**Creating a Decision Tree in R**

We have several equations in the model.

Recall that the model equations are costs<-c.treat+p.rec\*(1-p.rel)\*c.rec+p.rec\*p.rel\*c.rel+(1-p.rec)\*c.norec effects<-p.rec\*(1-p.rel)\*q.rec+p.rec\*p.rel\*q.rel+(1-p.rec)\*q.norec

Look at the values of the matrix parameters (e.g. p.rel, c.treat) going into this equation using the colMeans() function. This takes a mean of the columns matrices; for example, colMeans(p.rel) will give the mean probability of relapse on each of the three treatment options. Look at the mean of vectors (e.g. c.rec, c.rel) using the mean() function. A quick way to check if a data structure is a matrix or vector is to use dim(), the dimensions of a matrix, as this will be NULL for a vector.

1. a)  Can you tell which treatment has the highest average probability of recovery or lowest probability of relapse?
2. b)  Of cost of no recovery, relapse, and recovery, which has the highest mean?
3. c)  Of QALY associated with no recovery, relapse, and recovery, which has the highest

mean?

Now that you understand the inputs to the costs and effects, use the colMeans function to find the treatment with lowest costs and highest effects.