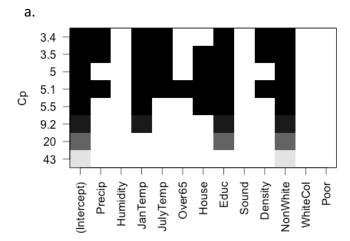
Name: Parth Pareek

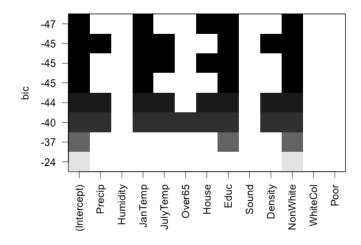
UNI: PP2547 Date: 4/6/2016 Assignment: HW8

1.



Smallest Cp = 3.443

Model variables: Precip, JanTemp, JulyTemp, Educ, Density, NonWhite



Smallest BIC = 453

Model variables: JanTemp, House, Educ, NonWhite

After adding pollution variables F = ((66518-52712)/3)/(52712/50) = 4.365 (p-value = .0083)

b. Stepwise regression leads to same model

F= ((74,651-63018)3)/(63018/52) = 3.2 (p-value = .03)

There is a difference in p-values however, the result doesn't change.

2. The data set is separated into Native and Non-Native. After taking log transformation, we use best subset methodology. It is noticed that the best subset has only 1 variable, *Area*.

```
lm(formula = Native ~ ., data = dat.native)
Residuals:
              10 Median
                               30
    Min
                                       Max
-2.11603 -0.29983 0.09883 0.36696 1.00491
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 3.06730 1.49763 2.048 0.05164
        Area
                    0.29019 -0.468 0.64423
0.10371 -0.566 0.57688
Flev
           -0.13572
DistNear -0.05866
DistSc -0.01637 0.11973 -0.137 0.89237
AreaNear -0.03634 0.04141 -0.878 0.38881
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.7022 on 24 degrees of freedom
Multiple R-squared: 0.7127, Adjusted R-squared: 0.6529
F-statistic: 11.91 on 5 and 24 DF, p-value: 7.223e-06
```

A model with all parameter also suggests that only Area is of significance (all other parameters have p-value > 0.005)

```
Subset selection object
Call: regsubsets.formula(Native ~ ., data = dat.native, method = "forward")
5 Variables (and intercept)
       Forced in Forced out
          FALSE
                     FALSE
Area
           FALSE
                     FALSE
Elev
DistNear
           FALSE
                     FALSE
           FALSE
                     FALSE
DistSc
AreaNear FALSE
                     FALSE
1 subsets of each size up to 5
Selection Algorithm: forward
       Area Elev DistNear DistSc AreaNear
1 (1) "*" " " "
2 (1)"*" """
                               "*"
3 (1) "*" " "*" ""
                              "*"
4 (1) "*" "*" "*"
                              "*"
5 (1) "*" "*" "*"
```

```
3.
a.
Call:
glm(formula = Failure ~ ., family = "binomial", data = dat)
Deviance Residuals:
    Min
         1Q Median
                               3Q
                                       Max
-1.2125 -0.8253 -0.4706 0.5907
                                    2.0512
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) 10.87535 5.70291 1.907 0.0565.
Temperature -0.17132
                       0.08344 -2.053
                                       0.0400 *
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 28.975 on 23 degrees of freedom
Residual deviance: 23.030 on 22 degrees of freedom
AIC: 27.03
Number of Fisher Scoring iterations: 4
b. One sided p-value = 0.04/2 = 0.02
c. Drop in deviance = 28.975 - 23.030 = 5.94
Analysis of Deviance Table
Model: binomial, link: logit
Response: Failure
Terms added sequentially (first to last)
           Df Deviance Resid. Df Resid. Dev
                                    28.975
NULL
                             23
                             22
                                    23.030
Temperature 1 5.9441
d. CI = -0.3348 to -0.0078
```

e. Logit = 5.5644; Probability = 0.9962

f. Can't say for sure since data available is not in range of explanatory variable is not in range of the dataset used for regression.

```
4.
k = 1, p-value = 0.00048
k = 2, p-value = 0.01163
k = 3, p-value = 0.00003
k = 4, p-value = 0.00462
k = 5, p-value = 0.00014
k = 6, p-value = 0.00026
k = 7, p-value = 0.24819
b.
Call:
glm(formula = Site ~ ., family = "binomial", data = dat)
Deviance Residuals:
     Min
               10
                     Median
                                           Max
-2.39021 -0.74745 -0.01854 0.72308
                                      1.90308
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) 9.80304
                     3.38934
                               2.892 0.00382 **
PctRing1
           -0.05708
                       0.03713 -1.537 0.12422
PctRing2
            0.11730
                       0.04990
                                2.351
                                       0.01873
PctRing3
            -0.12181
                       0.05199
                               -2.343
                                       0.01913 *
PctRing4
            0.01694
                       0.04277
                                0.396 0.69201
PctRing5
           -0.03296
                       0.03905 -0.844 0.39875
                       0.06631 -1.642 0.10051
PctRing6
           -0.10891
PctRing7
           0.05157
                       0.03619 1.425 0.15415
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 83.178 on 59 degrees of freedom
Residual deviance: 52.107 on 52 degrees of freedom
AIC: 68.107
Number of Fisher Scoring iterations: 6
```

Simple logistic regression suggests that Ring 2 and 3 are critical covariates for regression. However, 1 cannot be ignored.

Taking hint into account, ring percentages is converted to circle percentages by cumulative addition of rings.

Adding a ring at a time, we can conclude that ring 1,2,3 and 5 (between 1.6 and 1.78 km) are the most relevant.

```
#Question 1
library(Sleuth3)
library(leaps)
attach(ex1217)
dat <- ex1217
dat1 <- dat[,-(15:17)]
subset1 <- regsubsets(Mortality~.,dat1[,-1])</pre>
plot(subset1,scale = "Cp")
plot(subset1,scale = "bic")
min(leaps(x=dat1[,-(1:2)],y=dat1[,2])$Cp)
model11 <- lm(Mortality~Precip + JanTemp + JulyTemp + Educ + Density +
                 NonWhite, data = dat)
model12 <- lm(Mortality~Precip + JanTemp + JulyTemp + Educ + Density +
                 NonWhite + HC + NOX + SO2, data = dat)
anova(model11, model12)
subset2 <- regsubsets(Mortality~.,dat1[,-1])</pre>
bestmodel <- which.max(summary(subset2)$adjr2)</pre>
plot(subset2,scale = "Cp")
plot(subset2,scale = "bic")
summary(subset2)
model21 <- lm(Mortality~JanTemp + House + Educ + NonWhite, data = dat)</pre>
model22 <- lm(Mortality~JanTemp + House + Educ + NonWhite
               + HC + NOX + SO2, data = dat)
anova(model21, model22)
#Question 2
library(Sleuth3)
attach(ex1220)
dat <- ex1220
dat$DistSc <- dat$DistSc + 2</pre>
dat.native <- dat[,-(1:2)]
dat.native <- log(dat.native)</pre>
dat.nonnat <- cbind("NonNative" = (dat[,2] - dat[,3]), dat[,-(1:3)])
dat.nonnat <- log(dat.nonnat)</pre>
subset.native <- regsubsets(Native~., data = dat.native, method =
"forward")
best.sub.native <- which.max(summary(subset.native)$adjr2)</pre>
model1 <- lm(Native~.,data = dat.native)</pre>
summary(model1)
model2 <- lm(NonNative~.,data = dat.nonnat)</pre>
summary(model2)
```

```
#Question 3
library(MASS)
library(Sleuth3)
attach(ex2011)
dat <- ex2011
model1 <- glm(Failure~., data = dat, family = "binomial")</pre>
summary(model1) #z-value is -2.054; 2 sided p-value is 0.4
                 #therefore, one-sided would approximately be 0.2
model2 <- glm(Failure~.-1, data = dat, family = "binomial")</pre>
anova(model2,model1)
predict(model1, list(Temperature = 31))
(\exp(5.564414)-1)/\exp(5.564414)
#Question 4
library(MASS)
library(leaps)
library(Sleuth3)
attach(ex2015)
dat <- ex2015
rr1 <- dat$PctRing1[which(dat$Site == "Random")]
rr2 <- dat$PctRing2[which(dat$Site == "Random")]</pre>
rr3 <- dat$PctRing3[which(dat$Site == "Random")]
rr4 <- dat$PctRing4[which(dat$Site == "Random")]</pre>
rr5 <- dat$PctRing5[which(dat$Site == "Random")]</pre>
rr6 <- dat$PctRing6[which(dat$Site == "Random")]</pre>
rr7 <- dat$PctRing7[which(dat$Site == "Random")]</pre>
rn1 <- dat$PctRing1[which(dat$Site == "Nest")]</pre>
rn2 <- dat$PctRing2[which(dat$Site == "Nest")]</pre>
rn3 <- dat$PctRing3[which(dat$Site == "Nest")]</pre>
rn4 <- dat$PctRing4[which(dat$Site == "Nest")]</pre>
rn5 <- dat$PctRing5[which(dat$Site == "Nest")]</pre>
rn6 <- dat$PctRing6[which(dat$Site == "Nest")]</pre>
rn7 <- dat$PctRing7[which(dat$Site == "Nest")]</pre>
t.test(rr1,rn1, alternative = "less")$p.value
t.test(rr2,rn2, alternative = "less")$p.value
t.test(rr3,rn3, alternative = "less")$p.value
t.test(rr4,rn4, alternative = "less")$p.value
t.test(rr5,rn5, alternative = "less")$p.value
t.test(rr6,rn6, alternative = "less")$p.value
t.test(rr7,rn7, alternative = "less")$p.value
model <- glm(Site~., data = dat, family = "binomial")</pre>
model1 <- glm(Site~PctRing1, data = dat, family = "binomial")</pre>
R1 <- PctRing1
R2 <- R1+PctRing2
```

```
R3 <- R2+PctRing3
R4 <- R3+PctRing4
R5 <- R4+PctRing5
R6 <- R5+PctRing6
R7 <- R6+PctRing7

sub <- regsubsets(dat$Site~R1+R2+R3+R4+R5+R6+R7, data = dat)
summary(sub)

#Question 6
library(MASS)
library(leaps)
X <- c(-2,-1,1,2)
Y <- c(0,0,1,1)
dat <- data.frame(X,Y)
model <- glm(Y~X-1,data = dat, family = binomial)
summary(model)</pre>
```