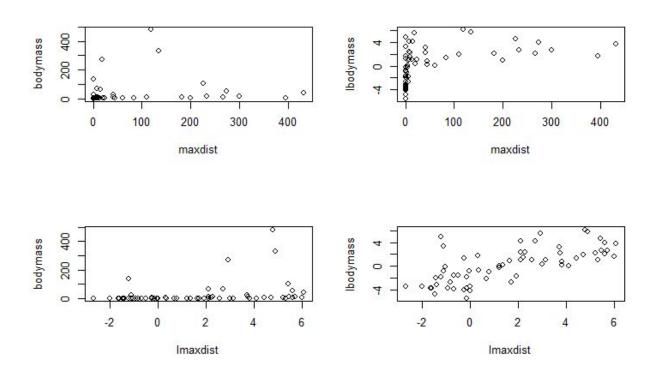
```
Assignment 4
Part 3
dir = "..."
file1 = "ex1124.csv"
dfEx1124 = read.table(file=paste(dir,file1, sep=""), header=TRUE, sep=',')
type = dfEx1124[,"type"]
bodymass = dfEx1124[,"bodymass"]
maxdist = dfEx1124[,"maxdist"]
# Create indicator variables for diet type.
omni = herbi = carni = rep(0,64) # make 3 variables of length 64
# all values equal to 0
omni[type=="O"] = 1 # if type ==O, then omni <- 1; else omni <- 0;
herbi[type=="H"] = 1
carni[type=="C"] = 1
lbodymass = log(bodymass)
lmaxdist = log(maxdist)
# Attach new variables to data frame
dfEx1124 = data.frame(dfEx1124,omni,herbi,carni,lbodymass,lmaxdist)
#attach(dfEx1124,pos=1)
```

3a)
par(mfrow=c(2,2))
plot(maxdist,bodymass)
plot(maxdist,lbodymass)
plot(lmaxdist,bodymass)
plot(lmaxdist,lbodymass)



The relationship between Ibodymass and Imaxdist appears to be linear and certainly the most linear of the four relationships.

```
3b)
M1 = Im(Imaxdist~Ibodymass*type, data=dfEx1124)
summary(M1)
```

OUTPUT

Call:

lm(formula = lmaxdist ~ lbodymass * type, data = dfEx1124)

Residuals:

Min 1Q Median 3Q Max -3.9221 -0.6731 0.0952 0.7020 4.2592

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)		
(Intercept)	3.01854	0.35649	8.467	1.01e-11	***	
1bodymass	0.70771	0.14168	4.995	5.72e-06	***	
typeH	-2.41569	0.42694	-5.658	4.95e-07	***	
type0	-1.13373	0.65608	-1.728	0.0893		
<pre>lbodymass:typeH</pre>	-0.27648	0.16140	-1.713	0.0921		
1bodymass:type0	-0.09824	0.21802	-0.451	0.6540		
Signif. codes:	0 '***' (0.001 '**' (0.01 '*'	0.05 '.'	0.1 '	' 1

Residual standard error: 1.425 on 58 degrees of freedom Multiple R-squared: 0.7049, Adjusted R-squared: 0.6794 F-statistic: 27.7 on 5 and 58 DF, p-value: 3.232e-14

```
3c)
M2 = Im(Imaxdist~Ibodymass+type, data=dfEx1124)
summary(M2)
anova(M2)
OUTPUT
Call:
lm(formula = lmaxdist ~ lbodymass + type, data = dfEx1124)
Residuals:
    Min
            1Q Median 3Q
                                  Max
-4.3571 -0.6168 -0.0674 0.9038 4.1355
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
                       0.3439 9.258 3.64e-13 ***
(Intercept)
             3.1839
                       0.0635 8.049 4.04e-11 ***
lbodymass
             0.5112
            -2.5381
typeH
                       0.4216 -6.020 1.14e-07 ***
type0
                       0.6133 -1.903 0.0618 .
            -1.1672
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 1.441 on 60 degrees of freedom
Multiple R-squared: 0.6878, Adjusted R-squared: 0.6722
F-statistic: 44.07 on 3 and 60 DF, p-value: 3.546e-15
> anova(M2)
Analysis of Variance Table
Response: lmaxdist
         Df Sum Sq Mean Sq F value Pr(>F)
Tbodymass 1 198.024 198.024 95.323 5.250e-14 ***
          2 76.622 38.311 18.442 5.715e-07 ***
Residuals 60 124.643 2.077
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' '1
```

```
3d)
anova(M2,M1)
Fcritical = qf(0.95, df1=2, df2=58) = 3.1559

Table
> anova(M2,M1)
Analysis of Variance Table

Model 1: lmaxdist ~ lbodymass + type
Model 2: lmaxdist ~ lbodymass * type
Res.Df RSS Df Sum of Sq F Pr(>F)
1 60 124.64
2 58 117.85 2 6.7972 1.6727 0.1967
```

5 Step Hypothesis test:

- 1. H0: The Parallel Lines model is sufficient to describe the data H1: The Three-Lines model is necessary to describe the data
- 2. Significance level, a = 0.05
- 3. From Table 1 we can see that our Fobs value for the Three-Lines model is 1.6727
- 4. We will reject the null hypothesis if Fobs > Fcritical. We can see that 1.6727 < 3.1559 so we do not have evidence to reject the null.
- 5. There is not enough evidence to reject the null hypothesis and so we can see that the parallel lines model is sufficient to describe the data.

```
3e)
M3=Im(Imaxdist~lbodymass, data=dfEx1124)
summary(M3)
anova(M3)
Call:
lm(formula = lmaxdist ~ lbodymass, data = dfEx1124)
Residuals:
    Min
            10 Median
                            3Q
                                   Max
-5.6635 -1.0135 -0.1455 1.3091 3.4661
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
                       0.22531 6.762 5.55e-09 ***
(Intercept) 1.52351
                       0.07663 7.810 8.44e-11 ***
           0.59854
lbodymass
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 1.802 on 62 degrees of freedom
Multiple R-squared: 0.4959, Adjusted R-squared: 0.4878
F-statistic:
              61 on 1 and 62 DF, p-value: 8.444e-11
> anova(M3)
Analysis of Variance Table
Response: lmaxdist
         Df Sum Sq Mean Sq F value Pr(>F)
lbodymass 1 198.02 198.024 61.002 8.444e-11 ***
Residuals 62 201.26
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
3f)
anova(M3,M2)
Feritical = qf(0.95, df1=2, df2=60) = 3.1504
Table 2:
> anova(M3,M2)
Analysis of Variance Table
Model 1: lmaxdist ~ lbodymass
Model 2: lmaxdist ~ lbodymass + type
  Res.Df
            RSS Df Sum of Sq
                                        Pr(>F)
                                F
      62 201.26
      60 124.64 2
                       76.622 18.442 5.715e-07 ***
2
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

5 Step Hypothesis test:

- H0: The SLR is sufficient to describe the data
 H1: The Parallel Lines model is necessary
- 2. Significance level, a = 0.05
- 3. From Table 2 we can see that our F value for Parallel Lines model is 18.442.
- 4. We will reject the null hypothesis if Fobs > Fcritical. We can see that 18.442 > 3.1504 so we have evidence to reject the null.
- 5. There is evidence to reject the null hypothesis and so we can see that the SLR Model is not sufficient to describe the data.

3g)

B1 = 0.5112, the coefficient on Ibodymass, is the expected change of Imaxdistance if we increase Ibodymass by 1 unit while holding the type variable constant.

B2 = -2.5381, the coefficient on typeH, is the expected difference of Imaxdistance between typeH and typeO if we hold lbodymass constant.

B3 = -1.1672, the coefficient on typeO is the expected difference in Imaxdistance between typeO and typeH if we hold lbodymass constant.