

Problem 1

Max.

:17.500

a) The data set contains 3 numerical variables; Mass, Period and Eccentricity of 101 observations. Following is the summery of the data set.

summary(planet) Mass Period Eccentricity :0.0000 Min. : 0.050 Min. : 2.985 Min. 1st Qu.: 0.930 44.280 1st Qu.: 1st Qu.:0.1000 Median : 337.110 Median : 1.760 Median : 0.2700 : 3.327 : 666.531 :0.2815 3rd Qu.: 4.140 3rd Qu.:1089.000 3rd Qu.: 0.4100

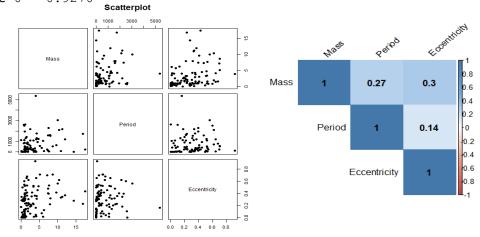
:5360.000

Max.

Three variables are ranged differently. Period has the largest range 2.985 - 5360.000 and Eccentricity has the smallest range 0 - 0.9270

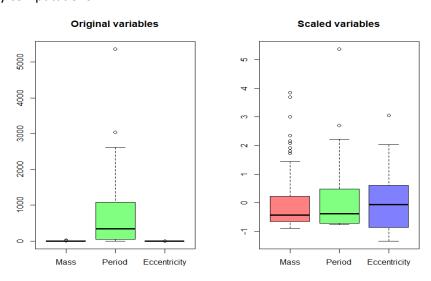
:0.9270

Max.



Scatter plots show the correlations between the 3 variables, but their values are small.

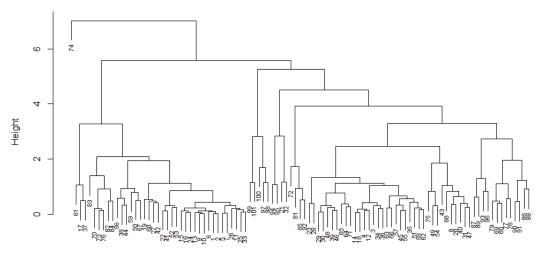
b) Since the range of the period variable is too large compared to the other variables, its good to standardize them before doing any computations.



c) Since the variables are related to dynamics of the exoplanet bodies and the correlations between the variables are low its best to use metric-based distance to cluster the exoplanets.

d) Data is clustered hierarchically using complete linkage and Euclidean distance. Following is the dendrogram of the result.

Complete Linkage

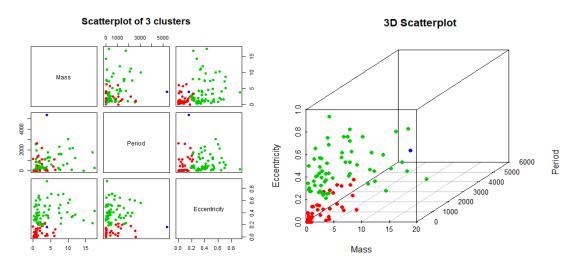


Dendrogram gives 3 clusters as follows.

[1]	1	1	2	2	1	1	1	2	1	1	1	2	1	2	1	1	1	2	1	2	2	1	2	1	1	1	1	2	2	2	2	2	1	2	2	2
[37]	1	1	2	2	1	1	2	1	2	2	2	2	2	1	2	1	1	2	2	1	2	2	1	1	1	2	2	2	2	2	1	2	2	1	2	2
r 7 2 1	-1	\sim	_	-1	_	_	_	_	_	-1	-1	-1	_	_	_	_	_	_	_	_	_	_	_	\circ	_	\circ	_	_	_							

Summary of the cluster-specific means:

	Group.1	Mass	Period	Eccentricity
1	1	1.703316	488.7479	0.07077105
2	2	4.311774	699.7941	0.41269355
3	3	4.000000	5360,0000	0.16000000



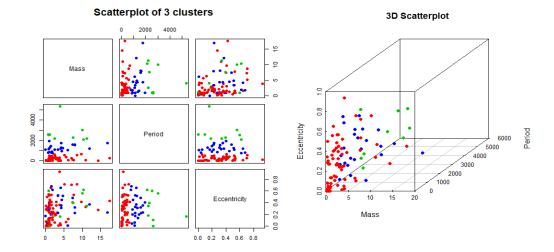
e) When the exoplanets are clustered with K-means, following results are found.

Cluster means:

	Mass	Period	Eccentricity
1	2.734500	187.5163	0.2606221
2	5.390000	2767.2444	0.3283333
3	4 233333	1235 9729	0 3232917

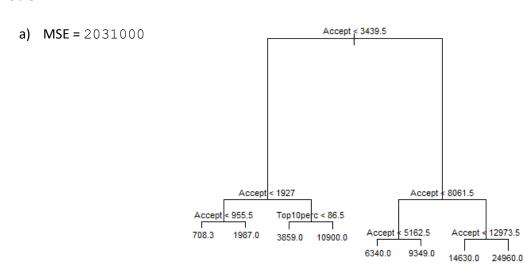
Clustering vector:

[1]	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	3	1	2	1	3	1	1	1	1	3	1	1	1	3	1	1	1	1
[37]	2	3	1	1	1	1	1	3	1	1	1	1	3	3	1	1	1	3	1	3	1	1	3	1	2	1	1	1	1	1	3	1	3	1	1	1
[73]	1	2	3	1	3	3	3	3	1	1	3	1	1	3	1	2	1	3	3	1	1	2	2	1	2	3	1	3	1							



Since the Hierarchical clustering was able to cluster only one exoplanet for the 3rd cluster, K-means clustering works better when you need 3 clusters out of the data set. Also the pairwise scatterplots of the K-means shows somewhat clear separation of these three clusters.

Problem 2



Region	Expression	Mean(Predicted Applications)
1	Accept < 955.5	708.3
2	955.5 < Accept < 1927	1987.0
3	1927 < Accept and Top10per < 86.5	3859.0
4	1927 < Accept and Top10per > 86.5	10900.0
5	3439.5 < Accept < 5162.5	6340.0
6	3439.5 < Accept < 8061.5	9349.0
7	8061.5 < Accept < 12973.5	14630.0
8	12973.5 < Accept	24960.0

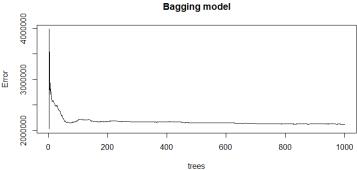
b) When pruning is done for the tree, with LOOCV, best pruning size is found to be 8. Thus pruning is not useful for this tree and the pruned tree is exactly the same as the full tree. So is the MSE.

MSE of the pruned tree = 2031000

Most important predictors are Accept and Top10per

c) Bagging approach has MSE = 2124209 and the top important predictor is Accept. Bellow are the top 5 important predictors.

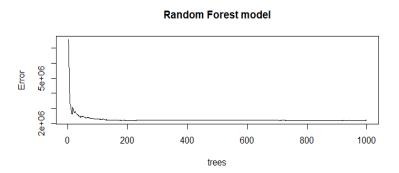
	X.IncMSE	IncNodePurity
Accept	22016845.6518	10598466352
Top10perc	349136.3838	286343989
Enroll	295881.2979	245209919
Top25perc	188104.5242	161109658
Expend	122938.0253	88231957



After 200 trees, there is not much change in terms of error.

d) Random forest approach has MSE = 2213661 and the top two important predictors are Accept and Enroll. Bellow are the top 5 important predictors.

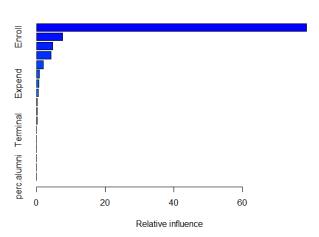
	X.IncMSE	IncNodePurity
Accept	9357061.39	4787760962
Enroll	3622110.84	2533886881
F.Undergrad	2260502.82	1745082241
P.Undergrad	178029.66	369345190
Top25perc	302858.86	320552183



Again after 200 trees, there is not much change in terms of error.

e) Boosting approach has MSE = 3724476 and the top important predictor is Accept. Bellow are the top 5 important predictors.

	var	rel.inf
Accept	Accept	78.79257671
Enroll	Enroll	7.55712464
F.Undergrad	F.Undergrad	4.68956879
Top10perc	Top10perc	4.22216126
Top25perc	Top25perc	2.01856968



f) Out of three methods, minimum MSE = 2124209 gives from Bagging method. Thus the best approach for this data set is Bagging method.

```
Section 2
# problem 1
planet <- read.csv("planet.csv", header = T)</pre>
attach (planet)
head(planet)
summary(planet)
                                 Eccentricity
      Mass
                    Period
# Min. : 0.050 Min. : 2.985 Min. :0.0000
# 1st Qu.: 0.930 1st Qu.: 44.280 1st Qu.:0.1000
# Median : 1.760 Median : 337.110 Median :0.2700
# Mean : 3.327 Mean : 666.531 Mean :0.2815
# 3rd Ou.: 4.140 3rd Ou.:1089.000 3rd Ou.:0.4100
# Max. :17.500 Max. :5360.000 Max. :0.9270
library(corrplot)
plot(planet, main="Scatterplot", pch=19)
col <- colorRampPalette(c("#BB4444", "#EE9988", "#FFFFFF", "#77AADD", "#4477AA"))
corrplot(cor(planet), method="color", col = col(200),
        type="upper",
        addCoef.col = "black", # Add coefficient of correlation
        tl.col="black", tl.srt=45, sig.level = 0.01, insig = "blank")
# part b)
# standardizing the data
planet.scaled <- scale(planet)</pre>
apply(planet.scaled, 2, mean)
apply(planet.scaled, 2, sd)
par(mfrow=c(1,2))
boxplot(planet, col = rainbow(3, s = 0.5), main="Original variables")
boxplot(planet.scaled, col = rainbow(3, s = 0.5), main="Scaled variables")
par(mfrow=c(1,1))
# part d)
# hierarchical cluster using complete linkage and Euclidean distance.
hc.complete <- hclust(dist(planet.scaled), method = "complete")</pre>
plot(hc.complete, main = "Complete Linkage", xlab = "", sub = "",
    cex = 0.7)
hc.clusters <- cutree(hc.complete, 3)</pre>
m{\#} [1] 1 1 2 2 1 1 1 2 1 1 1 2 1 2 1 2 1 1 1 2 2 2 2 2 2 1 2
a <- cbind(planet,hc.clusters)</pre>
aggregate(a[, 1:3], list(a$hc.clusters), mean)
# Group.1
             Mass Period Eccentricity
# 1
        1 1.703316 488.7479 0.07077105
# 2
       2 4.311774 699.7941 0.41269355
# 3
        3 4.000000 5360.0000 0.16000000
```

```
library(scatterplot3d)
scatterplot3d(Mass, Period, Eccentricity, color = (hc.clusters + 1), main="3D
Scatterplot", pch = 16)
plot(planet, main="Scatterplot of 3 clusters", col = (hc.clusters + 1), pch=19)
# part e)
set.seed(3)
km.out <- kmeans(planet, 3, nstart = 20)</pre>
\# K-means clustering with 3 clusters of sizes 68, 9, 24
# Cluster means:
     Mass Period Eccentricity
# 1 2.734500 187.5163 0.2606221
# 2 5.390000 2767.2444 0.3283333
# 3 4.233333 1235.9729 0.3232917
# Clustering vector:
 # Within cluster sum of squares by cluster:
  [1] 2526577 8224052 2492267
# (between SS / total SS = 82.7 %)
scatterplot3d(Mass, Period, Eccentricity, color = (km.out$cluster+ 1), main="3D
Scatterplot", pch = 16)
plot(planet, main="Scatterplot of 3 clusters", col = (km.out$cluster+ 1), pch=19)
# problem 2
library(ISLR)
train.data <- College
str(train.data)
attach(train.data)
# part a)
library(tree)
tree.College <- tree(Apps ~ ., train.data)</pre>
# node), split, n, deviance, yval
      * denotes terminal node
   1) root 777 1.162e+10 3002.0
#
     2) Accept < 3439.5 651 1.732e+09 1736.0
#
       4) Accept < 1927 532 3.251e+08 1182.0
        8) Accept < 955.5 335 3.457e+07 708.3 *
        9) Accept > 955.5 197 8.769e+07 1987.0 *
#
#
       5) Accept > 1927 119 5.130e+08 4213.0
       10) Top10perc < 86.5 113 1.883e+08 3859.0 *
       11) Top10perc > 86.5 6 4.255e+07 10900.0 *
     3) Accept > 3439.5 126 3.461e+09 9541.0
#
       6) Accept < 8061.5 101 6.351e+08 7770.0
       12) Accept < 5162.5 53 1.439e+08 6340.0 *
       13) Accept > 5162.5 48 2.632e+08 9349.0 *
```

```
7) Accept > 8061.5 25 1.229e+09 16700.0
        14) Accept < 12973.5 20 1.172e+08 14630.0 *
        15) Accept > 12973.5 5 6.849e+08 24960.0 *
summary(tree.College)
# Regression tree:
# tree(formula = Apps ~ ., data = train.data)
# Variables actually used in tree construction:
# [1] "Accept"
                "Top10perc"
# Number of terminal nodes: 8
# Residual mean deviance: 2031000 = 1.562e+09 / 769
# Distribution of residuals:
   Min. 1st Qu. Median Mean 3rd Qu.
# -8371.0 -429.3 -104.3 0.0 286.7 23140.0
plot(tree.College)
text(tree.College, pretty = 0, cex = 0.7)
# part b)
cv.College <- cv.tree(tree.College, FUN = prune.tree, K=777)
# $size
# [1] 8 7 6 5 4 3 2 1
# $dev
# [1] 2381430909 2667272688 3129789615 3196896546 3251213689
# [6] 4065549912 5778625446 12478016777
# $k
# [1]
           -Inf 202873515 228050501 282105525 426616632 893815939
# [7] 1596851915 6430760151
# $method
# [1] "deviance"
# attr(,"class")
# [1] "prune"
                     "tree.sequence"
plot(cv.College$size, cv.College$dev, type = "b")
# get the best size
cv.College$size[which.min(cv.College$dev)]
# [1] 8
prune.College <- prune.tree(tree.College, best = 8)</pre>
summary(prune.College)
# Regression tree:
# tree(formula = Apps ~ ., data = train.data)
# Variables actually used in tree construction:
# [1] "Accept"
                "Top10perc"
# Number of terminal nodes: 8
# Residual mean deviance: 2031000 = 1.562e+09 / 769
# Distribution of residuals:
   Min. 1st Qu. Median Mean 3rd Qu.
# -8371.0 -429.3 -104.3 0.0 286.7 23140.0
```

```
plot(prune.College)
text(prune.College, pretty = 0)
# part c)
library(randomForest)
set.seed(1)
bag.College <- randomForest(Apps ~ ., data = College, mtry = 17,</pre>
                            ntree = 1000, importance = TRUE)
# Call:
  randomForest(formula = Apps ~ ., data = College, mtry = 17, ntree = 1000,
importance = TRUE)
# Type of random forest: regression
# Number of trees: 1000
# No. of variables tried at each split: 17
# Mean of squared residuals: 2124209
# % Var explained: 85.8
bag.imp <- data.frame(bag.College$importance)</pre>
bag.imp[order(bag.imp$IncNodePurity, decreasing = T),]
#
                   X.IncMSE IncNodePurity
# Accept 22016845.6518 10598466352
# Top10perc
               349136.3838
                               286343989
# Enroll
              295881.2979
                               245209919
# Top25perc
              188104.5242
                              161109658
           122938.0253 88231957
# Expend
plot(bag.College, main = "Bagging model")
# part d)
set.seed(1)
forest.College <- randomForest(Apps ~ ., data = College, mtry = 6,</pre>
                            ntree = 1000, importance = TRUE)
# Call:
   randomForest(formula = Apps ~ ., data = College, mtry = 6, ntree = 1000,
importance = TRUE)
# Type of random forest: regression
# Number of trees: 1000
# No. of variables tried at each split: 6
# Mean of squared residuals: 2213661
# % Var explained: 85.2
forest.imp <- data.frame(forest.College$importance)</pre>
forest.imp[order(forest.imp$IncNodePurity, decreasing = T),]
              X.IncMSE IncNodePurity
# Accept
            9357061.39
                           4787760962
# Enroll
             3622110.84
                           2533886881
# F.Undergrad 2260502.82 1745082241
# P.Undergrad 178029.66
                           369345190
                           320552183
# Top25perc
             302858.86
plot(forest.College, main = "Random Forest model")
```

```
# part e)
library(gbm)
set.seed(1)
boost.College <- gbm(Apps ~ ., data = College, distribution = "gaussian",</pre>
                   n.trees = 1000, interaction.depth = 1, shrinkage = 0.01, cv.folds =
777)
# gbm(formula = Apps ~ ., distribution = "gaussian", data = College,
     n.trees = 1000, interaction.depth = 1, shrinkage = 0.01,
      cv.folds = 777)
# A gradient boosted model with gaussian loss function.
# 1000 iterations were performed.
# The best cross-validation iteration was 999.
# There were 17 predictors of which 14 had non-zero influence.
summary(boost.College)
# var rel.inf
# Accept
                   Accept 78.79257671
                  Enroll 7.55712464
# Enroll
# F.Undergrad F.Undergrad 4.68956879
# Top10perc Top10perc 4.22216126
# Top25perc Top25perc 2.01856968
# P.Undergrad P.Undergrad 0.88111834
mean(boost.College$cv.error)
# [1] 3724476
```