AR(1) of Hospitalization
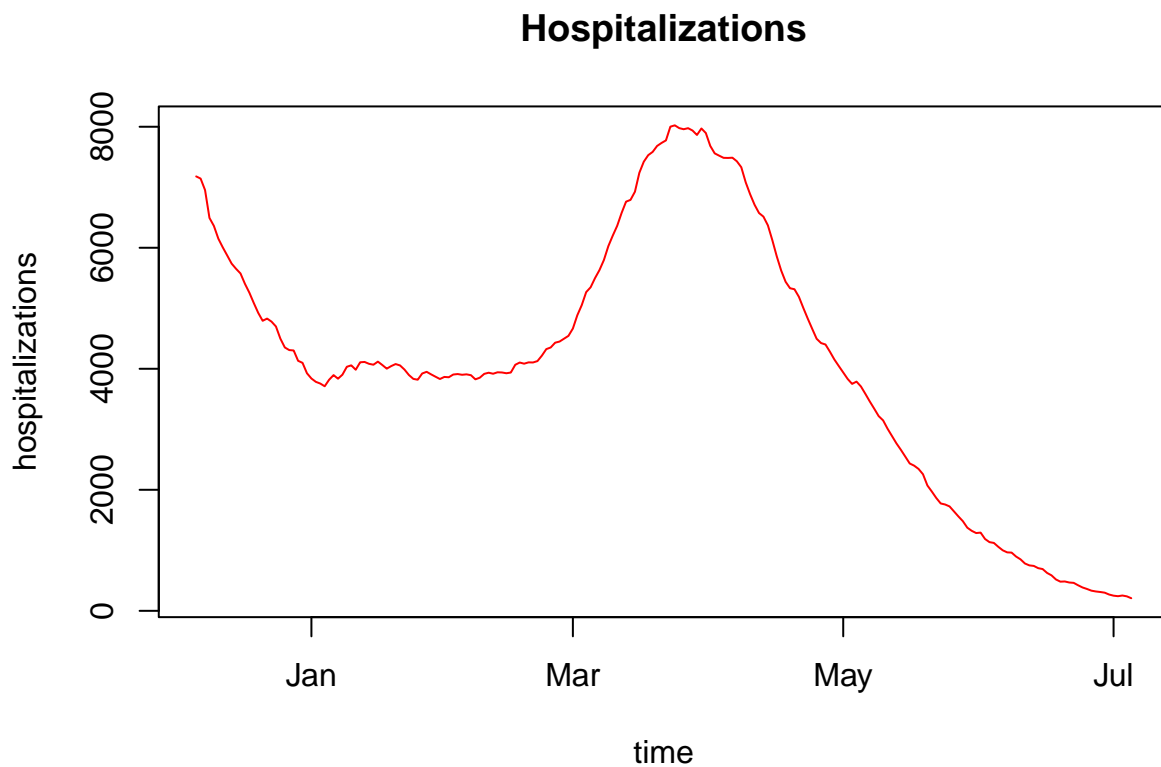
Load Data

```
rm(list=ls())
library(rjags)
```

```
## Loading required package: coda
```

```
## Linked to JAGS 4.3.1
```

```
## Loaded modules: basemod,bugs
```

```
setwd("~/Downloads/BLMS/BLMS")
dataset = readRDS("dataset.rds")
```

Data Plot

```
plot(dataset$date,
     dataset$total_hosp,
     type="l",
     ylab="hospitalizations",
     xlab="time",
     col='red',
     main="Hospitalizations")
```

Hospitalizations

Prior

$$\alpha \sim \mathcal{N}(0.5, 100)$$
$$\mu \sim \mathcal{N}(0, 1000)$$
$$\tau = \frac{1}{\sigma^2} \sim \mathcal{G}(0.001, 0.001)$$

Jags Model Formulation

```
modelAR.string <-"model {
  ## parameters: alpha,tau,m0
  #likeliohood
  mu[1] <- Y[1]
  for (i in 2:N) {
    Y[i] ~ dnorm(mu[i],tau)
    Yp[i] ~ dnorm(mu[i],tau) # prediction
    mu[i] <- m0 + alpha*Y[i-1]
  }
  sigma2<-1/tau
  #prior
  alpha ~ dnorm(0.5,100)
  tau ~ dgamma(1.0E-3, 1.0E-3)
  m0 ~ dnorm(0.0, 1.0E-4)
}"
```

## Run the chain

```
line_data =  list("Y" = dataset$total_hosp, "N"=length(dataset$total_hosp))

jagsAR = jags.model(textConnection(modelAR.string),
                    data=line_data,
                    n.chains = 1,
                    n.adapt = 300)
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 211
##    Unobserved stochastic nodes: 214
##    Total graph size: 846
##
## Initializing model
```

```
update(jagsAR,5000)

outputmcmcAR=coda.samples(jagsAR,
                    c('alpha',"sigma2","mu","Yp"),
                    n.iter=10000, progress.bar="none")
```
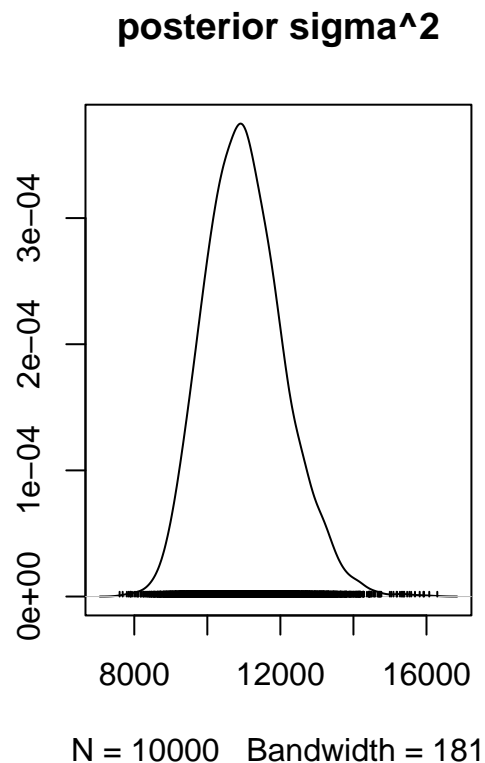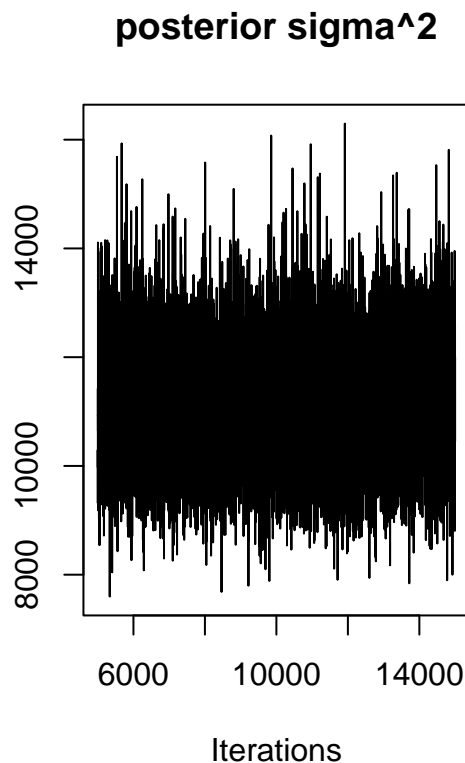
Trace Plots α

```
alpha.mcmc=outputmcmcAR[,c("alpha")]
plot(alpha.mcmc,main="posterior alpha")
```

posterior alpha   **posterior alpha**

Iterations   N = 10000   Bandwidth = 0.0005472
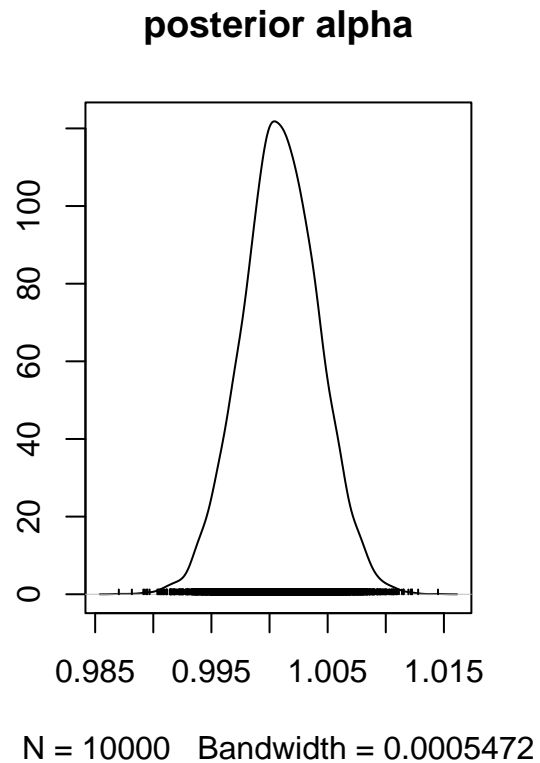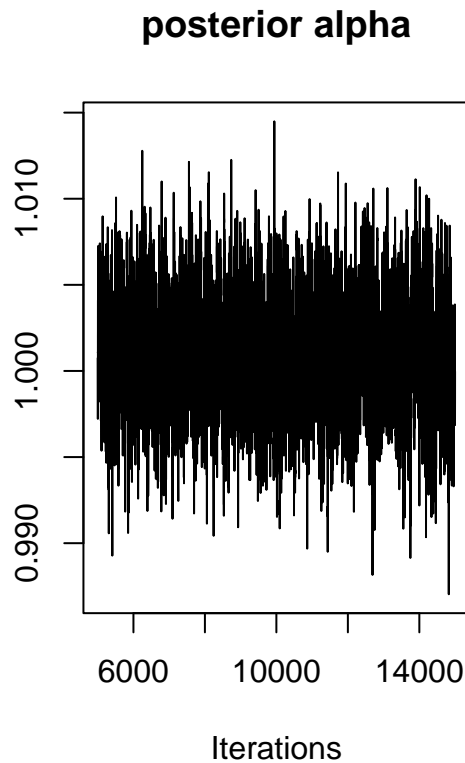
Trace Plots σ^2

```
sigma.mcmc=outputmcmcAR[,c("sigma2")]
plot(sigma.mcmc,main="posterior sigma^2")
```

posterior sigma^2   **posterior sigma^2**

Iterations   N = 10000   Bandwidth = 181

True Data and Sample Estimates With Corresponding Confidence Intervals

```r
suAR=summary(outputmcmcAR)
n = length(dataset$total_hosp)
t=seq(1,n)
yp=suAR$statistics[1:n-1]

q1=suAR$quantiles[,1][1:n-1]
q2=suAR$quantiles[,5][1:n-1]
muest=suAR$statistics[1:n]

plot(dataset$date,
     dataset$total_hosp,
     col="red",
     ylab="hospitalizations",
     main="Hospitalizations",
     xlab="time")
lines(dataset$date,q1[1:n])
lines(dataset$date,q2[1:n])
lines(dataset$date,muest,type="p",col="green")
```


Hospitalizations