Model Based Statistics in Biology.

Part III. The General Linear Model.

Chapter 9.1 Regression. Explanatory Variable Fixed by Experiment

ReCap.	Part I (Chapters 1,2,3,4)
ReCap	Part II (Ch 5, 6, 7)
ReCap	Part III (Ch 8 GLM components)
9.1	Explanatory Variable Fixed by Experiment
9.2	Explanatory Variable Fixed into Classes
9.3	Explanatory Variable Measured with Error
9.4	Exponential Functions
9.5	Power Laws. Linear Regression
9.6	Model Revision

Data files & analysis
SC_9_3_1.out
Ch9.xls

on chalk board

ReCap Part I (Chapters 1,2,3,4)
Quantitative reasoning: Example of scallops,
which combined models (what is the relation of scallop density to substrate?)
with statistics (how certain can we be?)

ReCap Part II (Chapters 5,6,7)
Data equations summarize pattern in data as a series of parameters (means, slopes).
Frequency distributions, a key concept in statistics, are used to quantify uncertainty.
Hypothesis testing uses the logic of the null hypothesis to make a decision about an unknown population parameter.
Estimation is concerned with the specific value of an unknown population parameter.

Today: The General Linear Model
Regression: Single explanatory variable fixed by experiment.
Work through this example, using a generic recipe.

Wrap-up

Going to use the General Linear Model.
The GLM consists of familiar and new components.
Regression a special case of the general linear model.
Response variable as a function of a single explanatory variable.
Relation between variables expressed as a slope.
H_A/H_o pair about this parameter.
Model evaluated by partitioning variance in the data according to the model.
Decision declared about F = ratio of explained (model)
to unexplained (residual) variance.

GLM, applied to regression X variable fixed. Experimental studies.

Example 9.3.1 from Snedecor and Cochran (1989). Quantity of interest is the phosphorus content of corn (*Pcorn* in ppm), in relation to the phosphorus levels in samples of soils with experimentally fixed levels of phosphorus (*Psoil* in ppm).

Psoil	Pcorn
1	64
4	71
5	54
9	81
13	93
11	76
23	77
23	95
28	109

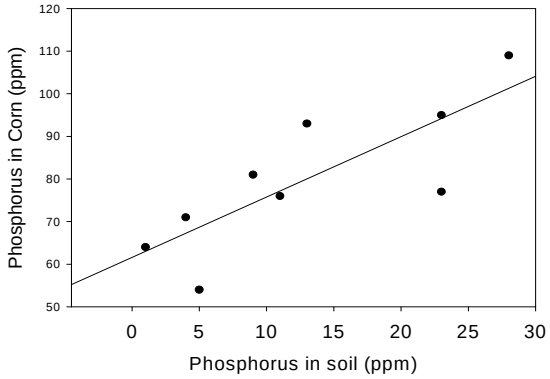
Does the phosphorus content of corn increase when soil phosphorus is increased ?

1. Construct model

Constructing a model can appear formidable, but it is not, if taken step by step. We will proceed around the triangle, starting with verbal model, proceeding to graphical, and finally formal model.

Verbal model: Phosphorus content of corn depends on Phosphorus content of soil.

Graphical model.



The verbal and graphic model help us to distinguish the response from the explanatory variables.

First, distinguish response variable from the explanatory variable or variables.
Response variable is

Pcorn = Phosphorus content of corn (ppm).
Continuous variable on a ratio type of scale.
This is also called the dependent variable.

The explanatory variable is

Psoil = phosphorus content of prepared sample of soil (ppm).
The levels of *Psoil* are fixed in this experimental study.

This is an important step. Separating the response from explanatory variables is the first and most important step in statistical analysis. If someone comes to you for statistical advice, the best way to help is often to ask them to state the response variables, and to separate these from the explanatory variables. This clears away the fog that surrounds the search for the "right statistical test."

1. Construct model

State type of measurement scale for response variable and explanatory variable(s).
Assign symbols, state units and type of measurement scale.

		Units	Dimensions	Type of measurement scale
Response	*Pcorn*	(ppm)	dimensionless	ratio
Explanatory	*Psoil*	(ppm)	dimensionless	ratio

This helps in deciding on the statistical model to use.

Response variable
- if nominal–> frequencies, then Generalized Linear Model GzLM
- if nominal then median test, binomial tests, etc
- if ordinal then "non-parametric" tests. e.g. Kruskal-Wallis
- if ratio then GLM

Explanatory variable in GLM
- if nominal then ANOVA
- if ordinal then ANOVA
- if ratio then regression
- if ratio and otherwise then ANCOVA

Explanatory variable in GzLM
- if nominal then G-tests and extensions
- if ordinal then G-tests and extensions
- if ratio then logistic regression etc

Now write the model using names of quantities.

Pcorn = f(*Psoil*).

"Phosphorus in soil depends on phosphorus in the soil"

Finally, write the model in more abstract form, which is what the computer will use to carry out the analysis.

$Pcorn = \alpha + \beta_{PSoil} \cdot Psoil + \varepsilon$

With practice, this sequence becomes practically automatic.

This is the model for the population

α and β_{PSoil} are parameters for the population.

	Units	Dimensions	Type of measurement scale
α	same as *Pcorn*	none (mass/mass)	ratio
β_{PSoil}	(ppm/ppm)	none	ratio

1. Construct model

Here is the model for the sample. It uses parameter estimates from data.

$$Pcorn = \hat{\alpha} + \hat{\beta}_{Psoil} \cdot Psoil + residual$$

$\hat{\alpha}$ and $\hat{\beta}_{PSoil}$ are estimates of the parameters α and β_{PSoil}

We will use greek letters for the population parameters, and the hats on top of the greek symbols for estimates of these parameters. An alternative convention is to use greek letters for population parameters, roman letters for estimates.
Using this convention, the model for the sample is written as:

$$Pcorn = a + b_{Psoil} \cdot Psoil + residual$$

2. Execute analysis. Place data in model format:

Column of data for response variable labelled *Pcorn*
Column of data for explanatory variable labelled *Psoil*

Code model statement in statistical package according to the GLM

$$Pcorn = \alpha + \beta_{PSoil} \cdot Psoil + \varepsilon$$

```
MTB> regress 'Pcorn' 1 'Psoil'
MTB> GLM Pcorn = Psoil.
```

All packages use a model statement to code the GLM. In some packages this model statement is typed (SAS, Minitab, R). In other packages it is present but not obvious. The example in the box shows the coding in Minitab for two different commands that produce the same result. Some packages have a graphics interface that allows you to code this model (e.g., SPSS). If you are using the graphics interface, it helps to look at the code produced, so that you understand how the model you produce with the graphic interface translates into a model statement.

2. Execute analysis. Compute fitted values and residuals.

The model statement is similar across statistical packages.
Extracting the residuals and fits differs among packages.

```
MTB > GLM Pcorn = Psoil;
SUBC> fits fits;
SUBC> res resisuals.    Minitab
```

```
Proc GLM;
   Model Pcorn = Psoil      SAS
```

```
CornModel <- lm(Pcorn ~ Psoil)
                            R
```

```
Regress Pcorn Psoil,
                        Stata
```

```
MTB > print 'Pcorn' 'fits' 'residuals'
  ROW  Pcorn     fits      res
    1     64   62.997    1.0031
    2     71    67.248    3.7524
    3     54    68.665  _14.6645
    4     81    74.332    6.6679
    5     93    80.000   13.0003
    6     76    77.166   _1.1659
    7     77    94.169  _17.1687
    8     95    94.169    0.8313
    9    109   101.253    7.7468
```

2. Execute analysis. Compute fitted values and residuals.

Here is the computional sequence:

1. Estimate the parameters
2. Calculate fitted values from the parameter estimates, for each data equation.
3. Calculate the residuals (response variable – fitted value).

These are readily obtained in from model based routines in statistical packages. We depend on the package to make these calculations correctly. Here is a brief tour of the machinery, for those who are interested.

1. Estimate parameters α and β_{PSoil} from the sample. The least squares estimate of β_{PSoil} minimizes the sum of the squared residuals (deviations of the data from the line).

$$SSE = \sum_{i=1}^{n} \left(Y - \hat{Y}\right)^2 = \sum_{i=1}^{n} \left(Y - \hat{\alpha} - \hat{\beta} X\right)^2$$

where there are *n* observations indexed by *i*. Some routines use iterative search: make a guess, compute the SS_{error}, make another guess, compute SS_{error} for this guess, compare to previous SS_{error}, continue until SS_{error} is as small as possible.

For a simple straight line model most routines obtain the estimate of $\hat{\beta}$ from the following formula.

$$\hat{\beta} = \frac{\sum_{i=1}^{n} \left(X_i - \overline{X}\right)\left(Y_i - \overline{Y}\right)}{\sum_{i=1}^{n} \left(X_i - \overline{X}\right)^2}$$

For the Corn data the estimate is $\hat{\beta}_{Psoil} = 1.4169$

To estimate the y-intercept α we use the mean values of the response and explanatory variable.

mean(*Pcorn*) = $\hat{\beta}_0$ = 80 ppm

mean(*Psoil*) = 13.0 ppm

$\hat{\alpha} = \hat{\beta}_0 - \hat{\beta}_{Psoil}$ (mean(*Psoil*) = 80 – 1.42(13)

$\hat{\alpha}$ = 61.58 ppm

Here is the relation of the regression equation (which has the y-intercept α) to the GLM (which has β_o the mean value of the response variable).

GLM:	*Pcorn*	– 80.0 =		1.42	(*Psoil* – 13.0)	+ res
Regression Eq:	*Pcorn*	=	61.58 +	1.42	*Psoil*	+ res

2. Calculate the fitted values from the parameter estimates,

Fitted values: Fits = E[*Pcorn*] = $\hat{\alpha}$ + $\hat{\beta}_{Psoil} \cdot Psoil$

3. Calculate the residuasl from the fitted values:

Residuals: Res = *Pcorn* – Fits

3. Evaluate Model.

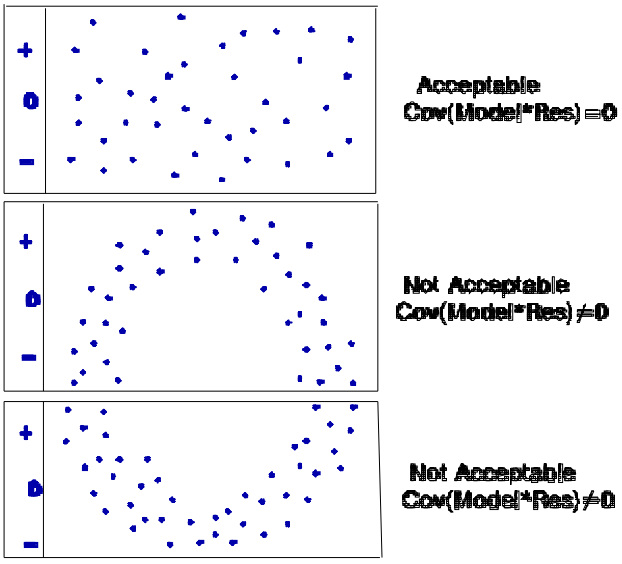
We use the residuals to evaluate the model.

We begin by examining the straight line assumption. Is this valid?
We use the residual versus fit plot to evaluate this assumption.
If the assumption is valid, the plot will show a band from left to right. If the assumption is not valid, the plot will show either a bowl or an arch pattern. The residual fit plot shows that the straight line model is acceptable for the corn data.

```
MTB > plot 'res' 'fits'
          _                                *
          _
        10+
          _                                                    *
 res      _                    *
          _           *
          _      *
          _
         0+                                                    *
          _                   *
          _
          _
          _
        -10+
          _
          _           *
          _
          _                                                    *
          _
            ______+_________+_________+_________+_________+_________+fits
                64.0      72.0      80.0      88.0      96.0     104.0
```

The accompanying diagram contrasts an acceptable plot with two unacceptable plot. One shows an arch, where residuals are too low at high or low fitted values. The other diagram shows a bowl, where residuals are too high at high or low fitted values. Bowls or arches result if the relation of the response to explanatory variable is curvilinear.

If this assumption is violated we go back to step 1 and reformulate the model to something other than a straight line.



3. Evaluate model.

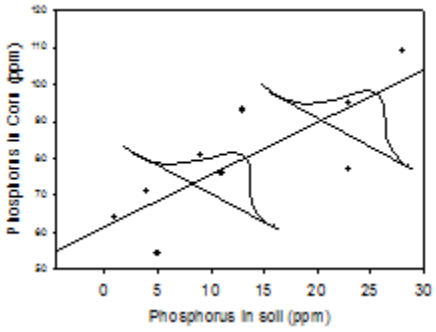
Next, we evaluate the error model that was used to estimate the parameters and likelihood ratios that will be used to calculate p-values (Type I error) from a statistical distribution (chisquare or *t* or *F*).

These distributions assume:

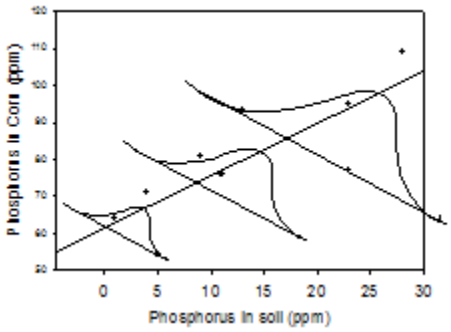
Fixed variance (errors homogeneous)
Normally distributed errors.
Independent errors
Unbiased estimate (errors sum to zero)

In practice the first assumption is the most important. The second assumption is more often mentioned and often incorrectly diagnosed (i.e diagnosed before estimating parameters and computing residuals). The third assumption is best diagnosed if we know the order in which samples were gathered or we know the spatial arrangement of samples. The fourth assumption does not need to be checked when parameters are estimated by statistical packages that automatically produce unbiased estimates. We will focus on the first two assumptions, unless we have information allowing us to diagnose the independent error assumption.

To evaluate the fixed error assumption we again examine the residual versus fit plot. If the assumption is valid the plot will show a horizontal band. The dispersion around zero will be uniform across the plot. If the assumption is not valid the plot will show dispersion around zero changes from left to right in the plot, usually with an obvious cone, fan, or spindle pattern. The residual fit plot for the corn data shows an acceptable band, with no evidence of change in dispersion going from left to right. The assumption of homogeneous error is acceptable for the corn data.



The accompanying diagram shows acceptably homogenous residuals in idealized form, superimposed on the corn data. The dispersion around the regression line is equal all along the line. As a result, the residual versus fit plot shows a uniform band running from left to right.



The next diagram shows a pattern of heterogeneity in which the dispersion increases from left to right along the regression line. This pattern, which is common, will result in a cone opening out to the right in the plot of residuals versus fitted values. The opposite pattern, of a cone opening out to the left due to high variance at small fitted value, is rare.

3. Evaluate model. Normal Errors

The next assumption is that the errors are normal. The histogram of residuals for the corn data looks "somewhat" normal, but there is evidence of skew to low values.

Another diagnostic is comparison of the observed distribution to a normal distribution with the same mean and standard error.

```
MTB > hist 'res'
 Histogram of res   N = 9

 Midpoint   Count
      -15       2  **
      -10       0
       -5       0
        0       3  ***
        5       2  **
       10       1  *
       15       1  *
```

Add diagram

The most useful plot for diagnosing normality shows each residual, transformed to a normal score, plotted against the (untransformed) residual. If the residuals are normal, this normal probability plot will exhibit a straight line rising from left to right.

```
MTB > nscores 'res' c7
 MTB > plot c7 'res'
 C7      -
         -                                                    *
         -
      1.0+                                              *
         -
         -                                           *
         -
         -                                      *
      0.0+                                   *
         -                                 *
         -
         -                              *
         -
     -1.0+          *
         -
         -    *
         -
           --+---------+---------+---------+---------+---------+---------+----res
         -18.0     -12.0      -6.0       0.0       6.0      12.0
```

The normal probability plot for the *Pcorn* analysis shows some deviation from the diagonal at strongly negative residuals.

3. Evaluate model. Independent Errors

This is a text example, we do not have information on spatial layout of samples, or on collection sequence. We will assume independent errors. Just because our observations come from a single location, we do not assume that our data are 'not independent.' See Hurlbert (1984) for an example of this fallacy.

3. Evaluate error model. Conclusion.

Residuals appear to be homogeneous with some departure from normal distribution. We do not have enough information to evaluate the assumption of independent errors.
We may need to use an empirical distribution to compute p-values or confidence limits.

4. Partition df and SS according to model.

Compute total degrees of freedom $df_{total} = n - 1 = 9 - 1 = 8$

Partition df_{total} according to model, using rules $df_{model} = 1$ regression line

$df_{res} = df_{total} - df_{model}$ $df_{res} = 8 - 1 = 7$

Model	$Pcorn - \beta_o$	=	$\beta_{PSoil} \cdot Psoil$	+	ε
Source	Total	=	$Psoil$	+	Resid
df	9 – 1	=	1	+	7

General linear model routines estimate the total sum of squares, partition it, and produce an ANOVA table with the partitioned SS_{tot}

GLM	$Pcorn - \beta_o$	=	$\beta_{PSoil} \cdot P_{Soil}$	+	ε
Source	Total	=	$PSoil$	+	Resid
df	9 – 1	=	1	+	7
SS	2274	=	1473	+	800.4
	SS_{tot}	=	SS_{regr}	+	SS_{res}

Here are calculations from data equations.

Data Equations for null model, Pcorn = mean(Pcorn)

	Data =	Model	+ Res	Res^2	
	64.00	80.00	-16.00	256.0000	
	71.00	80.00	-9.00	81.0000	
	54.00	80.00	-26.00	676.0000	
	81.00	80.00	1.00	1.0000	
	93.00	80.00	13.00	169.0000	
	76.00	80.00	-4.00	16.0000	
	77.00	80.00	-3.00	9.0000	
	95.00	80.00	15.00	225.0000	
	109.00	80.00	29.00	841.0000	
Sums	720.00	720.00	0.00	2274.0000	= sum(res^2)
	720/9 = 80				

Data Equations for regression model

Pcorn = 61.58 + 1.417*Psoil

Psoil	Data =	Model	+ Res	Res^2			
1	64.00	63.00	1.00	1.0055			
4	71.00	67.25	3.75	14.0778			
5	54.00	68.66	-14.66	215.0578			
9	81.00	74.33	6.67	44.4566			
13	93.00	80.00	13.00	169.0000			
11	76.00	77.17	-1.17	1.3601			
23	77.00	94.17	-17.17	294.7724			
23	95.00	94.17	0.83	0.6907			
28	109.00	101.25	7.75	60.0097			
						2274.00	SS total, from above
intercept	61.5804		0.00	800.4305	= sum(res^2)	800.43	SS residual
slope	1.4169					1473.57	SS improvement

4. What is the evidence? Calculate likelihood ratio for the overall model

The overall (omnibus) model includes all of the terms in the model.
The analytic model isolates a single term for comparison.
The omnibus and analytic models are the same for single variable models.

$$LR = (SS_{res} / SS_{total})^{-n/2}$$
$$LR = (800.4 / 2274)^{-9/2} = 110$$

The alternative model is 110 times more likely than the full (null) model.

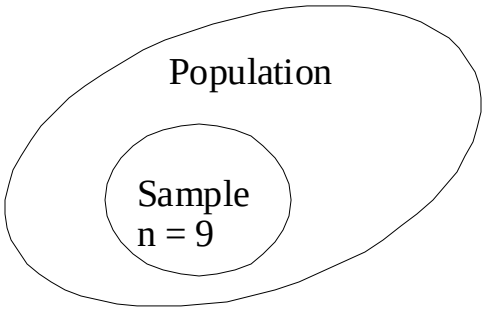
5. Mode of inference.

This is an experiment under controlled conditions with a measurement protocol that could be repeated many times. We expect the results to vary from run to run due to many sources of variation including measurement error. From the law of large numbers (Bernoulli 1713) we expect better and better estimates of the true value of the parameters as we increase the number of repeats. This is called frequentist inference. In other examples we will encounter two other forms of inference, priorist and evidentialist.

5. State population and whether sample is representative.

The population is a very large number of repeats of the experiment. The population is represented by the model

$$Pcorn = \alpha + \beta_{PSoil} \cdot PSoil + \varepsilon$$



Running the experiment thousands of times, while conceivable, is hardly feasible. We are will use the law of large number to infer from the measurements we have (the sample) to the larger population (thousands of runs). We will infer from our sample to the true value of the relation of phosphorus in corn to phosphorus in soil, as represented by the parameters β_{PSoil} and α. This view of inference emphasizes the importance of the experimental protocol. From this point of view, the population is all possible measurements, given the experimental protocol.

The population is not an enumerable population. It is not all corn plants in the world nor is it all corn plants in Iowa, where the experiment was conducted. It is not even all corn plants at the agricultural station where the experiment was conducted.

Looking beyond the results from an experimental agriculture station, can we make and inference about the relation between phosphorus in corn and in soil in the state of Iowa? To do this, we need more information. For example do the experimental results vary among the 17 soils types in Iowa ? If so, we would have some basis for inference beyond the research station.

5. Decide on mode of inference. Is hypothesis testing appropriate? If yes step 6, otherwise, calculate and report the likelihood ratio with parameter estimates.

Based on the law of large numbers we can use the likelihood ratio to calculate the probability of drawing a correct conclusion from the sample. *LR* -- > *LR* test ? Yes. What is the cost (or risk) of drawing a false conclusion? In an applied context, such as this, one cost is recommending an agricultural practice, such as adding phosphorus to soil. In such a context, we control our false conclusion rate at a fixed value. By convention this is 5%.

6. State H_A / H_o , test statistic, and α

There is one term in the model, $\beta_{Psoil} \cdot Psoil$

The research hypothesis for this term is that phosphorus in corn depends on phosphorus in the soil, and hence variation in $\beta_{Psoil} \cdot Psoil$ term. In the absence of evidence for a relation of phosphorus in corn to phosphorus in soil, the null or state of science hypothesis is no relation hence no variance in $\beta_{Psoil} \cdot Psoil$ term, beyond chance variation.

H_A: $\text{var}(\beta_{Psoil} \cdot Psoil) > 0$

H_o: $\text{var}(\beta_{Psoil} \cdot Psoil) = 0$

Hypotheses about terms in the model are equivalent to hypotheses about the parameters in the model.

H_A:	$\text{var}(\beta_{Psoil} \cdot Psoil) > 0$	Equivalent to	H_A: $\beta_{Psoil} \neq 0$
H_o:	$\text{var}(\beta_{Psoil} \cdot Psoil) = 0$	Equivalent to	H_o: $\beta_{Psoil} = 0$

The test statistic will be the F-statistic, a variance ratio, which we will construct in the next step.

The distribution will be the F-distribution, which is readily calculated.

There is some evidence that the errors are not normal, so later we will evaluate whether we should obtain a randomized pvalue, free of assumptions.

Tolerance for Type I error is 5%

7. ANOVA. Table Source, SS, df, MS, F-ratio.

```
Establish relation of model to ANOVA table.
GLM on left side of chalk board, with df and SS
ANOVA table headings at top, to right.
Fill in below GLM, then move Source, df, SS to table.
Move Source, df, and SS to ANOVA table
Complete calculations of MS, F,
```

7. ANOVA: Table SS and degrees of freedom df.

Move Source, df, and SS to table. An ANOVA table is a GLM turned on its side.

Source	df	SS	MS	F	---->	p
PSoil	1	1473.6				
Res	7	800.4				
Total	8	2274.0				

7. ANOVA: Complete the ANOVA table

```
Computational flow is left to right,
  compute MS from SS and df in ANOVA table
  compute F from MS
```

MS = SS/df

MS_{model} = 1473.6/1 = 1473.6

MS_{res} = 800.4/7 = 114.34

F = MS_{model} / MS_{res} = 12.89

Source	df	SS	MS	F ---->	p
PSoil	1	1473.6	1473.6	12.89	
Res	7	800.4	114.34		
Total	8	2274.0			

Here are some additional statistics.

r^2 = explained variance = SS_{model} / SS_{tot}

r is the correlation coefficient

SS_{model} / SS_{tot} = coefficient of determination, for any GLM

1 – coefficient of determination = coefficient of non-determination.

Here is a summary, before moving on to the next step in the recipe.

The ANOVA table represents a sequence of computations from left to right.

Factors are listed, based on the model that was written.

df are listed, for each factor, and for the residuals. df_{tot} = df_{model} + df_{res}

SS_{tot} is estimated as the sum of the squared deviations of the response variable from the grand mean of the reponse variable. This is partitioned into a component for each factor in the model, and one residual component.

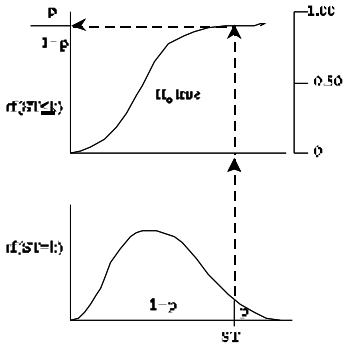
MS means squares are computed for each source (model factors + residuals).

F ratios are formed as ratios of mean squares MS

7. ANOVA: Calculate Type I error from F distribution.

Packages compute and place the p-value in the ANOVA table. p = 0.00885

```
MTB > cdf 12.89 k3;
SUBC> f 1 8.
MTB > print k3
K3       0.991146
MTB > let k3 = 1-k3
MTB > print k3
K3       0.00885403
```



8. Recompute p-value if necessary.

Confidence limits and p-values are computed from statistical distributions (chisquare, *F*, *t*, and normal). However, these calculations can be inaccurate if assumptions for these distributions are violated. The distortion depends on sample size. As a rule of thumb distortion can be serious if $n < 30$, less serious if $30 \leq n \leq 100$, and usually not serious if $n > 100$. In this example $n = 9$, so violations are potentially serious.

When assumptions are not met, recomputed Type I error is worth considering if:

n small (Yes, n = 9)

p near α (No, p = 0.00885)

The p-value is far from α and hence recomputing the p-value can easily change our estimate of Type I error, but will not change our decision. Randomized p-values generally differ from the theoretical p-values by less than a factor of two, rarely by a factor of 5 or more. This choice is a matter of judgement, through experience with randomized p-values. In this case, a factor of 5 would leave the p-value less than 5%, and hence not alter the decision. So we might well judge at this point not to recompute the p-value. But while good judgement will suffice in day to day practice, it is not adequate when we must defend our conclusion from critical scrutiny. If we publish the result then we may well decide to compute a p-value free of assumptions, rather than appealing to personal judgement. If we had to defend our conclusion in court, then we would certainly use a p-value free of assumptions rather than appealing to judgement.

For the example at hand, it is of interest to find out whether our judgement was correct, that the p-value is so small that a better estimate won't change the decision at a 5% level.

In 4000 randomizations there were 27 instances of an F-ratio greater than 12.89. The randomized p-value is somewhat smaller than the p-value from the F-distribution. The p-value from the theoretical distribution was high by a factor of

0.008854 / 0.00675 = 1.3

```
MTB > let k2 = 27/4000
MTB > print k2
K2        0.00675000
```

This is consistent with experience with randomization, which shows that the recalculated p-value will generally differ from that from the F-distribution by less than a factor of 2 (and rarely by more than a factor of 5).

We will report the randomized p-value because it is free of assumptions. But in the future we will be less likely to undertake randomization unless *p* is near α.

9. Declare and report decision about model terms.

p = 0.006750 (via randomization, hence no assumptions)

$p < \alpha = 5\%$ so reject H_o : $\text{var}(\beta_{PSoil} \cdot Psoil) = 0$

Rejecting the null on the variance is equivalent to rejecting the null on the parameter, $\beta_{PSoil} \neq 0$

9. Report statistical conclusion.

We reject the no-effect hypothesis in favour of stastistically significant increase in available phosphorus with increase in soil phosphorus

We report the test statistic, the sample size (or equivalent) and the p-value ($F_{1,7} = 12.89$, $p = 0.0085$ by randomization)

10. Report science conclusion. Interpret parameters of biological interest.

In this example our interest was in whether or not phosphorus content in corn was related to phosphorus content in the soil. However, we can learn more from the analysis than just this yes/no decision about the relation.

We begin by interpreting the slope parameter, for which the estimate is: $\hat{\beta}_{Psoil} = 1.4$
The observed phosphorus content in corn increases by 1.4 units for each unit increase in soil phosphorus. Are the results consistent with amplification in corn relative to the soil? In other words, can we exclude the hypothesis ($\beta_{Psoil} = 1$) that there was no amplification?

To avoid repeated testing, we compute the confidence limits using the standard error of the estimate of the slope parameter $s_b = 0.3947$. This estimate is provided by the statistical package. It differs from the standard error of the mean.

95% confidence limits for parameters.

$P\{\text{Lower} < \beta_{Psoil} < \text{Upper}\} = 1 - \alpha = 95\%$

Lower =	$\hat{\beta}_{Psoil}$	–	$t_{0.025[7]} * s_b$	
Lower =	1.4169	–	2.3646 * 0.3947	= 0.484
Upper =	$\hat{\beta}_{Psoil}$	+	$t_{0.025[7]} * s_b$	
Upper =	1.4169	+	2.3646 * 0.3947	= 2.35

$0.484 \leq \beta_{PSoil} \leq 2.35$ for $\alpha = 5\%$.

These limits exclude the $\beta_{PSoil} = 0$ hypothesis. They do not exclude the hypothesis $\beta_{PSoil} = 1$ hypothesis. that available phosphorus increases in direct proportion to soil phosphorus. We cannot reject the hypothesis that phosphorus in corn increases in direction proporation to phosphorus in soil $\beta_{PSoil} = 1$.

Confidence limits allow us to exclude several hypotheses, not just the null of no relation.

For the sake of completeness, we report the regression equation with standard error of the slope parameter and sample size.

$$P_{corn} = 61.58 + 1.42\ P_{Soil} \quad s_b = 0.3947,\ n = 9$$

References

Bernoulli, Jakob (2005) [1713], The Art of Conjecturing, together with Letter to a Friend on Sets in Court Tennis (English translation), translated by Edith Sylla, Baltimore: Johns Hopkins Univ Press