Model Based Statistics in Biology.

Part II. Quantifying Uncertainty and Evidence.

Chapter 5 Data Equations

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Red chalk for residuals
Yellow chalk for model
White chalk for data
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on chalk board

Recap Part I

Ch1 Quantitative reasoning: Example of scallops, which combined stats and models
Ch2 Quantities: Five part definition
Ch3 Rescaling
Ch4 Equations express an idea or concept about the relation of one quantity to another

Today-- Data Equations
Defined, then an example to demonstrate the idea
and its application in statistical analysis.

Wrap-up. Data equations summarize pattern in data.
Data equations have 3 parts: the data, the model, and the residuals.
The sum of the residuals is a measure of bias in fit.
The sum of the squared residuals
measures the goodness of fit.
allows us to quantify the improvement in fit.
The likelihood ratio is calculated from the sum of squared residuals
It measures which of two models is more likely than the other.
Data equations apply to regression lines (ratio scale explanatory variable)
and to contrasting means among groups (nominal scale explanatory variable)
We will use likelihood ratios to make statistical tests of regression lines and
contrasting means (t-tests, F-tests, chisquare tests, *etc*).

5.1 Introduction

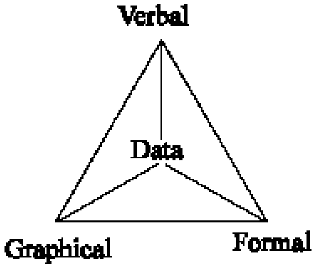
Statistics are often presented in the following sequence

Here are some statistics and how to compute them (means, variances)
Here is a little bit of probability theory (How many blue marbles do you expect to draw in 5 tries, from an urn with 5000 blue marbles and 5000 red marbles ?)
Here are some more probability distributions--normal, X^2, etc.
Here is how to do a t-test to compare two means.
Here is how to do a regression. Etc.

In this course we will take a different approach, one that will allow you to set up an appropriate analysis of data, without having to search for the 'right' test. This approach is readily learned. It allows you to accomplish far more than is possible by learning a series of tests. This model based approach begins with the concept of a set of data equations. We will use data equations to compare models to data.

$$\text{Data} = \text{Model} + \text{Residual}$$

This allows us to set up simple symbolic expressions to undertake statistical analysis of our data. In order to use these simple symbolic expressions with confidence, we will always link them with verbal and graphical expressions of the same idea.



We will use data equations to measure how well a model fits the data. We will use data equations to compare competing models. Later, we will use data equations to calculate the error rate if we assume the model to be true (hypothesis testing).

The goal of the equations lab (Lab 2) is to gain experience in working with models that relate one variable to another. The models in this lab expressed:

-metabolic rate as an allometric function of body mass (Kleiber's Law)
-hormone levels in mothers as a function of time before birth
-femur length as allometric function of body length
-survival rate of snails that host human parasites as a function of temperature

These equations provide ideal or expected values of one quantity, as a function of some other quantity. The model values will not match observed values perfectly. But the match should be close enough to be convincing. Data equations allow us to quantify the fit of data to models that express important concepts in biology.

Definition: A data equation has three parts: observed values *Y*, expected values *E(H)*, and the residual ε.

$$\text{Data } = \text{Model } + \text{ Residual}$$

$$\begin{array}{ccccc}\text{Data} & = & \text{Expected} & + & \text{Residual}\\ Y & = & E(H) & + & \varepsilon\end{array}$$

$$\begin{array}{ccccc}\text{Data} & = & \text{Fitted values} & + & \text{Residual}\\ Y & = & \hat{Y} & + & \varepsilon\end{array}$$

The data are a set of measured values.

Expected (model) values are calculated from an equation, such as those in the equations lab.

The residuals are the difference between the data and fitted value.

$$\text{Residuals } = \text{ Data } - \text{Fitted}$$

In following examples, keep the data, the graphics, and the stack of data equations coordinated.

In stack of Data Equations:
Keep data on board (white chalk)
Erase and replace the model (yellow)
Erase and replace residuals (in red)

Graphs:
Keep axes and data points on board (white)
Erase and replace model (yellow lines)
Erase and replace residuals (vertical lines in red)

Example of expected value from an equation: Metabolic rate of a non-passerine bird (Lasiewski and Dawson 1967)

$$\dot{E} = 78.3\ M^{0.723}$$

$$\frac{kcal}{day} = 78.3kg^{0.723}$$

Ostrich, 2.7 m tall. Weight = 115kg

$$Expected\ value(\dot{E}) = 78.3(115kg)^{0.723} = 2420\ kcal/day$$

For a single ostrich, with measured value of 2300 *kcal/day* the data equation is

$$2300 = 2420 - 120$$

5.2 Example: Fruit Fly Heterozygosity. Data from Brussard (1984)

To become familiar with data equations we will use data collected by Theodosius Dobzhansky, who was one of the pioneers of populations genetics. Dobzhansky, one of the founders of the ‘modern synthesis’ in evolutionary biology, established the fact that natural populations have high levels of genetic variation. Dobzhansky devoted his professional life to one of the central questions in population biology: the origin and maintenance of genetic variability. Dobzhansky worked on fruit flies in laboratory populations, but during the summer he would leave the lab and study wild populations of fruit flies in order to look at the ecological processes that generate or erode genetic variability in nature. Harsher environments at higher altitudes are expected to select for a narrower range of phenotypes, hence reduce genetic variability. One of the research questions Dobzhansky addressed was:

Does genetic variability decrease at higher altitude, due to stronger selection in extreme environments ?

To address this question Dobzhansky collected flies at different altitudes in Yosemite Park in the Sierra Nevada range, a spectacularly scenic location that offered pleasant relief from the hot summer conditions of urban Los Angeles. Dobzhansky used the best technique at the time, called inversion heterozygosity, to measure genetic variability. Here is Dobzhansky’s data on inversion heterozygosity (assuming Hardy Weinberg equilibrium) of 3rd chromosome inversions from the fruit fly *Drosophila persimilis*.

The data were reported by P.F. Brussard 1984. Geographic patterns and environmental gradients: The central-marginal model in Drosophila revisited.
Annual Review of Ecology and Systematics 15: 25-64.

```
   850  0.59  0.26
  3000  0.37  0.91
  4600  0.41  1.40
  6200  0.40  1.89
  8000  0.31  2.44
  8600  0.18  2.62
 10000  0.20  3.05

Elev    H(%)  Elev(km)
```

H = heterozygosity.
Elev = elevation in feet, converted to km

Under classical evolutionary theory, these values are high. For example, we expect heterozygosity no greater than 50%, with most loci at values less than 10%, corresponding to a gene frequency of 95% for a dominant allele at Hardy-Weinberg equilibrium. Are these values, for a single locus, typical?

5.3 Deviations from a Single Value Model. Model: $E(H) = \beta_{ext}$

Lewontin and Hubby (1966) showed that heterozygosity over many loci ran at an average of 30% in *D. persimilis*. This forces us to update our prior probability (circa 10% or less) to a much high value, on the order of 30%, corresponding to a dominant alleles at 80% or less. This approach, which Fisher called Bayesian inference, depends on a known prior probability from theory. However, when we look at Bayes' 1763 publication, we find only a rule for calculating a probability interval, given a binomial distribution. There is no theorem. Nor is there any way to apply this approach to non-binomial data, such as heterozygosity. The apparatus to do this was developed by Laplace (1774). Keynes (1921) developed the first proof of what is now called Bayes' theorem. This approach, that of updating a prior to a posterior probability is accurately described as "priorist."

Our model is $E(H) = \beta_{ext}$ where β_{ext} has a single value, 30%.

$$\begin{aligned} \text{Data} &= \text{Model} + \text{Residual} \\ H &= E(H) + \varepsilon \\ H &= \beta_{ext} \quad + \varepsilon \\ H &= 0.3 \quad + \varepsilon \end{aligned}$$

Using this simple model we form 7 data equations, one for each observed value.

Data	=	Model	Residual		
H	=	$\widehat{H}$	res		res^2
0.59	=	0.3	0.29		0.0841
0.37	=	0.3	0.07		0.0049
0.41	=	0.3	0.11		0.0121
0.40	=	0.3	0.10		0.01
0.31	=	0.3	0.01		0.0001
0.18	=	0.3	-0.12		0.0144
0.20	=	0.3	-0.10		0.01
			0.36		0.13560

$\Sigma\text{res} = \underline{\ 0.36}$

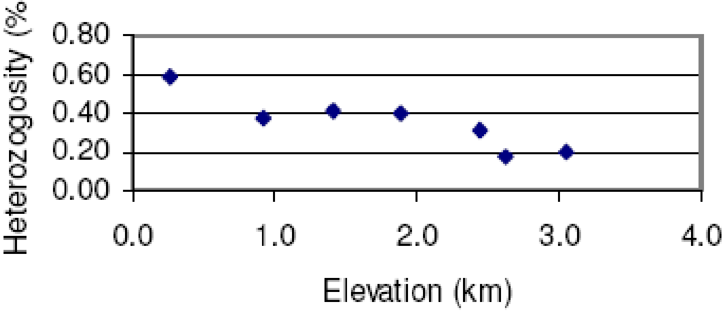
$\Sigma\text{res}^2 = \underline{\ 0.1356}$

$L(\beta_{ext} \mid H) = 0.1356^{-n/2}$

n = 7

The values tend to be more than 0.30 and hence the residuals sum to a positive value.

The summed residuals measure the bias in fit.
The sum of the squared residuals measures the goodness of fit.
$L(\beta_{ext} \mid H)$ is the likelihood of the parameter β_{ext} given the data *H*. We will use it to compare the weight of evidence for one model versus another.



Add the model value 0.30 to the graph as a horizontal line.

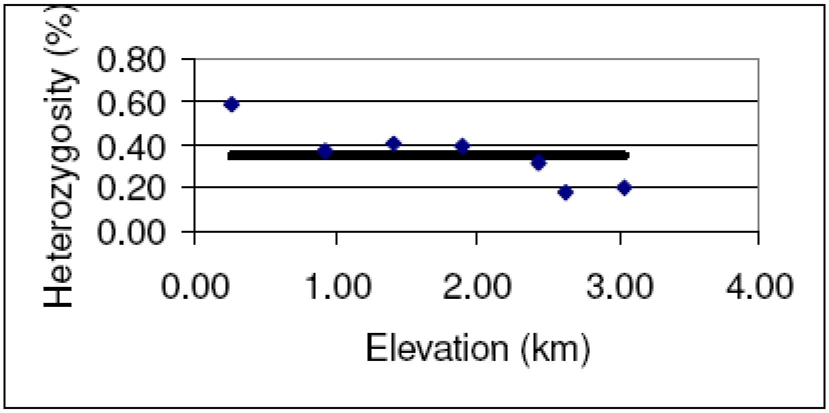
Run a perpendicular from the line to each point. These are the residuals.

5.4 Deviations from the Mean. Model: $E(H) = \overline{H}$ estimated from data

Often we have no prior parameter value, as in Fisher's "Bayesian" inference.
In such cases we estimate the parameter from the data we have.
We use "frequentist" inference to make the "best" estimate.

What does "best" mean ? There are several criteria. We will start with two statistical criteria: that the residuals sum to zero (the estimate is unbiased) and that the residuals be as small as possible. The number that meets both these criteria is the mean value.

$$\text{Mean}(H) = \overline{H} = n^{-1}\,\Sigma\,H = 7^{-1} \cdot 2.46 = 0.3514$$



```
Add the model value 0.3514
to the graph as a
horizontal line.
```

```
Run a perpendicular from
the line to each point.
These are the residuals.
```

```
White chalk for data,
yellow chalk for model =
straight line at 0.351
```

Our model is $E(H) = \overline{H}$ where $\overline{H}$ has a single value, 35.14%.

$$\text{Data} = \text{Model} + \text{Residual}$$
$$H = E(H) + \varepsilon$$
$$H = \beta_o + \varepsilon$$
$$H = 0.3514 + \varepsilon$$

Here are the data equations when the model value is the mean

Data	=	Model	+	Residual	
H	=		+	res	res^2
0.59	=	0.3514	+	0.2386	0.0569
0.37	=	0.3514	+	0.0186	0.0003
0.41	=	0.3514	+	0.0586	0.0034
0.40	=	0.3514	+	0.0486	0.0024
0.31	=	0.3514	–	0.0414	0.0017
0.18	=	0.3514	–	0.1714	0.0294

Σres = 0

Σres^2 = 0.1171

$L(\beta_o \mid H) = 0.1171^{-n/2}$

n = 7

The residuals sum to zero, meeting the criterion of no bias. It can be shown mathematically that the squared deviations sum to the smallest possible value.

This model is an improvement over our previous model ($H = 0.30$ + residual) because it is unbiased and has the minimum deviation of the data from the model. It is not necessarily an improvement from the point of view of the underlying biology. We have substituted a statistical criterion (best fit) for a biological criterion (prior knowledge).

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Keep Σres² on board for
each successive model
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5.5 Deviations from a Linear Trend: $\hat{H} = \hat{\beta}_E E + \hat{\beta}_I$ estimated from large scale data.

Our single value model of the data fails to capture the trend in heterozygosity relative to elevation. This shows up in the residuals when listed from low to high elevation: positive residuals early in the series, negative residuals later in the series. So we investigate a model that describes a decrease in heterozygosity with increase in elevation. We start with the simplest possible model, a straight line increase with altitude.

$$H = \hat{H} + \varepsilon$$
$$H = \hat{\beta}_E E + \hat{\beta}_I + \varepsilon$$

The parameterβ_E in this equation (model) is the heterozygosity gradient. It is the change in heterozygosity for each unit change in elevation. The gradient β_E has units of % /km . The product $\beta_E \cdot E$ has units of (%/km)(km) = %. Thus it has the same units as the response variable H, as it must for the equation to be dimensionally homogeneous.
β_I is the Y intercept.

We will start with the large scale heterozygosity gradient β_E. The large scale gradient is the difference in heterozyzosity from the lowest to highest elevation.

$$\hat{\beta}_E = \frac{(20 - 59)\ \%}{(3.05 - 0.26)\ \text{km}} = -13.98\ \%/\ \text{km}$$

$\hat{\beta}_E$ is an estimate of the slope of the line in the plot of heterozygosity versus elevation. The estimate is -13.98% per km increase in elevation. The hat over the symbol signifies that this is an estimate of the parameter.

Next we calculate an offset so that the line runs through the value at 0.26 km.

$$\begin{array}{lll} \hat{H} & = \hat{\beta}_E \cdot E & + \text{offset} \\ 0.59 & = (-13.98\ \%/\ \text{km})(0.26\ \text{km}) & + \text{offset} \end{array}$$

$$\text{offset} = 0.59 - (-13.98\ \%/\ \text{km})(0.26) = 0.6262$$

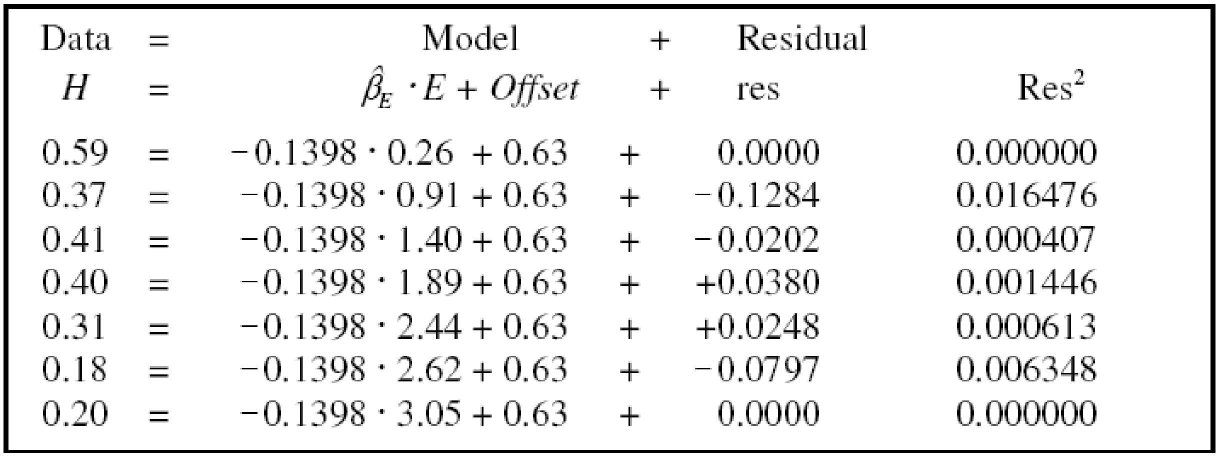
$$\hat{H} = -0.1398 \cdot E + 0.626$$

Here is the gradient model, with estimates from the highest and lowest elevation.

$$\begin{array}{lccl} H & = & \hat{H} & + \ \varepsilon \\ H & = & \beta_E \cdot E + \text{offset} & + \ \text{res} \\ H & = & -0.1398 \cdot E + 0.626 & + \ \text{res} \end{array}$$

5.4 Deviations from a Linear Trend: $\hat{H} = \hat{\beta}_E E + \hat{\beta}_I$ estimated from data

With this model we can calculate an expected value for each observation of heterozygosity, based on the elevation.



Data	=	Model	+	Residual	
H	=	$\hat{\beta}_E \cdot E + Offset$	+	res	Res^2
0.59	=	$-0.1398 \cdot 0.26 + 0.63$	+	0.0000	0.000000
0.37	=	$-0.1398 \cdot 0.91 + 0.63$	+	-0.1284	0.016476
0.41	=	$-0.1398 \cdot 1.40 + 0.63$	+	-0.0202	0.000407
0.40	=	$-0.1398 \cdot 1.89 + 0.63$	+	$+0.0380$	0.001446
0.31	=	$-0.1398 \cdot 2.44 + 0.63$	+	$+0.0248$	0.000613
0.18	=	$-0.1398 \cdot 2.62 + 0.63$	+	-0.0797	0.006348
0.20	=	$-0.1398 \cdot 3.05 + 0.63$	+	0.0000	0.000000

Note bias: Σres = –0.17 Σres^2 = 0.0253

$L(\beta_e \mid H) = 0.0253^{-7/2}$

The model exactly predicts the heterozygosity at the highest and lowest elevation. We examine the deviations at each elevation to determine whether this model is acceptable.

high and low residuals are interspersed.

there are about as many negative as positive residuals

the sum of the residuals is somewhat biased (negative): Σres = –0.17

The model is satisfactory in that there are no patterns in the residuals. The model is somewhat biased, leading to an estimate of the heterozygosity gradient that is more negative than an unbiased estimate.

A better estimate of the gradient β_E can be obtained from the formula for the least squares estimate, found in every book on statistics.

$$\hat{\beta}_E = \frac{\Sigma\,(H - \overline{H})(\mathrm{E} - \overline{\mathrm{E}})}{\Sigma\,(\mathrm{E} - \mathrm{E})^2}$$

We have already met the quantity $H - \overline{H}$. It is the deviation of the observed value from the average value of heterozygosity.

Similarly, the quantity $\left(E - \overline{E}\right)$ represents the deviations from the average elevation $\overline{\mathrm{E}}$.

And $\left(E - \overline{E}\right)^2$ represents the squared deviations from average elevation.

5.4 Deviations from a Linear Trend.

The formula produces an estimate of β_E that minimizes $\left(H-\overline{H}\right)^2$

With this formula, the estimate of the heterozygosity gradient comes to $\hat{\beta}_E = -12.73$ %/km, a value that is not quite as negative (as steep) as our crude estimate of −13.98%/km.

As before we compute an offset. This offset runs through the mean values (0.3514,1.796), which we use as our reference point because we always have more information about this point than we do about the *Y*-intercept, where *E* = 0).

$$\begin{aligned}
\overline{H} &= \hat{\beta}_E \cdot \overline{E} && + \text{offset} \\
0.3514 &= (-12.73\ \%/\ \text{km})(1.796) && + \text{offset}
\end{aligned}$$

$$\text{offset} = 0.3514 - (-12.73\ \%/\ \text{km})(1.796) = 0.58$$

$$\hat{H} = -0.1273 \cdot E + 0.58$$

Here is the gradient model, with unbiased estimates from the data.

$$H = -0.1273 \cdot E + 0.58 + \text{res}$$

The data equations based on this new estimate:

Data	=	Model	+	Residual	
H	=	$\beta \cdot E + Offset$	+	res	res^2
0.59	=	–0.1273 · 0.26 + 0.58	+	+0.0429	0.001842
0.37	=	–0.1273 · 0.91 + 0.58	+	–0.0937	0.008773
0.41	=	–0.1273 · 1.40 + 0.58	+	+0.0084	0.000071
0.40	=	–0.1273 · 1.89 + 0.58	+	+0.0605	0.003659
0.31	=	–0.1273 · 2.44 + 0.58	+	+0.0403	0.001626
0.18	=	–0.1273 · 2.62 + 0.58	+	–0.0664	0.004408
0.20	=	–0.1273 · 3.05 + 0.58	+	+0.0079	0.000063

$\Sigma\text{res} = \underline{0.0000}$ No bias

$\Sigma\text{res}^2 = \underline{0.0204}$ Much less than 0.1171, the value of the previous no bias model

$L(\beta_E \mid H) = 0.0204^{-7/2}$ More likely than previous no bias model based on β_o because a smaller fraction raised to the same power.

We examine the residuals to evaluate this model.

-residuals are all approximately the same magnitude

-about the same number of positive and negative residuals

-no pattern of low residuals followed by high residuals

-sum of residuals is zero

The fact that the residuals sum to zero is no accident: the least squares estimation method guarantees this. The estimation also produces the smallest possible value of the sum of squared residuals Σres^2.

5.5 Comparison of Models - Analysis of Variance and Analysis of Deviance

We have considered several models of the data. We use three measures to compare them.

First: The sum of the residuals. This measures bias.
We looked at several models. We find that some have biased estimates, two do not.

β from previous information.	$\Sigma \text{res} = \underline{-0.34}$	-0.36
$\hat{\beta}_o = \text{mean}(H)$ estimated from data (least squares)	$\Sigma \text{res} = \underline{0.00}$	
$\hat{\beta}_E$ estimated from data (using two data points)	$\Sigma \text{res} = \underline{-0.17}$	
$\hat{\beta}_E$ estimated from data (least squares)	$\Sigma \text{res} = \underline{0.00}$	

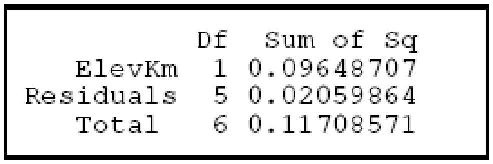
Those having unbiased estimates are preferable.

Second: The sum of the squared residuals. This measures goodness of fit.

H_o: $H = \hat{\beta}_o + \epsilon$	SS_{tot}	$\Sigma \text{res}^2 = \underline{0.1171}$
H_A: $H = \hat{\beta}_E \cdot E + Offset + \epsilon$		$\Sigma \text{res}^2 = \underline{0.0204}$
The reduction in squared deviation is:	SS_{model}	$\Sigma \text{res}^2 = \underline{0.0966}$

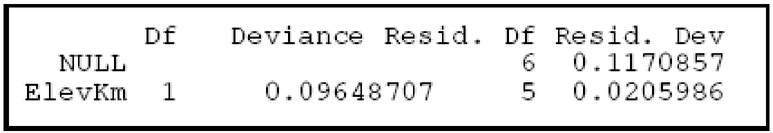
We conclude that the model that includes the gradient in heterozygosity β_E fits the data better than the model without the gradient.

This comparison is displayed in either of two different forms: the analysis of variance (ANOVA) table or the analysis of deviance (ANODEV) table.



```
           Df  Sum of Sq
   ElevKm   1 0.09648707
Residuals   5 0.02059864
    Total   6 0.11708571
```

Analysis of Variance (ANOVA) format



```
       Df   Deviance Resid. Df Resid. Dev
  NULL                       6  0.1170857
ElevKm  1   0.09648707       5  0.0205986
```

Analysis of Deviance (ANODEV) format

Third: Likelihood. Which model is more likely?
The evidential support for the full (null) model of no gradient is $SS_{tot} = 0.1174^{-7/2}$

This is called the full model because it encompasses all of the variation in the data, relative to the simplest model, that of single value, in this case the mean.

The support for the reduced (alternative) model of a gradient is $SS_{tot} = 0.0204^{-7/2}$
This is called the reduced model because it encompasses the information in the data, after reducing the variance by including an explanatory variable, in this case a gradient.
The likelihood of the reduced to the full model is $LR = (0.0204/0.1174)^{-7/2} = 453$

The gradient model is 450 times more likely than the no gradient model.

5.5 Comparison of Models - Analysis of Variance and Analysis of Deviance

The evidence is stronger for the gradient model than the no-gradient model.

We have a measure of strength of evidence. $\text{Log}_{10}(453) = 2.66$ hartleys

The evidence is better than 100:1 odds ($\log_{10}(100) = 2$

The evidence is not as strong as 1000:1 odds ($\log_{10}(1000) = 3$

Later we will use the *LR* to develop a statistical test of whether the no-gradient model could have arisen by chance.

Statistical results report degrees of freedom (df).What is a degree of freedom ?

We started with 7 observations. We have 7 degrees of freedom.

If we know 6 values, the 7th is still free to vary.

We lose 1 degree of freedom when we estimate the mean from the data.

If we know 6 values and the mean, the 7th is not free to vary. We only have 6 df

Hence the total sum of squares (ANOVA) and null model (ANODEV) has 6 df.

We lose another degree of freedom when we estimate the slope parameter.

We assign this degree of freedom to the regression term in the model

Hence the residual term has $7-1-1 = 5$ df

We will use the ANOVA table for the general linear model, which assumes normal errors. We use the ANODEV table for the generalized linear model (any error structure)

Lewontin, R. C.; Hubby, J. L. (1966). "A molecular approach to the study of genic heterozygosity in natural populations. II. Amount of variation and degree of heterozygosity in natural populations of Drosophila pseudoobscura". Genetics. 54 (2): 595–609.

* * * *

Next, we will look at the data equations for another common situation in biology, where we wish to compare mean values in two or more groups.

5.7 Deviations from the Means of Two or More Groups $Y = \beta_0 + \beta_x \cdot X$
Oat Yield data from Steel and Torrie (1960)

To illustrate the idea of data equations for two or more groups we will use data from Steel and Torrie 1960 (p237) who reported yield (bushels/acre) of oats (Vicland variety, infected with *H. victoriae*) with or without a chemical seed treatment (Panogen).

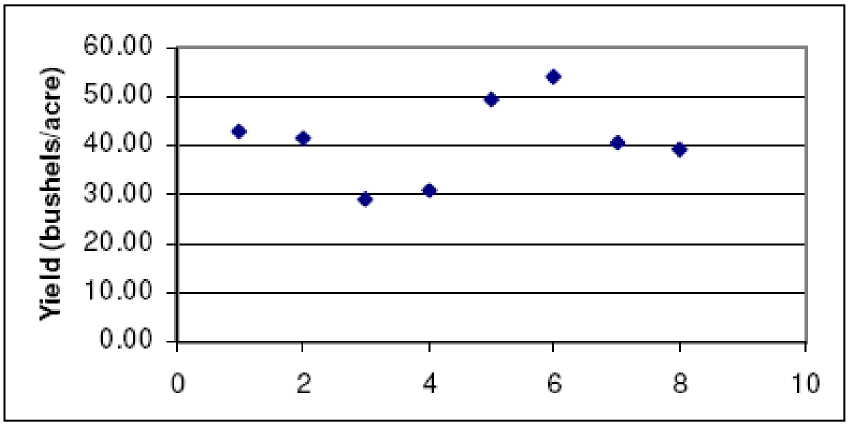
−1	42.9	untreated
−1	41.6	untreated
−1	28.9	untreated
−1	30.8	untreated
+1	49.5	treated
+1	53.8	treated
+1	40.7	treated
+1	39.4	treated
Grp	Y	

Y = Yield of oats (bushels / acre)
X = group (−1 = control, +1 = treated)

<u>Null Model.</u> $\hat{Y} = \hat{\beta}_o$ estimated from data

As is often the case we do not have a parameter value from prior evidence. We estimate the parameter from the data we have. The 'best' estimate is the overall mean, which is unbiased (residuals sum to zero) with smallest deviation (smallest sum of squared residuals).

$$\text{Mean}(Y) = \overline{Y} = \text{n}^{-1}\, \Sigma\, Y = 8^{-1} \cdot 327.6 = 40.95$$



Draw in, as horizontal line, the model value of 40.95.

Connect each dot to the line with a perpendicular. These are the residuals.

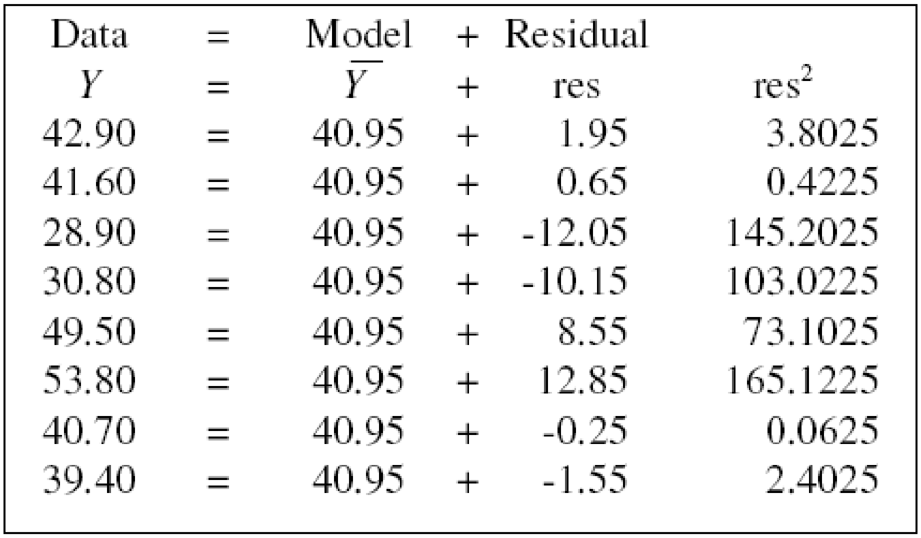
White chalk for data, yellow chalk fro model = horizontal line at 40.95

Null Model (continued) $\hat{Y} = \hat{\beta}_o$ from data

Our model is $\hat{Y} = \hat{\beta}_o$ where $\hat{\beta}_o$ is an estimate, 40.95 bushels / acre

$$\begin{aligned} \text{Data} &= \text{Model} + \text{Residual} \\ Y &= Y + \epsilon \\ Y &= \hat{\beta}_o + \epsilon \\ Y &= 40.95 + \epsilon \end{aligned}$$

Here are the data equations when the model value is the mean.



Data	=	Model	+	Residual	
Y	=	$\overline{Y}$	+	res	res^2
42.90	=	40.95	+	1.95	3.8025
41.60	=	40.95	+	0.65	0.4225
28.90	=	40.95	+	-12.05	145.2025
30.80	=	40.95	+	-10.15	103.0225
49.50	=	40.95	+	8.55	73.1025
53.80	=	40.95	+	12.85	165.1225
40.70	=	40.95	+	-0.25	0.0625
39.40	=	40.95	+	-1.55	2.4025

Σres = 0

Σres^2 = 493.14

$$L(\hat{\beta}_o | Y) = (493.14)^{-8/2}$$

Keep Σres^2 on board for each successive model

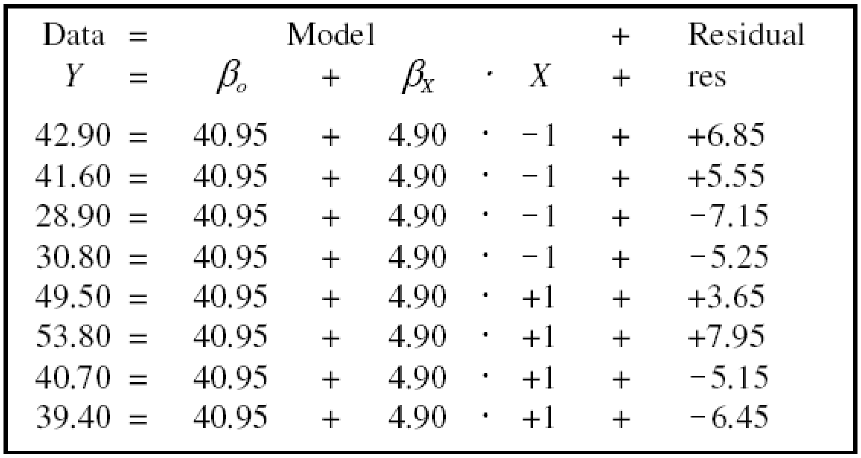
Alternative Model $Y = \beta_0 + \beta_x \cdot X$

where X = two groups

We have no prior information to tell us the expected value for treated and untreated oats, so we use means estimated from the data in each group.

For untreated oats the mean value is $\hat{\beta}_o + \hat{\beta}_x(-1) = 40.95 - 4.90 = 36.05,$

For treated oats the mean value is $\hat{\beta}_o + \hat{\beta}_x(+1) = 40.95 + 4.90 = 45.85$



Data	=		Model				+	Residual
Y	=	β_o	+	β_X	·	X	+	res
42.90	=	40.95	+	4.90	·	−1	+	+6.85
41.60	=	40.95	+	4.90	·	−1	+	+5.55
28.90	=	40.95	+	4.90	·	−1	+	−7.15
30.80	=	40.95	+	4.90	·	−1	+	−5.25
49.50	=	40.95	+	4.90	·	+1	+	+3.65
53.80	=	40.95	+	4.90	·	+1	+	+7.95
40.70	=	40.95	+	4.90	·	+1	+	−5.15
39.40	=	40.95	+	4.90	·	+1	+	−6.45

Σres = 0

Σres^2 = 301.06

$$L(\hat{\beta}_X | Y) = (301.06)^{-8/2}$$

Data Equations. $Y = \beta_0 + \beta_x{\cdot}X$ two groups

The data equations are written using the overall mean $\hat{\beta}_o$= 40.95 bushels/acre, together with the group means expressed as deviations $\hat{\beta}_X$ from the grand mean.

Comparing models

How does our two group model (treated versus control) compare to the single value (no effect) model?

To draw a conclusion about the effects of panogen on oat yields, we compare the model with the group means ($Y = \beta_o + \beta_x X$) to the model without the group means ($Y = \beta_o$).

That is, we compare the fit of the model having the explanatory term (X = presence or absence of panogen) to the simpler model, in which the explanatory term X is absent. The no effect model -- the one with no explanatory term -- is called the null model. We have already met the null model H_o. It is the model based on the grand mean β_o, for which the estimate was $\hat{\beta}_o$ = 40.95 bushels/acre. The alternative model H_A includes the explanatory variable X, as shown in the above data equations.

We apply three criteria.

First: Sum of the residuals. Σres = 0 for both models. Both are unbiased.

Second: Sum of the squared residuals. This measures goodness of fit.

H_o:	$Y = \beta_o$	$\Sigma\text{res}^2 = 493.14$	= SStotal
H_A:	$Y = \beta_o + \beta_x X$	$\Sigma\text{res}^2 = 301.06$	

H_A is a better fit than the null model, H_o .

The improvement in fit (reduction in squared deviation) is:

$\Sigma\text{res}^2 = 493.14 - 301.06 = 192.08$ = SSmodel

The improvement in fit as a percentage is 192.08/493.14 = 32%

Third: Likelihood. Which model is more likely, given the data ?

The likelihood ratio is $LR = (301.06/493.14)^{(-8/2)} = 7.2$

The model with treatment effects is only 7 times more likely than the no effect model.

The weight of evidence ($LR < 20$) is not in favor of the treatment effect model.

Could this improvement in fit and in likelihood have been due to chance variation in measurements ?

Later, we will use the likelihood to develop a test for deciding whether the improvement in fit and is attributable to chance.

See worksheet (ST237.xls)

5.8 Review Questions

1. Here are the 7 values of fly heterozygosity assigned randomly to the 7 values of altitude .

ft	km	Random sample of H
850	0.25908	0.37
3000	0.91440	0.59
4600	1.40208	0.18
6200	1.88976	0.20
8000	2.43840	0.40
8600	2.62128	0.31
10000	3.04800	0.41

Calculate the sum of the residuals and the sum of the squared residuals for the null and alternative model.

How does the random improvement in fit compare to that for the unrandomized data?

Calculate the likelihood ratio for the gradient model compared to the no gradient model (no change with increasing altitude) for the random data.

How does the likelihood ratio for the random data compare to that before randomization? (take LR for unrandomized compared to randomized).

2. Here are the heterozygosity values for *Drosophila pseudoobscura*, measured at the same locations as *D. persimilis*.

ft	km	H
850	0.25908	0.70
3000	0.91440	0.69
4600	1.40208	0.71
6200	1.88976	0.70
8000	2.43840	0.70
8600	2.62128	0.62
10000	3.04800	0.68

Calculate the sum of the residuals and the sum of the squared residuals for the null and alternative model.

Calculate the likelihood ratio for the gradient model compared to the no gradient model (no change with increasing altitude)

How does the likelihood ratio for this species compare to that for *D. persimilis*? (take LR for *D. persimilis* compared to *D. pseudoobscura*).

```
       *** Linear Model ***

Call: lm(formula = H ~ Alt.km., data = Brussard, subset = 1:7, na.action = 
       na.exclude)
Residuals:
       1        2        3       4       5       6        7 
 0.04292 -0.09367 0.008411 0.06049 0.04032 -0.0664 0.007921

Coefficients:
               Value Std. Error  t value Pr(>|t|) 
(Intercept)   0.5801   0.0529    10.9711   0.0001
    Alt.km.  -0.1273   0.0262    -4.8619   0.0046

Residual standard error: 0.06394 on 5 degrees of freedom
Multiple R-Squared: 0.8254 
F-statistic: 23.64 on 1 and 5 degrees of freedom, the p-value is 0.004625 

Analysis of Variance Table
Response: H
Terms added sequentially (first to last)
          Df  Sum of Sq    Mean Sq  F Value       Pr(F) 
  Alt.km.  1 0.09664358 0.09664358 23.63833 0.004625356
Residuals  5 0.02044213 0.00408843


       *** Generalized Linear Model ***

Call: glm(formula = H ~ Alt.km., family = gaussian, data = Brussard, subset = 1:7, na.action 
= na.exclude, control = list(epsilon = 0.0001, maxit = 50, 
trace = F))
Deviance Residuals:
          1           2           3          4          5           6 
 0.04291757 -0.09366627 0.008410879 0.06048802 0.04032481 -0.06639626

           7 
 0.007921242

Coefficients:
                 Value Std. Error    t value 
(Intercept)  0.5800609 0.05287169  10.971105
    Alt.km. -0.1272907 0.02618113  -4.861927

(Dispersion Parameter for Gaussian family taken to be 0.0040884 )

    Null Deviance: 0.1170857 on 6 degrees of freedom
Residual Deviance: 0.0204421 on 5 degrees of freedom

Number of Fisher Scoring Iterations: 1 
Analysis of Deviance Table
Gaussian model
Response: H

Terms added sequentially (first to last)
        Df   Deviance Resid. Df Resid. Dev 
   NULL                      6  0.1170857
Alt.km.  1 0.09664358         5  0.0204421
```