Data Transformation

- Transformations in R
  - General overview
  - Log transformation
  - Power transformation
- The pitfalls of interpreting interactions in transformed data

Transformations in R

"Data transformation" is a fancy term for changing the values of observations through some mathematical operation. Such transformations are simple in R and assume a form that should be very familiar to you by now:

```
data_dat$trans_Y <- sqrt(data_dat$Y)
```

The above code tells R to create a new variable (or column in the data_dat dataset) named "trans_Y" that is equal to the square root of the original response variable Y. We've seen this basic trick before (e.g. appending residual and predicted values to a dataframe).

While R can handle just about any mathematical operation you can throw at it, the syntax for such things is not always intuitive. So here are some other examples that we could have used in the above sample code:

```
data_dat$trans_Y <- (data_dat$Y)^3          Raises Y to the power of 3
data_dat$trans_Y <- (data_dat$Y)^(1/9)      Takes the ninth root of Y
data_dat$trans_Y <- log(data_dat$Y)         Takes the natural logarithm (ln) of Y
data_dat$trans_Y <- log10(data_dat$Y)       Takes the base-10 logarithm of Y
data_dat$trans_Y <- exp(data_dat$Y)         Raises the constant e to the power of Y
data_dat$trans_Y <- abs(data_dat$Y)         Finds the absolute value of Y
data_dat$trans_Y <- sin(data_dat$Y)         Calculates the sine of Y
data_dat$trans_Y <- asin(data_dat$Y)        Calculates the inverse sine (arcsine) of Y
Etc…
```

You can create as many derived variables as you wish; and you can calculate new variables that refer to other derived variables, e.g.

```
data_dat$trans1_Y <- sqrt(data_dat$Y)
data_dat$trans2_Y <- sin(data_dat$trans1_Y)
```

But now for some real examples.

Log Transformation

Example 1 *From Little and Hills [Lab6ex1.R]*

In this experiment, the effect of vitamin supplements on weight gain is being investigated in three animal species (mice, chickens, and sheep). The experiment is designed as an RCBD with one replication (i.e. animal) per block*treatment combination. The six treatment levels are MC (mouse control), MV (mouse + vitamin), CC (chicken control), CV (chicken + vitamin), SC (sheep control), and SV (sheep + vitamin). The response variable is the weight of the animal at the end of the experiment.

trtmt	block	weight
MC	I	0.18
MC	II	0.3
MC	III	0.28
...	...	...
SV	II	153
SV	III	148
SV	IV	176

```
#read in, re-classify, and inspect the data
vit_dat<-as.data.frame(vit_dat)
vit_dat$block<-as.factor(vit_dat$block)
vit_dat$trtmt<-as.factor(vit_dat$trtmt)
str(vit_dat, give.attr = F)

#The ANOVA
vit_mod<-lm(weight ~ trtmt + block, vit_dat)
anova(vit_mod)

#Need to assign contrast coefficients
#Notice from str() that R orders the Trtmt levels this way: CC,CV,MC,etc...
# Our desired contrasts:
# Contrast 'Mam vs. Bird'         2,2,-1,-1,-1,-1
# Contrast 'Mouse vs. Sheep'      0,0,1,1,-1,-1
# Contrast 'Vit'                  1,-1,1,-1,1,-1
# Contrast 'MamBird*Vit'           2,-2,-1,1,-1,1
# Contrast 'MouShe*Vit'           0,0,1,-1,-1,1

contrastmatrix<-cbind(c(2,2,-1,-1,-1,-1),c(0,0,1,1,-1,-1),c(1,-1,1,-1,1,-1),c(2,-2,-
1,1,-1,1),c(0,0,1,-1,-1,1))
contrasts(vit_dat$trtmt)<-contrastmatrix

log_contrast_mod<-aov(weight ~ trtmt + block, vit_dat)
summary(log_contrast_mod, split = list(trtmt = list("MvsB" = 1, "MvsS" = 2, "Vit" = 3,
"MB*Vit" = 4, "MS*Vit" = 5)))

#TESTING ASSUMPTIONS
#Generate residual and predicted values
vit_dat$resids <- residuals(vit_mod)
```

```
vit_dat$preds <- predict(vit_mod)
vit_dat$sq_preds <- vit_dat$preds^2

#Look at a plot of residual vs. predicted values
plot(resids ~ preds, data = vit_dat,
       xlab = "Predicted Values",
       ylab = "Residuals")

#Perform a Shapiro-Wilk test for normality of residuals
shapiro.test(vit_dat$resids)

#Perform Levene's Test for homogenity of variances
#install.packages("car")
library(car)
leveneTest(weight ~ trtmt, data = vit_dat)

#Perform a Tukey 1-df Test for Non-additivity
log_1df_mod<-lm(weight ~ trtmt + block + sq_preds, vit_dat)
anova(log_1df_mod)
```

The ANOVA

```
                 Df Sum Sq Mean Sq F value   Pr(>F)
trtmt             5 108714   21743 174.433 9.77e-13 ***
  trtmt: MvsB     1  25780   25780 206.821 3.51e-10 ***
  trtmt: MvsS     1  82541   82541 662.193 7.97e-14 ***
  trtmt: Vit      1    142     142   1.140   0.3025
  trtmt: MB*Vit   1     57      57   0.459   0.5084
  trtmt: MS*Vit   1    193     193   1.550   0.2322
block             3    984     328   2.631   0.0881 .
Residuals        15   1870     125
```

Test for normality of residuals

```
        Shapiro-Wilk normality test

data:  vit_dat$resids
W = 0.9536, p-value = 0.3236
```

NS

Test for homogeneity of variance among treatments

```
Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
group   5  3.3749 0.0252 *
```

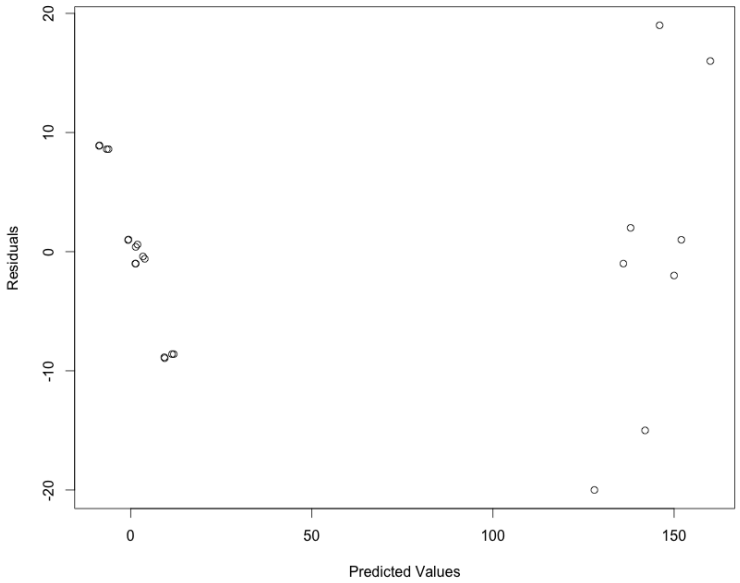
Levene's Test is significant.
The res vs. pred plot will illustrate this.

Test for nonadditivity

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
~~trtmt~~	~~5~~	~~108714~~	~~21742.7~~	~~6506.417~~	~~< 2.2e-16~~	~~***~~
~~block~~	~~3~~	~~984~~	~~328.0~~	~~98.153~~	~~1.222e-09~~	~~***~~
sq_preds	1	1823	1822.9	545.507	1.301e-12	***
Residuals	14	47	3.3			

DANGER DANGER WILL ROBINSON!!!
SIGNIFICANT NON-ADDITIVE EFFECT! MUST TRANSFORM DATA!

Status: We violated our assumption of additivity,
and Levene's Test for Treatment is significant.
What to do? First thing's first: Read your tea leaves…



It's smiling at you.

Now take a look at the means, standard deviations, and variances:

Trtmt	Mean	Std Dev	Variance
MC	0.3000000	0.1070825	0.0114667
MV	0.4000000	0.0588784	0.0034667
CC	2.4000000	0.5887841	0.3466667
CV	2.9000000	0.4618802	0.2133333
SC	137.0000000	23.3666429	546.0000000
SV	151.0000000	20.1163284	404.6666667

Between mice and sheep, the mean increases by a factor of about 400, the standard deviation increases by a factor of about 270, and the variance increases by a factor of about 73,000!

The situation we face is this:

1. Significant Tukey Test for Nonadditivity
2. The standard deviation scales with the mean
3. The Res vs. Pred plot is smiling tauntingly at you

The best transformation under these conditions is a LOG transformation.

Example 1 (continued) *[Lab5ex1.R]*

```
#Create a log-transformed variable
vit_dat$trans_weight<-log10(10*vit_dat$weight)
```

Output

The ANOVA of the log-transformed data

```
                 Df Sum Sq Mean Sq  F value   Pr(>F)
trtmt             5 28.632   5.726 1859.571  < 2e-16 ***
  trtmt: MvsB     1  0.969   0.969  314.750 1.78e-11 ***
  trtmt: MvsS     1 27.603  27.603 8963.598  < 2e-16 ***
  trtmt: Vit      1  0.050   0.050   16.355 0.001060 **
  trtmt: MB*Vit   1  0.000   0.000    0.012 0.913524
  trtmt: MS*Vit   1  0.010   0.010    3.140 0.096717 .
block             3  0.120   0.040   13.043 0.000186 ***
Residuals        15  0.046   0.003
```

Test for normality of residuals of the transformed data

```
Shapiro-Wilk normality test

data:  vit_dat$trans_resids
W = 0.966, p-value = 0.5694 NS
```

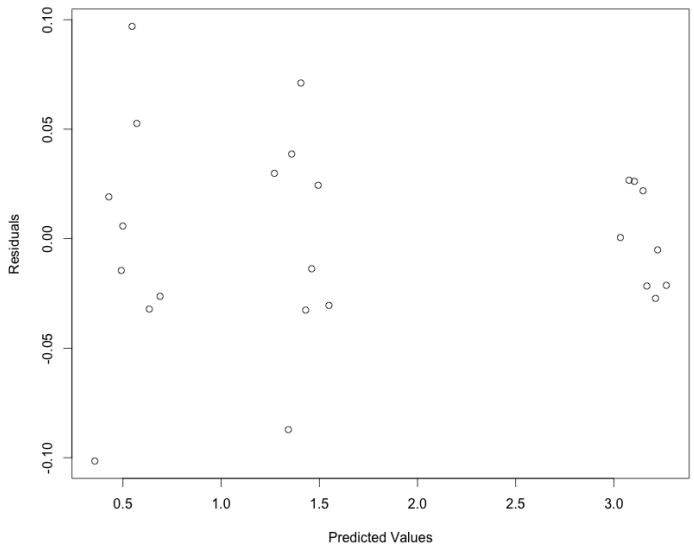
Test for homogeneity of variance among transformed treatments

```
Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  5  1.0094 0.4407 NS
```

Test for nonadditivity in the transformed data

```
                Df  Sum Sq Mean Sq   F value    Pr(>F)
trtmt            5 28.6323  5.7265 1950.9256 < 2.2e-16 ***
block            3  0.1205  0.0402   13.6838 0.0001906 ***
sq_trans_preds   1  0.0051  0.0051    1.7369 0.2086908 NS
Residuals       14  0.0411  0.0029
```

All of our tests are good. Notice how much better the residuals look now:



At this point, you may make conclusions about differences among treatments, etc. But be careful how you state your conclusions because you are making them based on *transformed data*. It is also customary to use the *detransformed* means in your final conclusions. "But aren't the detransformed means just the original means reclaimed?" NO:

When the mean of the logarithms is detransformed back to the original scale, what results is a geometric mean (not arithmetic mean) of the original data:

						Mean
Y	20	40	50	60	80	50
log(Y)	2.9957	3.6889	3.9120	4.0943	3.820	3.8146

The geometric mean of the original data $G = (20*40*50*60*80)^{1/5} = 45.3586$, exactly what you get if you detransform the log(Y) mean: $10^{3.8146} = 45.3586$.

Some final remarks about the Log transformation

Data with negative values cannot be transformed this way. If there are zeros in the data, we are faced with the problem that $\text{Log}(0) = -\infty$. To get around this, it is recommended that 1 be added to every data point before transforming. Logarithms to any base can be used, but log10 is most common. Before transforming, it is also legitimate to multiply all data points by a constant since this has no effect on subsequent analyses. This is a good idea if any data points are less than 1, for in this way you can avoid negative logarithms (Little and Hills).

Power Transformation

Example 2 *[Lab5ex2.R]*

This experiment is a generic CRD with six treatments and five replications per treatment.

trtmt	response
A	220
B	96
C	62
…	…
D	265
E	131
F	101

```
#read in, re-classify, and inspect the data
power_dat<-as.data.frame(power_dat)
power_dat$trtmt<-as.factor(power_dat$trtmt)
str(power_dat, give.attr = F)

#The ANOVA
power_mod<-lm(response ~ trtmt, power_dat)
anova(power_mod)

library(agricolae)
tukey<-HSD.test(power_mod, "trtmt")

#Generate residual and predicted values
power_dat$resids <- residuals(power_mod)
power_dat$preds <- predict(power_mod)
power_dat$sq_preds <- power_dat$preds^2

#Look at a plot of residual vs. predicted values
plot(resids ~ preds, data = power_dat, xlab = "Predicted Values",
      ylab = "Residuals")

#Perform a Shapiro-Wilk test for normality of residuals
shapiro.test(power_dat$resids)

#Perform Levene's Test for homogenity of variances
leveneTest(response ~ trtmt, data = power_dat, center = mean)
leveneTest(response ~ trtmt, data = power_dat, center = median)
```

Note: There is no Tukey 1-df Test for Nonadditivity because this is a CRD.

Output

The ANOVA

```
           Df Sum Sq Mean Sq F value    Pr(>F)
trtmt       5 143273 28654.6  13.437 2.641e-06 ***
Residuals 24  51180  2132.5
```

Test for normality of residuals

```
        Shapiro-Wilk normality test

data:  power_dat$resids
W = 0.9827, p-value = 0.891 NS
```

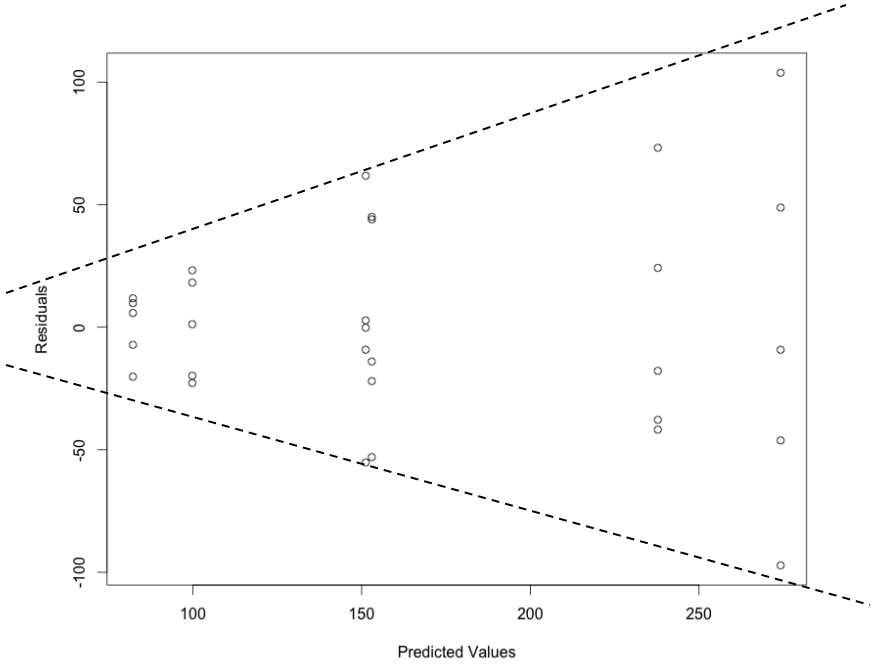
Test for homogeneity of variances among treatments

```
Levene's Test for Homogeneity of Variance (center = mean)
       Df F value  Pr(>F)
group   5  2.9164 0.03396 *
       24

Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
group   5  1.7915 0.1527
```

DANGER DANGER!!!
Wonky Levene's Test! Transform data!

The tea leaves



The significant Levene's Test is reflected in the Res*Pred plot above. The funnel shape of the data indicates that the magnitude of the residuals is increasing as the mean increases. This is verified by the table of means and standard deviations shown below:

	response	std	r	Min	Max	
A	237.8	48.57160	5	196	311	
B	151.2	41.70971	5	96	213	
C	82.2	13.49815	5	62	94	MIN mean and stdev
D	274.2	78.77627	5	177	378	MAX mean and stdev
E	153.0	43.15669	5	100	198	
F	99.8	21.11161	5	77	123	

In this situation, a power transformation will likely restore the data; but what is the appropriate power to use? There is a slick procedure for finding this information, and it involves performing a regression of the logarithms of the variances vs. the logarithms of the means of the original data. The code:

Example 2 (continued) *Calculating the power for a power transformation [Lab6ex2.R]*

```
# ----- Finding the exponent for a power transformation ----

means <- aggregate(power_dat$response, list(power_dat$trtmt), mean)
vars <- aggregate(power_dat$response, list(power_dat$trtmt), var)

logmeans <- log10(means$x)
```

```
logvars <- log10(vars$x)

power_mod<-lm(logvars ~ logmeans)
summary(power_mod)
```

Output

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.5353     0.8463  -2.996  0.04010 *
logmeans      2.5814     0.3864   6.680  0.00261 **
```

Locate the slope of the regression. In this case, slope = 2.5814. Now calculate the appropriate power of the transformation, where Power = 1 – (b/2). In this case,

$$\text{Power} = 1 - (2.5814/2) = -0.29$$

To use this magic number, return to R and continue coding:

```
#Create power-tranformed variable
power_dat$trans_response<-(power_dat$response)^(-0.29)

#The ANOVA
trans_power_mod<-lm(trans_response ~ trtmt, power_dat)
anova(trans_power_mod)

trans_tukey<-HSD.test(trans_power_mod, "trtmt")

#TESTING ASSUMPTIONS
#Generate residual and predicted values
power_dat$trans_resids <- residuals(trans_power_mod)
power_dat$trans_preds <- predict(trans_power_mod)

#Look at a plot of residual vs. predicted values
plot(trans_resids ~ trans_preds, data = power_dat,
     xlab = "Predicted Values",
     ylab = "Residuals")

#Perform a Shapiro-Wilk test for normality of residuals
shapiro.test(power_dat$trans_resids)

#Perform Levene's Test for homogenity of variances
leveneTest(trans_response ~ trtmt, data = power_dat, center = mean)
leveneTest(trans_response ~ trtmt, data = power_dat, center = median)
```

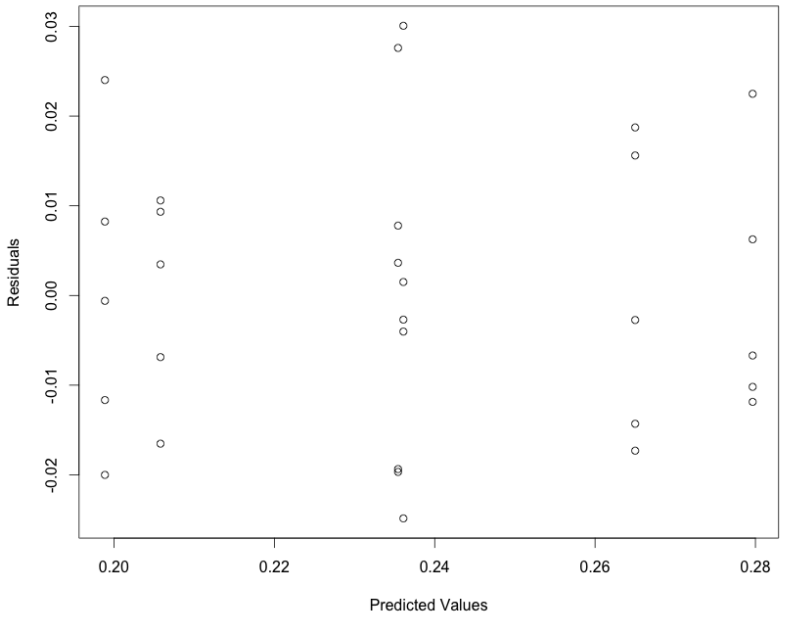
Output

Again, we have a significant ANOVA and a NS Shapiro-Wilk test. But our Levene's Test results have changed dramatically:

```
Levene's Test for Homogeneity of Variance (center = mean)
       Df  F value  Pr(>F)
group   5    0.279    0.92  NS!

Levene's Test for Homogeneity of Variance (center = median)
       Df  F value  Pr(>F)
group   5   0.2125  0.9538  NS!
```

And this result is confirmed by the Res*Pred plot for the transformed data, shown below. Notice that the strong funnel shape is now gone and the variances have lost their previous correlation to the means.



The suggested power transformation restored the homogeneity of variances and eliminated the obvious correlation between means and dispersion. Mean comparisons based on the transformed data are valid, *but those based on the untransformed (i.e. original) data are not*. This is because in the ANOVA of the original data, you used an average variance (MSE) that is not really representative of the different variances present across the different treatments.

To present a table of mean comparisons from this experiment, first perform the mean comparison analysis on the *transformed* data. The results:

	trt	means	M
1	C	0.2796530	a
2	F	0.2650037	ab
3	B	0.2360917	bc
4	E	0.2354292	bc
5	A	0.2057988	cd
6	D	0.1988690	d

While the Tukey Groupings (i.e. significance groups) shown in this table are correct, it is customary to present the means in the original data scale. To do this, you should *detransform* the means of the transformed data, using the inverse operation of the original transformation:

[e.g. For Treatment C, the detransformed mean is (0.27965)^(-1/0.29) = 80.95147]

	trt	means	M
1	D	262.2567	a
2	A	233.0396	ab
3	E	146.5527	bc
4	B	145.1448	bc
5	F	97.45572	cd
6	C	80.95147	d

Notice how it was necessary to flip the sequence of the treatments and shuffle the letters of the significance groupings in order to keep the means listed from largest to smallest. For reference, here is what the Tukey means separation table looked like for the original data:

	trt	means	M
1	D	274.2	a
2	A	237.8	ab
3	E	153.0	bc
4	B	151.2	bc
5	F	99.8	c
6	C	82.2	c

THE TAKE-HOME MESSAGE

USE THE DATA THAT BETTER FIT THE ANOVA ASSUMPTIONS,
NOT THE DATA THAT BETTER FIT **YOUR** ASSUMPTIONS ABOUT NATURE

The Pitfalls of
Interpreting Interactions in Transformed Data

	0	A	B	AB
Y	20	30	35	45
Y^2	400	900	1225	2025