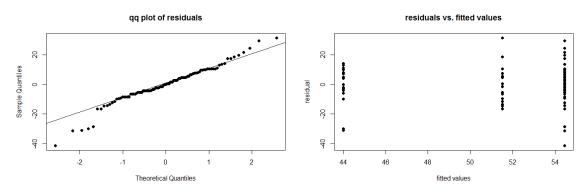
- 1. Revisit the analysis of the data from the study of effects of exposure to lead on the psychological and neurological well-being of children from the previous HW. Recall that the data are given in the lead.csv data set.
 - a. Use a residual analysis to assess whether the assumptions of the ANOVA model (on the untransformed, full data set) are met. What remedies do you recommend and why (Note: you will use a nonparametric method in the next part of this problem so there is no need to complete the analysis using your recommended remedy).

The exploratory analysis and the residual plots below are used to assess the assumptions of normality and equal variances, and to identify outliers. There are small deviations from normality in the two exposure groups and this is apparent in the QQ plot of the residuals – which suggest deviations in both tails of the distribution of the residuals. The plot of residuals vs. fitted values highlight some outliers, particularly in the current exposed group but generally suggest the equal variances assumption is met (although, without the two outliers in the current exposure group, the data are no longer consistent with the equal variances assumption). Independence is reasonably met based on the study design although as this is an observational study, I would hesitate to draw causal conclusions from these results.



These outliers are of some concern to me. There are a number of approaches to address this. I would consider a transformation of the data to attempt to downplay the outliers (likely a square root or perhaps a log transformation.) I would also consider holding out the most extreme of these (I would also use a nonparametric procedure (such as the Kruskal-Wallis Test), which you will do in part (b)! No need to actually carry out the transformation at this point.

b. Use nonparametric methods to address the research questions of interest. Restate how the hypotheses of interest from the last HW will be addressed using the nonparametric methods. Carry out the analysis (on untransformed data) and clearly state the conclusions. For pairwise comparisons, use the Bonferroni method. How would you conduct a one-sided test?

Based on the Kruskal-Wallis test of Ho: equal population distributions of MAXFWT across all three exposure groups vs. Ha: at least one exposure group's population distribution of MAXFWT is shifted away from the others, there is evidence (p-value = 0.005) of at least one of the exposure groups having a population distribution of MAXFWT scores shifted away from the others.

> kruskal.test(maxfwt~factor(leadgrp))

```
Kruskal-Wallis rank sum test
```

```
data: maxfwt by factor(leadgrp)
Kruskal-Wallis chi-squared = 10.587, df = 2, p-value = 0.005024
```

The pairwise comparisons (using a Bonferroni correction given in the output below suggests that there is evidence of a difference between the control group (1) and the currently exposed group (2). Continuing with the remaining two comparisons, there is no convincing evidence of a difference in the distribution of MAXFWT scores in the previously exposed group (3) versus the currently exposed group (2). Finally, there is no convincing evidence that the distribution of MAXFWT scores in the previously exposed group (3) is below the distribution of MAXFWT scores for the control group (1). Both of these p-values are quite large.

```
> pairwise.wilcox.test(lead$MAXFT,factor(lead$lead_typ),p.adjust.method="bonf
erroni",exact=F)
```

Pairwise comparisons using Wilcoxon rank sum test with continuity correction

data: lead\$MAXFT and factor(lead\$lead_typ)

```
1 2
2 0.004 -
3 0.562 0.718
```

P value adjustment method: Bonferroni

For the one-sided tests, note that I did not ask you to *conduct* the one-sided tests but only *how* you would do this. You can conduct the individual Wilcoxon Rank Sum test for any one-sided hypothesis of interest to make sure you are getting the correct p-value (i.e. the correct direction).

To see this, note that the pairwise.wilxoc.test() without any adjustment for multiple comparisons is equivalent to the three separate applications of the wilcox.test() on two groups at a time. The code to see this is below:

```
pairwise.wilcox.test(sublead$MAXFT,sublead$lead_typ,exact=F,p.adjust.method="
none") # two-sided with no adjustment
maxft1 <- sublead$MAXFT[sublead$lead_typ==1] # create MAXFT by group vars
maxft2 <- sublead$MAXFT[sublead$lead_typ==2]
maxft3 <- sublead$MAXFT[sublead$lead_typ==3]
wilcox.test(maxft1,maxft2, exact = F, alternative="two.sided")
wilcox.test(maxft1,maxft3, exact = F, alternative="two.sided")
wilcox.test(maxft2,maxft3, exact = F, alternative="two.sided")</pre>
```

The output is on the next page where you can see the two functions align. Thus we can use the more generous output from the wilcox.test() function to properly determine the one-sided tests of interest (control has higher average MAXFT than either previous or current exposure groups):

```
wilcox.test(maxft1,maxft2, exact = F, alternative="greater")
wilcox.test(maxft1,maxft3, exact = F, alternative="greater")
```

If you need the adjusted p-values, then you can use the pairwise.wilcox.test() with the appropriate alternative (less or greater) indicated by the choice used in wilcox.test().

```
p.adjust.method="none") # two-sided

    Pairwise comparisons using Wilcoxon rank sum test with continuity
correction

data: sublead$MAXFT and sublead$lead_typ

1     2
2 0.0013 -     3 0.1873 0.2394

P value adjustment method: none

> wilcox.test(maxft1,maxft2, exact = F, alternative="two.sided")
        Wilcoxon rank sum test with continuity correction

data: maxft1 and maxft2
W = 904, p-value = 0.001347
alternative hypothesis: true location shift is not equal to 0
> wilcox.test(maxft1,maxft3, exact = F, alternative="two.sided")
```

> pairwise.wilcox.test(sublead\$MAXFT,sublead\$lead_typ,exact=F,

data: maxft1 and maxft3
W_= 622, p-value = 0.1873

alternative hypothesis: true location shift is not equal to 0

Wilcoxon rank sum test with continuity correction

> wilcox.test(maxft2,maxft3, exact = F, alternative="two.sided")

Wilcoxon rank sum test with continuity correction

data: maxft2 and maxft3
W = 116, p-value = 0.2394

alternative hypothesis: true location shift is not equal to 0

2. Chapter 5 #17

	Degrees of	Sum of Squares	Mean Square		
Source	Freedom (df)	(SS)	(MS)	F-statistic	P-value
Between Groups	7	35819	5117	3.5	0.009941808
Within Groups	24	35088	1462		
Total	31	70907			

3. This hypothesis was determined *after* seeing the data. Ideally, a new study would be designed, and new data would be collected to test this hypothesis. This is an example of data dredging or data snooping. The familywise significance level should be controlled as this is an unplanned comparison and the uncertainty measure must incorporate the process of searching for important comparisons. Scheffe's method controls for *all possible linear contrasts among means* (including this one) so would be the best choice of a method to use.