

MCMC using JAGS

Applied Bayesian Statistics

Winter term 2018

MCMC using
JAGS

Susumu Shikano

Introduction

JAGS

Beta-Binomial

Core part: model set up

Obtaining information

Storing posterior

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GSDS

This session

- Using JAGS to set up MCMC
- ... with beta-binomial and bivariate regression models

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Just Another Gibbs Sampler

- The name is a bit confusing since it utilizes not only Gibbs sampling, but also MH, slice sampling etc.
- Free available under:
`http://mcmc-jags.sourceforge.net/`
- Or: simply google with “JAGS”
 - Download the latest version and install it.
 - currently
Download JAGS-4.3.0.exe (about 30 MB)
- You can use `rjags` to use JAGS from R.

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Why JAGS?

- Easy, intuitive and flexible in programming.
- Main Code = Likelihood + Prior
- One of the most popular tools (at least in Social Sciences).

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Why JAGS?

- Easy, intuitive and flexible in programming.
- Main Code = Likelihood + Prior
- One of the most popular tools (at least in Social Sciences).

Some drawbacks

- Slow if the posteriors are correlated.
- Alternative: `stan` via `rstan` using the hybrid Monte Carlo algorithm (or Hamilton MC).
- ... Installation a bit tricky (see the preparation document of this course).

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Markov-Chain-Monte-Carlo (MCMC) using JAGS

- Installation of JAGS
- Basic procedure
 - Specifying a model
 - Reading data
 - Giving initial values
 - Running MCMC
 - Describing the posterior
- Example 1: beta binomial model
- Example 2: bivariate regression model

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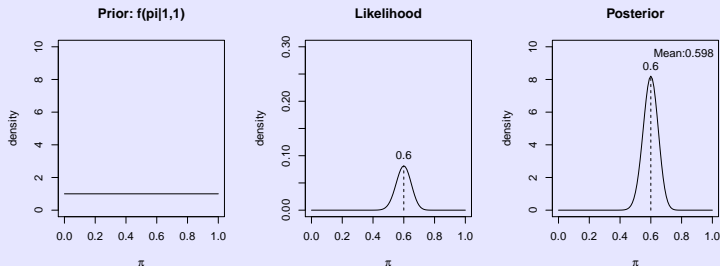
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Beta-Binomial Model

Hopefully you still remember...



- The more certain $p(\theta)$ is,

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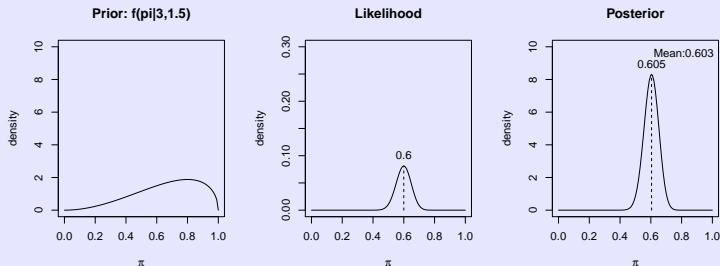
Core part: model set up

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Beta-Binomial Model

Hopefully you still remember...



- The more certain $p(\theta)$ is,

... the more the prior distribution influences the posterior.

→ A more different result from ML.

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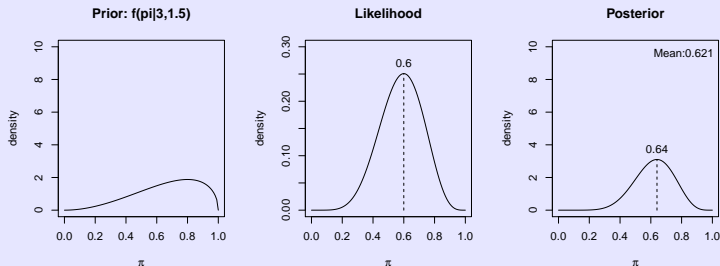
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Beta-Binomial Model

Hopefully you still remember...



- The more certain $p(\theta)$ is,
- The smaller n is,*

... the more the prior distribution influences the posterior.
→ A more different result from ML.

* Here, 6 out of 10 are correct judgement.

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JAGS-Code

```
library(rjags)

# JAGS Modell
beta.binom.model <- "model{
  y ~ dbin(p,N)  # Likelihood
  p ~ dbeta(1,1) # Prior
}"

write(beta.binom.model, "Bayes_Beta_Binom.bug")

# Data
jags.data <- list(y = 60,N=100)
```

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JAGS-Code

```
# Running JAGS
jags.binom <- jags.model(file="Bayes_Beta_Binom.bug",
                        data=jags.data, n.chains=3)

update(jags.binom, 1000)
parameters <- c("p")
jags.out <- coda.samples(jags.binom,
                        variable.name= parameters,
                        n.iter=1000, thin=1)
```

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JAGS-Code

```
# Simple description of posterior
summary(jags.out)
plot(jags.out)

# Which percentage of posterior  $p > 0.5$  ?
p <- unlist(jags.out)

table(p > 0.5)

hist(p)
plot(density(p))
```

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How to set up a model

An example: Regression model

$$(\mathbf{y}|\beta_0, \beta_1, \sigma^2, \mathbf{X}) \sim N(\beta_0 + \beta_1 \mathbf{X}, \sigma^2) \quad (1)$$

...is equivalent to...

$$\begin{aligned} y_i &\sim N(\mu_i, \sigma^2) \\ \mu_i &= \beta_0 + x_i \beta_1 \\ &\text{for all } i = 1, \dots, n \end{aligned}$$

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An example: Regression model

$$(y|\beta_0, \beta_1, \sigma^2, X) \sim N(\beta_0 + \beta_1 X, \sigma^2) \quad (1)$$

...is equivalent to...

$$\begin{aligned} y_i &\sim N(\mu_i, \sigma^2) \\ \mu_i &= \beta_0 + x_i \beta_1 \\ &\text{for all } i = 1, \dots, n \\ \beta_0 &\sim \text{prior distribution} \\ \beta_1 &\sim \text{prior distribution} \\ \sigma^2 &\sim \text{prior distribution} \end{aligned}$$

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How to set up a model

JAGS-Code

```
for (i in 1:N){  
  y[i] ~ dnorm(mu[i],tau)  
  mu[i] <- beta0 + beta1 * x[i]  
}  
  
beta0 ~ dnorm(0,0.0001)  
beta1 ~ dnorm(0,0.0001)  
tau ~ dgamma(0.001,0.001)  
sigma <- 1/sqrt(tau)
```

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2nd parameter of normal distribution

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How to set up a model

JAGS-Code

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2nd parameter of normal distribution

- Precision
- = Inverse of variance

Example data

Bayes_Student_Survey.RData

A reduced dataset of Student Survey during the Lecture in
Introduction to Political Methodology Winter term 2016/2017

poleff: Political Efficacy (Likert Score based on 7 items)

- A larger value → A higher level of efficacy

friend: Number of alteri in friendship network

poldisc: Number of alteri in political discussion network

lr.self: Ideological orientation (left right self-placement)

- 1: Left <- -> 11: Right

lr.self.2: Ideological orientation (left right self-placement, 2nd measurement with the same scale above)

univ.election: Vote intention at the next university election

- 1: Yes; 0: other (No and DK)

polint: interest at university politics

- 1: not interested at all <- -> 5 strongly interested

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Example data

Bayes_Student_Survey.RData

tuition: opinion on the general tuition fee for German universities

- 1: support; 2: reject; 3: indifferent

acceptable: acceptable level of the tuition fee (in Euro per Semester)

- (Only those who support the tuition fee or indifferent)

protest1 - protest6: willingness to participate a protest action against the general tuition fee

- 1: yes; 0: no

- 1 demonstration in Konstanz
- 2 demonstration in Stuttgart
- 3 giving signature at petitions
- 4 strike
- 5 occupation of university buildings
- 6 legal dispute at courts

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Step by Step

- 1 Specify and save your model
- 2 Read your data
- 3 Select/generate initial values for unknown parameters
- 4 Compile your model with data
- 5 Determine the parameter of interest
- 6 Run Gibbs Sampling
- 7 Observe posterior distribution to check the convergence
- 8 Repeat Step 6-7 if needed
- 9 Describe posterior and save the results

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Basic Procedure in rjags: Step by step

Specify your model

```
reg.model <- "model{
  for (i in 1:N){
    y[i] ~ dnorm(mu[i],tau)
    mu[i] <- beta0 + beta1 * x[i]
  }

  beta0 ~ dnorm(0,0.0001)
  beta1 ~ dnorm(0,0.0001)

  tau ~ dgamma(0.001,0.001)
  sigma <- 1/sqrt(tau)
}"

write(reg.model,
      "Bayes_Bivariate_Reg_Student_Survey.bug")
```

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Basic Procedure in rjags: Step by step

Prepare the Sampler

```
y <- dat$poleff
x <- log(dat$friend+1)
N <- length(y)
jags.data <- list(y=y,x=x,N=N)

jags.inits <- function(){list(sigma=runif(1,0,100))}

jags.reg <- jags.model(file=
  "Bayes_Bivariate_Reg_Student_Survey.bug")
  inits=jags.inits,
  data=jags.data, n.chains=3)
```

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Basic Procedure in rjags: Step by step

Run Gibbs Sampler

```
# setting the parameters
parameters <- c("beta0", "beta1", "sigma")

# running Gibbs sampler (for burn-in)
update(jags.reg, 2000)

# random draw from the posterior
jags.reg.out <- coda.samples(jags.reg,
                             variable.names=parameters,
                             n.iter=2000, thin=1)
```

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Basic Procedure in rjags: Step by step

Describe the result

```
# Summary Statistics
summary(jags.reg.out)

# plotting posterior
plot(jags.reg.out)

# Gelman-Rubin-Statistics
gelman.plot(jags.reg.out)

# Deviance Information Criterion
jags.reg.dic.out <- dic.samples(jags.reg,
                               variable.names=parameters,
                               n.iter=2000, thin=1)

jags.reg.dic.out
```

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Two possibilities in `rjags` to sample from the posterior

```
jags.post <- coda.samples(jags.mcmc,  
  variable.names=c("beta0", "beta1", "sigma"),  
  n.iter=5000, thin=1)
```

```
jags.post <- jags.samples(jags.mcmc,  
  variable.names=c("beta0", "beta1", "sigma"),  
  n.iter=5000, thin=1)
```

They are same in sampling, but differ in the output form.

- `coda.samples:mcmc.list-object`
- `jags.samples:marray-object`

Below, only `coda.sample` will be discussed.

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Structure of the output (`mcmc.list-object`)

- It is a list of individual chains.
- It is quite easy to get a summary statistics:
 - `summary(jags.post)`

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To extract a single chain

- e.g. 1st chain: `jags.post[[1]]`
- ... A matrix (row: iterations; column: parameters)

	beta0	beta1	sigma
[1,]	139.8247	-24.99645	15.70429
[2,]	142.4995	-26.94930	17.77505
[3,]	139.0966	-26.15395	18.35460
[4,]	138.6545	-24.32788	17.88755
[5,]	137.4641	-24.57537	15.34373
...			

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To obtain information of a specific parameter

- Obtained posterior by e.g. `jags.post[, "beta1"]` is a list:

```
[[1]]
Markov Chain Monte Carlo (MCMC) output:
Start = 4001
End = 5000
Thinning interval = 1
[1] -0.858293314  0.040098476 -0.698333929 -0.829177717
    ...

[[2]]
Markov Chain Monte Carlo (MCMC) output:
Start = 4001
End = 5000
Thinning interval = 1
[1] 0.432260841  0.149573781  0.238826681  0.014094765
    ...
```

- The list can be transformed into vector by using e.g. `unlist(jags.post[, "beta1"])`

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To obtain information of multiple parameters

- E.g. `beta0` and `beta1`
- `jags.post[,c("beta0", "beta1")]` can also work.
- The list can be transformed into a matrix:
 - by using e.g.
`as.matrix(jags.post[, "beta0", "beta1"])`.
 - Do not use here `unlist`. The matrix structure would be lost.

Sometimes working with `mcmc.list`-object is annoying

- A better way: transform the object into a matrix:
 - `post.mat <- as.matrix(jags.post)`
 - with parameters in columns
 - with iterations in rows
- Some advantages:
 - Different calculation is easier.
 - Easily extract parameters with similar names:
 - `posterior.mat[,grep("beta", colnames(post.mat))]`
 - Extract all variables with a name including `beta`
 - `grep` returns which elements of an object include a character pattern is included.

Some possibilities

- `save(jags.post, file=c:xxx.RData")`
 - By using `load(file=c:xxx.RData")` you can restore the same object.
 - Only for R
- `write.dta(xxx)` `write.csv(xxx)`.
 - In the formats readable in the other softwares.
 - You have to first convert the `mcmc.list`-object into a data frame.

Storing posterior

You have to care:

- Sometimes your posterior information requires a large disk space.
- You do not have to save all iterations.
 - The number of iterations and the MC-standard error is not in a linear relationship.
- You can thin the posterior information post-hoc.

```
post.mat <- as.matrix(jags.post)
thinned <- seq(1,nrow(post.mat),by=10)
post.mat.thinned <- post.mat[thinned,]
```

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Cleaning up trash

- `rjags` produces bug-files in your working directory.
- bug-files: files for the JAGS-model
- They can be cleaned up by the following commands.

```
all.files <- dir()
      # list up the name of all files in WD
bug.files <- all.files[grep(".bug", all.files)]
      # choose only the file names with ".bug"
file.remove(bug.files)
      # delete the specified files
```