau[k])
    df[k]  ~ dexp(1/30)
 }
}'
merT.jags<-run.jags(model=merT.model,data=dataList,inits=ini,
                 monitor=c("beta","sd","df"))
```

```
summary(merT.jags)

           Lower95      Median    Upper95        Mean            SD
beta[1] -0.0493220  0.004837055  0.0509028  0.003700867  0.0250550490
beta[2] -0.0960694 -0.040110150  0.0178689 -0.041406342  0.0308381995
sd[1]    0.0331850  0.060982700  0.1111170  0.065790069  0.0223915061
sd[2]    0.0328871  0.063878400  0.1197580  0.069951338  0.0277873651
sd[3]    0.0144714  0.015668700  0.0169331  0.015681810  0.0006299104
df[1]    0.4971880 26.123050000 94.2885000 34.566629536 30.2471683403
df[2]    0.7022430 25.942500000 97.1656000 35.097635586 31.1035258239
df[3]    5.2444700  9.762580000 17.3171000 10.483894742  3.5377769451
                Mode          MCerr MC%ofSD SSeff       AC.10     psrf
beta[1]   0.003432674 0.005109977706    20.4    24 0.98770168 1.320518
beta[2]  -0.041339950 0.001840556101     6.0   281 0.86671243 1.052037
sd[1]     0.055387662 0.000356107964     1.6  3954 0.16613637 1.014166
sd[2]     0.057080212 0.000423452140     1.5  4306 0.20049416 1.012595
sd[3]     0.015670532 0.000006221029     1.0 10253 0.00404767 1.000094
df[1]    14.391761211 0.319857854448     1.1  8942 0.01981948 1.000398
df[2]    14.082360315 0.328853639540     1.1  8946 0.02401787 1.000086
df[3]     8.850137918 0.039238723328     1.1  8129 0.02614337 1.000066
```

Here is the posterior density of the degrees of freedom.

```
merT.df<-data.frame(as.mcmc(merT.jags))
xx<-melt(merT.df[,grep("^df",names(merT.df))])
xx<-rbind.fill(xx,data.frame(list(variable="prior",value=qexp(((1:100)-1/2)/100,1/30))))
densityplot(~value,group=variable,data=xx,plot.points=FALSE,
            auto.key=list(space="top",columns=4),xlim=c(-10,100))
```

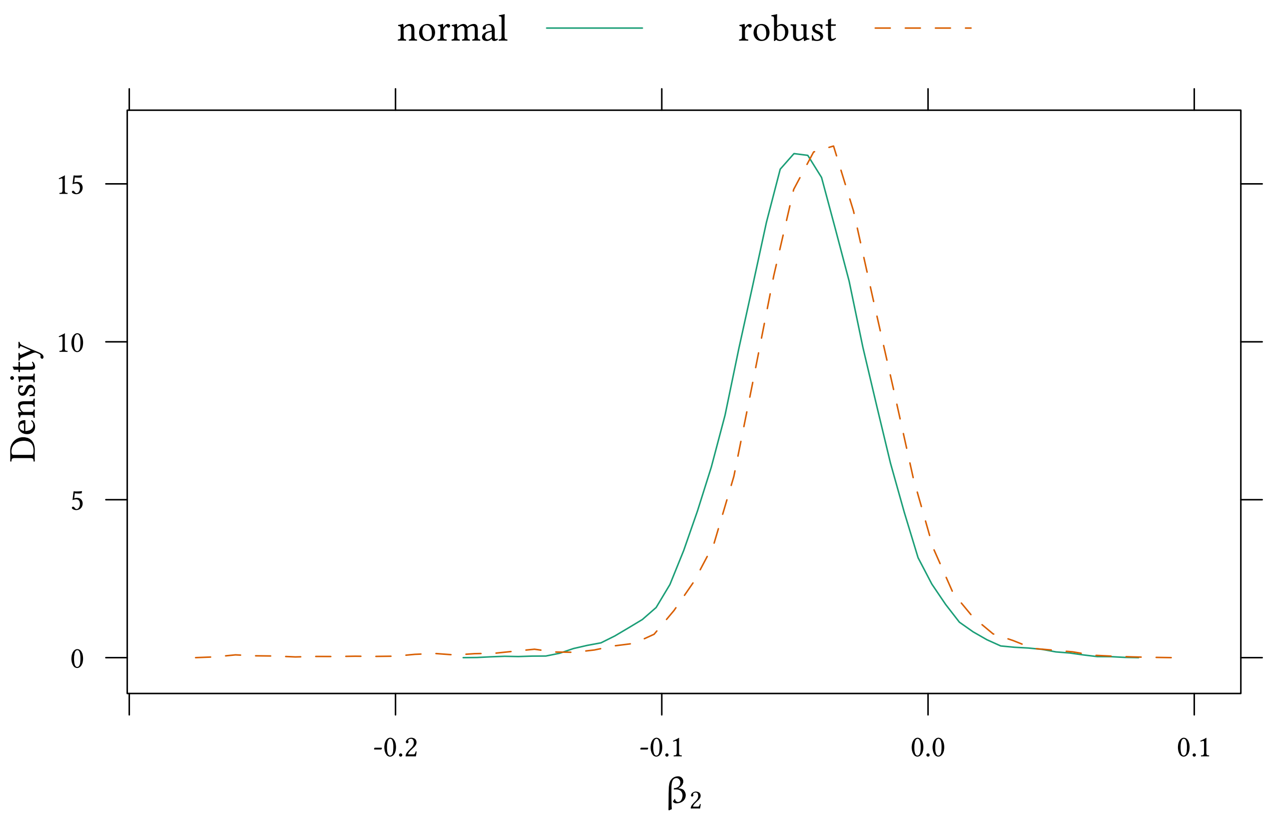


We see that, in particular, the residual (`df[3]`) needs some robustness.

For `df[1]` and `df[2]`, i.e. for the random effects for intercept and slope, the posterior is very similar to the prior, i.e. the data does not provide a lot of extra information in this respect.

On the other hand, the estimate for `beta[2]` does not seem to change much with the robust model:

```
mer.df<-data.frame(as.mcmc(mer.jags))
densityplot(~mer.df$beta.2.+merT.df$beta.2. ,plot.points=FALSE,
            xlab="$\\beta_2$",auto.key=list(space="top",columns=2,text=c("normal","robust"
```



17.5 Exercises

Consider the data set *LaborSupply* from *Ecdat*.

1. Which variables could explain labor supply?
2. Estimate your model, taking into account a random effect for the intercept?
3. Include a random effect for the slope.

18 Model Comparison

- Several models (at least two).
- Discrete variable selects among the models.
- $\rightarrow$ posterior probability for each model.

Preliminaries

- F: Null-Hypothesis-Testing: $\Pr(X|H_0)$.
- B: Model comparison: $\Pr(H_0|X)$ versus $\Pr(H_1|X)$ versus $\Pr(H_2|X)$ …
  - Models can be nested, they need not be nested.

  - Models can be of different complexity (automatic penalty).

Are these the only plausible models? (similar to a very strong prior)

18.1 Example 1

- Data:

```
set.seed(123)
x <- rnorm(5,5,1)
```

- $x \sim N(\mu, 1)$ where N is the normal distribution.

  We compare three models:

  $\mu_1 = 3.8$, $\mu_2 = 4$, $\mu_3 = 6$.

```
c.model <- 'model {
for (i in 1:length(x)) {
   x[i] ~ dnorm(mu[m],1)
}
 m ~ dcat(modelProb)
}'
c.data<-list(x=x,modelProb=c(1,1,1),mu=c(3.8,4,6))
c.jags<-run.jags(c.model,c.data,monitor=c("m"))
with(data.frame(as.mcmc(c.jags)),table(m)/length(m))

m
      1       2       3
0.03415 0.12255 0.84330
```

What is, actually, a vague prior in this context? Can we give more flexibility to the prior for m?

```
c.model2 <- 'model {
for (i in 1:length(x)) {
   x[i] ~ dnorm(mu[m],1)
}
 m ~ dcat(mP)
 mP ~ ddirch(modelProb)
}'
c.jags<-run.jags(c.model2,c.data,monitor=c("m"))
with(data.frame(as.mcmc(c.jags)),table(m)/length(m))

m
      1       2       3
0.03390 0.12455 0.84155
```

```
c.model3 <- 'model {
for (i in 1:length(x)) {
   x[i] ~ dnorm(mu[m],1)
}
m ~ dcat(modelProb)
for (i in 1:length(modelProb)) {
   mSel[i] <- ifelse(m==i,1,0)
}
}'
c.jags<-run.jags(c.model3,c.data,monitor=c("mSel"))
summary(c.jags)[,c("Mean","SSeff","psrf")]
```

```
           Mean SSeff     psrf
mSel[1] 0.03585 19745 1.000177
mSel[2] 0.12605 18986 1.000027
mSel[3] 0.83810 19409 1.000064
```

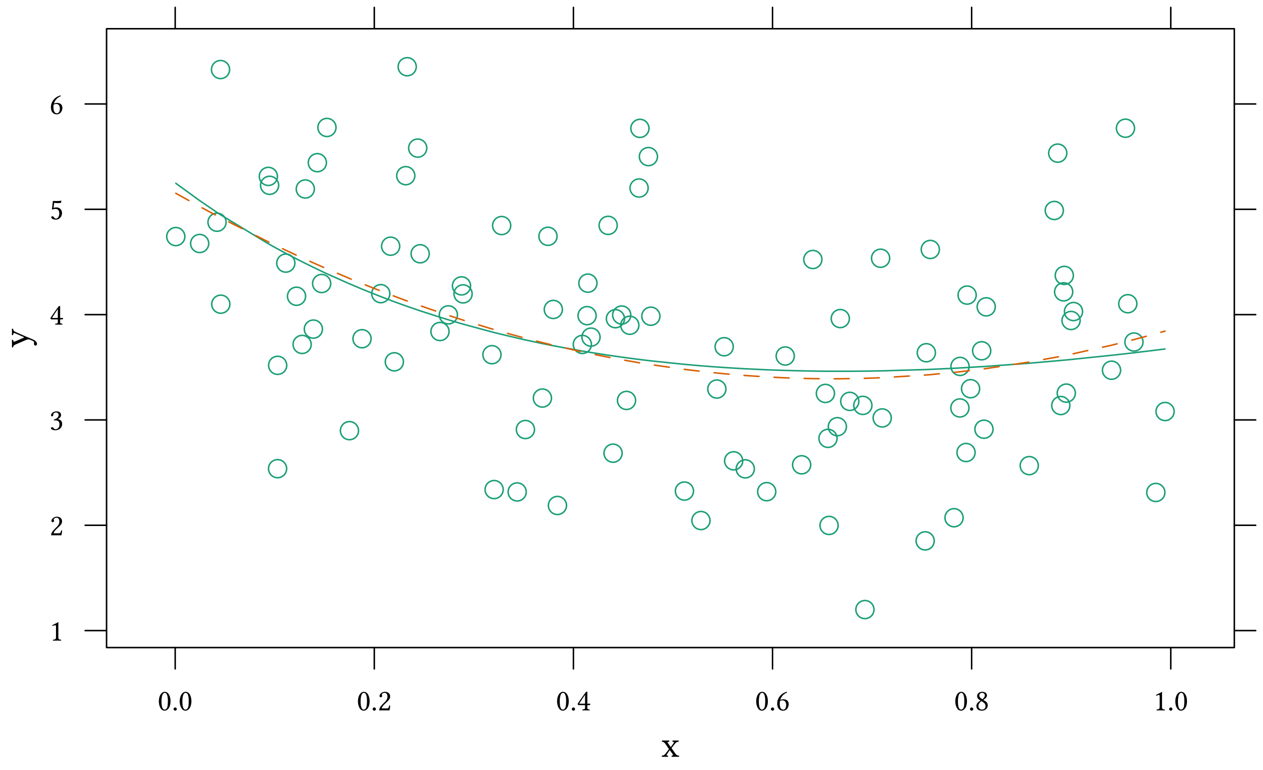
18.2 Example 2

Should we better use a polynomial or a fractional polynomial model to describe the relation in the following simulated data:

```
set.seed(123)
N<-100
x<-runif(N)
y<-5-4.3*x+3.1*x^2+rnorm(N)
mData<-data.frame(y=y,x=x)
quad<-predict(lm(y ~ x + I(x^2),data=mData))
hyp<-predict(lm(y ~ x + I(1/(x+1)),data=mData))
```

- Model 1: $y = \beta_0 + \beta_1 x + \beta_2 x^2 + u$
- Model 2: $y = \beta_0 + \beta_1 x + \beta_2 \frac{1}{x+1} + u$

```
xplot(y~x,data=mData,type="p")+
    xyplot(hyp+quad~x,data=mData,type="a",ylab="y")
```



AIC

$$\mathrm{AIC} = -2\log(L) + 2k$$

- AIC is a measure of information loss of a model (Akaike, 1973).
- AIC is asymtotically equivalent to leave one out cross-validation (Stone, 1977; Fang, Yixin, 2011).

```
extractAIC(lm(y ~ x + I(1/(x+1)),data=mData))

[1]  3.000000 -1.199884

extractAIC(lm(y ~ x + I(x^2),data=mData))

[1]  3.000000 -2.757703
```

DIC Deviance information criterion:

$$\begin{array}{ll} \text{Deviance} & D(\theta) = -2\log(P(X|\theta)) + C \\ & \bar{D} = E[D(\theta)], \qquad \bar{\theta} = E[\theta] \\ \text{eff. \# parameters} & p_D = \bar{D} - D(\bar{\theta}) \quad \text{(Spiegelhalter et al., 2002)} \\ & \mathrm{DIC} = D(\bar{\theta}) + 2p_D \end{array}$$

18.3 Model 1

```
model1.model <- 'model {
 for (i in 1:length(y)) {
    y[i] ~ dnorm(inprod(beta,X[i,]),tau)
 }
 for (k in 1:K) {
    beta[k] ~ dnorm (0,.0001)
 }
    tau ~ dgamma(m^2/d^2,m/d^2); m ~ dexp(1); d ~ dexp(1);
}'
model1.data<-with(mData,list(y=y,K=4,X=cbind(1,x,x^2,1/(x+1))))
model1.data<-within(model1.data,{X<-sweep(X,2,apply(X,2,mean));X[,1]<-1})
ini<-genInit(4)
model1.jags<-run.jags(model=model1.model,data=within(model1.data,beta<-c(NA,NA,0,NA)),inits=in
                      monitor=c("beta","tau","dic","popt"))
```

```
model1.jags


JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

          Lower95 Median Upper95   Mean       SD   Mode      MCerr MC%ofSD
beta[1]    3.6282 3.8227  4.0158  3.822 0.098466 3.8199 0.00049776     0.5
beta[2] -0.058831 3.9502  7.9823 3.9875   2.0602 3.9891   0.085904     4.2
beta[3]         0      0       0      0        0      0         --      --
beta[4]    2.8239 11.055  19.542 11.117    4.288 11.428    0.17664     4.1
tau        0.7631 1.0402   1.343 1.0472    0.149 1.0325  0.0011955     0.8

        SSeff       AC.10    psrf
beta[1] 39132 -0.0033029 0.99999
beta[2]   575    0.74862  1.0046
beta[3]    --         --      --
beta[4]   589    0.74929  1.0045
tau     15534   0.021715       1

Model fit assessment:
DIC = 295.7388
PED = 299.9781
Estimated effective number of parameters:  pD = 4.10993, pOpt = 8.34924

Total time taken: 3.3 seconds
```

18.4 Model 2

```
model2.jags<-run.jags(model=model1.model,data=within(model1.data,beta<-c(NA,NA,NA,0)),inits=in
                      monitor=c("beta","tau","dic","popt"))
```

```
JAGS model summary statistics from 40000 samples (chains = 4; adapt+burnin = 5000):

        Lower95  Median Upper95    Mean        SD    Mode      MCerr MC%ofSD
beta[1]  3.6304   3.822  4.0128  3.8225 0.097745  3.8181 0.00049109     0.5
beta[2] -8.1456 -5.3772 -2.5942 -5.3861   1.4185 -5.3932   0.040147     2.8
beta[3]  1.4144  4.0777  6.7505  4.0861   1.3666  4.0514   0.038833     2.8
beta[4]       0       0       0       0        0       0         --      --
tau     0.78073  1.0592  1.3684  1.0647  0.15076  1.0485  0.0011949     0.8

        SSeff      AC.10   psrf
beta[1] 39616 0.00046172      1
beta[2]  1248    0.53816  1.004
beta[3]  1238    0.53725 1.0039
beta[4]    --         --     --
tau     15919   0.024424 1.0001

Model fit assessment:
DIC = 294.1368
PED = 298.4162
Estimated effective number of parameters:  pD = 4.07012, pOpt = 8.34955

Total time taken: 3.3 seconds
```

18.5 A joint model

Different from the models so far we use parameters (*priBetaMean, priBetaTau, priTM, priTD*) to describe priors. These priors are defined as part of the *data* argument to *run.jags*.

We also restrict the matrix *beta* to describe the different models.

```
modelSel0.model <- 'model {
 for (i in 1:length(y)) {
    y[i] ~ dnorm((yy[i,mod]),tau[mod])
    for (m in 1:2) {
       yy[i,m] <- inprod(beta[,m],X[i,])
    }
 }
 for (m in 1:2) {
    for (k in 1:K) {
      beta[k,m] ~ dnorm (priBetaMean[k,m],priBetaTau[k,m])
   }
   tau[m] ~ dgamma(priTauAlpha[m],priTauBeta[m])
 }
 mod ~ dcat(modelProb)
}'
modelSel0.data<-within(model1.data,{
    beta <- matrix(NA,K,2); beta[3,1]<-0; beta[4,2]<-0;
    priBetaMean <- matrix(0,K,2);priBetaTau <- matrix(.0001,K,2)
    priTauAlpha <- c(.01,.01);     priTauBeta <- c(.01,.01)
    modelProb   <- c(1,1)})
ini<-genInit(4)
```

Convergence in model comparison Unfortunately, in the above specification the model (even if we guide *partTauAlpha* and *priTauBeta*) does not converge too well:

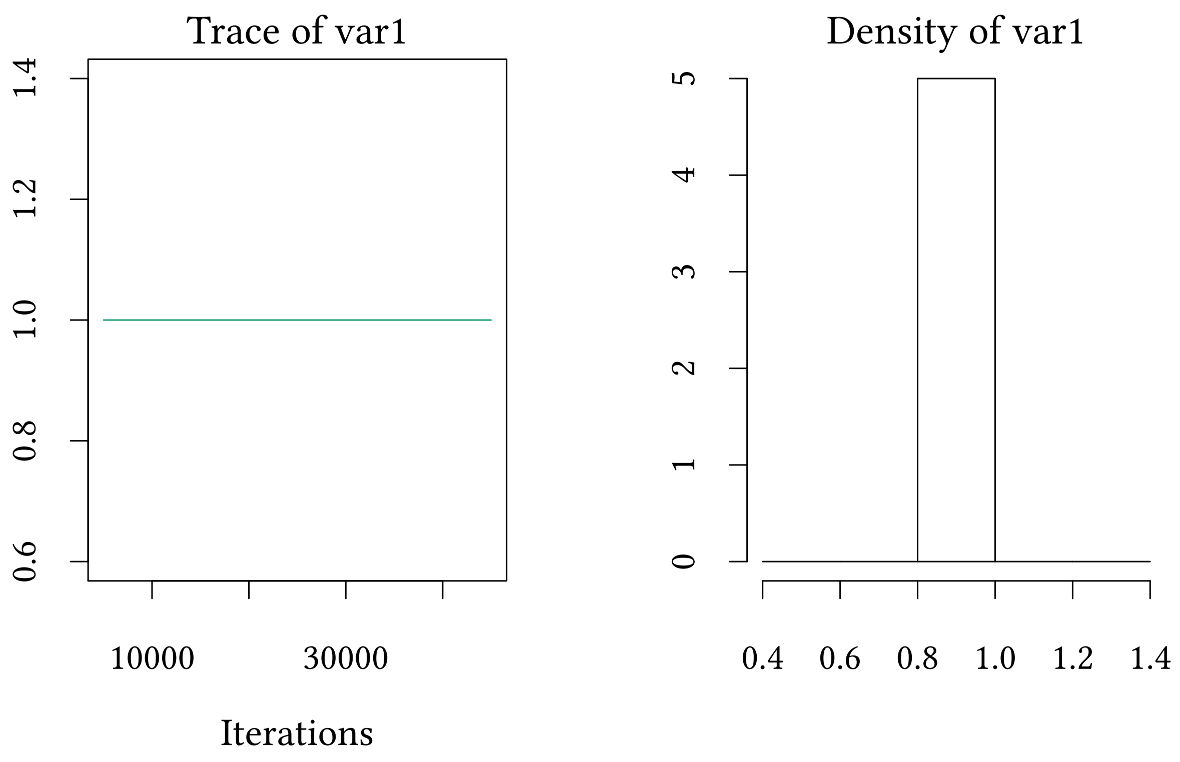
```
modelSel0.jags<-run.jags(model=modelSel0.model,
   data=modelSel0.data,inits=ini,monitor=c("beta","tau","mod"))
```

```
summary(modelSel0.jags)[,c("Mean","SD","SSeff","psrf")]

                 Mean           SD SSeff      psrf
beta[1,1]   3.8217968   0.09815767 40186 1.0000236
beta[2,1]   3.9348496   1.98008024   619 1.0020974
beta[3,1]   0.0000000   0.00000000    NA        NA
beta[4,1]  11.0058461   4.12504235   628 1.0021217
beta[1,2]  -0.3627482 100.25173235 40260 1.0002285
beta[2,2]   0.4437219  99.88351859 41634 1.0002128
beta[3,2]  -0.1120987  99.46382220 40591 0.9999999
beta[4,2]   0.0000000   0.00000000    NA        NA
tau[1]      1.0417498   0.14984201 36746 1.0000176
tau[2]      0.9247774   9.62548329 40000 1.0045433
mod         1.0000000   0.00000000    NA        NA
```

(if *partTauAlpha* and *priTauBeta* are left to *NA*, then simulations crash with *Error in node priTauAlpha[2]. Slicer stuck at value with infinite density*).

The main reason for the lack of convergence is: chains do not mix:

```
plot(as.mcmc(modelSel0.jags)[,"mod"])
```



What happens if the chain selects one model:

- coefficients for this model adjust.
  - likelihood for this model is good.
- coefficients of the other model still follow prior distribution.
  - likelihood of the other model is bad.
- $\rightarrow$ the sampler will almost never switch (model selection is correlated).

Convergence is very slow, we have to help the sampler.

$\rightarrow$ Pseudopriors (Carlin, Chib, 1995).

- When model is selected: use vague priors (as before).
- When model is not selected: use pseudopriors (posteriors from previous estimation).

```
modelSel.model <- 'model {
 for (i in 1:length(y)) {
    y[i] ~ dnorm((yy[i,mod]),tau[mod])
    for (m in 1:2) { yy[i,m] <- inprod(beta[,m],X[i,]) }
 }
 for (m in 1:2) {
    for (k in 1:K) {
      beta[k,m] ~ dnorm (priBetaMean[k,m,mod],priBetaTau[k,m,mod])
   }
   tau[m] ~ dgamma(priTM[m,mod]^2/priTD[m,mod]^2, priTM[m,mod]/priTD[m,mod]^2)
   for(modI in 1:2) {
      priTM[m,modI] ~ dgamma(1,1); priTD[m,modI] ~ dgamma(1,1);
   }
 }
 mod ~ dcat(modelProb)
}'
modelSel.data<-within(model1.data,{
    beta <- matrix(NA,K,2); beta[3,1]<-0; beta[4,2]<-0;
    priBetaMean <- array(0,c(K,2,2)); priBetaTau <- array(.0001,c(K,2,2))
    priTM <- matrix(NA,2,2);          priTD <- matrix(NA,2,2)
    modelProb   <- c(1,1)})
ini<-genInit(4)
```

Digression: We can use the above (flexible) model to estimate the previous (specific) models:

```
model1B.jags<-run.jags(model=modelSel.model,within(modelSel.data,mod<-1),inits=ini,
                 monitor=c("beta","tau","mod"))
summary(model1B.jags)[c(1:4,9),c("Mean","SD","SSeff","psrf")]

               Mean         SD SSeff     psrf
beta[1,1]  3.822052 0.09835104 40000 1.000074
beta[2,1]  3.833818 2.01108758   634 1.004135
beta[3,1]  0.000000 0.00000000    NA       NA
beta[4,1] 10.793066 4.18976062   637 1.004153
tau[1]     1.047556 0.14930482 14775 1.000149

summary(model1.jags)[,c("Mean","SD","SSeff","psrf")]

             Mean         SD SSeff      psrf
beta[1]  3.822043 0.09846607 39132 0.9999892
beta[2]  3.987455 2.06018110   575 1.0045649
beta[3]  0.000000 0.00000000    NA        NA
beta[4] 11.117199 4.28800888   589 1.0044837
tau      1.047170 0.14899855 15534 0.9999992
```

```
model2B.jags<-run.jags(model=modelSel.model,within(modelSel.data,mod<-2),inits=ini,
                 monitor=c("beta","tau","mod"))
summary(model2B.jags)[c(5:8,10),c("Mean","SD","SSeff","psrf")]

               Mean         SD SSeff     psrf
beta[1,2]  3.822396 0.09806754 39853 1.000000
beta[2,2] -5.304239 1.45780548  1152 1.000958
beta[3,2]  4.009177 1.40370489  1163 1.000993
beta[4,2]  0.000000 0.00000000    NA       NA
tau[2]     1.062206 0.14953725 16640 1.000211

summary(model2.jags)[,c("Mean","SD","SSeff","psrf")]
```

```
               Mean          SD SSeff     psrf
beta[1]  3.822521 0.09774548 39616 1.000005
beta[2] -5.386093 1.41847995  1248 1.004034
beta[3]  4.086113 1.36658457  1238 1.003926
beta[4]  0.000000 0.00000000    NA       NA
tau      1.064744 0.15075710 15919 1.000054
```

To avoid coding mistakes it might be better to use one (single) flexible model for all calculations.

18.6 Pseudopriors

Extract pseudopriors from previous estimates:

$$\beta \sim N(\mu, \tau) \qquad \mu = \texttt{Mean}, \quad \tau = 1/\texttt{SD}^2$$

```
sum2prior <- function(jags,pattern,var) {
    x <- summary(jags)
    x[grep(pattern,rownames(x)),var]
    }
sum2prior(model1B.jags,"beta\\[.,1\\]","Mean")

beta[1,1] beta[2,1] beta[3,1] beta[4,1]
 3.822052  3.833818  0.000000 10.793066

sum2prior(model1B.jags,"beta\\[.,1\\]","SD")

 beta[1,1]  beta[2,1]  beta[3,1]  beta[4,1]
0.09835104 2.01108758 0.00000000 4.18976062
```

We construct the pseudopriors here one by one, so that we can see each step:

```
within(modelSel.data,{
    priBetaMean[,1,2]<-sum2prior(model1B.jags,"beta\\[.,1\\]","Mean")
    priBetaMean[,2,1]<-sum2prior(model2B.jags,"beta\\[.,2\\]","Mean")
})[["priBetaMean"]]

, , 1

     [,1]      [,2]
[1,]    0  3.822396
[2,]    0 -5.304239
[3,]    0  4.009177
[4,]    0  0.000000

, , 2

          [,1] [,2]
[1,]  3.822052    0
```

```
[2,]  3.833818    0
[3,]  0.000000    0
[4,] 10.793066    0
```

```
within(modelSel.data,{
    priBetaTau[,1,2] <-1/sum2prior(model1B.jags,"beta\\[.,1\\]","SD")^2
    priBetaTau[,2,1] <-1/sum2prior(model2B.jags,"beta\\[.,2\\]","SD")^2
    priBetaTau[3,1,] <-100
    priBetaTau[4,2,] <-100
})[["priBetaTau"]]

, , 1

         [,1]         [,2]
[1,]   0.0001 103.9799166
[2,]   0.0001   0.4705447
[3,] 100.0000   0.5075144
[4,]   0.0001 100.0000000

, , 2

             [,1]     [,2]
[1,] 103.38131591   0.0001
[2,]   0.24725099   0.0001
[3,] 100.00000000   0.0001
[4,]   0.05696677 100.0000
```

```
within(modelSel.data,{
    priTM[1,2]<-sum2prior(model1B.jags,"tau\\[1\\]","Mean")
    priTM[2,1]<-sum2prior(model2B.jags,"tau\\[2\\]","Mean")
})[["priTM"]]

         [,1]     [,2]
[1,]       NA 1.047556
[2,] 1.062206       NA
```

```
within(modelSel.data,{
    priTD[1,2]<-sum2prior(model1B.jags,"tau\\[1\\]","SD")^2
    priTD[2,1]<-sum2prior(model2B.jags,"tau\\[2\\]","SD")^2
})[["priTD"]]

           [,1]       [,2]
[1,]         NA 0.02229193
[2,] 0.02236139         NA
```

Now we do all the pseudopriors in one step:

```
pseudo.data<-within(modelSel.data,{
    priBetaMean[,1,2]<-sum2prior(model1B.jags,"beta\\[.,1\\]","Mean")
    priBetaMean[,2,1]<-sum2prior(model2B.jags,"beta\\[.,2\\]","Mean")
    priBetaTau[,1,2] <-1/sum2prior(model1B.jags,"beta\\[.,1\\]","SD")^2
    priBetaTau[,2,1] <-1/sum2prior(model2B.jags,"beta\\[.,2\\]","SD")^2
    priBetaTau[3,1,] <-100; priBetaTau[4,2,] <-100
    priTM[1,2]<-sum2prior(model1B.jags,"tau\\[1\\]","Mean")
    priTM[2,1]<-sum2prior(model2B.jags,"tau\\[2\\]","Mean")
    priTD[1,2]<-sum2prior(model1B.jags,"tau\\[1\\]","SD")^2
    priTD[2,1]<-sum2prior(model2B.jags,"tau\\[2\\]","SD")^2
})
```

```
modelSelPP.jags<-run.jags(model=modelSel.model,data=pseudo.data,inits=ini,
                          monitor=c("beta","tau","mod"))
```

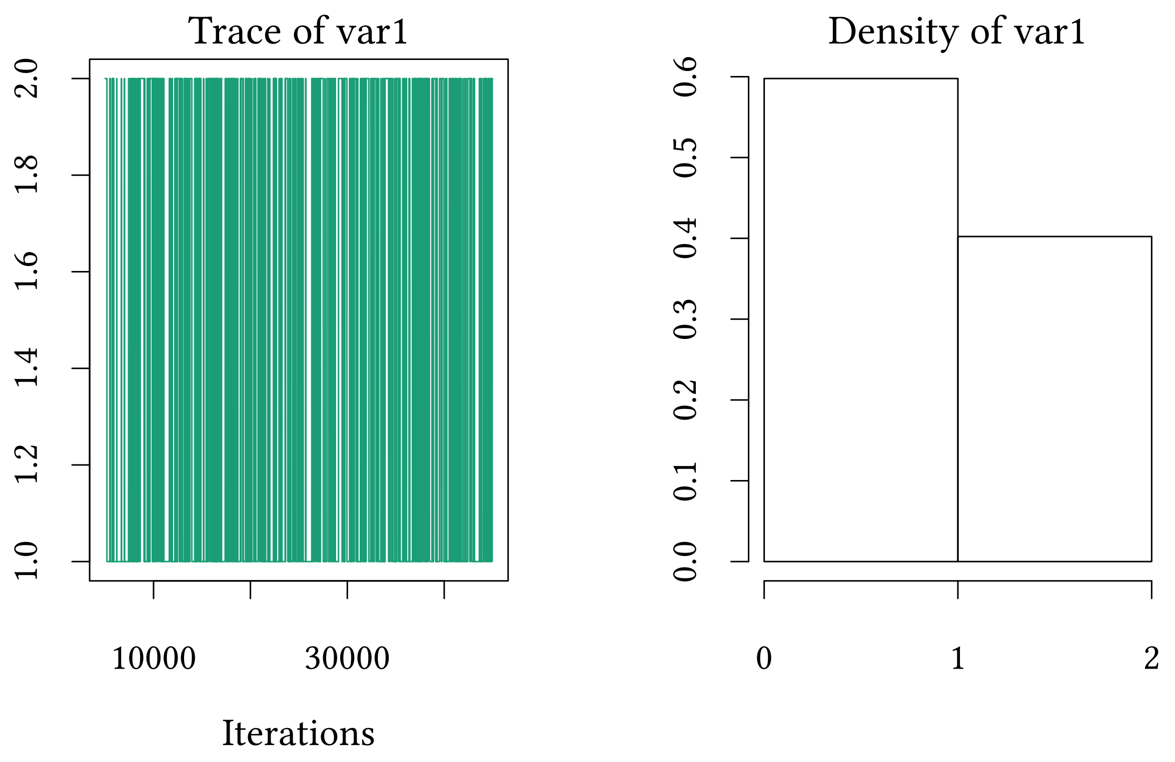
```
summary(modelSelPP.jags)[,c("Mean","SD","SSeff","psrf")]

                Mean          SD SSeff      psrf
beta[1,1]   3.821997 0.09871367 38950 1.0000209
beta[2,1]   4.002512 1.98414304  1377 1.0005341
beta[3,1]   0.000000 0.00000000    NA        NA
beta[4,1]  11.193314 4.12112634  1298 1.0006789
beta[1,2]   3.822861 0.09832232 41560 0.9999652
beta[2,2]  -5.298587 1.44274116  3594 1.0017140
beta[3,2]   4.006381 1.38483622  3343 1.0013366
beta[4,2]   0.000000 0.00000000    NA        NA
tau[1]      1.047751 0.11587482 15748 1.0013711
tau[2]      1.063313 0.09624414 16621 1.0032096
mod         1.402250 0.49035798   517 1.0103870
```

Compare with, e.g., model 2:

```
summary(model2B.jags)[5:8,c("Mean","SD","SSeff","psrf")]

                Mean          SD SSeff     psrf
beta[1,2]   3.822396 0.09806754 39853 1.000000
beta[2,2]  -5.304239 1.45780548  1152 1.000958
beta[3,2]   4.009177 1.40370489  1163 1.000993
beta[4,2]   0.000000 0.00000000    NA       NA
```

With pseudopriors convergence is good and the chains mix well:

```
plot(as.mcmc(modelSelPP.jags)[,"mod"])
```



```
summary(modelSelPP.jags)["mod",]

    Lower95      Median     Upper95        Mean          SD        Mode
 1.00000000  1.00000000  2.00000000  1.40225000  0.49035798  1.00000000
      MCerr    MC%ofSD       SSeff        AC.10        psrf
 0.02156391  4.40000000 517.00000000  0.77285590  1.01038703
```

The mean coefficient of *mod* is 1.402.

→ the second (polynomial) model has a posterior probability of 40.2%.

- The first (fractional polynomial) model has a posterior probability of 59.8%.
- The fractional polynomial model is 1.49 times more probable than the polynomial one.

Are these two models the only relevant models?

18.7 Model uncertainty

- F: inference is based on one model.
- B: composite inference from model posteriors.

  What if there is a large number of possible models?
  - Occam's window: consider a subset of plausible and not too complex models.
  - Markov Chain Monte Carlo Model Composition (MC^3).

18.8 Bayes factors

Posterior probability of Model H_1:

$$\Pr(H_1|X) = \Pr(H_1) \cdot \Pr(X|H_1) \frac{1}{\Pr(X)}$$

Hence

$$\frac{\Pr(H_1|X)}{\Pr(H_2|X)} = \frac{\Pr(H_1) \cdot \Pr(X|H_1)}{\Pr(H_2) \cdot \Pr(X|H_2)}$$

For uninformed priors $\Pr(H_1) = \Pr(H_2)$ we have the *Bayes factor*

$$K = \frac{\Pr(X|H_1)}{\Pr(X|H_2)} = \underbrace{\frac{\int \Pr(\theta_1|H_1) \Pr(X|\theta_1, H_1)\, d\theta_1}{\int \Pr(\theta_2|H_2) \Pr(X|\theta_2, H_2)\, d\theta_2}}_{\text{Bayes factor}} \neq \underbrace{\frac{\Pr(X|\theta_1^*, H_1)}{\Pr(X|\theta_2^*, H_2)}}_{\text{LR-test}}$$

Interpreting K: Harold Jeffreys (1961):

10^0 $10^{0.5}$ 10^1 $10^{1.5}$ 10^2

barely worth mentioning — substantial — strong — very strong — decisive

Robert E. Kass and Adrian E. Raftery (1995):

e^0 $e^1 \approx 2.7$ $e^3 \approx 20$ $e^5 \approx 150$

barely worth mentioning — positive — strong — very strong

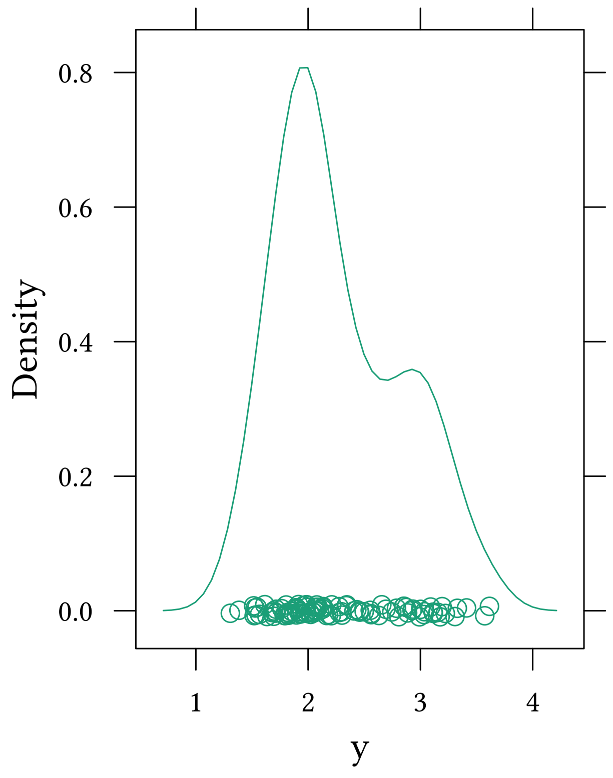
19 Mixture Models

19.1 Example

Sometimes we assume that our population can be described as a mixture of two distributions. Here we construct such a mixture with means $\mu = 2$ and $\mu = 3$ respectively:

```r
set.seed(123)
N <- 100
group <- rbinom(N,1,.3)
y <- rnorm(N,mean=2+group,sd=.3)
```

```
densityplot(~y)
```



We first consider a model with exactly 2 groups:

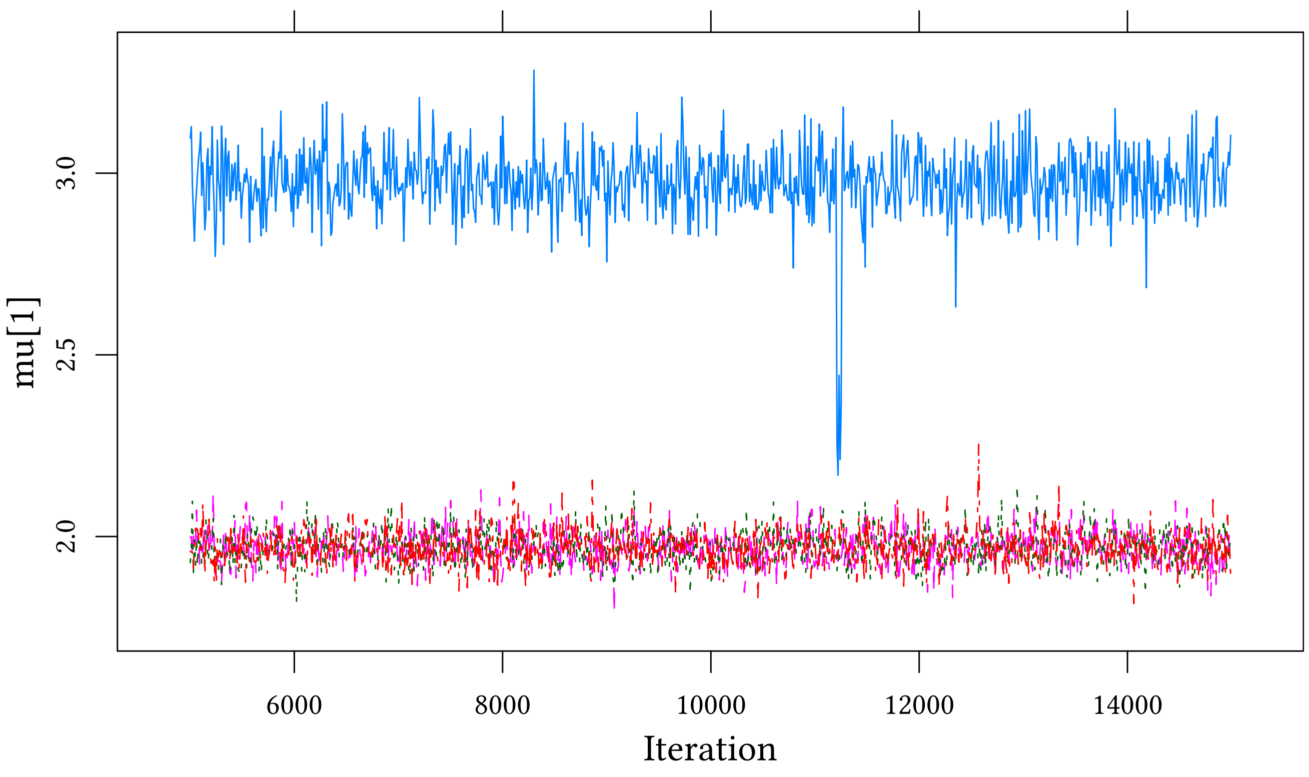
```
mix0.model <- 'model {
   for (i in 1:length(y)) {
      y[i] ~ dnorm(mu[group[i]+1],tau)
      group[i] ~ dbern(p)
   }
   for (g in 1:2) {
     mu[g] ~ dnorm(0,.0001)
   }
   p     ~ dbeta(1,1)
   tau   ~ dgamma(m^2/d^2,m/d^2)
   m     ~ dgamma(1,1)
   d     ~ dgamma(1,1)
   sd   <- 1/sqrt(tau)
}'
mix0.jags<-run.jags(mix0.model,data=list(y=y),
         inits=genInit(4,function(i) list(mu0=rnorm(2,0,100))),
         monitor=c("mu","p","sd"))
```

The model does not seem to converge well:

```
summary(mix0.jags)

       Lower95    Median  Upper95      Mean         SD      Mode         MCerr
mu[1] 1.877390 1.9871800 3.059580 2.2209454 0.44060046 1.9662915 0.0044379631
```

```
mu[2] 1.905170 2.9490500 3.113520 2.7281157 0.44324581 2.9795342 0.0042013182
p     0.203301 0.3279260 0.757267 0.4026280 0.17679597 0.3032847 0.0014272437
sd    0.256232 0.3105675 0.382061 0.3149543 0.03439059 0.3045459 0.0004583154
      MC%ofSD SSeff       AC.10      psrf
mu[1]     1.0  9856 0.075288824 11.405622
mu[2]     0.9 11131 0.049729473 11.204242
p         0.8 15344 0.005118556  4.415163
sd        1.3  5631 0.118850843  1.002810
```

```
plot(mix0.jags,plot.type="trace",vars="mu[1]")
```



19.2 Labels and sorting

The problem has to do with *labels*. We have two `mu`s, a large one and a small one. But which is which? We need a convention, e.g. that the smaller one is always *`mu[1]`*. There are different ways to implement this convention. One is `sort`.

```
mix.model <- 'model {
   for (i in 1:length(y)) {
      y[i] ~ dnorm(mu[group[i]+1],tau)
      group[i] ~ dbern(p)
   }
   for (g in 1:2) {
     mu0[g] ~ dnorm(0,.0001)
   }
   p     ~ dbeta(1,1)
   mu[1:2] <- sort(mu0)
   tau   ~ dgamma(m^2/d^2,m/d^2)
   m     ~ dgamma(1,1)
   d     ~ dgamma(1,1)
   sd   <- 1/sqrt(tau)
}'
mix.jags<-run.jags(mix.model,data=list(y=y),
         inits=genInit(4,function(i) list(mu0=rnorm(2,0,100))),
         monitor=c("mu","p","sd"))
```

```
summary(mix.jags)

       Lower95   Median  Upper95      Mean          SD      Mode         MCerr
mu[1] 1.876640 1.968230 2.061600 1.9697203 0.04709826 1.9644642 0.0004521677
mu[2] 2.835250 2.981240 3.133600 2.9811188 0.07645630 2.9851922 0.0007250130
p     0.198150 0.303486 0.410794 0.3050988 0.05439289 0.3013208 0.0004569694
sd    0.253974 0.311317 0.382210 0.3156051 0.03377336 0.3048141 0.0004575182
      MC%ofSD SSeff      AC.10     psrf
mu[1]     1.0 10850 0.03118628 1.000599
mu[2]     0.9 11121 0.01767753 1.000999
p         0.8 14168 0.01796723 1.000584
sd        1.4  5449 0.10259628 1.000359
```

19.3 More groups

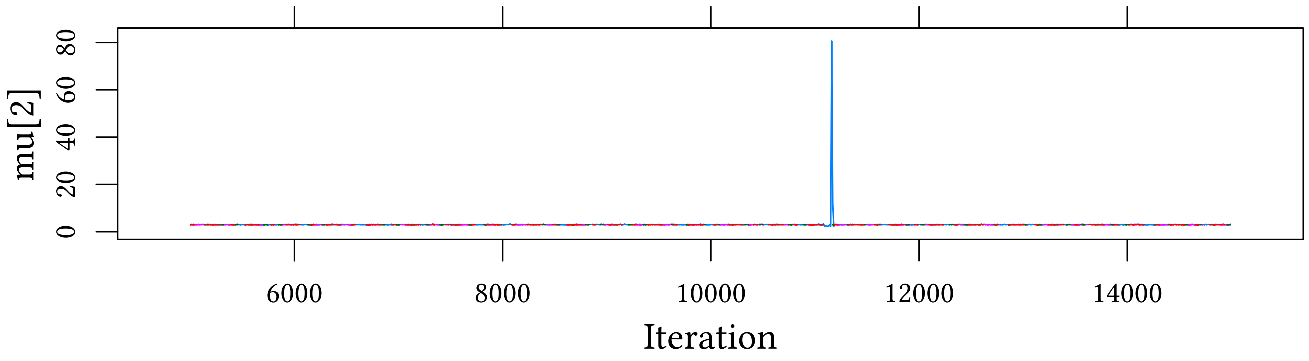
For a potentially larger number of groups we replace *dbern* with *dcat* and *dbeta* with *ddirch* (the Dirichlet distribution).

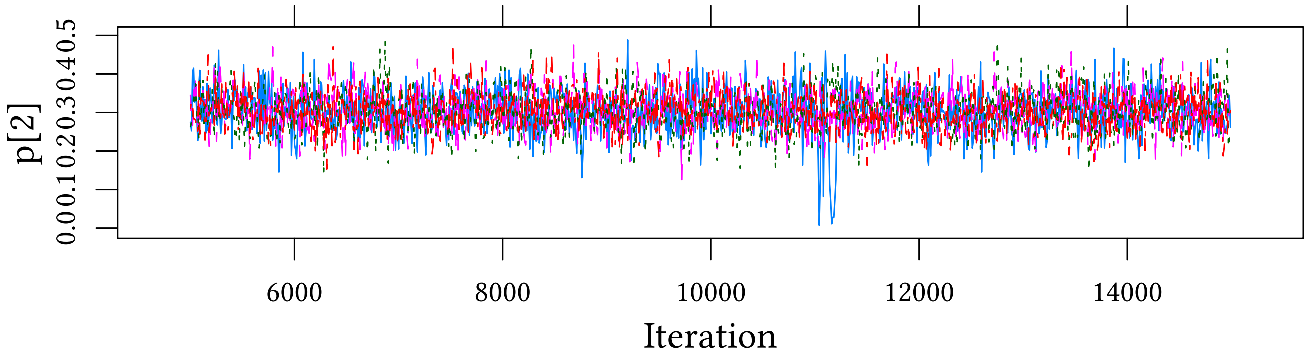
```
mixGen.model <- 'model {
   for (i in 1:length(y)) {
      y[i] ~ dnorm(mu[group[i]],tau)
      group[i] ~ dcat(p)
   }
   for (g in 1:G) {
     mu0[g] ~ dnorm(0,.0001)
     alpha[g] <- alphaD # concentration paramter
   }
   p[1:G] ~ ddirch(alpha)
   mu[1:G] <- sort(mu0)
   tau   ~ dgamma(m^2/d^2,m/d^2)
   m     ~ dgamma(1,1)
   d     ~ dgamma(1,1)
   sd   <- 1/sqrt(tau)
}'
```

```
mixGen.jags<-run.jags(mixGen.model,data=list(y=y,G=2,alphaD=1),
         inits=genInit(4,function(i) list(mu0=rnorm(2,0,100))),
         monitor=c("mu","p","sd"))
summary(mixGen.jags)

        Lower95   Median  Upper95      Mean         SD      Mode         MCerr
mu[1] 1.877140 1.968090 2.063090 1.9697448 0.04897114 1.9669813 0.0004923403
mu[2] 2.829740 2.979530 3.128850 3.0112581 1.42819031 2.9762628 0.0140909891
p[1]  0.587668 0.695937 0.800762 0.6949947 0.05529482 0.6959666 0.0004975720
p[2]  0.199238 0.304063 0.412332 0.3050053 0.05529482 0.3040298 0.0004975720
sd    0.257106 0.310959 0.384815 0.3157564 0.03597221 0.3062316 0.0004999398
      MC%ofSD SSeff       AC.10     psrf
mu[1]     1.0  9893 0.08963486 1.006286
mu[2]     1.0 10273 0.11200784 1.252197
p[1]      0.9 12350 0.04021071 1.002042
p[2]      0.9 12350 0.04021071 1.002042
sd        1.4  5177 0.15989207 1.013997
```

Convergence is not too exciting. Let us have a look at p:

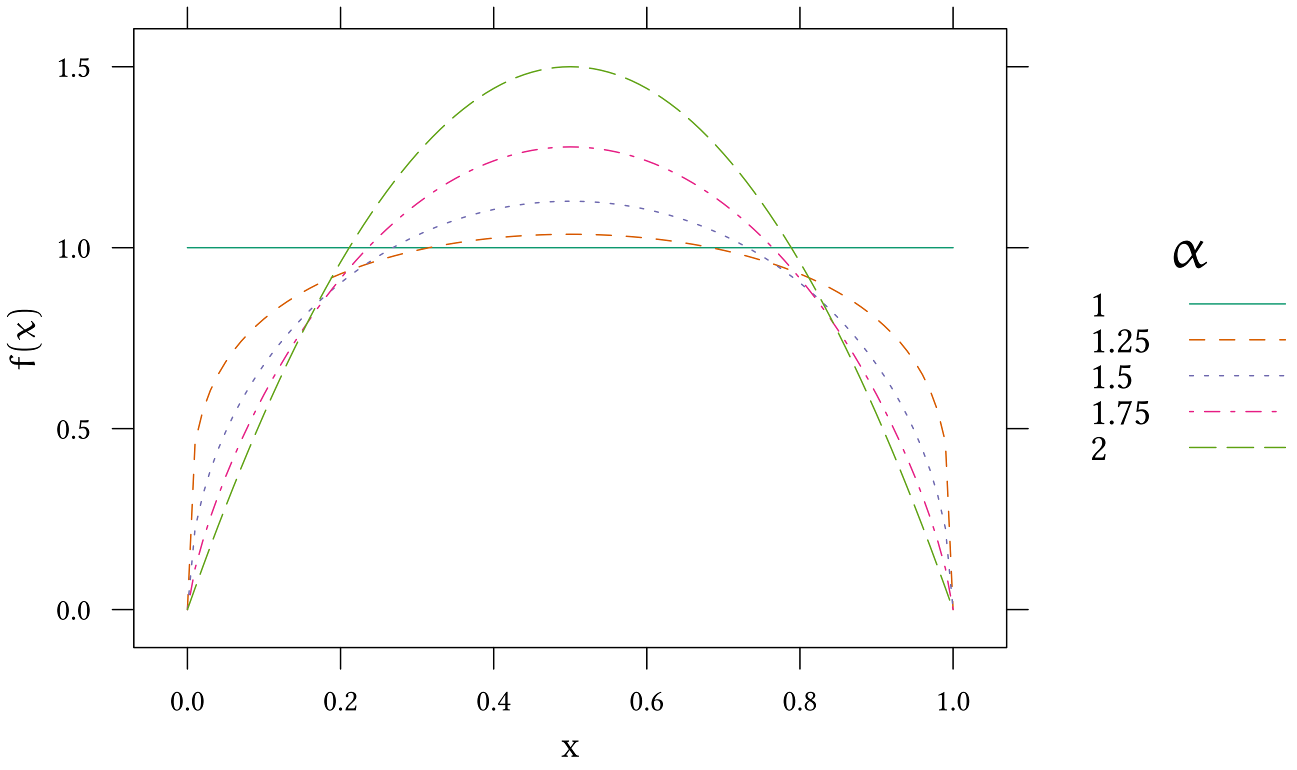
```
plot(mixGen.jags,plot.type="trace",var=c("p[2]","mu[2]"))
```





We see that sometimes p reaches extreme values. As a consequence, if, e.g. *p[2]*=0, there is no pressure on *mu[2]*, so *mu[2]* starts drifting. Increasing the concentration parameter for the Dirichlet distribution helps:

Here is the symmetric Dirichlet distribution for different values of α:



```
mixGen3.jags<-run.jags(mixGen.model,data=list(y=y,G=2,alphaD=1.2),
         inits=genInit(4,function(i) list(mu0=rnorm(2,0,100))),
         monitor=c("mu","p","sd"))
summary(mixGen3.jags)

       Lower95    Median  Upper95      Mean         SD      Mode        MCerr
mu[1] 1.877330 1.9679100 2.062510 1.9695937 0.04778520 1.9661304 0.0004995502
mu[2] 2.829810 2.9791450 3.130150 2.9784262 0.07777156 2.9811662 0.0008417142
p[1]  0.586327 0.6946925 0.799249 0.6932889 0.05462998 0.6982235 0.0004613692
p[2]  0.200751 0.3053075 0.413673 0.3067111 0.05462998 0.3017765 0.0004613692
sd    0.255730 0.3115115 0.384091 0.3160652 0.03533687 0.3057062 0.0005375619
      MC%ofSD SSeff      AC.10     psrf
mu[1]     1.0  9150 0.06431488 1.001063
mu[2]     1.1  8537 0.05781594 1.002620
p[1]      0.8 14021 0.01870416 1.000145
p[2]      0.8 14021 0.01870416 1.000145
sd        1.5  4321 0.16758452 1.002422
```

19.4 Ordering, not sorting

Above we made sure that the sampler used the sorted *mu*s. This is not necessary. An alternative way to make sure that the *mu[1]* we observe is always the smaller one is to only sort the variables we monitor. We have to make sure that we sort *p* and *mu* in the same way.

```
mixord.model <- 'model {
   for (i in 1:length(y)) {
      y[i] ~ dnorm(mu0[group[i]],tau)
      group[i] ~ dcat(p1)
   }
   for (g in 1:G) {
     mu0[g] ~ dnorm(0,.0001)
     alpha[g] <- alphaD # concentration parameter
   }
   p1[1:G] ~ ddirch(alpha)
   oo    <- order(mu0)
   for (g in 1:G) {
      mu[g] <- mu0[oo[g]]
      p[g]  <- p1[oo[g]]
   }
   tau   ~ dgamma(m^2/d^2,m/d^2)
   m     ~ dgamma(1,1)
   d     ~ dgamma(1,1)
   sd   <- 1/sqrt(tau)
}'
```

```
mixord.jags<-run.jags(mixord.model,data=list(y=y,G=2,alphaD=1.2),
         inits=genInit(4,function(i) list(mu0=rnorm(2,0,1))),
         monitor=c("mu","p","sd"))
summary(mixord.jags)

       Lower95    Median  Upper95      Mean         SD      Mode         MCerr
mu[1] 1.879690 1.9680000 2.066400 1.9701441 0.04910953 1.9670927 0.0005196924
mu[2] 2.829970 2.9789400 3.132580 2.9774925 0.08441752 2.9798676 0.0008158677
p[1]  0.581688 0.6946910 0.798163 0.6930490 0.05849335 0.6956936 0.0005359130
p[2]  0.201837 0.3053090 0.418312 0.3069510 0.05849335 0.3043064 0.0005359130
sd    0.256746 0.3113765 0.385527 0.3166895 0.03712381 0.3043649 0.0005840915
      MC%ofSD SSeff       AC.10     psrf
mu[1]     1.1  8930 0.05240630 1.003782
mu[2]     1.0 10706 0.09789146 1.026120
p[1]      0.9 11913 0.04975953 1.009397
p[2]      0.9 11913 0.04975954 1.009397
sd        1.6  4040 0.21573679 1.013792
```

19.5 Using *dnormmix*

We can also use a special “mixture” distribution: *dnormmix*.

```
mixmix.model <- 'model {
   for (i in 1:length(y)) {
      y[i] ~ dnormmix(mu0,tau0,p1)
   }
   for (g in 1:G) {
     mu0[g] ~ dnorm(0,.0001)
     alpha[g] <- alphaD
     tau0[g] <- tau
     mu[g] <- mu0[oo[g]]
     p[g]  <- p1[oo[g]]
   }
   p1[1:G] ~ ddirch(alpha)
   oo    <- order(mu0)
   tau  ~ dgamma(m^2/d^2,m/d^2)
   m     ~ dgamma(1,1)
   d     ~ dgamma(1,1)
   sd   <- 1/sqrt(tau)
}'
```

```
mixmix.jags<-run.jags(mixmix.model,data=list(y=y,G=2,alphaD=1),
         inits=genInit(4),
         monitor=c("mu","p","sd"),modules="mix",
         factories="mix::TemperedMix sampler off")
summary(mixmix.jags)

       Lower95   Median  Upper95       Mean         SD      Mode        MCerr
mu[1] 1.878860 1.968770 2.068290 1.9709513 0.04869615 1.9652007 0.0005009737
mu[2] 2.829440 2.980690 3.135510 2.9798318 0.08093398 2.9801064 0.0007983197
p[1]  0.582950 0.696652 0.797185 0.6947085 0.05714018 0.7015553 0.0008381321
p[2]  0.202815 0.303348 0.417050 0.3052915 0.05714018 0.2984410 0.0008381321
sd    0.256532 0.312209 0.388559 0.3172079 0.03657474 0.3060555 0.0005409398
      MC%ofSD SSeff      AC.10     psrf
mu[1]     1.0  9448 0.06863096 1.000358
mu[2]     1.0 10278 0.06463824 1.002544
p[1]      1.5  4648 0.11796077 1.002673
p[2]      1.5  4648 0.11796078 1.002673
sd        1.5  4572 0.17138468 1.001610
```

19.6 Exercises

Consider the following data:

```
N<-100
set.seed(123)
group <- rbinom(N,1,.3)
x <- rnorm(N)
y <- rnorm(N,mean=x*group-group,sd=.3)
```

group can not be observed. Estimate a mixture model where $Y = X'\beta_g + \epsilon$ and where β_g is a group specific coefficient.

20 Summary

- Probability: objective vs. subjective.

- Priors, how to get them?
- Results: F: depend on intention of the experimenter

  B: depend on prior.
- Flexible modelling: F. has only a limited number of models.

  F: precise models which are sometimes not such a good representation of the problem.

  B: approximate models which can be a more precise representation of the problem.
- Interpretation: p-values versus posteriors.

  B. predicts (posterior) probability of a hypothesis.

  F. writes carefully worded statements which are wrong 5% of the time (or any other probability) provided H_0 is true.
- Quality of decisions: p-values are only a heuristics for a decision rule.

  B.'s decisions are better in expectation.

21 Exercises

Exercise 21.1 *You assume that* $X \sim N(\mu, \tau)$.
Your prior is $\mu \sim N(10, 1)$, $\tau = 2$.
Your sample is $X = \{8, 9, 10\}$.
What is your posterior for μ *and* τ*?*

Exercise 21.2 (Female labour supply) *Have a look at the dataset* `Mroz` *in* `Ecdat`*. Estimate the following model*

$$\texttt{hoursw} = \beta_0 + \beta_1 \texttt{educw} + \beta_2 \texttt{income} + \epsilon_i$$

Compare two specifications:

- *First assume that* `hoursw` *is not censored. Use standard OLS and a Bayesian specification.*
- *Then assume that* `hoursw` *is censored at zero. Use a standard ML model and a Bayesian specification.*
- *Next make this a robust regression, taking into account the censoring.*

Exercise 21.3 (Young males) *Have a look at the dataset* `Males` *in* `Ecdat`.

1. *Estimate a mixed effects model that explains* `wage` *as a function of* `exper` *and* `school`*. Include a random effect on the intercept for the identity of the male. Use Maximum Likelihood and a Bayesian Model. Check convergence.*

2. *Use a robust model.*