S&DS 563 / F&ES 758b - Multivariate Statistics Homework #5
MANOVA and Multivariate GLM

Lanxin Jiang (lj345), Grace Sun (ys544), Chenglin Lu (cl939)

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The dataset obtained from the UCI Machine Learning Repository describes the chronic kidney disease status and blood measurement of patients from Apollo Hospitals in India. There are 400 observations in this dataset. For this homework, we will use two categorical factors: specific gravity(sg) of urine, and red blood cells(rbc); and two continuous: blood glucose random(bgr) and serum creatinine(sc). In problem 4, we will add another continuous variable: hemoglobin (hemo). All observations with missing values will be excluded, so there will be 203 patients for the analysis.

1. For two categorical factors, make interaction plots for each of your response variables. Discuss what you see. If you only have one categorical factor, then provide some plot/discussion of which means are different for which response variables

```
library(ggplot2)
multiplot <- function(..., plotlist=NULL, file, cols=1, layout=NULL) {
  library(grid)

  # Make a list from the ... arguments and plotlist
  plots <- c(list(...), plotlist)

  numPlots = length(plots)

  # If layout is NULL, then use 'cols' to determine layout
  if (is.null(layout)) {
    # Make the panel
    # ncol: Number of columns of plots
    # nrow: Number of rows needed, calculated from # of cols
    layout <- matrix(seq(1, cols * ceiling(numPlots/cols)),
                     ncol = cols, nrow = ceiling(numPlots/cols))
  }

 if (numPlots==1) {
    print(plots[[1]])

  } else {
    # Set up the page
    grid.newpage()
    pushViewport(viewport(layout = grid.layout(nrow(layout), ncol(layout))))
```

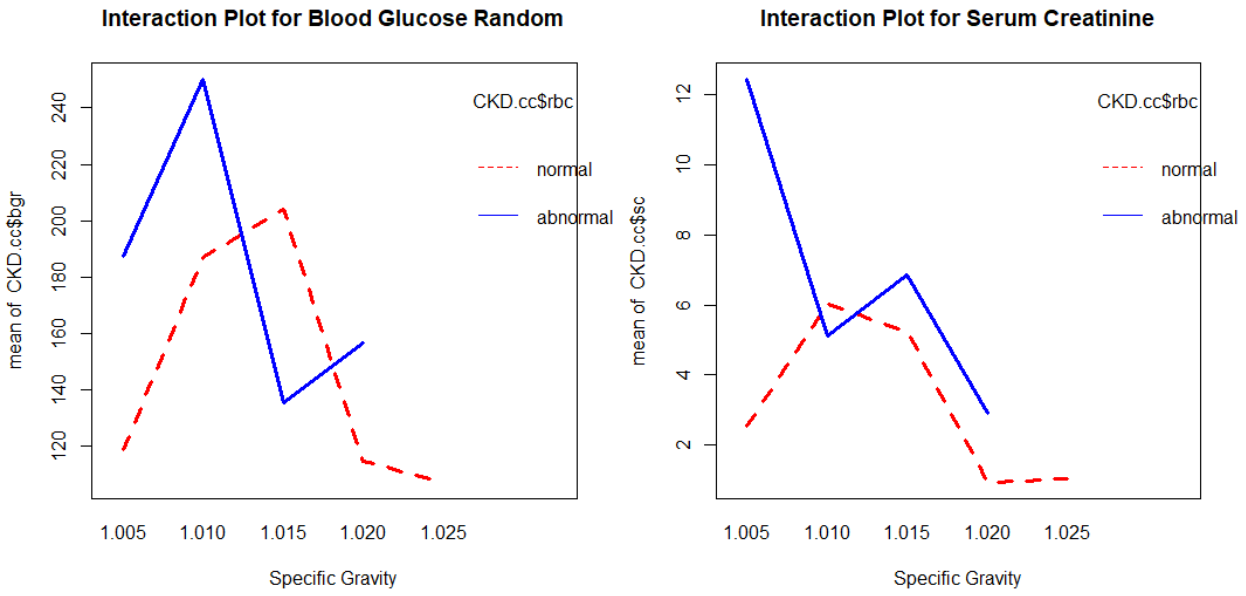
```
    # Make each plot, in the correct location
    for (i in 1:numPlots) {
      # Get the i,j matrix positions of the regions that contain this subplot
      matchidx <- as.data.frame(which(layout == i, arr.ind = TRUE))

      print(plots[[i]], vp = viewport(layout.pos.row = matchidx$row,
                                      layout.pos.col = matchidx$col))
    }
  }
}
Sys.setenv(JAVA_HOME="C:\\Program Files\\Java\\jre-9.0.4\\")
library(rJava)
library(RWeka)
CKD <- read.arff("C:/Users/lanxin/Documents/GitHub/Chronic_Kidney_Disease/Chr
onic_Kidney_Disease/chronic_kidney_disease_full.arff")

#import dataset

CKD_hw5<-CKD[,c(3,6,10,12,15)]
CKD.cc<-CKD_hw5[complete.cases(CKD_hw5),]
CKD.cc$rbc<-as.factor(CKD.cc$rbc)
write.csv(CKD.cc,file="C:/Users/lanxin/Documents/GitHub/Chronic_Kidney_Diseas
e/HW5/CKDCC.csv")

par(mfrow=c(1,2))
#this makes the plots
interaction.plot(CKD.cc$sg,CKD.cc$rbc,CKD.cc$bgr,  lwd=3,col=c("red","blue"),
xlab="Specific Gravity",main="Interaction Plot for Blood Glucose Random")
interaction.plot(CKD.cc$sg,CKD.cc$rbc,CKD.cc$sc,  lwd=3,col=c("red","blue"),x
lab="Specific Gravity",main="Interaction Plot for Serum Creatinine")
```



Red blood cells(rbc) is a binary variable (normal or abnormal) and specific gravity of urine (sg) is an ordinal variable.

These plots suggest that there may be an interaction between specific gravity and red blood cells on serum creatinine and blood glucose. Also suggests that there may not be much difference of RBC on serum creatinine and glucose value. Overall, it seems that normal red blood cells have higher serum creatinine concentration and specific gravity of urine. Two plots also indicate that When SG=1.025, there is no observation where red blood cell is abnormal.

2. Run Two-Way MANOVA for these two categorical factors. Discuss your results, both univariate and multivariate. If only one categorical predictor, do one-way MANOVA.

```
#fit linear model
mod1=manova(as.matrix(CKD.cc[,3:4])~CKD.cc$sg + CKD.cc$rbc +CKD.cc$sg*CKD.cc$
rbc)
#get univariate results
summary.aov(mod1)

##  Response bgr :
##                       Df Sum Sq Mean Sq F value    Pr(>F)
## CKD.cc$sg              4 301474   75368 21.6350 8.944e-15 ***
## CKD.cc$rbc             1  16413   16413  4.7116  0.031174 *
## CKD.cc$sg:CKD.cc$rbc   3  58801   19600  5.6264  0.001019 **
## Residuals            194 675824    3484
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Response sc :
##                       Df  Sum Sq Mean Sq F value    Pr(>F)
## CKD.cc$sg              4  946.77 236.692 39.1767 < 2.2e-16 ***
## CKD.cc$rbc             1   35.49  35.493  5.8748 0.0162770 *
## CKD.cc$sg:CKD.cc$rbc   3  131.88  43.960  7.2762 0.0001193 ***
## Residuals            194 1172.08   6.042
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#get multivariate results summary.manova(mod1)
summary.manova(mod1,test="Wilks")

##                       Df   Wilks approx F num Df den Df    Pr(>F)
## CKD.cc$sg              4 0.40169  27.8795      8    386 < 2.2e-16 ***
## CKD.cc$rbc             1 0.94029   6.1279      2    193  0.002629 **
## CKD.cc$sg:CKD.cc$rbc   3 0.82604   6.4506      6    386 1.704e-06 ***
## Residuals            194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

mod1$coefficients
```

```
##                                              bgr         sc
## (Intercept)                           118.666667   2.533333
## CKD.cc$sg1.010                         68.196970   3.471212
## CKD.cc$sg1.015                         85.500000   2.700000
## CKD.cc$sg1.020                         -3.857843  -1.602451
## CKD.cc$sg1.025                        -11.393939  -1.524242
## CKD.cc$rbcabnormal                     68.833333   9.916667
## CKD.cc$sg1.010:CKD.cc$rbcabnormal     -5.543124 -10.798135
## CKD.cc$sg1.015:CKD.cc$rbcabnormal   -137.750000  -8.300000
## CKD.cc$sg1.020:CKD.cc$rbcabnormal    -26.864379  -7.958660
## CKD.cc$sg1.025:CKD.cc$rbcabnormal           NA         NA
```

Univariate Results : For blood glucose, there are significant differences between either sg or rbc. Also, there, there is evidence on an interaction effect. The coefficients suggest that sg =1.010 or 1.015 have quite difference impact on bgr from sg=1.025.

Similar results are observed for serum creatinine, but rbc is no longer a significant factor. The coefficients also suggest when sg is higher if rbc is normal then the influence becomes negative, but the trend is different if rbc is abnormal.

Multivariate Results : The coefficient for sg=1.025*rbc=abnormal is NA, which corresponds to that When SG=1.025, there is no observation where red blood cell is abnormal. Either predictor and the interaction term are significant. Thus, there is strong interaction effect between specific gravity and the normality of red blood cells.

3. Perform (multivariate) contrasts to compare levels of a particular factor or combinations of factors. Discuss your results. If you're using SPSS/R, you won't be able to do the multivariate contrasts.

From the above coefficients, we can see that each category varies a lot. Thus, contrast for each pair is conducted is SAS. Also, since SG is an ordinal variable, we also test its linear effect via contrast. Following are the codes:

```
data CKDCC; set CKDCC;
trtcombine=trim(trim(sg) || trim(rbc)); run;

proc sort data=CKDCC;
by trtcombine;

ods rtf
file="C:\Users\lanxin\Documents\GitHub\Chronic_Kidney_Disease\HW5\contrast.rt
f";
proc glm data=CKDCC;
class trtcombine;
model bgr sc=trtcombine;
contrast 'Red blood cell: abnormal vs normal' trtcombine 1 -1 1 -1 1 -1 1 -1
0;
contrast 'Specific Gravity: 1.005 vs 1.010' trtcombine 1 1 -1 -1 0 0 0 0 0;
contrast 'Specific Gravity: 1.005 vs 1.015' trtcombine 1 1 0 0 -1 -1 0 0 0;
contrast 'Specific Gravity: 1.005 vs 1.020' trtcombine 1 1 0 0 0 0 -1 -1 0;
contrast 'Specific Gravity: 1.005 vs 1.025' trtcombine 1 1 0 0 0 0 0 0 -2;
contrast 'Specific Gravity: 1.010 vs 1.015' trtcombine 0 0 1 1 -1 -1 0 0 0;
```

```
contrast 'Specific Gravity: 1.010 vs 1.020' trtcombine 0 0 1 1 0 0 -1 -1 0;
contrast 'Specific Gravity: 1.010 vs 1.025' trtcombine 0 0 1 1 0 0 0 0 -2;
contrast 'Specific Gravity: 1.015 vs 1.020' trtcombine 0 0 0 0 1 1 -1 -1 0;
contrast 'Specific Gravity: 1.015 vs 1.025' trtcombine 0 0 0 0 1 1 0 0 -2;
contrast 'Specific Gravity: 1.020 vs 1.025' trtcombine 0 0 0 0 0 0 1 1 -2;
contrast 'Specific Gravity linear effect' trtcombine 1 1 0.5 0.5 0 0 -0.5 -
0.5 -2;
contrast 'Specific Gravity: 1.010 vs the other ' trtcombine -1 -1 3.5 3.5 -1
-1 -1 -1 -1;
run;
ods rtf close;
```

The results are:

Contrast when dependent variable is bgr	DF	Contrast SS	Mean Square	F Value	Pr > F
Red blood cell: abnormal vs normal	1	8576.0814	8576.0814	2.46	0.1183
Specific Gravity: 1.005 vs 1.010	1	17915.3916	17915.3916	5.14	0.0244
Specific Gravity: 1.005 vs 1.015	1	1061.3400	1061.3400	0.30	0.5816
Specific Gravity: 1.005 vs 1.020	1	1246.7086	1246.7086	0.36	0.5504
Specific Gravity: 1.005 vs 1.025	1	9390.3978	9390.3978	2.70	0.1022
Specific Gravity: 1.010 vs 1.015	1	28804.3655	28804.3655	8.27	0.0045
Specific Gravity: 1.010 vs 1.020	1	110265.7943	110265.7943	31.65	<.0001
Specific Gravity: 1.010 vs 1.025	1	270482.0584	270482.0584	77.64	<.0001
Specific Gravity: 1.015 vs 1.020	1	13769.0057	13769.0057	3.95	0.0482
Specific Gravity: 1.015 vs 1.025	1	57978.9349	57978.9349	16.64	<.0001
Specific Gravity: 1.020 vs 1.025	1	17453.2728	17453.2728	5.01	0.0263
Specific Gravity linear effect	1	31792.51932	31792.51932	9.13	0.0029
Specific Gravity: 1.010 vs the other	1	95140.73831	95140.73831	27.31	<.0001

Contrast when the dependent variable is sc	DF	Contrast SS	Mean Square	F Value	Pr > F
Red blood cell: abnormal vs normal	1	123.2759346	123.2759346	20.40	<.0001
Specific Gravity: 1.005 vs 1.010	1	15.5554427	15.5554427	2.57	0.1102
Specific Gravity: 1.005 vs 1.015	1	8.0736000	8.0736000	1.34	0.2491
Specific Gravity: 1.005 vs 1.020	1	129.9328323	129.9328323	21.51	<.0001
Specific Gravity: 1.005 vs 1.025	1	188.0386466	188.0386466	31.12	<.0001
Specific Gravity: 1.010 vs 1.015	1	2.7618784	2.7618784	0.46	0.4998
Specific Gravity: 1.010 vs 1.020	1	215.1726299	215.1726299	35.61	<.0001
Specific Gravity: 1.010 vs 1.025	1	453.4934807	453.4934807	75.06	<.0001
Specific Gravity: 1.015 vs 1.020	1	204.3584967	204.3584967	33.82	<.0001

Contrast when the dependent variable is sc	DF	Contrast SS	Mean Square	F Value	Pr > F
Specific Gravity: 1.015 vs 1.025	1	376.6918395	376.6918395	62.35	<.0001
Specific Gravity: 1.020 vs 1.025	1	17.4105315	17.4105315	2.88	0.0912
Specific Gravity linear effect	1	288.9091801	288.9091801	47.82	<.0001
Specific Gravity: 1.010 vs the other	1	18.5395747	18.5395747	3.07	0.0814

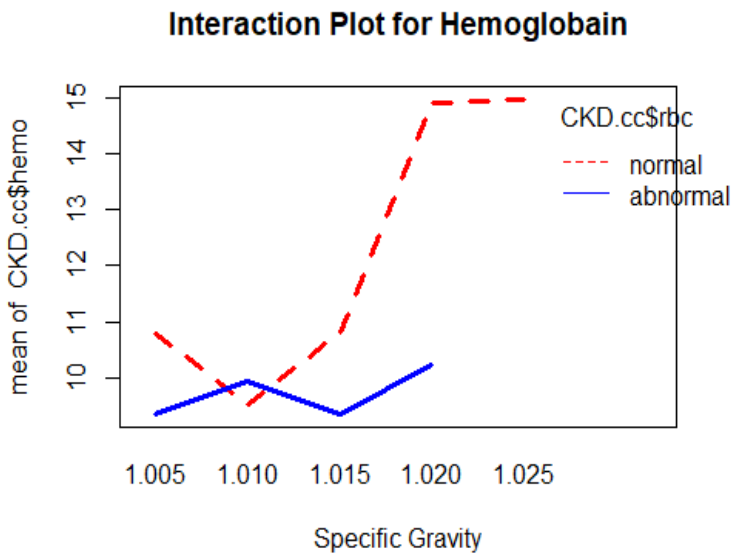
The above contrast results suggest that when the dependent variable is blood glucose random, then sg =1.010 is quite different from all the other values of sg. Specific gravity = 1.015 is significantly different from sg=1.020 and sg=1.025.

When the dependent variable is serum creatinine, the normality of red blood cells is a significant factor. Sg= 1.005, 1.020 and 1. 025 is quite different from each other . Sg = 1.010 is significantly different from higher gravity.

Also, there is significantly linear effect of sg on both sc and bgr which indicates that we could treat sg as a continuous variable when it is necessary to reduce degrees of freedom.

4. **If applicable, add a continuous variable to your model and fit as a multiple-response generalized linear model. Before you fit the model, make some plots to see if there are linear relationships between your covariates and your responses.**

```
#relationship
interaction.plot(CKD.cc$sg,CKD.cc$rbc,CKD.cc$hemo,  lwd=3,col=c("red","blue")
,xlab="Specific Gravity",main="Interaction Plot for Hemoglobain")
```



The above interaction plot shows that there may also be an interaction between specific gravity and red blood cells on hemoglobin. Generally patients with normal red blood cells will have higher concentration of hemoglobin.

```r
#fit linear model
mod1=lm(as.matrix(CKD.cc[,3:5])~CKD.cc$sg + CKD.cc$rbc +CKD.cc$sg*CKD.cc$rbc)
#get univariate results
mod1
```

```
##
## Call:
## lm(formula = as.matrix(CKD.cc[, 3:5]) ~ CKD.cc$sg + CKD.cc$rbc +
##     CKD.cc$sg * CKD.cc$rbc)
##
## Coefficients:
##                                       bgr         sc          hemo
## (Intercept)                         118.66667    2.53333    10.76667
## CKD.cc$sg1.010                       68.19697    3.47121    -1.24394
## CKD.cc$sg1.015                       85.50000    2.70000     0.04167
## CKD.cc$sg1.020                       -3.85784   -1.60245     4.14510
## CKD.cc$sg1.025                      -11.39394   -1.52424     4.20152
## CKD.cc$rbcabnormal                   68.83333    9.91667    -1.41667
## CKD.cc$sg1.010:CKD.cc$rbcabnormal    -5.54312  -10.79814     1.84009
## CKD.cc$sg1.015:CKD.cc$rbcabnormal  -137.75000   -8.30000    -0.04167
## CKD.cc$sg1.020:CKD.cc$rbcabnormal   -26.86438   -7.95866    -3.27288
## CKD.cc$sg1.025:CKD.cc$rbcabnormal          NA         NA          NA
```

```r
summary(mod1)
```

```
## Response bgr :
##
## Call:
## lm(formula = bgr ~ CKD.cc$sg + CKD.cc$rbc + CKD.cc$sg * CKD.cc$rbc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -171.154  -23.309   -5.809   17.459  309.191
##
## Coefficients: (1 not defined because of singularities)
##                                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)                          118.667     34.077   3.482 0.000614 ***
## CKD.cc$sg1.010                        68.197     36.326   1.877 0.061967 .
## CKD.cc$sg1.015                        85.500     38.099   2.244 0.025951 *
## CKD.cc$sg1.020                        -3.858     34.820  -0.111 0.911895
## CKD.cc$sg1.025                       -11.394     34.842  -0.327 0.744010
## CKD.cc$rbcabnormal                    68.833     53.880   1.278 0.202939
## CKD.cc$sg1.010:CKD.cc$rbcabnormal     -5.543     57.700  -0.096 0.923566
## CKD.cc$sg1.015:CKD.cc$rbcabnormal   -137.750     60.239  -2.287 0.023292 *
## CKD.cc$sg1.020:CKD.cc$rbcabnormal    -26.864     57.804  -0.465 0.642633
## CKD.cc$sg1.025:CKD.cc$rbcabnormal         NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 59.02 on 194 degrees of freedom
```

```
## Multiple R-squared:  0.3579, Adjusted R-squared:  0.3314
## F-statistic: 13.52 on 8 and 194 DF,  p-value: 1.705e-15
##
##
## Response sc :
##
## Call:
## lm(formula = sc ~ CKD.cc$sg + CKD.cc$rbc + CKD.cc$sg * CKD.cc$rbc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.1500 -0.4309 -0.1309  0.1909 10.8955
##
## Coefficients: (1 not defined because of singularities)
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                          2.533      1.419   1.785  0.07580 .
## CKD.cc$sg1.010                       3.471      1.513   2.295  0.02283 *
## CKD.cc$sg1.015                       2.700      1.587   1.702  0.09041 .
## CKD.cc$sg1.020                      -1.602      1.450  -1.105  0.27049
## CKD.cc$sg1.025                      -1.524      1.451  -1.050  0.29481
## CKD.cc$rbcabnormal                   9.917      2.244   4.420 1.64e-05 ***
## CKD.cc$sg1.010:CKD.cc$rbcabnormal  -10.798      2.403  -4.494 1.20e-05 ***
## CKD.cc$sg1.015:CKD.cc$rbcabnormal   -8.300      2.509  -3.309  0.00112 **
## CKD.cc$sg1.020:CKD.cc$rbcabnormal   -7.959      2.407  -3.306  0.00113 **
## CKD.cc$sg1.025:CKD.cc$rbcabnormal       NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.458 on 194 degrees of freedom
## Multiple R-squared:  0.4873, Adjusted R-squared:  0.4662
## F-statistic: 23.05 on 8 and 194 DF,  p-value: < 2.2e-16
##
##
## Response hemo :
##
## Call:
## lm(formula = hemo ~ CKD.cc$sg + CKD.cc$rbc + CKD.cc$sg * CKD.cc$rbc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.4227 -1.0118  0.0318  1.1428  6.7500
##
## Coefficients: (1 not defined because of singularities)
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                       10.76667    1.05275  10.227  < 2e-16 ***
## CKD.cc$sg1.010                    -1.24394    1.12224  -1.108 0.269041
## CKD.cc$sg1.015                     0.04167    1.17701   0.035 0.971797
## CKD.cc$sg1.020                     4.14510    1.07572   3.853 0.000158 ***
## CKD.cc$sg1.025                     4.20152    1.07641   3.903 0.000131 ***
## CKD.cc$rbcabnormal                -1.41667    1.66454  -0.851 0.395772
```

```
## CKD.cc$sg1.010:CKD.cc$rbcabnormal  1.84009    1.78258   1.032 0.303234
## CKD.cc$sg1.015:CKD.cc$rbcabnormal -0.04167    1.86102  -0.022 0.982161
## CKD.cc$sg1.020:CKD.cc$rbcabnormal -3.27288    1.78579  -1.833 0.068375 .
## CKD.cc$sg1.025:CKD.cc$rbcabnormal       NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.823 on 194 degrees of freedom
## Multiple R-squared:  0.6416, Adjusted R-squared:  0.6268
## F-statistic: 43.42 on 8 and 194 DF,  p-value: < 2.2e-16
```

MANOVA tests from SAS output:

The SAS System

The GLM Procedure
Multivariate Analysis of Variance

Characteristic Roots and Vectors of: E Inverse * H, where
H = Type III SSCP Matrix for sg
E = Error SSCP Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1		
		bgr	sc	hemo
0.93766868	**87.92**	0.00065688	0.01168748	-0.02534888
0.09219276	**8.64**	-0.00019184	0.02924657	0.02382176
0.03659278	**3.43**	0.00102395	0.00393728	0.02417227

MANOVA Test Criteria and F Approximations for the Hypothesis of No Overall sg Effect
H = Type III SSCP Matrix for sg
E = Error SSCP Matrix

S=3 M=0 N=95

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.45584060	14.64	12	508.28	<.0001
Pillai's Trace	0.60362762	12.22	12	582	<.0001
Hotelling-Lawley Trace	1.06645422	16.99	12	331.71	<.0001
Roy's Greatest Root	0.93766868	45.48	4	194	<.0001

NOTE: F Statistic for Roy's Greatest Root is an upper bound.

Characteristic Roots and Vectors of: E Inverse * H, where
H = Type III SSCP Matrix for rbc
E = Error SSCP Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1		
		bgr	sc	hemo
0.14737327	**100.00**	0.00048444	0.02249137	-0.01420354
0.00000000	**0.00**	0.00112373	-0.00690377	0.00435981
0.00000000	**0.00**	0.00013895	0.02130581	0.03966853

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall rbc Effect
H = Type III SSCP Matrix for rbc
E = Error SSCP Matrix

S=1 M=0.5 N=95

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.87155595	9.43	3	192	<.0001
Pillai's Trace	0.12844405	9.43	3	192	<.0001
Hotelling-Lawley Trace	0.14737327	9.43	3	192	<.0001
Roy's Greatest Root	0.14737327	9.43	3	192	<.0001

Characteristic Roots and Vectors of: E Inverse * H, where
H = Type III SSCP Matrix for sg*rbc
E = Error SSCP Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1		
		bgr	**sc**	**hemo**
0.16792369	**46.35**	0.00017914	0.00273790	0.04027821
0.10979577	**30.31**	0.00045144	0.03076418	0.01073294
0.08453706	**23.34**	0.00113176	-0.00731644	-0.00753726

MANOVA Test Criteria and F Approximations for the Hypothesis of No Overall sg*rbc Effect
H = Type III SSCP Matrix for sg*rbc
E = Error SSCP Matrix

S=3 M=-0.5 N=95

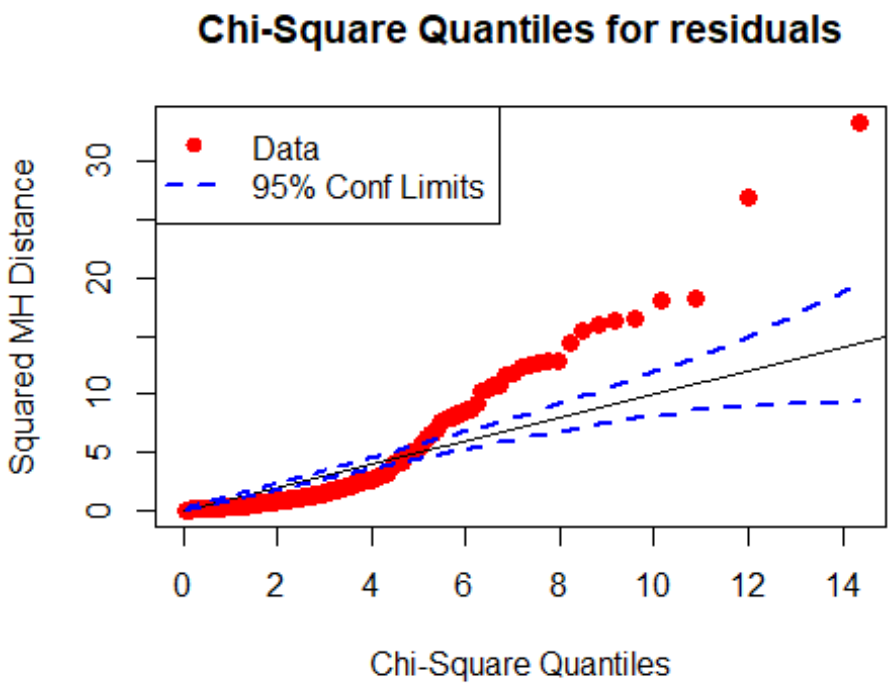
Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.71137413	7.80	9	467.43	<.0001
Pillai's Trace	0.32066059	7.74	9	582	<.0001
Hotelling-Lawley Trace	0.36225652	7.70	9	298.55	<.0001
Roy's Greatest Root	0.16792369	10.86	3	194	<.0001

NOTE: F Statistic for Roy's Greatest Root is an upper bound.

The above results show that rbc and sg has significant effect on hemoglobin univariately, and also it would affect the multivariate model significantly..

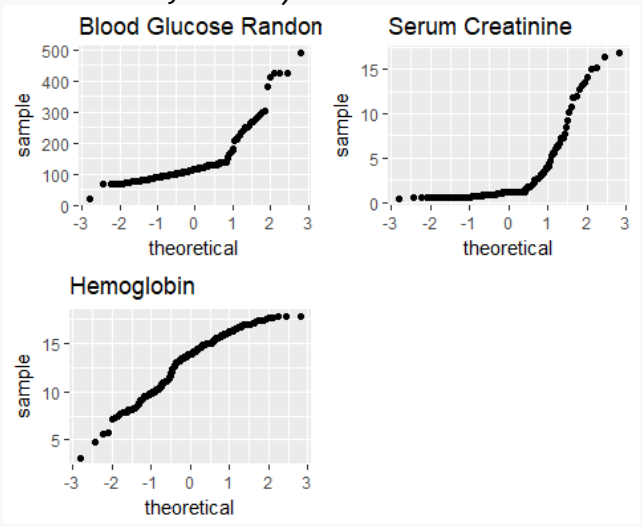
5. Check model assumptions by making a chi-square quantile plot of the residuals. Modify your model as appropriate based on your findings.

```r
source("http://www.reuningscherer.net/STAT660/R/CSQPlot.r.txt")
#run the function
CSQPlot(mod1$residuals, label="residuals")
```



The above chi-square quantiles plot for residuals show that the residuals don't follow a multivariate distribution. Then we check normality for each variable.

```
#check normality for each variable
#check QQ plot for some numeric variables
gg.qqplot <- function (variable, title, data) {
ggplot(data, aes_string(sample=variable)) + ggtitle(title) + stat_qq()
}
p2 <- gg.qqplot("bgr", "Blood Glucose Random",CKD.cc)
p3 <- gg.qqplot("hemo", "Hemoglobin",CKD.cc)
p4 <- gg.qqplot("sc", "Serum Creatinine",CKD.cc)
```




```
multiplot( p2, p3, p4, cols=2)
```

The above plots indicate that none of the response is normal. Then we perform power transformations which uses the MLE approach of Box and Cox (1964) to select a transformation of multivariate response for normality.

```
library(car)
trans <- powerTransform(as.matrix(CKD.cc[,3:5])~CKD.cc$sg + CKD.cc$rbc +CKD.c
c$sg*CKD.cc$rbc, family="bcPower")
summary(trans)
```

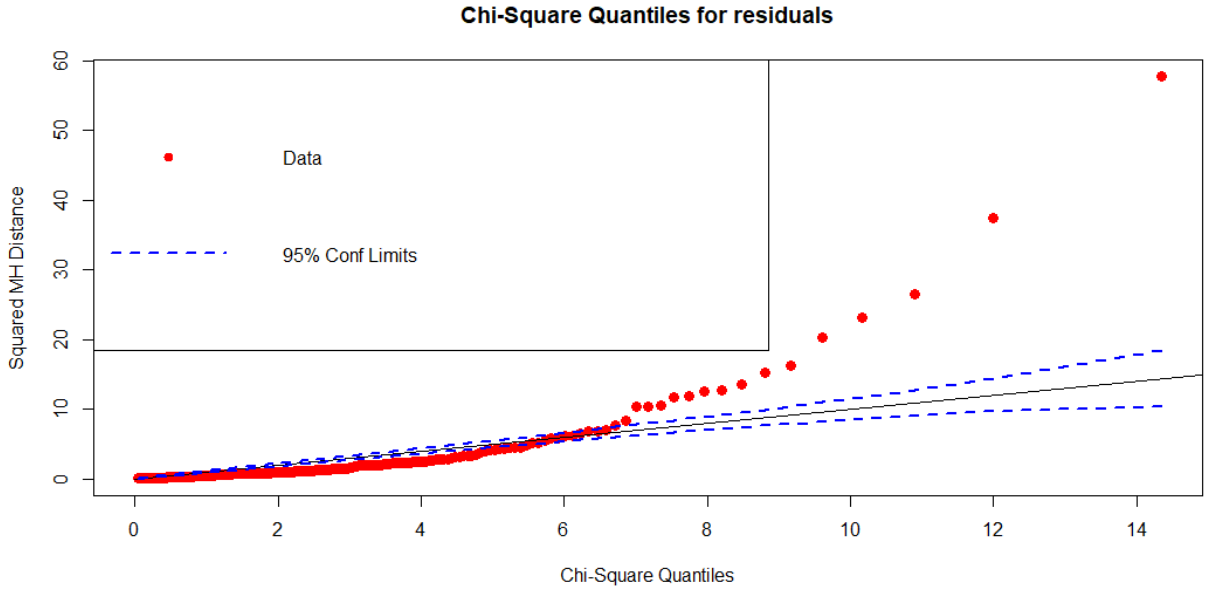
```
## bcPower Transformations to Multinormality
##      Est Power Rounded Pwr Wald Lwr bnd Wald Upr Bnd
## bgr    -0.1808       -0.33      -0.3587      -0.0028
## sc     -0.3608       -0.33      -0.4848      -0.2368
## hemo    1.5556        1.56       1.1639       1.9473
##
## Likelihood ratio tests about transformation parameters
##                                 LRT df pval
## LR test, lambda = (0 0 0) 124.7737  3    0
## LR test, lambda = (1 1 1) 630.0641  3    0
```

```
transformedY <- bcPower(with(CKD.cc, cbind(sc,hemo,bgr)),coef(trans, round=TR
UE))
 colnames(transformedY)<-c("sc","hemo","bgr")
 mod3=lm(transformedY~CKD.cc$sg + CKD.cc$rbc +CKD.cc$sg*CKD.cc$rbc)
 summary(mod3)
```

```
## Response sc :
##
## Call:
## lm(formula = sc ~ CKD.cc$sg + CKD.cc$rbc + CKD.cc$sg * CKD.cc$rbc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.97649 -0.32389  0.04737  0.33153  1.63983
##
## Coefficients: (1 not defined because of singularities)
##                                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)                          0.6234     0.2553   2.442  0.01551 *
## CKD.cc$sg1.010                       0.4998     0.2722   1.836  0.06786 .
## CKD.cc$sg1.015                       0.3951     0.2855   1.384  0.16790
## CKD.cc$sg1.020                      -0.8084     0.2609  -3.098  0.00223 **
## CKD.cc$sg1.025                      -0.7780     0.2611  -2.980  0.00325 **
## CKD.cc$rbcabnormal                   1.0572     0.4037   2.619  0.00952 **
## CKD.cc$sg1.010:CKD.cc$rbcabnormal  -1.2039     0.4323  -2.785  0.00589 **
## CKD.cc$sg1.015:CKD.cc$rbcabnormal  -0.7664     0.4514  -1.698  0.09110 .
## CKD.cc$sg1.020:CKD.cc$rbcabnormal  -0.1700     0.4331  -0.392  0.69519
## CKD.cc$sg1.025:CKD.cc$rbcabnormal       NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4422 on 194 degrees of freedom
```

```
## Multiple R-squared:  0.6475, Adjusted R-squared:  0.633
## F-statistic: 44.55 on 8 and 194 DF,  p-value: < 2.2e-16
##
##
## Response hemo :
##
## Call:
## lm(formula = hemo ~ CKD.cc$sg + CKD.cc$rbc + CKD.cc$sg * CKD.cc$rbc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.61918 -0.02703  0.00592  0.04029  0.27639
##
## Coefficients: (1 not defined because of singularities)
##                                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)                         1.646261   0.048654  33.836  < 2e-16
## CKD.cc$sg1.010                     -0.082886   0.051865  -1.598  0.11165
## CKD.cc$sg1.015                     -0.005325   0.054397  -0.098  0.92213
## CKD.cc$sg1.020                      0.138253   0.049715   2.781  0.00596
## CKD.cc$sg1.025                      0.139641   0.049747   2.807  0.00551
## CKD.cc$rbcabnormal                 -0.068429   0.076928  -0.890  0.37483
## CKD.cc$sg1.010:CKD.cc$rbcabnormal  0.109832   0.082384   1.333  0.18404
## CKD.cc$sg1.015:CKD.cc$rbcabnormal -0.029846   0.086009  -0.347  0.72896
## CKD.cc$sg1.020:CKD.cc$rbcabnormal -0.105898   0.082532  -1.283  0.20098
## CKD.cc$sg1.025:CKD.cc$rbcabnormal        NA         NA      NA       NA
##
## (Intercept)                        ***
## CKD.cc$sg1.010
## CKD.cc$sg1.015
## CKD.cc$sg1.020                     **
## CKD.cc$sg1.025                     **
## CKD.cc$rbcabnormal
## CKD.cc$sg1.010:CKD.cc$rbcabnormal
## CKD.cc$sg1.015:CKD.cc$rbcabnormal
## CKD.cc$sg1.020:CKD.cc$rbcabnormal
## CKD.cc$sg1.025:CKD.cc$rbcabnormal
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08427 on 194 degrees of freedom
## Multiple R-squared:  0.5628, Adjusted R-squared:  0.5448
## F-statistic: 31.22 on 8 and 194 DF,  p-value: < 2.2e-16
##
##
## Response bgr :
##
## Call:
## lm(formula = bgr ~ CKD.cc$sg + CKD.cc$rbc + CKD.cc$sg * CKD.cc$rbc)
##
## Residuals:
```

```
##     Min      1Q  Median      3Q     Max
## -3254.1  -368.2  -122.2   207.4  6771.7
##
## Coefficients: (1 not defined because of singularities)
##                                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)                         1137.92     693.06   1.642   0.1022
## CKD.cc$sg1.010                      1230.37     738.80   1.665   0.0975 .
## CKD.cc$sg1.015                      1593.37     774.86   2.056   0.0411 *
## CKD.cc$sg1.020                       -52.91     708.18  -0.075   0.9405
## CKD.cc$sg1.025                      -198.74     708.63  -0.280   0.7794
## CKD.cc$rbcabnormal                  1150.54    1095.82   1.050   0.2951
## CKD.cc$sg1.010:CKD.cc$rbcabnormal    310.21    1173.52   0.264   0.7918
## CKD.cc$sg1.015:CKD.cc$rbcabnormal -2460.62    1225.16  -2.008   0.0460 *
## CKD.cc$sg1.020:CKD.cc$rbcabnormal  -447.76    1175.63  -0.381   0.7037
## CKD.cc$sg1.025:CKD.cc$rbcabnormal       NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1200 on 194 degrees of freedom
## Multiple R-squared:  0.334,  Adjusted R-squared:  0.3065
## F-statistic: 12.16 on 8 and 194 DF,  p-value: 4.834e-14
```



By power transformation, the modified model doesn't fulfill the model assumptions because the above chi-square plot becomes better, but still indicates the residuals deviate from normal distribution. But we didn't come up with better approaches to modify our model. Thus, we suggest that non-parametric MANOVA (MRPP) should be a reasonable approach.