Using JAGS in R with the R2jags package

1. Download and Install JAGS

   a) Go to the following website http://sourceforge.net/projects/mcmc-jags/files/
   b) Download the JAGS from folder "***3.x***", and install it on your computer.
   c) Open R Studio, and install package "***R2jags***", which will allow you to run JAGS model from R.

   Note:
   The latest JAGS version is 4.0.0, however, it requires separate download of rjags from the above website (*R2jags* package in R currently available in R is not compatible with JAGS 4.0.0).

2. Run a JAGS model from R

   Running a JAGS model refers to generating samples from the posterior distribution of the model parameters, which include the following steps.
   ### a) *Define the model:*
       i. Write the model in a text format and save it as a txt file in your R working directory.
       ii. *Example*:

```
model{
  for (i in 1:n){
    y[i] ~ dnorm(beta.0, tau.sq)
  }

  beta.0 ~ dnorm(0, 0.0001)
  tau.sq <- 1/sigma.sq
  sigma.sq ~ dunif(0, 100)
}
```

       iii. ***Warning***: Distribution definition in JAGS is different than in R. R's *dnorm* takes a standard deviation for the dispersion parameter, whereas, JAGS takes the precision that is the inverse of the variance parameter.
       iv. Once you complete your JAGS model, the rest of the work happens in R.

b) ***Run the model in R***
  i.   Define the data elements that are referenced in JAGS model in R.
  ii.   Set the initial values for all of the parameters.
  iii.   Use ***jags*** function to specify data, initial values, parameter, model, number of chains, burn-in and thinning.

c) ***Convergence Diagnostics***
  i.   Traceplots on each parameter to look for convergence
  ii.   Geweke's Diagnostics
  iii.   Heidelberg and Welch Diagnostics
  iv.   Raferty-Lewis Diagnostics