

MAST30027 Assignment 4

Tianyi Mo

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

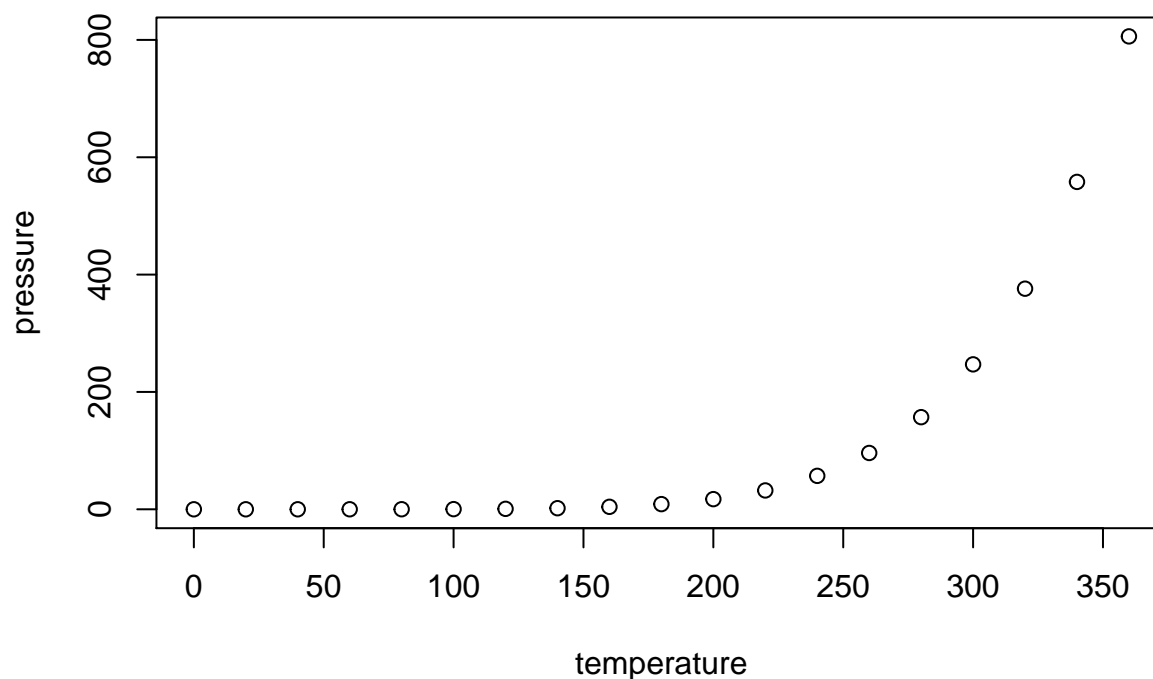
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed      dist
##  Min.   : 4.0    Min.   :  2.00
##  1st Qu.:12.0    1st Qu.: 26.00
##  Median :15.0    Median : 36.00
##  Mean   :15.4    Mean   : 42.98
##  3rd Qu.:19.0    3rd Qu.: 56.00
##  Max.   :25.0    Max.   :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

load data

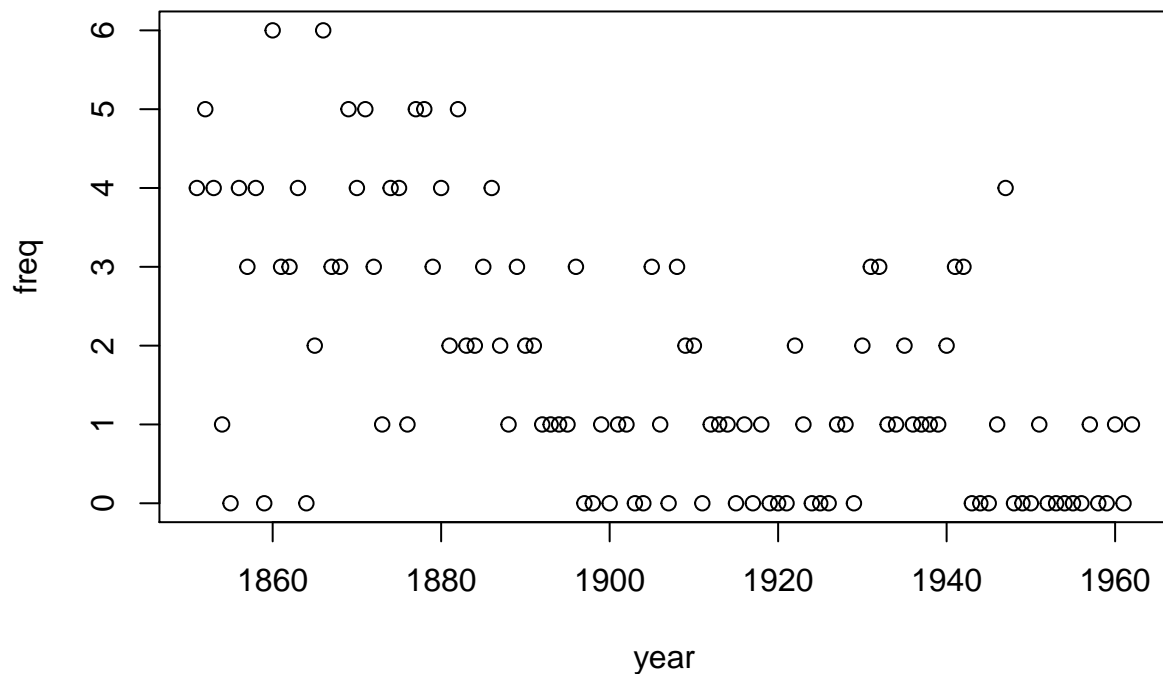
```
library(boot)
data(coal)
str(coal)

## 'data.frame': 191 obs. of 1 variable:
## $ date: num 1851 1852 1852 1852 1852 ...

when <- floor(coal)
year <- 1851:1962
freq <- sapply(year, function(x, y) sum(y==x), y=when)
str(freq)

## int [1:112] 4 5 4 1 0 4 3 4 0 6 ...

n <- length(freq)
plot(year, freq)
```



Implement Gibbs Sampler

```
GibbsS <- function(la1, la2, M, nreps, freq){

  # priors; uniform for M
  a1 <- .5
  b1 <- .001
  a2 <- .5
  b2 <- .001

  Gsamples <- matrix(nrow=nreps, ncol=3)
  Gsamples[1,] <- c(la1, la2, M)

  # main loop
  cfreq <- cumsum(freq)
  for (i in 2:nreps) {
    la1 <- rgamma(1, a1 + cfreq[M], b1 + M)
    la2 <- rgamma(1, a2 + cfreq[n] - cfreq[M], b2 + n - M)
    M <- sample(1:n, 1, prob=(la1/la2)^cfreq*exp((la2-la1)*(1:n)))
    Gsamples[i,] <- c(la1, la2, M)
  }

  return(Gsamples=Gsamples)
}
```

Simulate two Markov Chains (of length 500) using Gibbs Sampler

```
# sample size
nreps <- 500

# initial values
la1 <- 1
la2 <- 1
M <- 100

GibbsS1 = GibbsS(la1, la2, M, nreps, freq)

# initial values
la1 <- 3
la2 <- 3
M <- 50

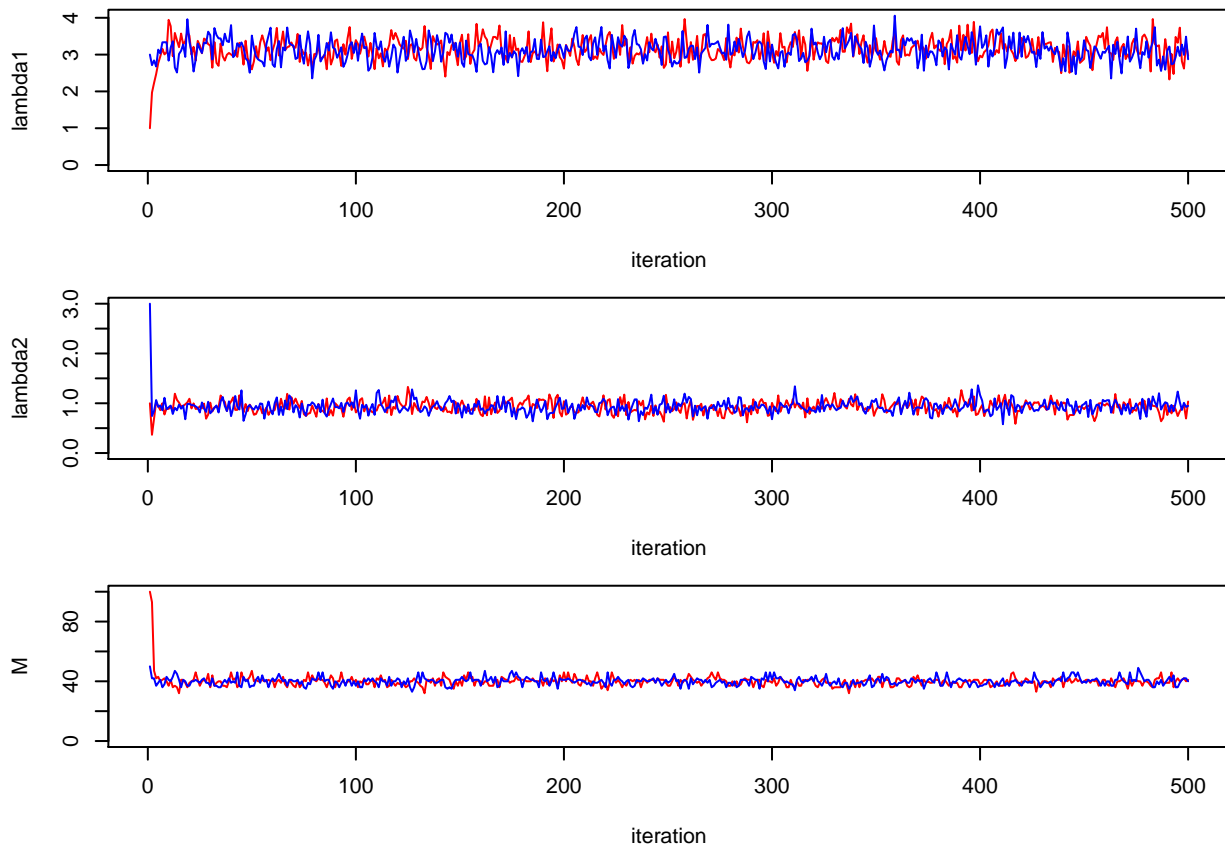
GibbsS2 = GibbsS(la1, la2, M, nreps, freq)
```

trace plot

```
par(mfrow=c(3,1), mar=c(4,4,1,1))
plot(1:nreps, GibbsS1[,1], type="l", col="red", ylim = c(0, max(GibbsS1[,1],GibbsS2[,1])), xlab = "iteration",
points(1:nreps, GibbsS2[,1], type="l", col="blue")

plot(1:nreps, GibbsS1[,2], type="l", col="red", ylim = c(0, max(GibbsS1[,2],GibbsS2[,2])), xlab = "iteration",
points(1:nreps, GibbsS2[,2], type="l", col="blue")
```

```
plot(1:nreps, GibbsS1[,3], type="l", col="red", ylim = c(0, max(GibbsS1[,3],GibbsS2[,3])), xlab = "iteration",
points(1:nreps, GibbsS2[,3], type="l", col="blue"))
```



Posterior distribution after discarding the first 50 samples as a burn-in.

```
par(mfrow=c(3,1), mar=c(4,4,1,1))
plot(density(GibbsS1[-(1:50),1]), ylab="posterior dist", xlab="lambda1", main="")
plot(density(GibbsS1[-(1:50),2]), ylab="posterior dist", xlab="lambda2", main="")
plot(table(GibbsS1[-(1:50),3])/nreps, ylab="posterior dist", xlab="M", main="")
```

