```r
#read in the data:
library(Stat2Data); data(BlueJays)


#ALL SUBSETS METHOD:

#install the leaps package
install.packages("leaps", repos="http://cran.r-project.org")

#load the leaps package
library(leaps)

#Ask for the best model of each size
all <- regsubsets(Mass~BillDepth+BillWidth+      Head+BillLength+Skull+Sex,data=BlueJays)

#Summary of results:
summary(all)

summary(all)$adjr2
plot(all,scale="adjr2")

summary(all)$cp
plot(all,scale="Cp")

#To see the facts about each "best" model:
cbind(as.data.frame(summary(all)$which), summary(all)$rsq, summary(all)$adjr2,
summary(all)$cp)

#Ask for the best 2 models of each size
all2 <- regsubsets(Mass~BillDepth+BillWidth+ BillLength+Head+Skull+Sex,data=BlueJays,nbest=2)
summary(all2)

#To get Cp value for ANY particular model:
#1 Fit the full model
full <- lm(Mass~BillDepth+BillWidth+BillLength+Head+Skull+Sex, data=BlueJays)
#2 Find the MSE for the full model
MSE <- (summary(full)$sigma)^2
#3 get the Cp (equivalent to AIC) for the particular model of interest
extractAIC(lm(Mass~BillDepth+BillLength+Skull, data=BlueJays), scale=MSE)


#STEPWISE REGRESSION METHODS:

#Backwards elimination
#1 Fit the full model
full <- lm(Mass~BillDepth+BillWidth+BillLength+Head+Skull+Sex, data=BlueJays)
#2 Find the MSE for the full model
MSE <- (summary(full)$sigma)^2
#3 Use the step() command for backward elimination
step(full, scale=MSE, direction="backward")

#Forwards selection
#1 Start with a model with no predictors
none <- lm(Mass~1,data=BlueJays)
#2 Define the full model and the MSE for that full model (we already did this above)
#3 Use the step() command for forward selection
step(none,scope=list(upper=full),scale=MSE,direction="forward")

#Stepwise regression
#Exactly like forwards selection, just get rid of the "direction" command
step(none,scope=list(upper=full),scale=MSE)
```