Topic 8. Data Transformations [ST&D section 9.16]

8.1 The assumptions of ANOVA

For ANOVA, the linear model for the RCBD is:

$$Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$

There are four key assumptions implicit in this model.

8.1.1. Additive effects

For the ANOVA to be valid, the treatment effects τ_i and block effects β_j must be additive (as opposed to, for example, multiplicative). Another way to say this is that "The treatment effects must be constant across blocks and the block effects must be constant across treatments." In terms of the model above, the treatment effects τ_i are independent of j, the index of blocks, and the block effects are independent of i, the index of treatments.

If multiplicative effects were present, the model would more appropriately be:

$$Y_{ij} = \mu(\tau_i)(\beta_j) + \varepsilon_{ij}$$

Tukey's 1-df Test for Nonadditivity is a tool for testing if the departure from additivity is statistically significant in an RCBD with one observation per cell (i.e. block-treatment combination).

8.1.2. Independence of errors

For the ANOVA to be valid, the values of the ε_{ij} (i.e. the *errors* or *residuals*) must be statistically independent from one another. Failure to meet this assumption is often the result of failing to randomize properly.

Similarity among experimental units adjacent in space or time is called **positive autocorrelation**. The regular alternation of positive and negative errors is a manifestation of **negative autocorrelation**. While independence of errors in a sequence of continuous variates may be tested using the differences between adjacent values (Biometry 394 –395), the process of randomly allocating the treatments to the experimental units usually ensures that the ε_{ij} will be independent. One ordinarily does not need to do more than a true randomization to satisfy this requirement. If another assumption is violated, however, it is often found that the assumption of independence of errors is also violated.

8.1.3. Normal distribution of errors

For the ANOVA to be valid, the error terms ε_{ij} (i.e. residuals) must be normally distributed. *This is the least influential assumption on the F test*, and some people do not worry too much about it. That being said, it is good practice to verify normality since all statements of probability are based on normal distributions. For small to medium sample sizes, the Shapiro-Wilk test is recommended. If the sample size is ≥ 2000, the Kolmogorov-Smirnov statistic (ST&D 564-568) is recommended.

8.1.4. Homogeneity of Variance

For the ANOVA to be valid, the variance among experimental units receiving the same treatment must be uniform across all levels of treatment. *This is the most influential assumption on the F test, and no conclusions should be drawn from the ANOVA if this assumption is violated.* The reason this assumption is so influential on the F test is because MSE, the denominator of the F test, is the *average* within-treatment variance. The very act of taking an average assumes that all within-treatment variances are estimates of the same value.

It is possible to fail this assumption. For example, the variance among EUs within a treatment level may scale with the treatment mean. This is often the case when the treatments have substantial effects on the response variable. The variances may also be unequal but have no apparent relation to the treatment means. The following example, based on one from Little and Hills, shows what can happen when homogeneity of variance is violated.

	Replicate							
Treatment	**1**	**2**	**3**	**4**	**5**	**Total**	**Mean**	**s^2**
A	3	1	5	4	2	15	3	2.5
B	6	8	7	4	5	30	6	2.5
C	12	6	9	3	15	45	9	22.5
D	21.5	15.5	12.5	18.5	9.5	77.5	15.5	22.5

The result of the ANOVA:

Source of variation	df	SS	MS	F
Treatments	3	428.4	142.8	11.4 ***
Error	16	200	12.5	

A Tukey means separation ($\alpha = 0.05$) uses a minimum significant difference of 6.3974. Therefore, the difference between means A and B is declared not significant while that between C and D is declared significant.

When analyzed *separately*, however, (i.e. with two separate ANOVAs), one obtains the exact opposite result:

Source of variation	df	SS	MS	F	p
Treatments A B	1	22.5	22.5	9.00 *	0.02
Error	8	20.0	2.5		
Source of variation	**df**	**SS**	**MS**	**F**	
Treatments C D	1	105.6	105.6	4.69 NS	0.06
Error	8	180	22.5		

Here, the difference between A and B *is* significant while that between C and D *is not*. The reason for this is that the variance for treatments C and D is larger than that for A and B. More specifically, by taking an average of all the variances (the MSE), those treatments with smaller variances were being unfairly penalized and those treatments with larger variances were being tested with an unreasonably small error.

> The consequences of moderate heterogeneity of variances are not too serious for the overall test of significance, but single degree-of-freedom comparisons (contrasts, means separations) may be far from accurate.

Among the different tests for homogeneity of variances, Bartlett's Test (S&TD 471) and Levene's Test are the most widely used. Bartlett's is a chi-square goodness of fit test and Levene's is an ANOVA of the squares or absolute values of the residuals.

If Levene's test is significant and the problem of heterogeneity of variances cannot be corrected by transformation, you can perform a **Welch's variance-weighted ANOVA** to test for differences among group means. The other alternative in this case is to analyze the data using **non-parametric statistics**.

8.2. Transformations

If the evidence indicates that the assumptions for an analysis of variance cannot be satisfied, two courses of action are available. The first is to carry out a different test which does not require the rejected assumptions, such as a non-parametric test or a variance-weighted ANOVA. The second is to transform the response variable in such a manner that the resulting *transformed variable* meets the assumptions of the analysis. Once this is accomplished, you can perform the analysis on the transformed variable.

When a statistical test that was not significant with the original data suddenly becomes significant after a data transformation, people may feel suspicious. What is the justification for transforming the data?

To begin, there is really no scientific necessity to employ the common linear or arithmetic scale to which we are accustomed. If a relationship is multiplicative on a linear scale, it may make much more sense to think of it as an additive relationship on a logarithmic scale.

The square root of a variable is another frequent transformation. The square root of the surface area of an organism may be a more appropriate measure of the effects of physiological and evolutionary forces on some biological variable than is the area itself. Evidence of this is reflected in the fact that, often, the square root of the surface area is normally distributed while the surface areas themselves exhibit a skewed distribution. In many cases, experience has shown that is better to express some variables in terms of logarithms (pH values), square roots (areas), or reciprocals (microbiological titrations). As soon as one accepts the idea that *the scale of measurement is arbitrary*, it is becomes clear that is valid to transform a variable in order to satisfy the assumptions of the analysis.

A fortunate fact about transformations is that very often several departures from the assumptions of ANOVA are cured simultaneously by a single transformation to a new scale. Simply by making the data homoscedastic (i.e. having uniform variances), normality and additivity of main effects may also be restored.

Four transformations will be discussed here: the logarithmic transformation, the square root transformation, the angular or arcsine transformation, and the power transformation.

8.2.1 The log transformation [Little and Hills]

Whenever the **standard deviations** (not the variances) of samples are roughly proportional to the means, an effective transformation may be a log transformation. Another criterion for deciding on this transformation is the evidence of multiplicative rather than additive main effects, as evidenced by significant Tukey's test. Finally, frequency distributions skewed to the right are often made more symmetrical by transformation to a logarithmic scale.

While logarithms to any base can be used, common logarithms (base 10) or natural logarithms (base e) are generally the most convenient. Data with values ≤ 0 cannot be transformed using logarithms, because the log of negative numbers is undefined and the log of zero is $-\infty$. In such cases, one may add a constant number to every data point so that the lowest value in the dataset becomes 1. Data containing a large number of zeros would probably be handled better by some other method.

Also before transforming, it is legitimate to multiply all data points by a constant, since this has no effect on the subsequent analyses. This is particularly useful if any of the data points are between 0 and 1, to avoid negative logarithms.

The following data set (Little and Hills 1978) will be used as an example of the effects of the log transformation on the assumptions of the ANOVA. The dependent variable is weight (lbs) of vitamin-treated and control animals; the design is an RCBD.

Data table for an RCBD with 4 blocks and 6 treatments.

	Block						
Species—Treatment	**I**	**II**	**III**	**IV**	**Total**	**Mean**	**s_i^2**
Mice—control	0.18	0.30	0.28	0.44	1.2	0.3	0.0115
Mice—vitamin	0.32	0.40	0.42	0.46	1.6	0.4	0.0035
Subtotals	**0.50**	**0.70**	**0.70**	**0.90**	**2.8**	**0.35**	
Chickens—control	2.0	3.0	1.8	2.8	9.6	2.40	0.3467
Chickens—vitamin	2.5	3.3	2.5	3.3	11.6	2.90	0.2133
Subtotals	**4.5**	**6.3**	**4.3**	**6.1**	**21.2**	**2.65**	
Sheep—control	108.0	140.0	135.0	165.0	548.0	137.0	546.0
Sheep—vitamin	127.0	153.0	148.0	176.0	604.0	151.0	425.3
Subtotals	**235.0**	**293.0**	**283.0**	**341.0**	**1152.0**	**144.0**	
Totals	240.0	300.0	288.0	348.0	1176.0	49.0	

See the lecture notes for the full R code for this analysis. First, the analysis is performed on the original data. Then, the analysis is performed on log transformed data. In this data, there are no zeros; but since the lowest value is 0.18, the data was multiplied by 10 before log transforming. Notice how the transformed variable (here called "LogWeight") is generated in the data input routine.

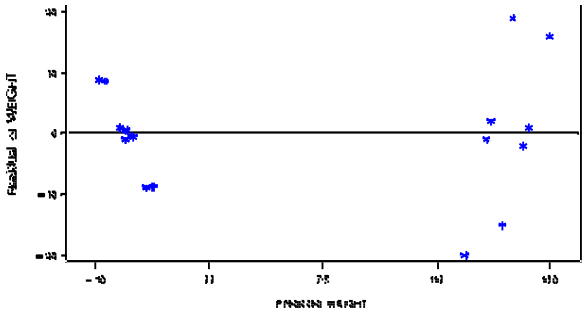
The next table compares the results of the analyses of the original and transformed response variables.

	Original data		Transformed data	
	F	**p**	**F**	**p**
Shapiro-Wilk	W = 0.95	0.32	W = 0.97	0.56
Levene's Test	3.37	0.03	1.01	0.44
Tukey's Nonadditivity Test	545.5	< 0.0001	1.74	0.21
Treatment F test	174.4	< 0.0001	1859.6	< 0.0001
"Bird/Mam" Contrast	206.8	< 0.0001	314.8	< 0.0001
"Mouse/Sheep" Contrast	662.2	< 0.0001	8964	< 0.0001
"Vitamin" Contrast	142.1	**0.3025**	16.4	**0.0011**
"B/M*Vit" Interaction	57.2	0.5084	0.01	0.9135
"M/S*Vit" Interaction	1.55	0.2322	3.14	0.0967

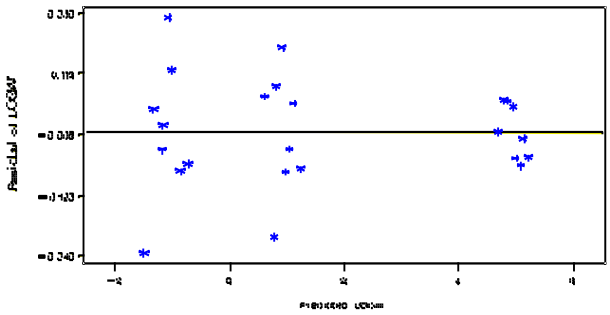
When this data was analyzed without any transformation, no significant effect of the vitamin treatment was detected. This seems very strange, because every animal in every replicate receiving the vitamin showed a greater weight than the corresponding control animal. It also seems strange that no significant differences were detected for the interaction between vitamin effects and species, since the apparent response to vitamins is so different in the different species.

These unexpected results suggest that there is something wrong with the ANOVA, and indeed there is. When the assumptions of the ANOVA are checked, significant Tukey's and Levene's tests demonstrate that there is significant nonadditivity of main effects as well as

significant heterogeneity of variances. A quick look at the residuals confirms these violations of the ANOVA assumptions:



Res vs. Pred **(Original data)**



Res vs. Pred **(Transformed data)**

The presence of multiplicative effects (see the smiley pattern in the above plot) and a rough proportionality between standard deviations and means suggest that a logarithmic transformation may be appropriate. Indeed, the transformed data meet all the ANOVA assumptions. Also, the results using the transformed data make more sense, particularly in terms of the significant effect of the vitamin treatment. The interaction between species and vitamins is still not significant, which may seem puzzling. But recognize that the question is now different. With the original data, the interaction question was, "Does the amount of change in weight due to vitamins vary from species to species?" With the log-transformed data, the question is now, "Does the ***proportion*** **or** ***percent*** change in weight due to vitamins vary from species to species?"

Did we get more satisfying results with the transformed data because we were simply playing with the numbers, fishing around until we got a result we liked? Or was the transformation we used justified and is the new analysis valid? Values for Tukey's and Levene's tests were significant for the original data but non-significant for the transformed data (even Shapiro-Wilk improved under the log transformation). The new analysis is valid because the transformed data satisfies *all* the assumptions of the ANOVA. But as you see with the interaction question, *interpretation* of results using transformed data can be tricky.

Effect of log transformation on means and variances

The data below illustrate the effect of the *ln* transformation on a multiplicative effect of a treatment that increases control values by 50% (*1.5). Notice the similar variance of 0.2740 after the *ln* transformation.

			Control			**Mean**	**Var**
Y	20	40	50	60	80	50	500
ln(Y)	2.9957	3.6889	3.9120	4.0943	3.820	3.8146	0.2740
			Treatment (1.5*Control)			**Mean**	**Var**
Y	30	60	75	90	120	75	1125
ln(Y)	3.4012	4.0943	4.3175	4.4998	4.7875	4.2201	0.2740

8.2.2. The square root transformation [Little and Hills]

Whenever the response variable is a count of relatively rare events (e.g. insects on a leaf, blood cells within a gridded region of a hematocytometer, etc.), the data tend to follow a special distribution called a *Poisson distribution*. In this context, a "rare event" is an event that has a very low probability of occurring in any individual. For example, suppose that in a lot of lettuce seed, 0.1% of the seed carries mosaic disease virus. The probability that any individual seed carries the virus is then only 1/1000; so as far as a single seed is concerned, this is a very rare event. If we take 100 samples of 1000 seeds each from such a lot, we will obtain approximately these results:

37	samples will contain 0 infected seeds
37	samples will contain 1 infected seed
18	samples will contain 2 infected seeds
6	samples will contain 3 infected seeds
2	samples will contain 4 infected seeds

It is obvious that this looks very little like a normal distribution. This Poisson distribution has a very interesting characteristic — the **variance** is equal to the mean. In actual practice, the variance is generally somewhat larger than the mean because other factors, in addition to sampling variation, are affecting the occurrence of the events being counted. At any rate, the variance tends to be proportional to the mean, thus violating the assumption that the variances and means are not correlated.

Another example of data of this kind is found in insect counts, such as those made from a standard number of sweeps with a net. The probability of finding an insect at a particular spot selected at random at one particular time is indeed a rare event.

Data of this kind can be made more nearly normal and at the same time the variances can be made relatively independent of the means by using a square root transformation. Actually, for count values near or less than 10, it is better to use:

$$Y_{transformed} = \sqrt{Y_{original} + \frac{1}{2}}$$

Example: Number of lygus bugs per 50 sweeps with a net. The experiment is an RCBD, testing 10 insecticides (A – J) and a control (K).

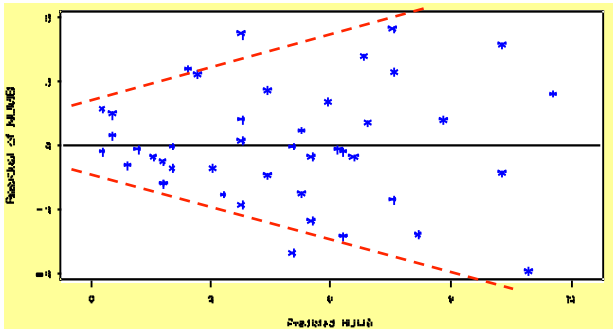
Treatment	Block						
	I	II	III	IV	Total	Mean	s_i^2
A	7	5	4	1	17	4.25	6.25
B	6	1	2	1	10	2.50	5.67
C	6	2	1	0	9	2.25	6.92
D	0	1	2	0	3	0.75	0.92
E	1	0	1	2	4	1.00	0.67
F	5	14	9	15	43	10.75	21.58
G	8	6	3	6	23	5.75	4.25
H	3	0	5	9	17	4.25	14.25
I	4	10	13	5	32	8.00	18.00
J	6	11	5	2	24	6.00	14.00
K	8	11	2	6	27	6.75	14.25

See the lecture notes for the full R code for this example. Again, we run an ANOVA on the original variable and on the transformed variable.

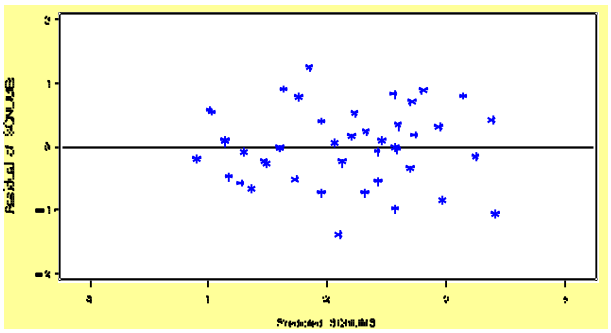
A comparative summary of the results:

	Original data		Transformed data	
	F	p	F	p
Shapiro-Wilk	W = 0.98	0.8204	W = 0.99	0.9790
Levene's Test	1.5	0.1729	0.6	0.8259
Tukey's Nonadditivity Test	0.6	0.4351	0.1	0.7892
Treatment F test	3.7	0.0026	4.0	0.0014

Though the data do not violate any of the assumptions, we can see that the transformed data meet the assumptions better than the original data (look particularly at Levene's Test, which moved from a low p-value of 0.1729 to a much stronger 0.8259). This improvement in the data can be seen in the scatterplots of residual vs. predicted values, shown below. Evidence of a correlation between treatment means and treatment variances manifests itself in the plot of the original data as a funnel shape. This funnel pattern is not visible in the plot of the transformed data:



Res vs. Pred (Original data)
Correlation mean-variance **r = 0.89 **** (p=0.001)



Res vs. Pred (Transformed data)
Correlation mean-variance **r = 0.37 NS** (p=0.1)

And while the two analyses are not very different from one another (e.g. both show a highly significant treatment effect, though the F value is about 10% higher after transformation), some differences do appear when separating means.

The *weighted means* shown are obtained by "detransforming" the means of the transformed data back to the original units. This is done by squaring the transformed means and subtracting one-half (i.e. by performed the inverse of the transformation function). The means obtained in this way are smaller than those obtained directly from the raw data because more weight is given to the smaller variates. This is as it should be, since in a Poisson distribution the smaller variates are measured with less sampling error (i.e. contain more information) than the larger ones. In presenting the results of any experiment in which a data transformation is used for analysis, it is best to present the *detransformed* means, making it clear in the report how they were obtained. Here are the Tukey mean separations performed on the original data and the transformed data ($\alpha = 0.05$):

Original Data

Tukey Grouping			Means	N	Trtmt
	A		10.750	4	F
B	A		8.000	4	I
B	A		6.750	4	K
B	A		6.000	4	J
B	A		5.750	4	G
B	A		4.250	4	H
B	A		4.250	4	A
B			2.500	4	B
B			2.250	4	C
B			1.000	4	E
B			0.750	4	D

Transformed Data ***Detransformed***

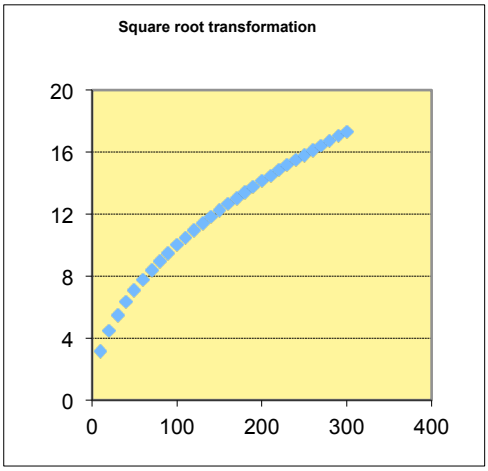
Tukey Grouping			Means	N	Trtmt
	A		10.3445	4	F
B	A		7.5957	4	I
B	A	C	6.3084	4	K
B	A	C	5.6073	4	J
B	A	C	5.5851	4	G
B	A	C	3.9416	4	H
B	A	C	3.5052	4	A
B	A	C	2.2060	4	B
B		C	1.7970	4	C
B		C	0.9028	4	E
		C	0.6130	4	D

Note the differences in significance groupings in this example. (As in all cases, the groupings derived from the transformed data are more reliable because the transformed data satisfy the assumptions of the analysis better than the original data.)

F and **B** are declared different in the original data, but not in the transformed data.

D and **I** are declared different in the transformed data, but not in the original data.

This is a nice illustration of the fact that **the general effect of the square root transformation is to increase the precision with which we measure differences between *small* means.** This is a direct result of the shape of the square root function, shown below.



Small values are spread out relative to large values, making them easier to discriminate from one another. This is highly desirable in insect control work, where we are generally not as interested in differences between two relatively ineffective treatments as we are in comparing treatments that give good control.

Note that the values of the *detransformed* means are smaller than the original means. This is also due to the shape of the curve and is what makes this transformation appropriate for data following a Poisson distribution. The square root transformation essentially gives higher weight to smaller values, those values with higher information content (lower variance).

In general, we can say that data requiring the square root transformation do not violate the ANOVA assumptions nearly as drastically as data requiring a log transformation. Consequently, the changes in the analysis brought about by the transformation are not nearly as spectacular.

8.2.3. The arcsine or angular transformation [Little and Hills]

Another kind of data that may require transformation is that based on counts expressed as percentages or proportions of the total sample. Such data generally exhibit what is called a *binomial distribution* rather than a normal distribution. One of the characteristics of such a distribution is that the variances are related to the means, though in quite a different way than discussed before. Data discussed in 8.2.1 and 8.2.2 showed a positive correlation between means and variances. In binomial data, variances tend to be small at the two ends of the range of values (close to zero and 100%) but larger in the middle (around 50%).

The data below are from a completely randomized experiment on lettuce seed with 24 treatments, each replicated three times. Treatments are arranged in order of magnitude of their means. Note that there is a strong tendency for the variances at the extremes to be smaller than those in the middle of the range. This is typical of binomial data.

Number of lettuce seeds germinating in samples of 50

	Blocks				
Treatment	**1**	**2**	**3**	**Mean**	s_i^2
1	0	0	1	0.33	0.33
2	0	1	0	0.33	0.33
3	0	0	1	0.33	0.33
4	0	2	0	0.67	1.33
5	2	0	0	0.67	1.33
6	0	2	3	1.67	2.33
7	7	10	7	8.00	3.00
8	11	12	15	12.67	4.33
9	13	18	18	16.33	8.33
10	22	16	13	17.00	21.00
11	24	13	18	18.33	30.33
12	23	21	29	24.33	17.33
13	24	29	29	27.33	8.33
14	37	28	27	30.67	30.33
15	42	41	40	41.00	1.00
16	39	41	45	41.67	9.33
17	41	45	40	42.00	7.00
18	47	41	43	43.67	9.33
19	45	42	48	45.00	9.00
20	46	42	48	45.33	9.33
21	49	46	48	47.67	2.33
22	48	49	48	48.33	0.33
23	50	49	48	49.00	1.00
24	49	49	50	49.33	0.33

The arcsine transformation involves taking the inverse sine of the square root of each observation, expressed as a proportion of a total:

$$Y_{transformed} = \arcsin\left(\sqrt{\frac{Y_{original}}{Total\ \ Possible\ Counts}}\right)$$

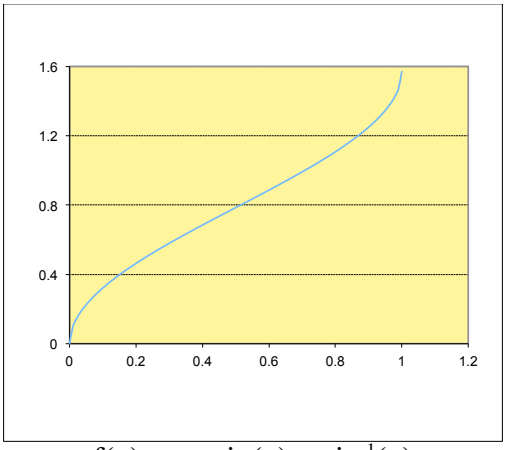
In this case, since the total number of seeds in each replication is 50, the arcsine transformation would be:

$$Y_{transformed} = \arcsin\left(\sqrt{\frac{Y_{original}}{50}}\right)$$

A comparative summary of the results (see lecture notes for R code):

	Original data		Transformed data	
	F	**p**	**F**	**p**
Levene's Test (center = mean)	2.64	0.0023	0.96	0.5255
Treatment F test	147.5	< 0.0001	98.59	< 0.0001

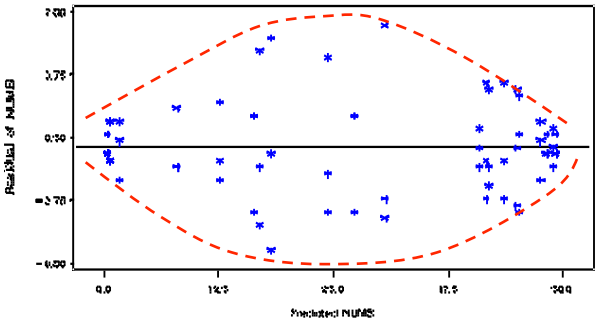
As indicated in the above table, the arcsine transformation is appropriate for this kind of data because it tends to spread the values at both ends of the distribution compared with the central region (i.e. it tends to homogenize variances). This effect is due to the shape of the arcsine function, a function which returns the number (in radians) whose sine is in the range 0 → 1:



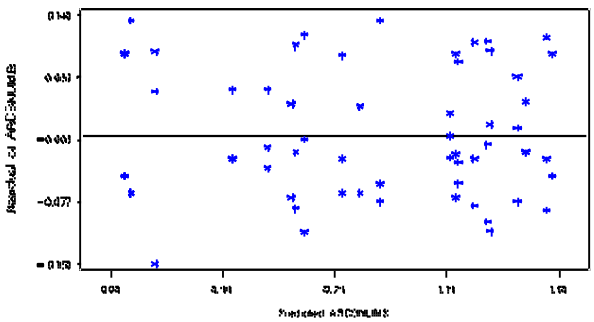
$f(x) = \arcsin(x) = \sin^{-1}(x)$

In general, proportion data of the sort described above should be transformed with the arcsine function if the range of percentages is greater than 0.40. Otherwise, it is scarcely necessary.

In this case, the arcsine transformation was successful is removing the correlation between treatment means and variances. Indeed, the pattern of the residuals observable in the raw data is no longer apparent in the transformed data:



Res vs. Pred **(Original data)**



Res vs. Pred **(Transformed data)**

As you've seen with other transformations, the ANOVA results of arcsine-transformed data are not necessarily different from those of the original data, at least at the level of the overall ANOVA F test. The important differences emerge in individual comparisons (e.g. contrasts and mean separations). A comparison of Tukey mean separations:

Original Data					**Transformed Data**				
			Original Means	**Trtmt**	**Detransformed Means**				
A			49.333	**24**	49.554	**A**			
A			49.000	**23**	49.348	**A**			
A			48.333	**22**	48.370	**A**	**B**		
A			47.667	**21**	47.827	**A**	**B**		
A			45.333	**20**	45.637	**A**	**B**		
A			45.000	**19**	45.302	**A**	**B**		
A			43.667	**18**	43.914	**A**	**B**		
A			42.000	**17**	42.134		**B**	**C**	
A			41.667	**16**	41.834		**B**	**C**	
A			41.000	**15**	41.015		**B**	**C**	
	B		30.667	**14**	30.789	**D**		**C**	
	B		27.333	**13**	27.341	**D**	**E**		
	B	**C**	24.333	**12**	24.333	**D**	**E**	**F**	
D		**C**	18.333	**11**	18.216	**D**	**E**	**F**	**G**
D		**C**	17.000	**10**	16.905	**D**	**E**	**F**	**G**
D	**E**	**C**	16.333	**9**	16.285		**E**	**F**	**G**
D	**E**		12.667	**8**	12.631			**F**	**G**
	E	**F**	8.000	**7**	7.952	**H**			**G**
		F	1.667	**6**	1.111	**H**	**I**		
		F	0.667	**5**	0.225		**I**		
		F	0.667	**4**	0.225		**I**		
		F	0.333	**1**	0.112		**I**		
		F	0.333	**3**	0.112		**I**		
		F	0.333	**2**	0.112		**I**		

Which set of conclusions should we accept? The answer is simple: we should accept the conclusions based on the more valid analysis. In this case, it is the analysis of the transformed data.

We do not transform data to give us results more to our liking. We transform data so that the analysis will be *valid* and the conclusions *correct*.

8.2.4. The power transformation

Hinz, PN and HA Eagles (1976) Estimation of a transformation for the analysis of some agronomic and genetic experiments. *Crop Science* **16**: 280-283.

Field experiments are commonly conducted using replicated trials over a broad range of locations and environmental conditions; and often, the means and the residual variances differ markedly across environments. Furthermore, there tends to be a positive correlation between the mean and the residual variance. In such instances, an analysis of the combined data over environments must contend with this heterogeneity in the residual variance. The transformation of the dependent variable is a well-known technique for reducing this relationship between the mean and the residual variance.

The choice of an optimal transformation from the many possible alternatives is not always obvious, especially if the functional relationship between mean and variance is unknown. The power transformation method (Hinz and Eagles 1976) provides a means of selecting an appropriate transformation from the broad class of power transformations by employing the dataset itself to estimate the exponent needed to transform the original measures.

A power transformation is any transformation in which the original measure is raised to some power "a":

$$Y_{transformed} = \left(Y_{original}\right)^{a}$$

The purpose of Hinz and Eagles' power transformation method is to find the value of "a" most appropriate for the data (i.e. most effective at minimizing the mean-variance correlation and variance heterogeneity). Generally, if the variances and means are positively correlated (i.e. as means increase, variance increases), the optimal value of "a" will be less than 1. If the variances and means are negatively correlated (i.e. as means increase, variance decreases, or vice versa), the optimal value of "a" will be greater than 1.

The square root transformation discussed previously is one specific case of a power transformation, where a = 1/2. If "a" is found to be approximately equal to 0, the log transformation is recommended. So:

$$Y_{transformed} = \left(Y_{original}\right)^{a} \text{ if } \mathbf{a} \neq 0$$
$$Y_{transformed} = \log\left(Y_{original}\right) \text{ if } \mathbf{a} \approx 0$$

And note that $Y = \sqrt{X}$ if $\mathbf{a} = ½$
$Y = 1 / X$ if $\mathbf{a} = -1$

A potentially effective value of the power of the transformation '**a**' can be determined by obtaining the slope '**m**' of the linear regression of $\log\left(s_i^2\right)$ versus $\log\left(\overline{Y}_i\right)$ (i.e. the best-fit slope of a log(Variance) * log(Mean) scatterplot), and then solving for **a** = 1 - **m**/2.

Suppose there are t groups of observations and s_i^2 and $\overline{Y}_i$ are the sample variance and sample mean, respectively, of the ith group. We want to find the slope **m** that best satisfies the linear equation:

$$\log\left(s_i^2\right) = m * \log\left(\overline{Y}_i\right) + b$$

See the lecture notes for R code that is useful for obtaining the treatment means and variances, and then performing a linear regression of the logarithms of those values in order to find the least squared estimate (**m**) of the slope.

Then, the data can be transformed using a power **a** = 1 - **m** /2.

See lecture notes for two power transformation examples.

8.3. Reporting results from transformed data

When a transformation is applied, tests of significance are performed on the transformed data, but estimates of means are usually given in the familiar, untransformed scale. It is best to calculate means using the transformed data and then detransform them to the original units. In this way, we obtain correctly weighted means.

Since all the transformations discussed here are non-linear, confidence limits computed in the transformed scale will become asymmetrical when detransformed into the original scale. Stating the standard error in the original scale is therefore misleading. So, in reporting results of research with variables that require transformation, it is better to report detransformed means (i.e. estimates of means in the original scale) followed by their asymmetrical confidence limits, rather than by a standard error.

Example: Using log transformed data, the mean of Treatment B is found to be 1.176. The Tukey minimum significant difference is found to be 0.023. In the transformed scale, the confidence interval about the mean of Treatment B is symmetric:

$$\mu_B = \overline{Y}_B \pm MSD = 1.176 \pm 0.023 = \textbf{[1.153 , 1.199]}$$

The proper way to report this confidence interval is by detransforming these confidence limits:

$$\mu_B = [10^{1.153} , 10^{1.199}] = \textbf{[14.223 , 15.812]}$$

Notice that this is an asymmetric interval about the detransformed mean $10^{1.176} = 14.997$.

8.3.1 Detransforming *ln* transformed means back to the original scale

The following example shows that when the mean of the logarithms is transformed back to the original scale, the result is the *Geometric Mean* of the original data:

						Mean	Variance
Y	20	40	50	60	80	50	500
ln(Y)	2.9957	3.6889	3.9120	4.0943	4.3820	3.8146	0.2740

Geometric mean $G = (Y_1 * Y_2 * \ldots * Y_n)^{1/n}$
Geometric mean $G = (20*40*50*60*80)^{1/5} = 45.3586$

Note that when you detransform the mean of the log-transformed data back to the original scale, **$e^{3.8146} = 45.3586$**. This is the geometric mean of the original data, NOT the arithmetic mean (50).