LEcTure Notes #2

Reading assignment

- Read MD ch 3 or G ch 6.

Goals for Lecture Notes #2

- Introduce decomposition of sum of squares
- Introduce the structural model
- Review assumptions and provide more detail on how to check assumptions

1. Fixed Effects One Way ANOVA

I will present ANOVA several different ways to develop intuition. The different methods I will present are equivalent—they are simply different ways of looking at and thinking about the same statistical technique. Each way of thinking about ANOVA highlights a different feature and provides different insight into the procedure.

(a) ANOVA as a generalization of the two sample $t$ test

Example showing $t^2 = F$ (Figure 2-1). This is not a transformation of the data, but a relationship between two different approaches to the same test statistic.

The null hypothesis for the one way ANOVA is:

$$
\mu_i = \mu \text{ for all } i
$$

(2-1)

In words, the means in each population $i$ are all assumed to equal the same value $\mu$. This is a generalization of the equality of two means that is tested by the two-sample $t$ test.
Figure 2-1: Example showing equivalence of $t$ test and ANOVA with two groups with SPSS and R syntax.

I’ll use the first two groups of the sleep deprivation data that we will discuss later.

data list file = "data.sleep" free/ dv group.

select if (group le 2).

TO SAVE SPACE I OMIT THE OUTPUT OF THE BOXPLOTS ETC

$t$-test groups=group
/variables=dv.

t-tests for independent samples of GROUP

<table>
<thead>
<tr>
<th>Variable</th>
<th>Number of Cases</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Standard Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>DV</td>
<td>8</td>
<td>19.3750</td>
<td>1.188</td>
<td>.420</td>
</tr>
<tr>
<td>GROUP 2</td>
<td>8</td>
<td>20.7500</td>
<td>1.282</td>
<td>.453</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Pooled Variance estimate</th>
<th>Separate Variance Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>F 2-tail</td>
<td>t Degrees of 2-tail</td>
<td>t Degrees of 2-tail</td>
</tr>
<tr>
<td>1.16</td>
<td>.846</td>
<td>-2.23</td>
</tr>
</tbody>
</table>

NOW WE’LL DO A ONE WAY ANOVA

oneway variables=dv by group.

ANALYSIS OF VARIANCE

<table>
<thead>
<tr>
<th>SOURCE</th>
<th>D.F.</th>
<th>SUM OF SQUARES</th>
<th>MEAN SQUARES</th>
<th>F</th>
<th>F</th>
<th>PROB.</th>
</tr>
</thead>
<tbody>
<tr>
<td>BETWEEN GROUPS</td>
<td>1</td>
<td>7.5625</td>
<td>7.5625</td>
<td>4.9532</td>
<td>.0430</td>
<td></td>
</tr>
<tr>
<td>WITHIN GROUPS</td>
<td>14</td>
<td>21.3750</td>
<td>1.5268</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOTAL</td>
<td>15</td>
<td>28.9375</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The value of the $t$ test squared ($-2.23^2$) equals the value of $F$ in the ANOVA table; the p-values are also identical (compare the two boxes).

R Version of ANOVA (data set has four groups, this example uses groups 1 and 2); same ANOVA $F = 4.9532$ as SPSS

> setwd("/Users/gonzo/rich/Teach/Gradst-1/unixfiles/lectnotes/lect2")
> data.sleep <- read.table("data.sleep",col.names=c("dv","group"))
> data.sleep <- data[sleep[2]<3,]
> data.sleep[,"group"] <- factor(data.sleep[,"group")
> summary(aov(dv ~ group, data=data.sleep))

<table>
<thead>
<tr>
<th>Df Sum Sq Mean Sq F value Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>group 1 7.562 7.562 4.953 0.043 *</td>
</tr>
<tr>
<td>Residuals 14 21.375 1.527</td>
</tr>
</tbody>
</table>

---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(b) Structural model approach

Let each data point be denoted by $Y_{ij}$, where $i$ denotes the group the subject belongs and $j$ denotes that the subject is the “$j$th” person in the group.

Consider the following example from Kirk (1982). You want to examine the effects of sleep deprivation on reaction time. The subject’s task is to press a key when he or she observes a stimulus light on the computer monitor. The dependent measure is reaction time measured in hundredths of a second. You randomly assign 32 subjects into one of four sleep deprivation conditions: 12 hrs, 24 hrs, 36 hrs, and 48 hrs. Your research hypothesis is that reaction time will slow down as sleep deprivation increases.

Here are the data:

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1st</td>
<td>20</td>
<td>21</td>
<td>25</td>
<td>26</td>
</tr>
<tr>
<td>2nd</td>
<td>20</td>
<td>20</td>
<td>23</td>
<td>27</td>
</tr>
<tr>
<td>3rd</td>
<td>17</td>
<td>21</td>
<td>22</td>
<td>24</td>
</tr>
<tr>
<td>4th</td>
<td>19</td>
<td>22</td>
<td>23</td>
<td>27</td>
</tr>
<tr>
<td>5th</td>
<td>20</td>
<td>20</td>
<td>21</td>
<td>25</td>
</tr>
<tr>
<td>6th</td>
<td>19</td>
<td>20</td>
<td>22</td>
<td>28</td>
</tr>
<tr>
<td>7th</td>
<td>21</td>
<td>23</td>
<td>22</td>
<td>26</td>
</tr>
<tr>
<td>8th</td>
<td>19</td>
<td>19</td>
<td>23</td>
<td>27</td>
</tr>
<tr>
<td>Group mean</td>
<td>19.38</td>
<td>20.75</td>
<td>22.63</td>
<td>26.25</td>
</tr>
<tr>
<td>St. dv.</td>
<td>1.19</td>
<td>1.28</td>
<td>1.189</td>
<td>1.28</td>
</tr>
</tbody>
</table>

See Appendix 1 for exploratory data analysis of these data.

The “grand mean”, i.e., the mean of the cell means, is denoted $\hat{\mu}$. For these data $\hat{\mu} = 22.25$. The grand mean is an unbiased estimate of the true population mean $\mu$. I will use the symbols $\hat{\mu}$ and $\bar{Y}$ interchangeably for the sample mean. When the cells have equal sample sizes, the grand mean can also be computed by taking the mean of all data, regardless of group membership. This will equal the (unweighted) mean of the cell means. However, when the cells have different sample sizes, then the grand mean is computed by taking the mean of the cell means. There are other definitions of “grand mean” that we’ll cover later, such as the sample-size weighted mean of cell means.

Obviously, if we don’t know how much sleep deprivation a particular subject had, our best prediction of his or her reaction time would be the grand mean. This is
not a very precise prediction, but if it's the only thing we have we can live with it. The simple model of an individual data point when you don’t know what condition subjects were assigned can be denoted as follows:

\[ Y_{ij} = \mu + \epsilon_{ij} \]  

(2-2)

where \( \epsilon_{ij} \) denotes the error. The error term is assumed to be normally distributed with mean 0 and variance \( \sigma^2 \). In this simple model, we attribute the deviation between \( Y_{ij} \) and \( \mu \) to the error \( \epsilon \). Maxwell and Delaney call Equation 2-2 the “reduced model.”

However, if we know the amount of sleep deprivation for an individual, then we can improve our prediction by using the group mean instead of the grand mean \( \mu \). The group mean can itself be considered a deviation from the grand mean. Thus, the mean of a particular group has two components. One component is the grand mean \( \mu \) itself, the other component is an “adjustment” that depends on the group the subjects was assigned. This adjustment will be denoted \( \alpha_i \) to convey the idea that the term is adjusting the “ith” group. An example will make this clearer. The group mean for the 12 hour sleep deprivation group is 19.38. We can define this as:

\[ Y_i = \hat{\mu} + \hat{\alpha}_i \]

19.38 = 22.25 + \hat{\alpha}_i

−2.88 = \hat{\alpha}_i

In words, everyone in the study has a “base” reaction time of 22.25 (the grand mean); being in the 12 hour sleep deprivation group “decreases” the reaction time by 2.88, yielding the cell mean 19.38. The estimate \( \hat{\alpha}_i \) represents the effect of being in treatment i, relative to the grand mean. The mean for group i, \( Y_i \), is an unbiased estimate of \( \mu_i \), the population mean of population i.

In one-way ANOVA’s the \( \alpha \)’s are easy to estimate. Simply take the difference between the observed group mean and the observed grand mean, i.e.,

\[ \bar{Y}_i - \bar{Y} = \hat{\alpha}_i \]  

(2-3)

The \( \hat{\alpha} \)'s are constrained to sum to zero, i.e., \( \sum \hat{\alpha}_i = 0 \). The treatment effect \( \alpha_i \) is not to be confused with the Type I error rate, which also uses the symbol \( \alpha \).

This gives us an interesting way to think about what ANOVA is doing. It shows that the one way ANOVA is fitting an additive model to data. That is,

\[ Y_{ij} = \mu + \alpha_i + \epsilon_{ij} \]  

(2-4)

So under this model, a given subject’s score consists of three components: grand mean, adjustment, and error. The grand mean is the same for all subjects, the
treatment adjustment is specific to treatment i, and the error is specific to the jth subject in the ith treatment. Equation 2-4 is what Maxwell and Delaney call the full model.

Understanding the underlying model that is fit provides interesting insights into your data. This is especially true when dealing with more complicated ANOVA designs as we will see later. Note that if additivity does not make sense in your domain of research, then you should not be using ANOVA.

Most textbooks state that the ANOVA tests the null hypothesis that all the group means are equal. This is one way of looking at it. An equivalent way of stating it is that the ANOVA tests the null hypothesis that all the $\alpha_i$ are zero. When all the $\alpha_i$ are zero, then all the cell means equal the grand mean. So a convenient way to think about ANOVA is that it tests whether all the $\alpha_i$s are equal to zero. The alternative hypothesis is that at least one of the $\alpha$s are not equal to zero.

A measurement aside: the structural model used in ANOVA implies that the scales (i.e., the dependent variable) should either be interval or ratio because of the notion of additive effects and additive noise (i.e., additive $\alpha$'s and $\epsilon$'s).

(c) A third way to formulate ANOVA: Variability between group means v. variability within groups

i. Recall the definitional formula for the estimate of the variance

$$\text{VAR}(Y) = \frac{\sum (Y_i - \bar{Y})^2}{N - 1} \quad (2-5)$$

The numerator of the right hand term is, in words, the sum of the squared deviations from the mean. It is usually just called “sum of squares”. The denominator is called degrees of freedom. In general, when you compute an estimate of a variance you always divide the sums of squares by the degrees of freedom,

$$\text{VAR}(Y) = \frac{\text{SS}}{\text{df}} \quad (2-6)$$

Another familiar example to drive the idea home. Consider the pooled standard deviation in a two sample $t$ test (lecture notes #1). It can also be written as sums of squares divided by degrees of freedom

$$\text{pooled st. dev.} = \sqrt{\frac{\sum (Y_{1j} - \bar{Y}_1)^2 + \sum (Y_{2j} - \bar{Y}_2)^2}{(n_1 - 1) + (n_2 - 1)}} \quad (2-7)$$
You can see the “pooling” in the numerator and in the denominator of Equation 2-7. We’ll see that Equation 2-7, which was written out for two groups, can be generalized to an arbitrary number of groups. In words, the pooled standard deviation in the classic $t$ test is as follows: one simply takes the sum of the sum of squared deviations from each cell mean (the numerator), divides by the total number of subjects minus the number of groups (denominator), and then computes the square root.

Returning to ANOVA, consider the variance of all the data regardless of group membership. This variance has the sum of squared deviations from the grand mean in the numerator and the total sample size minus one in the denominator.

$$\text{VAR}(Y) = \frac{\sum_i \sum_j (Y_{ij} - \bar{Y})^2}{N - 1}$$  \hspace{1cm} (2-9)

We call the numerator the sums of squares total (SST). This represents the variability present in the data with respect to the grand mean. This is identical to the variance form given in Equation 2-5.

SST can be decomposed into two parts. One part is the sums of squares between groups (SSB). This represents the sum of squared deviations between the group means and the grand mean (i.e., intergroup variability). The second part is the sum of squares within groups (SSW), or sum of squared errors. This represents the sum of squared deviations between individual scores and their respective group mean (i.e., intragroup variability). SSW is analogous to the pooled standard deviation we used in the $t$ test, but it generalizes the pooling across more than two groups.

The decomposition is such that $\text{SST} = \text{SSB} + \text{SSW}$. In words, the total variability (as indexed by sum of squares) of the data around the grand mean (SST) is a sum of the variability of the group means around the grand mean (SSB) and the variability of the individual data around the group mean (SSW).

I will now show the derivation of the statement $\text{SST} = \text{SSB} + \text{SSW}$. We saw earlier that

$$\text{SST} = \sum \sum (Y_{ij} - \bar{Y})^2$$  \hspace{1cm} (2-10)

With a little high school algebra, Equation 2-10 can be rewritten as

$$\text{SST} = \sum_i n_i (Y_i - \bar{Y})^2 + \sum_i \sum_j (Y_{ij} - \bar{Y}_i)^2$$  \hspace{1cm} (2-11)
\( \text{SS Total} = \text{SSB} + \text{SSW} \)  

(2-12)

(see, for example, Hays, section 10.8, for the proof).

A graphical way to see the decomposition is in terms of a pie chart where the entire pie represents SS total and the pie is decomposed into two pieces—SSB and SSW.

Thus, the analysis of variance performs a decomposition of the variances (actually, the sums of squares). This is why it is called “analysis of variance” even though “analysis of means” may seem more appropriate at first glance.

ii. Degrees of freedom and ANOVA source table

For one-way ANOVA’s computing degrees of freedom (df) is easy. The degrees of freedom corresponding to SSB is the number of groups minus 1 (i.e., letting T be the number of groups, T - 1). The degrees of freedom corresponding to SSW is the total number of subjects minus the number of groups (i.e., N - T). Of course, the degrees of freedom corresponding to SST is the total number of subjects minus one (N - 1). Thus, ANOVA also decomposes the degrees of freedom

\[
\text{df}_{\text{total}} = \text{df}_{\text{between}} + \text{df}_{\text{within}} \quad \text{(2-13)}
\]

\[
N - 1 = (T - 1) + (N - T) \quad \text{(2-14)}
\]

As always, a sums of squares divided by the degrees of freedom is interpreted as a variance (as per Equation 2-6). So, we can divide SSB and SSW by their appropriate degrees of freedom and end up with variances. These terms are given special names: mean squared between (\( \text{MSB} = \frac{\text{SSB}}{\text{df}_{\text{between}}} \)) and mean
squared within (MSW = \frac{SSW}{df_{within}}).

The F test is defined as the ratio MSB/MSW where the degrees of freedom for the F test correspond to the degrees of freedom used in MSB and MSW. You reject the null hypothesis if MSB/MSW is greater than the critical F value.

To summarize all of this information, the results of an ANOVA are typically arranged in a “source table.”

<table>
<thead>
<tr>
<th>source</th>
<th>SS</th>
<th>df</th>
<th>MS</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>between</td>
<td>T - 1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>within</td>
<td>N - T</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>total</td>
<td>N - 1</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The source table for the sleep deprivation example is below (the complete example is given in Appendix 1).

<table>
<thead>
<tr>
<th>SOURCE</th>
<th>D.F.</th>
<th>SUM OF SQUARES</th>
<th>MEAN SQUARES</th>
<th>F RATIO</th>
<th>PROB.</th>
</tr>
</thead>
<tbody>
<tr>
<td>BETWEEN GROUPS</td>
<td>3</td>
<td>213.2500</td>
<td>71.0833</td>
<td>46.5575</td>
<td>.0000</td>
</tr>
<tr>
<td>WITHIN GROUPS</td>
<td>28</td>
<td>42.7500</td>
<td>1.5268</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOTAL</td>
<td>31</td>
<td>256.0000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The conclusion we can draw from this p-value is that we can statistically reject the null hypothesis that the population means for the four groups are the same. This particular test does not provide information about which means are different from which means. We need to develop a little more machinery before we can perform those tests.

(d) Relating the structural model and the variance decomposition approaches to ANOVA

Let’s rewrite the structural model as

\[ \epsilon_{ij} = Y_{ij} - \mu - \alpha_i \]
\[ = Y_{ij} - (\mu + \alpha_i) \]
\[ = Y_{ij} - \mu_i \]

residual = observed score – expected score

That is, each subject has a new score \( \epsilon_{ij} \) that represents the deviation between the subject’s observed score and the score hypothesized by the structural model.
The variance of the $\epsilon_{ij}$ is equivalent to MSW (as long as you divide the sum of squares by $\text{df}_{\text{error}} = N - T$). See Appendix 2 for an example using the sleep deprivation data. MSW is an unbiased estimate of the true error variance $\sigma^2_{\epsilon}$. This holds whether or not the null hypothesis is true. A synonymous term for MSW is mean square error, MSE.

If the null hypothesis is true, then MSB is also an unbiased estimate of the variance of the residuals, or $\sigma^2_{\epsilon}$. However, if the null hypothesis is not true, MSB estimates

$$\sigma^2_{\epsilon} + \frac{\sum n_i \alpha^2_i}{T - 1} \quad (2-15)$$

The term on the right is essentially the variability of the treatment effects. Obviously, if the treatment effects are zero, the term vanishes. (This would occur when the null hypothesis is exactly true.) If the group means are far apart (in terms of location), then the group means have a relatively high variability, which will inflate the MSB. The ratio MSB/MSW is a test of how much the treatment effect has inflated the error term.

Putting all this together in the ANOVA application, the $F$ test statistic is simply a ratio of expected variances

$$F \sim \frac{\sigma^2_{\epsilon} + \sum n_i \alpha^2_i}{\frac{\sum n_i \alpha^2_i}{T - 1}} \quad (2-16)$$

In this context, the symbol $\sim$ means “distributed as”. So, Equation 2-16 means that the ratio of variances on the right hand side is “distributed as” an F distribution.

The F distribution has two degrees of freedom, one corresponding to the numerator term and another corresponding to the denominator term. I will give some examples of the F distribution in class. The F table appears in Maxwell and Delaney starting at page A-3. Here is an excerpt from those pages. Suppose we have an application with 3 degrees of freedom in the numerator, 28 degrees of freedom in the denominator, and wanted the Type I error cutoff corresponding to $\alpha = .05$. In this case, the tabled value for F for 3, 28 degrees of freedom for $\alpha = .05$ is 2.95. In the previous example the observed F was 46.56 (with 4 groups, so 3 & 28 degrees of freedom), which exceeds the tabled value of 2.95.
If you want to compute your own $F$ tables, you can use a spreadsheet such as Microsoft’s Excel. For instance, the excel function FINV gives the $F$ value corresponding to a particular $p$ value, numerator and denominator degrees of freedom. If you type “=FINV(.05,1,50)” (no quotes) in a cell of the spreadsheet, the number 4.0343 will appear, which is the $F$ value corresponding to a $p$ value of 0.05 with 1, 50 degrees of freedom. Check that you get 2.95 when you type =FINV(.05,3,28) in Excel. Newer versions of Excel (starting in 2010) have a new function called F.INV.RT for the right tail, so typing =F.INV.RT(.05,1,28) is the same as the old version FINV(.05,1,28). There is also an F.INV (a period between the F and the I) where one enters the cumulative probability rather than the right tail, so the command =F.INV(.95,1,28) is the same as =F.INV.RT(.05,1,28).

The command in R for generating $F$ values is qf(). For example, if you enter qf(.95,3,28) corresponding to two-tailed $\alpha = .05$, 3 degrees of freedom for the numerator, and 28 degrees of freedom for the denominator. R will return 2.95, just as the Excel example in the previous paragraph. Note that the qf command is defined by the cumulative probability, so we enter .95 rather than .05.

(e) Putting things into the hypothesis testing template

In Figure 2-3 I make use of the hypothesis testing template introduced in LN1. This organizes many of the concepts introduced so far in these lecture notes. We state the null hypothesis, the structural model, the computation for observed $F$, the critical $F$, and the statistical decision.

(f) Interpreting the $F$ test from a One Way ANOVA

The $F$ test yields an omnibus test. It signals that somewhere there is a difference between the means, but it does not tell you where. In research we usually want to be more specific than merely saying “the means are different.” In the next set of lecture notes (LN3) we will discuss planned contrasts as a way to make more
Null Hypothesis

- $H_0$: $\mu_i = \mu$
- $H_a$: $\mu_i \neq \mu$ (two-sided test)

Structural Model and Test Statistic

The structural model is that the dependent variable $Y$ consists of a grand population mean $\mu$, a treatment effect $\alpha$, and random noise $\epsilon_{ij}$. In symbols, for each subject $j$ in condition $i$ his or her individual observation $Y_{ij}$ is modeled as $Y_{ij} = \mu + \alpha_i + \epsilon_{ij}$.

The test statistic is a ratio of the mean square between groups (MSB) and the mean square within groups (MSW) from the ANOVA source table

$$F_{\text{observed}} = \frac{\text{MSB}}{\text{MSW}}$$

Critical Test Value The critical test value will be the table lookup of the $F$ distribution. We typically use $\alpha = 0.05$. The $F$ distribution has two degrees of freedom. The numerator df is number of groups minus 1 (i.e., $T - 1$) and the denominator df is total number of subjects minus number of groups (i.e., $N - T$).

Statistical decision If the observed $F$ exceeds the critical value $F_{\text{critical}}$, then we reject the null hypothesis. If the observed $F$ value does not exceed the critical value $F_{\text{critical}}$, then we fail to reject the null hypothesis.
specific statements such as “the difference between the means of group A and B is significant, but there is insufficient evidence suggesting the mean of Group C differs from the means of both Group A and B.” As we will see, planned contrasts also provide yet another way to think about ANOVA.

2. Power and sample size

Determining power and sample size needed to attain a given level of power is a nontrivial task requiring knowledge of noncentral distributions. Most people simply resort to rules of thumb. For most effect sizes in psychology 30-40 subjects per cell will do but much depends on the amount of noise in your data. You may need even larger cell sizes. Using such a heuristic commits us to a particular effect size that we are willing to deem statistically significant. In some areas where there is relatively little noise (or many trials per subject) fewer observations per cell is fine.

Different statistical tests have different computational rules for power. In general, if you are in doubt as to how to compute power (or needed sample size), a good rule of thumb is to consult an expert. A very preliminary discussion is given in Maxwell & Delaney, pages 120-. I’ll discuss power in more detail in the context of planned contrasts.

Power analyses can be misleading because they say something not just about the treatment effect but also about the specific context, experiment, subject pool, etc. Seems that psychological researchers would be better off worrying about reducing noise in their experiments and worrying about measurement issues, rather than concerning themselves exclusively with the needed sample sizes.

This discussion is moving in the direction of philosophy of science. If you are interested in learning about this viewpoint, see an article by Paul Meehl (1967, Philosophy of Science, 34, 103-115) where he contrasts data analysis as done by psychologists with data analysis as done in the physical sciences such as in physics.

3. Strength of Association

One question that can be asked is what percentage of the total variance is “accounted for” by having knowledge of the treatment effects (i.e., group membership). This percentage is given by

\[ R^2_{Y, \text{treatment}} = \frac{SSB}{SST} \]  \hspace{1cm} (2-17)

This ratio is interpreted as the percentage of the variability in the total sample that can be accounted for by the variability in the group means. For the sleep deprivation
data,
\[
R^2_{Y, \text{treatment}} = \frac{213.25}{256.00},
\] (2-18)
or 83% of the variability in the scores is accounted for by the treatments and the rest is error. In other words, \( R^2 \) denotes the percentage of total sum of squares corresponding to SSB. You can refer to the pie chart of sum of squares for this.

The phrase “percentage of variance accounted for” is always relative to a base model (or “reduced model”). In ANOVA, the base model is the simple model with only the grand mean other than the error term. Thus, \( R^2 \) in ANOVA refers to how much better the fit is by using individual group means (i.e., SSB) as opposed to the grand mean (i.e., SST). It does not mean that a theory predicts \( X \) amount of a phenomenon; all the phrase denotes is that a simple model of group means does better than a model of the grand mean. Most people don’t know this when they use the phrase “percentage of variance accounted for”.

A cautionary note about interpreting \( R^2_{Y, \text{treatment}} \). This percentage estimate refers only to the sample for which it was based, the particular experimental procedures, and the particular experimental context. Generalizations to other domains, treatments, and subjects must be made with care. We will deal with the issue of interpreting \( R^2 \) in more detail when discussing regression.

Several people have suggested a different measure, usually denoted \( \omega^2 \) (omega squared), which adjusts \( R^2_{Y, \text{treatment}} \) to yield a better estimate of the true population value. We will not review such measures in this class (I personally don’t think they are useful); they are discussed in Maxwell and Delaney if you want to learn about the details.

There are other measures of effect size that appear in the literature, such as Cohen’s d. These measures are all related to each other. They are just on different metrics and it is possible to convert one into another with simple formulas. Throughout these lecture notes I’ll use measures based on \( r \) to keep things simple. If a journal requires you to use a different measure of effect size, then it is a simple matter of converting \( r \) to that measure.

4. Computational formulae for the one way ANOVA.

Some people like to give computational formulae that are easier to work with than definitional formulae. In this course I will focus on the definitional formulae because they give insight into the techniques. One can still do the computations by hand using the definitional formulae. In this class the formula will facilitate understanding, the statistical computer program will perform the computations.
FYI: Hand computation of a one-way ANOVA using definitional formulae is fairly easy. First, compute the sum of squared deviations of each score from the grand mean. This yields SST. Second, compute the sum of squared deviations of scores from their group mean. This yields SSW. Third, figure out the degrees of freedom. Now you have all the pieces to complete the ANOVA source table. Be sure you understand this.

5. SPSS Syntax

The simple one-way ANOVA can be performed in SPSS using the ONEWAY command.

```
ONEWAY dv BY group.
```

More examples are given in the appendices.

6. R Syntax

The R command `aov()` performs basic ANOVA. For example, a one-way ANOVA is called by

```
out <- aov(dv ~ group)
summary(out)
```

where `dv` is the dependent variable and `group` is the grouping variable. The grouping variable should be defined as a factor.

7. Examining assumptions revisited: boxplots and normal-normal plots

(a) Boxplots defined

```
boxplot
```

a plot of the median, 1st & 3rd quartiles, and “whiskers.” (see LN1)

(b) Getting a feel for sampling variability—simulations with boxplots

The lesson here is that sample size matters. If cell sizes are large (say 100 in each cell) and the population variances are equal, then the boxplots look pretty
much the same across groups and minor deviations would not be tolerated (i.e.,
would lead to a rejection of the equal variance assumption). However, with
small sample sizes in each cell (say 10), then one should be more tolerant of
moderate discrepancies because they naturally occur even when sampling from
a distribution where all groups have the same population variance.

(c) Examining the equality of variance assumption

i. Examples of unequal variances.

I generated three samples of size 20 using these parameters:

A. normal with mean 10 and sd 4

B. normal with mean 40 and sd 16

C. normal with mean 300 and sd 64

These data are shown in boxplots. Figure 2-4 shows a clear violation of the
assumption of equal variances. Figure 2-5 shows how a log transformation
of the data improves the status of the assumption.

ii. The family of power transformations.

Consider the family of transformations of the form \(X^p\). This yields many sim-
ple transformations such as the square root (\(p = .5\)), the reciprocal (\(p = -1\)),
and the log (when \(p = 0\), see footnote\(^1\)).

Figure 2-6 shows the “ladder of power transformations”. Note how varying
the exponent \(p\) produces different curves, and these curves are continuous
variations of the continuously varying exponent \(p\).

\(^1\)Only for those who care… That \(p = 0\) yields the log transformation is not easy to prove unless you
know some calculus. Here’s the sketch of the proof. Consider this linear transformation of the power function
\[
\frac{X^p - 1}{p}
\]

We want to prove that the limit of this function is \(\log(X)\) as \(p\) approaches 0. Note that this limit is
indeterminate. Apply L’Hopital’s rule and solve for the limit. When \(p\) is negative, the scores \(X^p\) are
reversed in direction; thus, a side benefit of the form of Equation 2-19 is that it yields transformed data in
the correct order.
Figure 2-4: Raw data showing extreme violation of equality of variance assumption.
Figure 2-5: Log transform eliminates the unequal variance problem.
The SPSS syntax to compute these power transformations (i.e., \( x^p \)) is as follows: for \( p \) not equal to 0,

```spss
COMPUTE newx = x**p.
EXECUTE.
```

for \( p \) equal to 0,

```spss
COMPUTE newx = ln(x).
EXECUTE.
```

Transformations in R are computed more directly as in

```r
newx <- x^2
newxln <- ln(x)
```

iii. Spread and level plots for selecting the exponent

This plot exploits the relationship between measures of central tendency and measures of variability. By looking at, say, the relationship between the median and the interquartile ranges of each group we can “estimate” a suitable transformation in the family of the power functions. The spread
and level that SPSS generates plots the log of the medians and the log of the interquartile ranges.

In SPSS, the plot is generated by giving the \texttt{/plot=spreadlevel} subcommand to the \texttt{EXAMINE} command. That is,

\begin{verbatim}
EXAMINE variable = listofvars BY treatment 
/plot spreadlevel.
\end{verbatim}

The program finds the line of best fit (i.e., the regression line) through the points in that plot. If you limit yourself to power transformations, then the slope of the regression line is related to the power that will “best” transform the data (more precisely, power $= 1 - \text{slope}$). For example, if you find that the slope of the regression line is 0.5, then that suggests a square root transformation will probably do the trick (i.e., $1 - 0.5 = 0.5$). If you run the spread and level plot in SPSS on the sleep deprivation example it will suggest a transformation of -.095, or roughly a log transformation. More examples in the appendix.

The spread and level plot works well when the means and variances have a simple pattern (e.g., the variances increase linearly with means). If you the data don’t exhibit a simple pattern, then the spread and level plot will likely suggest strange transformations (e.g., $p = -8.54$). In cases where the patterns are not simple, then the spread and level plot should not be trusted.

In R the spread and level plot is available through the car package

\begin{verbatim}
library(car)
spreadLevelPlot(dv ~ group)
\end{verbatim}

This function complains if there are negative values or zeros in the dependent variable, and will add a constant to eliminate them.

For the sleep deprivation data we have

\verbatim
> library(car)
> # reread data because earlier I deleted two groups
> data.sleep <- read.table("data.sleep",col.names=c("dv","group"))
> data.sleep[,"group"] <- factor(data.sleep[,"group"])
> spreadLevelPlot(dv ~ group, data=data.sleep)
\end{verbatim}
### LowerHinge Median UpperHinge Hinge-Spread

<table>
<thead>
<tr>
<th></th>
<th>Lower Hinge</th>
<th>Median</th>
<th>Upper Hinge</th>
<th>Hinge-Spread</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>19.0</td>
<td>19.5</td>
<td>20.0</td>
<td>1.0</td>
</tr>
<tr>
<td>2</td>
<td>20.0</td>
<td>20.5</td>
<td>21.5</td>
<td>1.5</td>
</tr>
<tr>
<td>3</td>
<td>22.0</td>
<td>22.5</td>
<td>23.0</td>
<td>1.0</td>
</tr>
<tr>
<td>4</td>
<td>25.5</td>
<td>26.5</td>
<td>27.0</td>
<td>1.5</td>
</tr>
</tbody>
</table>

Suggested power transformation: 0.206773

If you round down, the R command suggests a log transform just like SPSS. The number is a little different than SPSS because this R command uses a different way to compute the IQR (that is, the hinge method). You’ll see that the IQRs computed by R are 1, 1.5, 1, and 1.5, but SPSS reports 1, 1.75, 1, 1.75 (run EXAMINE command to find out). This is due to different ways of interpolating when computing the IQR; see the help file for the quantile command in R for details. If you use type=6 as in `with(data.sleep,by(dv,group,IQR,type=6))` you reproduce the SPSS IQRs, and then can reproduce the SPSS spread and level plot if you do the appropriate regression on the logs. This is just a tiny point, and usually doesn’t make much difference in the suggested transformation.

See Box and Cox (1964, *Journal of the American Statistical Society, Series B, 26*, 211-243) for a derivation of why the slope of a spread and level plot tells you something about which transformation to use. They make their arguments from both maximum likelihood and Bayesian perspectives. A classic article in statistics! Note that the Box & Cox derivation is for a spread and level plot that uses log means and log standard deviations. The version that SPSS uses (log medians and log interquartile ranges) comes from arguments made by Tukey (1977) about the robustness of medians and interquartile ranges.

These procedures are merely guidelines—you should double-check the result of the transformation to make sure the transformation had the desired effect. In my opinion nothing beats a little common sense and boxplots—usually within a couple of tries you have a transformation that works at minimizing the violation to the equality of variances assumption.

(d) more examples given in class

Bank data, Norusis, SPSS Base manual (Appendix 3)

Helicopter data, KNNL.
Population in cities from 16 different countries–from UREDA’s boxplot chapter (Appendix 5)

Sometimes the spread and level plot doesn’t produce a good result (as seen in the helicopter data). The spread & level plot is merely a tool. When it yields strange results, the plot should be ignored. Recall that complicated patterns between means and variances cannot usually be corrected with a simple power transformation. You should always check that the transformation produced the desired result.

8. Checking the normality assumption

One way to check for normality is to examine the histogram. This is not necessarily the best thing to do because there is a lot of freedom in how one constructs a histogram (i.e., the sizes of the intervals that define each “bin”).

Another device is the trusty boxplot, which will tell you whether the distribution is symmetric (a necessary condition of normality). A suggestion of symmetry occurs if the median falls in the middle of the “box” and the two whiskers are similar in length.

A more sophisticated way to check normality is through a quantile-quantile plot. This is what SPSS calls the normal plot. The logic of this plot is quite elegant. Take your sample and for each point calculate the percentile. For example, one data point might be at the 50th percentile (i.e., the median). Then find the z scores from a normal distribution (μ = 0, σ = 1) that correspond to the each percentile. For example, if one data point had a percentile score of 95, then it corresponds to a z score of 1.645. Finally, plot the raw data points (y-axis) against their corresponding z scores (x-axis). If the points fall on a straight line, then the distribution is consistent with a normal distribution.

The way to calculate the percentile for purposes of this plot is to order your data from least to greatest so that the first data point is the least, . . . , the nth data point is the greatest. The percentile for the data point in the ith position is given by

\[ \frac{i - 0.5}{n} \]  

(2-20)

An example will illustrate. Suppose you observe these five data points: 30, 20, 40, 10, and 50. Create the following table:
The normal plot for these data appear in Figure 1. These five points fall on a straight line so a normal distribution cannot be ruled out.

The normal plot is useful in many situations. We will use it frequently when we look at residuals in the context of regression.
The quantile-quantile plot can be generalized to any theoretical or empirical distribution. For example, you can check whether your distribution matches a $\chi^2$ with df=3. Or, you can plot one observed distribution against another observed distribution to see whether the two distributions are similar. Unfortunately, the canned quantile-quantile plot that appears in SPSS only allows one distribution and compares it only to the normal distribution. The technique is more general than the specific SPSS implementation.

SPSS has the quantile-quantile plot (aka normal plot) in several of its commands. Today we'll discuss the subcommand in EXAMINE. Just enter the following:

```
EXAMINE variables = listofvariables
   /PLOT NPPLOT.
```

Appendix 6 shows an example.

To get separate normal plots for each cell enter:

```
EXAMINE variables = listofvariables BY treatment
   /PLOT NPPLOT.
```

It is okay to put all three plots (boxplot, spreadlevel, and normal probability plot) on one SPSS line as in:

```
EXAMINE variables = listofvariables BY treatment
   /PLOT BOXPLOT SPREADLEVEL NPPLOT.
```

Assumptions should usually be checked cell by cell (rather than for all cells combined).

SPSS also prints out the “detrended” plot. This is simply a plot of the residuals.

\[
\text{residual} = \text{observed} - \text{expected} = \text{raw score} - \text{linear model}
\]

If the straight line fits the data, then the detrended plot will look like a horizontal band. The intuition is that if the linear model captured all or most of the systematic variance, then just noise is left over. Noise is just as likely to be negative as positive
(and it should not be related, under the assumption of independence, to the level of the score). Some people like these detrended plots because it is easier to detect visually a discrepancy from a horizontal line than to detect discrepancy from a line with a non-zero slope.

There is also a command in SPSS called P PLOT, which allows you to compare your data to different distributions not just the normal. To get this plot for each of your groups you need to split your data into groups and get SPSS to run the command separately by group.

In R the quantile-quantile plot is produced by the qqnorm() and qqline() commands. The former sets up the plot, the latter prints the line.

```R
> #generate some non-normal data for illustration
> x <- rchisq(50,2)
> qqnorm(x)
> qqline(x)
```
As the name suggests, qqnorm and qqline compare the data distribution against the normal distribution. There is a more general function called qqplot, which compares data to an arbitrary distribution of your choosing. For example,

```r
> # some data but let's pretend we don't know the distribution
> # we hypothesize a theoretical distribution of chisq with 2 df
> # so set up a theoretical dataset of 10,000
> # compare data to the theoretical dist
> x <- rchisq(100, 2)
> theory.dist <- rchisq(10000, 2)
> qqplot(theory.dist, x)
> # draw line to guide the eye
> abline(0, 1)
```
Transformations can also be used to remedy violations of normality. But be careful because a transformation used to remedy one violation (e.g., to fix normality) may backfire and create problems for another assumption (e.g., equal variances).


The lesson here is that with large samples (say 250+) you can detect violations of normality and you should not be very tolerant of minor deviations from the straight line. However, with relatively small sample sizes (say 20) it is difficult to distinguish data that came from a normal distribution from data that came from a mildly skewed distribution.

Here is the rub: we know from the central limit theorem that as sample size increases, the sampling distribution of the mean approaches a normal distribution. Thus, the cases where we can be confident that we have found a violation of normality (a normal probability plot with large N), are the very cases where violations of normality
probably don’t matter much in terms of the effects on the t or F tests. The cases where we can’t be so confident that we have found a violation of normality (small N) are the very cases where the t or F test can break down if we violate normality. Simulations suggest that one needs to violate normality in a very major way before seeing adverse effects on the results of the t and F tests. [Note that the equality of variance assumption can create havoc even for moderately large N.]

10. Robustness

Maxwell and Delaney make an excellent point about violations of assumptions. The real issue about violations is whether they have an adverse effect on the results of the inferential tests. Will the width of our confidence intervals be wrong? Will the p-value of the t or F test be wrong? For the case of normality we can appeal to the central limit theorem for large N. But what about small N? What about violations of the equality of variance assumption?

Here we turn to simulation studies where we purposely create violations and find ways of measuring how “wrong” the t, the F and the CI turn out to be. Maxwell and Delaney review this work and you can read their take on it.

My take is that people who review the simulation work see what they want to see. The results are mixed. Sometimes violations matter, sometimes they don’t. Some people conclude that because there are cases where the ANOVA behaves well in the face of violations, we don’t need to worry so much about violations; other people conclude that because there are cases where ANOVA doesn’t behave well under violations, then we always need to worry about violations.

For me the issue is that for a specific dataset I don’t know what situation it falls in (i.e., I don’t know if that dataset will be in the “assumption violation probably doesn’t matter” camp or the “assumption violation probably matters” camp). Because I don’t know, then the best thing I can do is play it safe. Check the data to see if there are any gross discrepancies. If there are major violation assumptions, then I worry and try something remedial (a nonparametric test, a welch test if the problem is equal variances, a transformation). I’m not so worried about close calls because they probably won’t make much of a difference in my final results.

11. Explaining transformations in results sections

A transformation will add a sentence or two to your results section. You need to tell the reader that you checked the assumptions, that you had reason to believe violations were present, and that you believed it was necessary to transform the data.
It would be nice to report measures of central tendency (e.g., mean, median, etc.) and measures of variability (e.g., standard deviation, IQR) for both raw scores and transformed scores. But, if you have many measures, then you might want to trim down and only report the transformed scores. Hopefully, psychology journals will start publishing boxplots soon. Major journals such as *Science*, *Journal of the American Statistical Association*, *American Statistician*, and *New England Journal of Medicine* have started publishing papers with boxplots.

Some people will report the transformed means that have been “transformed back” into the original scale. For example, suppose you have the data 1, 2, 3, 4, and 5. You decide that a transformation is necessary and you use the square root. The mean on the square root scale is 1.676. The inferential test is computed on the transformed scores. Some people will transform the mean back to its original scale when reporting the cell means and cell standard deviations. In this example one would square the mean on the square root scale and report a mean of 2.81. So, they calculate their $p$ values on the transformed score but report means that have been transformed back to the original scale. Note that the mean on the original scale is 3 which is different from the re-transformed mean of 2.81.

You should not feel ashamed about having to report violations of assumptions. Actually, it reflects favorably on you because it shows how careful you are at data analysis. Remember that statistical assumptions are creations to make some derivations tractable (e.g., recall our discussion of the two-sample t test during the first Psych 613 lecture). If your data do not satisfy the assumptions of a statistical test, it does not mean you have inherently bad data. It simply means that one particular tool cannot be used because the conditions that make it possible to use that tool do not hold. The critical point is how you handle assumption violations. Do you do a transformation? a nonparametric test? a test like Welch’s that relaxes some of the assumptions? All three of these options are not always available in all applications of inferential tests. Careful consideration of all your options and careful examination of statistical assumptions are the most important aspects of data analysis.
Appendix 1

Example of One Way ANOVA: SPSS and R

First, we examine the describe statistics and boxplot. Then we present the ANOVA.

data list free /dv group.
begin data
[DATA OMITTED; SEE TEXT]
end data.

value labels group 1 '12hr' 2 '24hr' 3 '36hr' 4 '48hr'.

examine dv by group
/plot = boxplot.

DV
By GROUP 1.00 12hr
Valid cases: 8.0 Missing cases: .0 Percent missing: .0

Mean 19.3750 Std Err .4199 Min 17.0000 Skewness -.9698
Median 19.5000 Variance 1.4107 Max 21.0000 S E Skew .7521
5% Trim 19.4167 Std Dev 1.1877 Range 4.0000 Kurtosis 1.8718
   IQR 1.0000 S E Kurt 1.4809

DV
By GROUP 2.00 24hr
Valid cases: 8.0 Missing cases: .0 Percent missing: .0

Mean 20.7500 Std Err .4532 Min 19.0000 Skewness .6106
Median 20.5000 Variance 1.6429 Max 23.0000 S E Skew .7521
5% Trim 20.7222 Std Dev 1.2817 Range 4.0000 Kurtosis -.0212
   IQR 1.7500 S E Kurt 1.4809

DV
By GROUP 3.00 36hr
Valid cases: 8.0 Missing cases: .0 Percent missing: .0

Mean 22.6250 Std Err .4199 Min 21.0000 Skewness .9698
Median 22.5000 Variance 1.4107 Max 25.0000 S E Skew .7521
5% Trim 22.5833 Std Dev 1.1877 Range 4.0000 Kurtosis 1.8718
   IQR 1.0000 S E Kurt 1.4809

DV
By GROUP 4.00 48hr
Valid cases: 8.0 Missing cases: .0 Percent missing: .0

Mean 26.2500 Std Err .4532 Min 24.0000 Skewness -.6106
Median 26.5000 Variance 1.6429 Max 28.0000 S E Skew .7521
5% Trim 26.2778 Std Dev 1.2817 Range 4.0000 Kurtosis -.0212
HERE IS THE ANOVA

```
oneway dv by group
/statistics = all.

Variable DV
By Variable GROUP
```

### Analysis of Variance

<table>
<thead>
<tr>
<th>Source</th>
<th>D.F.</th>
<th>Sum of Squares</th>
<th>Mean Squares</th>
<th>F</th>
<th>F Ratio</th>
<th>Prob.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between Groups</td>
<td>3</td>
<td>213.2500</td>
<td>71.0833</td>
<td>46.5575</td>
<td>.0000</td>
<td></td>
</tr>
<tr>
<td>Within Groups</td>
<td>28</td>
<td>42.7500</td>
<td>1.5268</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>31</td>
<td>256.0000</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Group Statistics

<table>
<thead>
<tr>
<th>Group</th>
<th>Count</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Standard Error</th>
<th>Minimum</th>
<th>Maximum</th>
<th>95 Pct Conf Int for Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grp 1</td>
<td>8</td>
<td>19.3750</td>
<td>1.1877</td>
<td>.4199</td>
<td>17.0000</td>
<td>21.0000</td>
<td>18.3820 to 20.3680</td>
</tr>
<tr>
<td>Grp 2</td>
<td>8</td>
<td>20.7500</td>
<td>1.2817</td>
<td>.4532</td>
<td>19.0000</td>
<td>23.0000</td>
<td>19.6784 to 21.8216</td>
</tr>
<tr>
<td>Grp 3</td>
<td>8</td>
<td>22.6250</td>
<td>1.1877</td>
<td>.4199</td>
<td>21.0000</td>
<td>25.0000</td>
<td>21.6320 to 23.6180</td>
</tr>
<tr>
<td>Grp 4</td>
<td>8</td>
<td>26.2500</td>
<td>1.2817</td>
<td>.4532</td>
<td>24.0000</td>
<td>28.0000</td>
<td>25.1784 to 27.3216</td>
</tr>
<tr>
<td>Total</td>
<td>32</td>
<td>22.2500</td>
<td>2.8737</td>
<td>.5080</td>
<td>17.0000</td>
<td>28.0000</td>
<td>21.2139 to 23.2861</td>
</tr>
</tbody>
</table>

### Fixed Effects Model

- Estimate of Between Component Variance: 1.2356

### Random Effects Model

- Estimate of Between Component Variance: 1.4904

Tests for Homogeneity of Variances
Cochran's C = Max. Variance/Sum(Variances) = .2690, P = 1.000 (Approx.)
Bartlett-Box F = .025, P = .995
Maximum Variance / Minimum Variance = 1.165

Some notes about this output. The CI's in the printout are based on the individual cell standard deviations, not the pooled standard deviation. The CI around the "TOTAL" mean is the CI around the grand mean using the standard deviation computed from the entire sample (i.e., N - 1). The 1.2356 in the fixed effect model is the sqrt of MSW (i.e., √1.5268), the standard error of that estimate is 1.2356/√32 (the denominator contains the total sample size). Thus, the fixed effect is based on the pooled MSW. The CI given in the fixed effects column is the CI around the grand mean, using the square root of the pooled MSE term as the standard deviation estimate and having N - T degrees of freedom (rather than N - 1).

Basic ANOVA in R

```r
> setwd("/Users/gonzo/rich/Teach/Gradst1/unixfiles/lectnotes/lect2")
> data.sleep <- read.table("data.sleep",col.names=c("dv","group"))
> data.sleep[,"group"] <- factor(data.sleep[,"group")
> summary(aov(dv ~ group, data=data.sleep))

Df  Sum Sq Mean Sq F value Pr(>F)
group  3 213.25  71.08  46.56  5.22e-11 ***
Residuals 28  42.75  1.53
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

There are several ways to plot confidence intervals around means in R. LN1 mentions several; ggplot is probably the best approach but that requires learning more about R. Here I'll illustrate the plotmeans() command in the package gplots. You can look at the help file for plotmeans() for additional features.

```r
> library(gplots)
> plotmeans(dv ~ group,data=data.sleep)
```
To plot plus/minus one standard error just set the CI to be 68% (which is the CI corresponding to plus/minus one standard error).

> plotmeans(dv ~ group, data=data.sleep, p=.68)
Note that the y axis change slightly from the .95 to the .68 CI plot so if you want to put them side to side to compare the width of the intervals (in order to get an intuition of what plus/minus 1 vs plus/minus 2 looks like) be sure to set the ylim to be equal in both plots (e.g., add the argument ylim=c(18,28), or in both plotmeans calls, to set the y axis scale to range from, say, 18 to 28).

\begin{verbatim}
> par(mfcol=c(1,2))
> plotmeans(dv ~ group, data=data.sleep, p=.68, ylim=c(18,28))
> plotmeans(dv ~ group, data=data.sleep, ylim=c(18,28))
> par(mfcol=c(1,1))
\end{verbatim}
Lecture Notes #2: Introduction to Analysis of Variance

The image shows two line graphs with data points for each group, labeled as 1, 2, 3, and 4. Each group has a sample size of 8, indicated by "n=8" at the bottom of each graph. The graphs display the relationship between the independent variable (group) and the dependent variable (dv), with values ranging from 18 to 28 on the y-axis. The data points are connected by lines, and error bars are present, indicating variability within each group.
Appendix 2

Example showing how “variance of residuals” (with corrected df) is equal to MSW in the ANOVA source table.

RAW DATA: SLEEP DEPRIVATION DATA

<table>
<thead>
<tr>
<th>ROW</th>
<th>12hr</th>
<th>24hr</th>
<th>36hr</th>
<th>48hr</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>20</td>
<td>21</td>
<td>25</td>
<td>26</td>
</tr>
<tr>
<td>2</td>
<td>20</td>
<td>20</td>
<td>23</td>
<td>27</td>
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</tr>
<tr>
<td>8</td>
<td>19</td>
<td>19</td>
<td>23</td>
<td>27</td>
</tr>
</tbody>
</table>

ONEWAY ANOVA ON RAW SCORES (JUST FOR REFERENCE)

<table>
<thead>
<tr>
<th>SOURCE</th>
<th>DF</th>
<th>SS</th>
<th>MS</th>
<th>F</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>FACTOR</td>
<td>3</td>
<td>213.25</td>
<td>71.08</td>
<td>46.56</td>
<td>0.000</td>
</tr>
<tr>
<td>ERROR</td>
<td>28</td>
<td>42.75</td>
<td>1.53</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOTAL</td>
<td>31</td>
<td>256.00</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

POOLED STDEV = 1.236

SUBTRACT GROUP MEAN FROM EACH OBSERVED SCORE (CREATE NEW VARIABLES)

compute 12hrE = 12hr - 19.38.
compute 24hrE = 24hr - 20.75.
compute 36hrE = 36hr - 22.63.
compute 48hrE = 48hr - 26.25.
execute.

PRINT RESIDUALS

<table>
<thead>
<tr>
<th>ROW</th>
<th>12hrE</th>
<th>24hrE</th>
<th>36hrE</th>
<th>48hrE</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.62000</td>
<td>0.25</td>
<td>2.37000</td>
<td>-0.25</td>
</tr>
<tr>
<td>2</td>
<td>0.62000</td>
<td>-0.75</td>
<td>0.37000</td>
<td>0.75</td>
</tr>
<tr>
<td>3</td>
<td>-2.38000</td>
<td>0.25</td>
<td>-0.63000</td>
<td>-2.25</td>
</tr>
<tr>
<td>4</td>
<td>-0.38000</td>
<td>1.25</td>
<td>0.37000</td>
<td>0.75</td>
</tr>
<tr>
<td>5</td>
<td>0.62000</td>
<td>-0.75</td>
<td>-1.63000</td>
<td>-1.25</td>
</tr>
<tr>
<td>6</td>
<td>-0.38000</td>
<td>-0.75</td>
<td>-0.63000</td>
<td>1.75</td>
</tr>
<tr>
<td>7</td>
<td>1.62000</td>
<td>2.25</td>
<td>-0.63000</td>
<td>-0.25</td>
</tr>
<tr>
<td>8</td>
<td>-0.38000</td>
<td>-1.75</td>
<td>0.37000</td>
<td>0.75</td>
</tr>
</tbody>
</table>

DESCRIPTIVE STATISTICS ON THE RESIDUALS

<table>
<thead>
<tr>
<th>RESIDUAL</th>
<th>N</th>
<th>MEAN</th>
<th>MEDIAN</th>
<th>TRMEAN</th>
<th>STDEV</th>
<th>SEMEAN</th>
<th>MIN</th>
<th>MAX</th>
<th>Q1</th>
<th>Q3</th>
</tr>
</thead>
<tbody>
<tr>
<td>RESIDUAL</td>
<td>32</td>
<td>-0.002</td>
<td>0.000</td>
<td>-0.002</td>
<td>1.174</td>
<td>0.208</td>
<td>-2.380</td>
<td>2.370</td>
<td>-0.720</td>
<td>0.718</td>
</tr>
</tbody>
</table>

The standard deviation of the residual scores is 1.174, so the variance is 1.378. But, this variance was computed by SPSS using N - 1 in the denominator. We need N - T. So, multiply 1.378 by the “correction factor” \( \frac{N}{N-T} \) to yield 1.53—the MSE from the ANOVA source table.
Just to check our understanding let’s treat the residuals as the dependent variable and run an ANOVA. What do you expect the source table to look like? Try to think this through before looking at the answer below.

An ANOVA on the residuals yields MSB = 0 because the “effects” (that is, the treatment effects represented by each \( \alpha \)) have been subtracted out so there isn’t any SSB. The MSW = 1.53 is the same as the MSW for the raw data.

**ONE WAY ANOVA ON THE RESIDUALS**

<table>
<thead>
<tr>
<th>SOURCE</th>
<th>DF</th>
<th>SS</th>
<th>MS</th>
<th>F</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>FACTOR</td>
<td>3</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
<td>ERROR</td>
<td>28</td>
<td>42.75</td>
<td>1.53</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOTAL</td>
<td>31</td>
<td>42.75</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

POOLED STDEV = 1.236
Appendix 3

A more complete example of the bank data used by Norusis in the SPSS Base Manual.

```
select if (JOBCAT LE 5).

examine variables = salbeg by jobcat /plot=boxplot.
```

<table>
<thead>
<tr>
<th>JOBCAT</th>
<th>BEGINNING SALARY</th>
<th>Valid cases</th>
<th>Percent missing</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>CLERICAL</td>
<td>227.0</td>
<td>.0</td>
</tr>
<tr>
<td></td>
<td>Mean 5733.947</td>
<td>Std Err 84.4228</td>
<td>Min 3600.000 Skewness 1.2506</td>
</tr>
<tr>
<td></td>
<td>Median 5700.000</td>
<td>Variance 161767</td>
<td>Max 12792.00 S E Skew .1655</td>
</tr>
<tr>
<td></td>
<td>5% Trim 5661.713</td>
<td>Std Dev 1271.957 Range 9192.00 Kurtosis 4.4695</td>
<td></td>
</tr>
<tr>
<td></td>
<td>IQR 1500.000</td>
<td>SE Skew .1615</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>OFFICE TRAINEE</td>
<td>136.0</td>
<td>.0</td>
</tr>
<tr>
<td></td>
<td>Mean 5478.971</td>
<td>Std Err 80.3222</td>
<td>Min 3900.000 Skewness .3660</td>
</tr>
<tr>
<td></td>
<td>Median 5400.000</td>
<td>Variance 877424.1 Max 7800.00 S E Skew .2078</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5% Trim 5440.490</td>
<td>Std Dev 936.7092 Range 3900.00 Kurtosis -.9385</td>
<td></td>
</tr>
<tr>
<td></td>
<td>IQR 1800.000</td>
<td>SE Kurt .4127</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>SECURITY OFFICER</td>
<td>27.0</td>
<td>.0</td>
</tr>
<tr>
<td></td>
<td>Mean 6031.111</td>
<td>Std Err 103.2483</td>
<td>Min 3600.000 Skewness -3.8758</td>
</tr>
<tr>
<td></td>
<td>Median 6300.000</td>
<td>Variance 287825.6 Max 6300.00 S E Skew .4479</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5% Trim 6125.309</td>
<td>Std Dev 536.4938 Range 2700.00 Kurtosis 17.2035</td>
<td></td>
</tr>
<tr>
<td></td>
<td>IQR 300.0000</td>
<td>SE Kurt .8721</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>COLLEGE TRAINEE</td>
<td>41.0</td>
<td>.0</td>
</tr>
<tr>
<td></td>
<td>Mean 9956.488</td>
<td>Std Err 311.8593</td>
<td>Min 6300.000 Skewness .1221</td>
</tr>
<tr>
<td></td>
<td>Median 9492.000</td>
<td>Variance 3987506 Max 13500.00 S E Skew .3695</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5% Trim 9964.374</td>
<td>Std Dev 1996.874 Range 7200.00 Kurtosis -1.1850</td>
<td></td>
</tr>
<tr>
<td></td>
<td>IQR 3246.000</td>
<td>SE Kurt .7245</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>EXEMPT EMPLOYEE</td>
<td>32.0</td>
<td>.0</td>
</tr>
<tr>
<td></td>
<td>Mean 13258.88</td>
<td>Std Err 556.1423</td>
<td>Min 8496.000 Skewness 1.4015</td>
</tr>
</tbody>
</table>
```
The boxplot suggests a violation of the equality of variance assumption. The sample sizes are large enough that if the assumption was met we wouldn’t expect to see this degree of deviation, so we conclude that the equality of variance assumption is suspect. I’ll first perform an ANOVA on the raw data and then check out a possible transformation.

```
  oneway salbeg by jobcat
  /statistics all.
  
  Variable  SALBEG BEGINNING SALARY
By Variable  JOBCAT EMPLOYMENT CATEGORY

  ANALYSIS OF VARIANCE

  SOURCE     D.F.     SUM OF SQUARES     MEAN SQUARES   F  F
BETWEEN GROUPS     4   2230311013     557577753.4     266.5954 .0000
WITHIN GROUPS  458   957896695.7   2091475.318
TOTAL        462   3188206709

  STANDARD  STANDARD
GROUP   COUNT   MEAN   DEVIATION   ERROR MINIMUM   MAXIMUM   95 PCT CONF INT FOR MEAN
Grp 1   227  5733.9471   1271.9574 84.4228  3600.0000  12792.0000  5567.5907 TO 5900.3036
Grp 2  136  5478.9706   936.7092 80.3222  3900.0000  7800.0000  5320.1181 TO 5637.8231
Grp 3   27  6031.1111   536.4938 103.2483  3600.0000  6300.0000  5818.8812 TO 6243.3410
Grp 4   41  9956.4878  1996.8740 311.8593  6300.0000 13500.0000  9326.1966 TO 10586.7790
Grp 5   32 13258.8750  3146.0158 556.1423  8496.0000 24000.0000 12124.6153 TO 14393.1347
```
TOTAL 463 6570.3801 2626.9527 122.0848 24000.0000 6330.4697 TO 6810.2905

FIXED EFFECTS MODEL 1446.1934 67.2103 6438.3013 TO 6702.4589

RANDOM EFFECTS MODEL 1583.1406 2174.9485 TO 10965.8117

RANDOM EFFECTS MODEL - ESTIMATE OF BETWEEN COMPONENT VARIANCE 7300834.4825

It seems from running the spread and level plot that a -.5 slope (equivalent to the reciprocal of the square root transformation) will help with the equality of variance assumption.
compute tsalbeg = 1/sqrt(salbeg).
execute.

examine variables = tsalbeg by jobcat /plot = boxplot.

<table>
<thead>
<tr>
<th>TSALBEG By JOBCAT</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>TSALBEG By JOBCAT 1 CLERICAL</td>
<td>Valid cases:</td>
<td>Missing cases:</td>
<td>Percent missing:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean .0134 Std Err .0001 Min .0088 Skewness .1002</td>
<td>Median .0132 Variance .0000 Max .0167 S E Skew .1615</td>
<td>5% Trim .0134 Std Dev .0014 Range .0078 Kurtosis -.0697</td>
<td>IQR .0018 S E Kurt .3217</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean .0137 Std Err .0001 Min .0113 Skewness -.0638</td>
<td>Median .0136 Variance .0000 Max .0160 S E Skew .2078</td>
<td>5% Trim .0137 Std Dev .0011 Range .0047 Kurtosis -1.2928</td>
<td>IQR .0023 S E Kurt .4127</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean .0129 Std Err .0002 Min .0126 Skewness 4.4368</td>
<td>Median .0126 Variance .0000 Max .0167 S E Skew .4479</td>
<td>5% Trim .0128 Std Dev .0008 Range .0041 Kurtosis 21.3123</td>
<td>IQR .0003 S E Kurt .8721</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean .0102 Std Err .0002 Min .0086 Skewness .3008</td>
<td>Median .0103 Variance .0000 Max .0126 S E Skew .3695</td>
<td>5% Trim .0101 Std Dev .0010 Range .0040 Kurtosis -.8333</td>
<td>IQR .0016 S E Kurt .7245</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean .0088 Std Err .0002 Min .0065 Skewness -.2254</td>
<td>Median .0087 Variance .0000 Max .0108 S E Skew .4145</td>
<td>5% Trim .0089 Std Dev .0009 Range .0044 Kurtosis .2456</td>
<td>IQR .0012 S E Kurt .8094</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
The transformation didn’t do a perfect fix but with one exception (the middle group) the boxplots look better than the original data.

```
oneway tsalbeg by jobcat
/statistics all.
```

<table>
<thead>
<tr>
<th>Variable</th>
<th>TSALBEG</th>
</tr>
</thead>
<tbody>
<tr>
<td>By Variable</td>
<td>JOBCAT</td>
</tr>
</tbody>
</table>

### Analysis of Variance

<table>
<thead>
<tr>
<th>SOURCE</th>
<th>D.F.</th>
<th>SUM OF SQUARES</th>
<th>MEAN SQUARES</th>
<th>F RATIO</th>
<th>PROB.</th>
</tr>
</thead>
<tbody>
<tr>
<td>BETWEEN GROUPS</td>
<td>4</td>
<td>.0010</td>
<td>.0002</td>
<td>155.9406</td>
<td>.0000</td>
</tr>
<tr>
<td>WITHIN GROUPS</td>
<td>458</td>
<td>.0007</td>
<td>.0000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOTAL</td>
<td>462</td>
<td>.0017</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>GROUP</th>
<th>COUNT</th>
<th>MEAN</th>
<th>DEVIATION</th>
<th>ERROR</th>
<th>MINIMUM</th>
<th>MAXIMUM</th>
<th>95 PCT CONF INT FOR MEAN</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grp 1</td>
<td>227</td>
<td>.0134</td>
<td>.0014</td>
<td>.0001</td>
<td>.0088</td>
<td>.0167</td>
<td>.0132 TO .0136</td>
</tr>
<tr>
<td>Grp 2</td>
<td>136</td>
<td>.0137</td>
<td>.0011</td>
<td>.0001</td>
<td>.0113</td>
<td>.0160</td>
<td>.0135 TO .0138</td>
</tr>
<tr>
<td>Grp 3</td>
<td>27</td>
<td>.0129</td>
<td>.0008</td>
<td>.0002</td>
<td>.0126</td>
<td>.0167</td>
<td>.0126 TO .0132</td>
</tr>
<tr>
<td>Grp 4</td>
<td>41</td>
<td>.0102</td>
<td>.0010</td>
<td>.0002</td>
<td>.0086</td>
<td>.0126</td>
<td>.0098 TO .0105</td>
</tr>
<tr>
<td>Grp 5</td>
<td>32</td>
<td>.0088</td>
<td>.0009</td>
<td>.0002</td>
<td>.0065</td>
<td>.0108</td>
<td>.0085 TO .0092</td>
</tr>
<tr>
<td>TOTAL</td>
<td>463</td>
<td>.0129</td>
<td>.0019</td>
<td>.0001</td>
<td>.0065</td>
<td>.0167</td>
<td>.0127 TO .0130</td>
</tr>
</tbody>
</table>
FIXED EFFECTS MODEL  .0012  .0001  .0127  TO  .0130

RANDOM EFFECTS MODEL  .0010  .0100  TO  .0158

RANDOM EFFECTS MODEL - ESTIMATE OF BETWEEN COMPONENT VARIANCE  0.0000
Appendix 4: Helicopter data

examine variables = numemer by shift
/statistics=none
/plot=spreadlevel.

Thus the spread and level plot suggests somewhere between a square root transformation and the identity. Most likely a transformation is not needed in this case—not just because the spread and level plots says so but it is also obvious from the boxplots. First, let’s look at the raw helicopter data, then the transformed (square root).
Figure 2-8: Raw helicopter data. Transformation doesn’t seem to be needed here.
Figure 2-9: Square root of the helicopter data. The spread and level plot suggests that if a transformation is needed, then it might be the square root given that we limit ourselves to the “power family”. It isn’t clear that the transformed boxplot is any better than the original. So, we’d opt for not performing a transformation for these data.
Appendix 5: Population data

examine variables = pop by country
/statistics=none
/plot=spreadlevel.

* Plot of LN of Spread vs LN of Level.
Slope = .726    Power for transformation = .274
Test of homogeneity of variance   df1   df2   Significance
Levene Statistic        2.4580   15    144    .0031
Appendix 6: Transformations and Symmetry

Showing the use of transformation for satisfying the assumption of normality. I generated some random data. A normal plot follows. I know that such a distribution can be transformed, or re-expressed, into something that looks more normal by performing a log transformation. A second normal plot shows the “improvement” on the log scale.

data list free / dv.
begin data.
1.0355169
2.6118367
0.8492587
3.4192738
2.1297903
1.9830919
3.7556537
0.5049452
1.2166372
1.0311578
1.5835213
0.8411258
1.0442988
0.1184379
0.4746945
0.7125102
1.5810627
0.1060652
2.5585323
0.8339119
1.4155980
2.6909101
6.9099978
1.9278372
0.7376325
end data.

examine variables = dv
/plot = boxplot npplot.

DV
Valid cases: 25.0 Missing cases: 0.0 Percent missing: 0.0

Mean 1.6829 Std Err .2914 Min .1061 Skewness 2.1090
Median 1.2166 Variance 2.1221 Max 6.9100 S E Skew .4637
5% Trim 1.5151 Std Dev 1.4568 Range 6.8039 Kurtosis 6.0512
IQR 1.5584 S E Kurt .9017
**compute logdv = ln(dv).**

**execute.**

**examine variables = logdv**

`/plot = boxplot npplot.`

**LOGDV**

<table>
<thead>
<tr>
<th>Valid cases:</th>
<th>25.0</th>
<th>Missing cases:</th>
<th>.0</th>
<th>Percent missing:</th>
<th>.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>0.1630</td>
<td>Std Err</td>
<td>0.1918</td>
<td>Min</td>
<td>-2.2437</td>
</tr>
<tr>
<td>Median</td>
<td>0.1961</td>
<td>Variance</td>
<td>0.9199</td>
<td>Max</td>
<td>1.9330</td>
</tr>
<tr>
<td>5% Trim</td>
<td>0.2039</td>
<td>Std Dev</td>
<td>0.9591</td>
<td>Range</td>
<td>4.1787</td>
</tr>
<tr>
<td>IQR</td>
<td>1.0907</td>
<td>5 E Kurt</td>
<td>0.9017</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>