

8.使用R和JAGS的 贝叶斯数据分析

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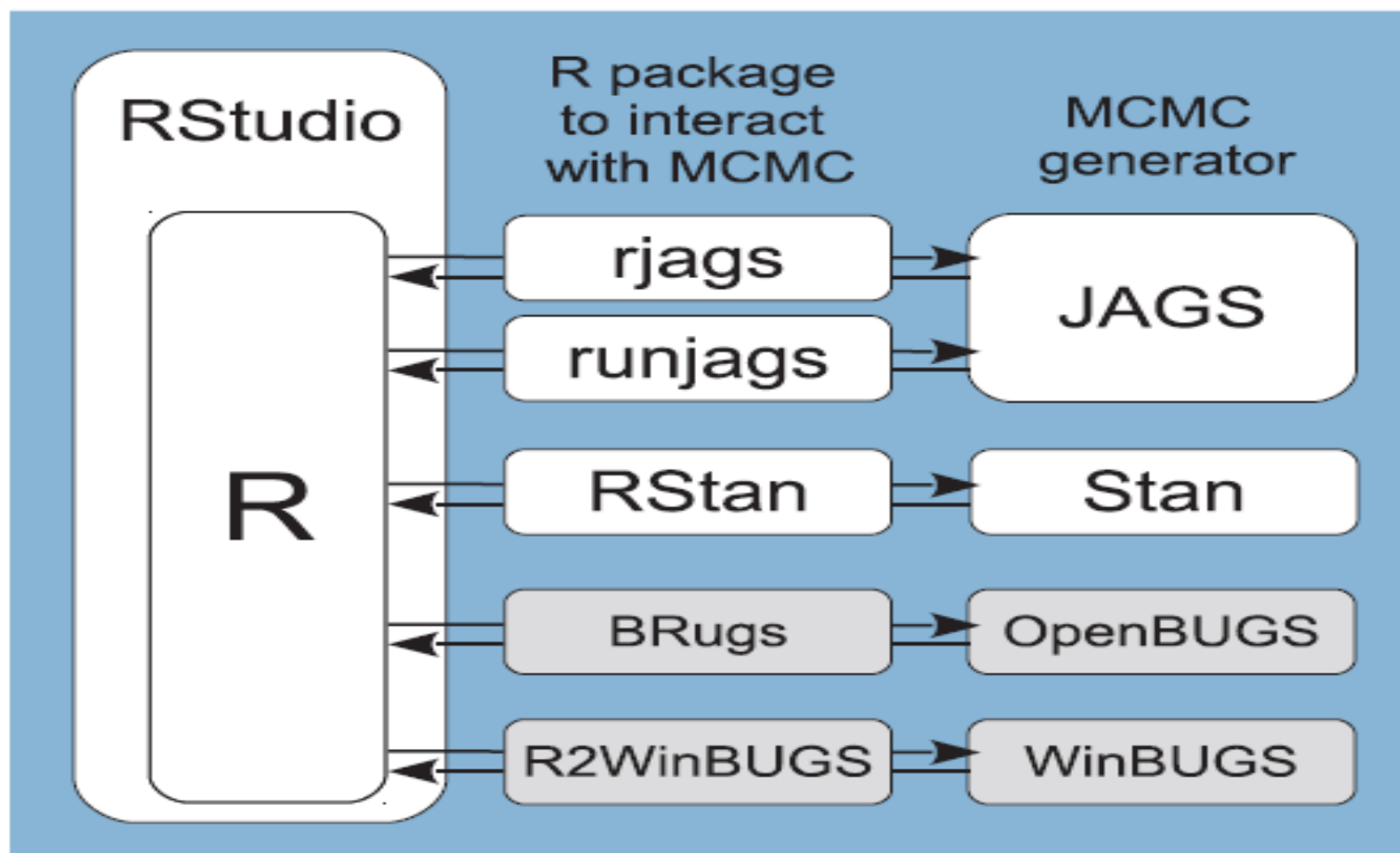


简介

- ❧ JAGS(Just Another Gibbs Sampler)是用于构建MCMC样本的系统
- ❧ 各种数据分析软件都有针对JAGS系统的界面，可以借助这些数据分析软件和相应界面，使用JAGS产生MCMC并做相应分析，例如基于R的rjags和runjags以及基于Matlab的matjags

简介

另外，R本身也有针对其他MCMC建构系统的界面

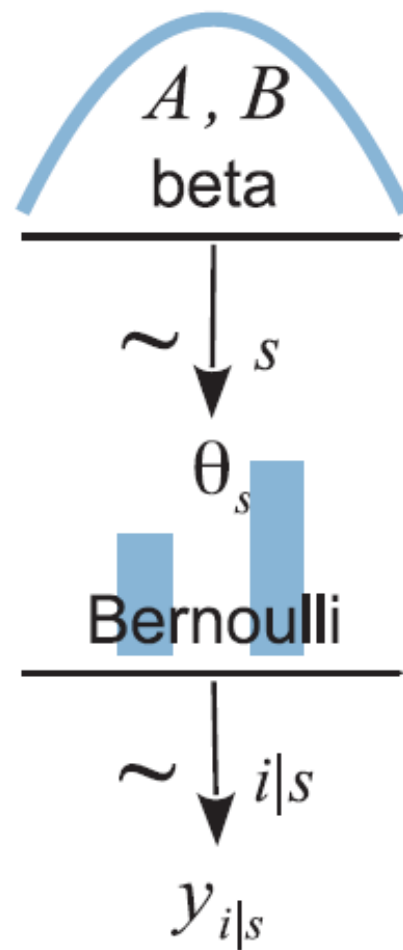
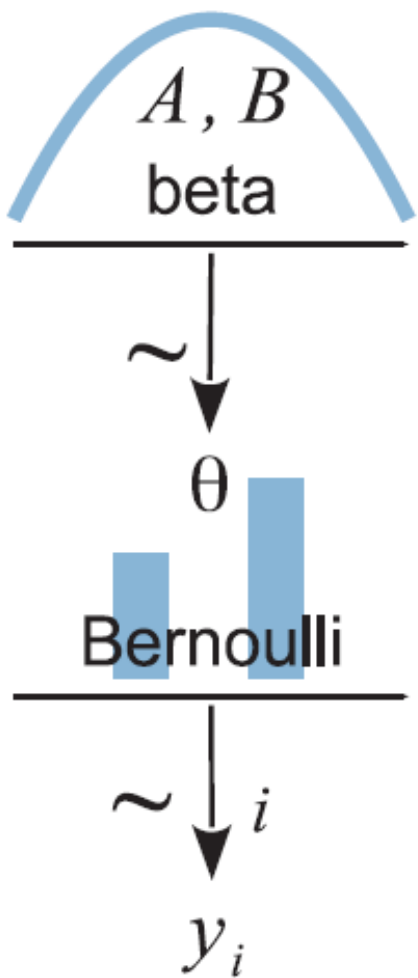


A decorative background image featuring a basket of white flowers, possibly tulips, with yellow centers. The basket is made of light-colored woven material and sits on a wooden surface. The flowers are in various stages of bloom, and some petals have fallen onto the surface. The overall tone is soft and natural.

使用JAGS的R代码

- ❧ 数据
- ❧ 模型
- ❧ MCMC初始值
- ❧ MCMC调试
- ❧ MCMC记录
- ❧ MCMC分析

模型示意图





数据代码

Load the data:

```
myData = read.csv("z15N50.csv") # Read data file; must be in curr. work. dir.
```

```
y = myData$y      # The y values are in the column named y.
```

```
Ntotal = length(y) # Compute the total number of flips.
```

```
dataList = list(  # Put the information into a list.
```

```
  y = y ,
```

```
  Ntotal = Ntotal
```

```
)
```

A decorative background image featuring a basket of white flowers, possibly tulips, with yellow centers, set against a light, airy background. The flowers are arranged in a basket, with some petals scattered around it.

模型代码

Define the model:

```
modelString = "
```

```
model {
```

```
  for ( i in 1:Ntotal ) {
```

```
    y[i] ~ dbern( theta )
```

```
  }
```

```
  theta ~ dbeta( 1 , 1 )
```

```
}
```

```
" # close quote for modelString
```

```
writeLines( modelString , con="TEMPmodel.txt" )
```



MCMC初始值代码

```
initsList = function() {  
  resampledY = sample( y , replace=TRUE )  
  thetaInit = sum(resampledY)/length(resampledY)  
  thetaInit = 0.001+0.998*thetaInit # keep away from 0,1  
  return( list( theta=thetaInit ) )  
}
```




MCMC调试代码

```
jagsModel = jags.model( file="TEMPmodel.txt" , data=dataList ,  
inits=initsList , n.chains=3 , n.adapt=500 )
```

```
update( jagsModel , n.iter=500 )
```



MCMC记录代码

```
codaSamples = coda.samples( jagsModel ,  
variable.names=c("theta"), n.iter=3334 )
```

```
save( codaSamples , file=pasteo(fileNameRoot,"Mcmc.Rdata") )
```



MCMC分析代码

```
source("DBDA2E-utilities.R")
```

```
# Convergence diagnostics:
```

```
diagMCMC( codaObject=codaSamples , parName="theta" )
```

```
saveGraph( file=pasteo(fileNameRoot,"ThetaDiag"), type="eps" )
```

```
# Posterior descriptives:
```

```
openGraph(height=3,width=4)
```

```
par( mar=c(3.5,0.5,2.5,0.5) , mgp=c(2.25,0.7,0) )
```

```
plotPost( codaSamples[, "theta"] , main="theta" , xlab=bquote(theta) )
```

```
saveGraph( file=pasteo(fileNameRoot,"ThetaPost"), type="eps" )
```



MCMC分析代码

Re-plot with different annotations:

```
plotPost( codaSamples[, "theta"], main="theta",  
xlab=bquote(theta),
```

```
  cenTend="median", compVal=0.5, ROPE=c(0.45,0.55),  
  credMass=0.90 )
```

```
saveGraph( file=pasteo(fileNameRoot,"ThetaPost2"), type="eps" )
```



常用分析的简易代码

- 🔗 Jags-Ydich-Xnom1subj-MbernBeta.r
- 🔗 Jags-Ydich-XnomSsubj-MbernBeta.r
- 🔗 Jags-BivariateNormalScript.r
- 🔗 Jags-Ymet-Xmet-Mrobust.r
- 🔗 Jags-Ybinom-Xnom1fac-Mlogistic.r
- 🔗