Forestry 430 Advanced Biometrics and
FRST 533 Problems in Statistical Methods
Course Materials 2007

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Course Objectives and Overview:
The objectives of this course are:

1. To be able to use simple linear and multiple linear regression to fit models using sample data;
2. To be able to design and analyze lab and field experiments;
3. To be able to interpret results of model fitting and experimental analysis; and
4. To be aware of other analysis methods not explicitly covered in this course.

In order to meet these objectives, background theory and examples will be used. A statistical package called "SAS" will be used in examples, and used to help in analyzing data in exercises. Texts are also important, both to increase understanding while taking the course, and as a reference for future applied and research work.

Course Content Materials:
These cover most of the course materials. However, changes will be made from year to year, including additional examples. Any additional course materials will be given as in-class handouts.
NOTE: Items given in Italics are only described briefly in this course.

These course materials will be presented in class and are essential for the courses. These materials are not published and should not be used as citations for papers. Recommendations for some published reference materials, including the textbook for the course, will be listed in the course outline handed out in class.

I. **Short Review of Probability and Statistics (pp. 9-37)**

- Descriptive statistics
- Inferential statistics using known probability distributions: normal, t , F, Chi-square, binomial, Poisson

II. **Fitting Equations (pp. 38-40)**

- Dependent variable and predictor variables
- Purpose: Prediction and examination
- General examples
- Simple linear, multiple linear, and *nonlinear regression*
- Objectives in fitting: Least squared error *or Maximum likelihood*

Simple Linear Regression (SLR) (pp. 41-96)

Definition, notation, and example uses

- dependent variable (y) and predictor variable (x)
- intercept, and slope, and error

Least squares solution to finding an estimated intercept and slope

- Derivation
- Normal equations
- Examples

Assumptions of simple linear regression and properties when assumptions are met

- Residual plots to visually check the assumptions that:
  - 1. Relationship is linear MOST IMPORTANT!!
  - 2. Equal variance of y around x (equal "spread" of errors around the line)
  - 3. Observations are independent (not correlated in space nor time)
- Normality plots to check assumption that:
  - 4. Normal distribution of y around x (normal distribution of errors around the line)
- Sampling and measurement assumptions:
  - 5. x values are fixed
  - 6. random sampling of y occurs for every x

Transformations and other measures to meet assumptions

- Common Transformations for nonlinear trends, unequal variances, percents, rank transformation
- Outliers: unusual observations
- Other methods: *nonlinear least squares, weighted least squares, general least squares, general linear models*

Measures of goodness-of-fit

- Graphs
- Coefficient of determination (r^2) [and Fit Index, I^2]
- Standard error of the estimate (SE_E) [and SE_E']

Estimated variances, confidence intervals and hypothesis tests

- For the equation
- For the intercept and slope
- For the mean of the dependent variable given a value for x
- For a single or group of values of the predicted dependent variable given a value for x

Selecting among alternative models

- Process to fit an equation using least squares regression
- Meeting assumptions
- Measures of goodness-of-fit: Graphs, Coefficient of determination (r^2) or I^2, and Standard error of the estimate (SE_E) or SE_E'
- Significance of the regression
- Biological or logical basis and cost

Multiple Linear Regression (pp. 97-173)

Definition, notation, and example uses

- dependent variable (y) and predictor variables (x's)
- intercept, and slopes and error

Least squares solution to finding an estimated intercept and slopes

- Least Squares and comparison to *Maximum Likelihood Estimation*
- Derivation
- Linear algebra to obtain normal equations; *matrix algebra*
- Examples: Calculations and SAS outputs

Assumptions of multiple linear regression

- Residual plots to visually check the assumptions that:

  - 1. Relationship is linear (y with ALL x's, not each x, necessarily); MOST IMPORTANT!!
  - 2. Equal variance of y around x's (equal "spread" of errors around the "surface")
  - 3. Observations are independent (not correlated in space nor time)
- Normality plots to check assumption that:
  - 4. Normal distribution of y around x's (normal distribution of errors around the "surface")
- Sampling and measurement assumptions:
  - 5. x values are fixed
  - 6. random sampling of y occurs for every combination of x values
- Properties when all assumptions are met versus some are not met

Transformations and other measures to meet assumptions: same as for SLR, but more difficult to select correct transformations

Measures of goodness-of-fit

- Graphs
- Coefficient of multiple determination (R^2) [and Fit Index, I^2]
- Standard error of the estimate (SE_E) [and SE_E']

Estimated variances, confidence intervals and hypothesis tests: Calculations and SAS outputs

- For the regression "surface"
- For the intercept and slopes
- For the mean of the dependent variable given a particular value for each of the x variables
- For a single or group of values of the predicted dependent variable given a particular value for each of the x variables

Methods to aid in selecting predictor (x) variables

- All possible regressions
- R^2 criterion in SAS
- Stepwise methods

Adding class variables as predictors

- Dummy variables to represent a class variable
- Interactions to change slopes for different classes

- Comparing two regressions for different class levels
- More than one class variable

(class variables as the dependent variable – covered in FRST 530; under generalized linear model).

Selecting and comparing alternative models

- Meeting assumptions
- Parsimony and cost
- Biological nature of the system modeled
- Measures of goodness-of-fit: Graphs, Coefficient of determination (R^2) [or Fit Index, I^2], and Standard error of the estimate (SE_E) [or SE_E']
- Comparing models when some models have a transformed dependent variable
- *Other methods using maximum likelihood criteria*

II. Experimental Design and Analysis (pp. 174-192)

- Sampling versus experiments
- Definitions of terms: experimental unit, response variable, factors, treatments, replications, crossed factors, randomization, sum of squares, degrees of freedom, confounding
- Variations in designs: number of factors, fixed versus random effects, blocking, split-plot, nested factors, subsampling, covariates
- Designs in use
- Main questions in experiments

Completely Randomized Design (CRD**) (pp. 193-293)**

Definition: no blocking and no splitting of experimental units

One Factor Experiment, Fixed Effects (pp. 193-237)

- Main questions of interest
- Notation and example: observed response, overall (grand mean), treatment effect, treatment means
- Data organization and preliminary calculations: means and sums of squares
- Test for differences among treatment means: error variance, treatment effect, mean squares, F-test

- Assumptions regarding the error term: independence, equal variance, normality, expected values under the assumptions
- Differences among particular treatment means
- Confidence intervals for treatment means
- Power of the test
- Transformations if assumptions are not met
- SAS code

Two Factor Experiment, Fixed Effects (pp. 238-273)

- Introduction: Separating treatment effects into factor 1, factor 2 and interaction between these
- Example layout
- Notation, means and sums of squares calculations
- Assumptions, and transformations
- Test for interactions and main effects: ANOVA table, expected mean squares, hypotheses and tests, interpretation
- Differences among particular treatment means
- Confidence intervals for treatment means
- SAS analysis for example

One Factor Experiment, Random Effects

- *Definition and example*
- *Notation and assumptions*
- *Least squares versus maximum likelihood solution*

Two Factor Experiment, One Fixed and One Random Effect (pp. 274-293)

- Introduction
- Example layout
- Notation, means and sums of squares calculations
- Assumptions, and transformations
- Test for interactions and main effects: ANOVA table, expected mean squares, hypotheses and tests, interpretation
- SAS code

Orthogonal polynomials – not covered

Restrictions on Randomization (pp. 294-397)

Randomized Block Design (RCB) with one fixed factor (pp. 294-319)

- Introduction, example layout, data organization, and main questions
- Notation, means and sums of squares calculations
- Assumptions, and transformations
- Differences among treatments: ANOVA table, expected mean squares, hypotheses and tests, interpretation
- Differences among particular treatment means
- Confidence intervals for treatment means
- SAS code

Randomized Block Design with other experiments (pp. 320-358)

- RCB with replicates in each block
- Two fixed factors
- One fixed, one random factor

Incomplete Block Design

- *Definition*
- *Examples*

Latin Square Design: restrictions in two directions (pp. 359-377)

- Definition and examples
- Notation and assumptions
- Expected mean squares
- Hypotheses and confidence intervals for main questions if assumptions are met

Split Plot and Split-Split Plot Design (pp. 378-397)

- Definition and examples
- Notation and assumptions
- Expected mean squares
- Hypotheses and confidence intervals for main questions if assumptions are met

Nested and hierarchical designs (pp. 398-456)

CRD: Two Factor Experiment, Both Fixed Effects, with Second Factor Nested in the First Factor (pp. 398-423)

- Introduction using an example
- Notation

- Analysis methods: averages, least squares, *maximum likelihood*
- Data organization and preliminary calculations: means and sums of squares
- Example using SAS

CRD: One Factor Experiment, Fixed Effects, with sub-sampling (pp. 424-449)

- Introduction using an example
- Notation
- Analysis methods: averages, least squares, *maximum likelihood*
- Data organization and preliminary calculations: means and sums of squares
- Example using SAS

RCB: One Factor Experiment, Fixed Effects, with sub-sampling (pp. 450-456)

- Introduction using an example
- Example using SAS

Adding Covariates (continuous variables) (pp. 457-468)

Analysis of covariance

- Definition and examples
- Notation and assumptions
- Expected mean squares
- Hypotheses and confidence intervals for main questions if assumptions are met
- Allowing for Inequality of slopes

Expected Mean Squares – Method to Calculate These (pp. 469-506)

- Method and examples

Power Analysis (pp. 507-524)

- *Concept and an example*

Use of Linear Mixed Models for Experimental Design (pp. 525-557)

- *Concept and examples*

Summary (pp. 558-572)

Probability and Statistics Review

Population vs. sample: N vs. n

Experimental vs. observational studies: in experiments, we manipulate the results whereas in observational studies we simple measure what is already there.

Variable of interest/ dependent variable/ response variable/ outcome: y

Auxilliary variables/ explanatory variables/ predictor variables/ independent variables/ covariates: x

Observations: Measure y's and x's for a census (all N) or on a sample (n out of the N)

x and y can be: 1) continuous (ratio or interval scale); or 2) discrete (nominal or ordinal scale)

Descriptive Statistics: summarize the sample data as means, variances, ranges, etc.

Inferential Statistics: use the sample statistics to estimate the parameters of the population

Parameters for populations:

1. Mean -- μ e.g. for N=4 and y_1=5; y_2=6; y_3=7 , y_4=6 μ=6

2. Range: Maximum value – minimum value

3. Standard Deviation σ and Variance σ^2

$$\sigma^2 = \sum_{i=1}^{N}(y_i - \mu)^2 \Big/ N$$

$$\sigma = \sqrt{\sigma^2}$$

4. Covariance between x and y: σ_{xy}

$$\sigma_{xy} = \left(\sum_{i=1}^{N}(y_i - \mu_y)(x_i - \mu_x)\right) \Big/ N$$

5. Correlation (Pearson's) between two variables, y and x: ρ

$$\rho_{xy} = \frac{\sigma_{xy}}{\sqrt{\sigma_x^{\ 2} \times \sigma_y^{\ 2}}}$$

Ranges from -1 to +1; with strong negative correlations near to -1 and strong positive correlations near to +1.

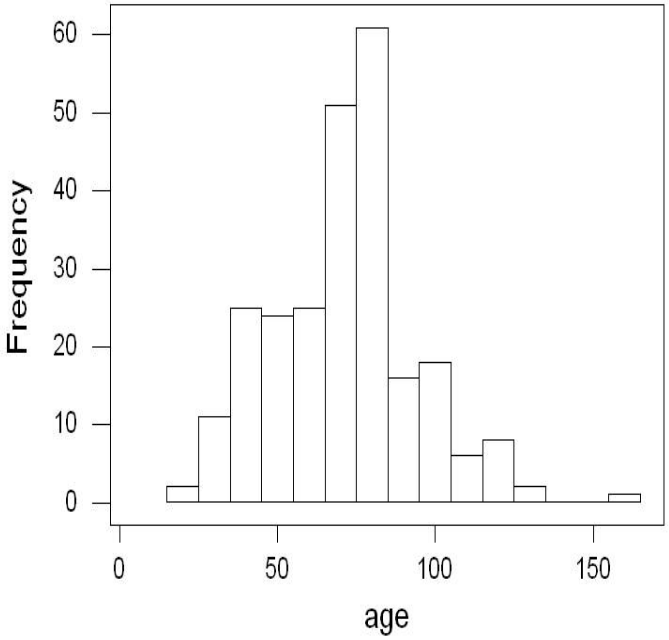
6. Distribution for y -- frequency of each value of y or x (may be divided into classes)

7. Probability Distribution of y or x – probability associated with each y value

8. Mode -- most common value of y or x

9. Median -- y-value or x-value which divides the distribution (50% of N observations are above and 50% are below)

Example: 250 aspen trees of Alberta



Descriptive Statistics: age

N=250 trees Mean = 71 years

Median = 73 years

25% percentile = 55 75% percentile = 82

Minimum = 24 Maximum =160

Variance = 514.7 Standard Deviation = 22.69

1. Compare mean versus median
2. Normal distribution?

Pearson correlation of age and dbh = 0.573 for the population of N=250 trees

Statistics from the Sample:

1. Mean -- $\bar{y}$ e.g. for n=3 and y_1=5; y_2=6; y_3=7 , $\bar{y}$ =6
2. Range: Maximum value – minimum value
3. Standard Deviation s and Variance s^2

$$s^2 = \sum_{i=1}^{n} (y_i - \bar{y})^2 \Big/ (n-1)$$

$$s = \sqrt{s^2}$$

4. Standard Deviation of the sample means (also called the Standard Error, short for Standard Error of the Mean) and it's square called the variance of the sample means are estimated by:

$$s_{\bar{y}}{}^2 = s^2/n \quad \text{and} \quad s_{\bar{y}} = \sqrt{s^2/n}$$

5. Coefficient of variation (CV): The standard deviation from the sample, divided by the sample mean. May be multiplied by 100 to get CV in percent.

6. Covariance between x and y: s_{xy}

$$s_{xy} = \left(\sum_{i=1}^{n} (y_i - \bar{y})(x_i - \bar{x}) \right) \Big/ (n-1)$$

7. Correlation (Pearson's) between two variables, y and x: r

$$r_{xy} = \frac{s_{xy}}{\sqrt{s_x{}^2 \times s_y{}^2}}$$

Ranges from -1 to +1; with strong negative correlations near to -1 and strong positive correlations near to +1.

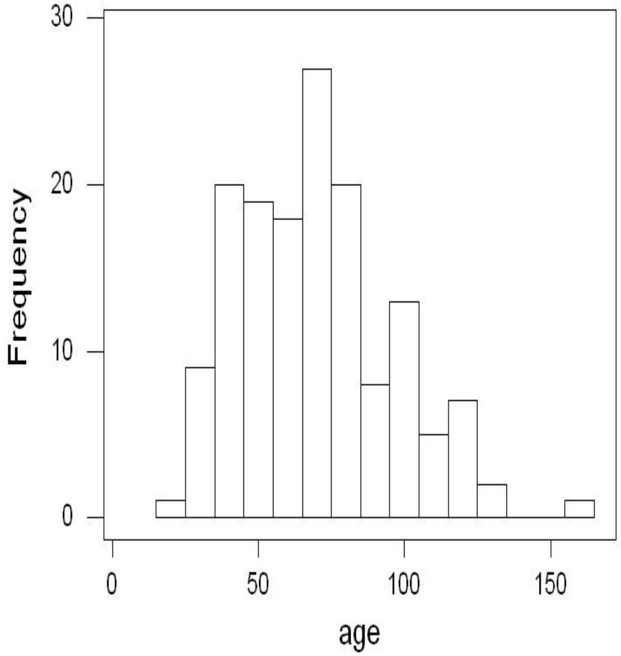
8. Distribution for y -- frequency of each value of y or x (may be divided into classes)

9. Estimated Probability Distribution of y or x – probability associated with each y value based on the *n* observations

10. Mode -- most common value of y or x

11. Median -- y-value or x-value which divides the estimated probability distribution (50% of N observations are above and 50% are below)

Example: n=150



n=150 trees Mean = 69 years

Median = 68 years

25% percentile = 48 75% percentile = 81

Minimum = 24 Maximum =160

Variance = 699.98
Standard Deviation = 25.69 years
Standard error of the mean =2.12 years

Good estimate of population values?

Pearson correlation of age and dbh = 0.66 with a p-value of 0.000 for the sample of n=150 trees from a population of 250 trees

Null and alternative hypothesis for the p-value?
What is a p-value?

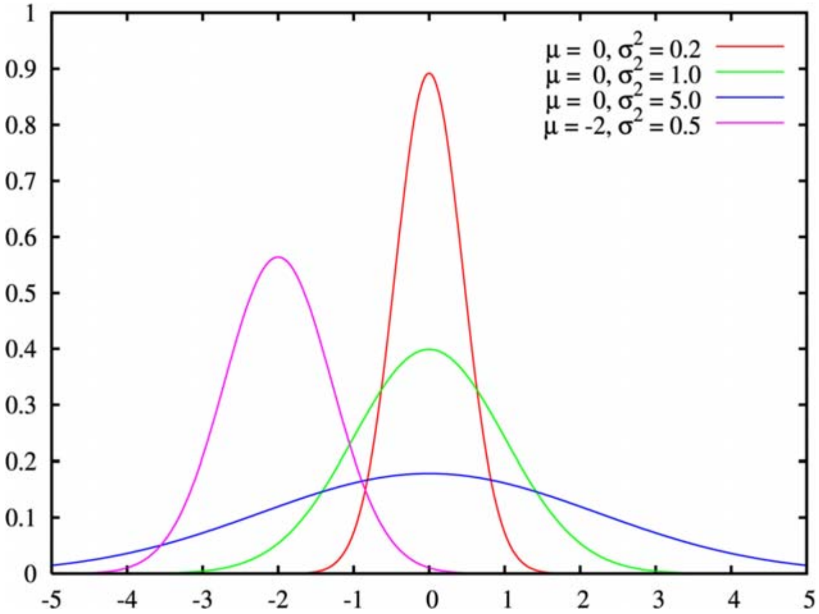
Sample Statistics to Estimate Population Parameters:

If simple random sampling (every observation has the same chance of being selected) is used to select n from N, then:

- Sample estimates are **unbiased estimates** of their counterparts (e.g., sample mean estimates the population mean), meaning that over all possible samples the sample statistics, averaged, would equal the population statistic.
- A particular sample value (e.g., sample mean) is called a "**point estimate**" -- do not necessarily equal the population parameter for a given sample.
- Can calculate an interval where the true population parameter is likely to be, with a certain probability. This is a **Confidence Interval**, and can be obtained for any population parameter, IF the distribution of the sample statistic is known.

Common continuous distributions:

Normal:



- Symmetric distribution around μ
- Defined by μ and σ^2. If we know that a variable has a normal distribution, and we know these parameters, then we know the probability of getting any particular value for the variable.

- Probability tables are for $\mu=0$ and $\sigma^2=1$, and are often called z-tables.

- Examples: $P(-1<z<+1) = 0.68$; $P(-1.96<z<1.96)=0.95$.
  Notation example: For $\alpha=0.05$,

$$z_{\alpha/2} = z_{0.025} = -1.96 \, .$$

- z-scores: scale the values for y by subtracting the mean, and dividing by the standard deviation.

$$z_i = \frac{y_i - \mu}{\sigma}$$

E.g., for mean=20, and standard deviation of 2 and y=10,
$z=-5.0$ (an extreme value)

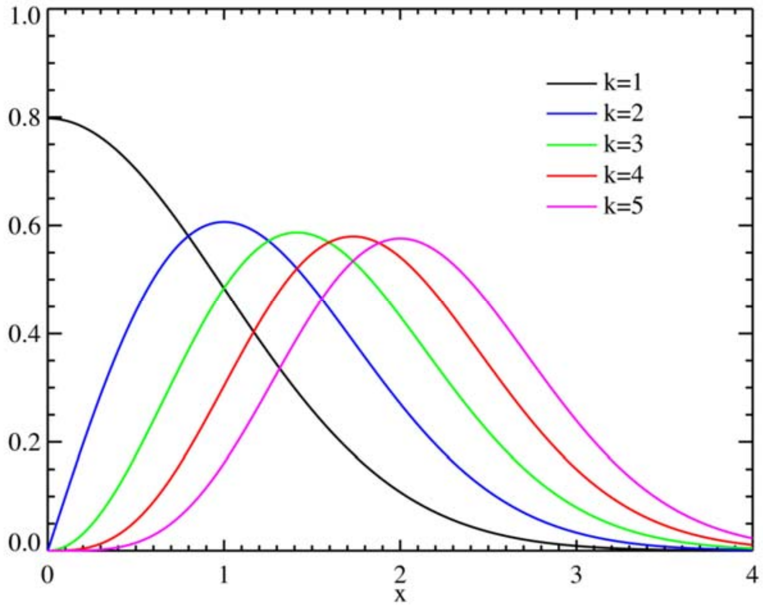
t-distribution:

- Symmetric distribution
- Table values have the center at 0. The spread varies with the *degrees of freedom*. As the sample size increases, the df increases, and the spread decreases, and will approach the normal distribution.
- Used for a normally distributed variable whenever the variance of that variable is not known.
- Notation examples:

$t_{n-1,\,1-\alpha/2}$ where n-1 is the degrees of freedom, in this case, and we are looking for the $1-\alpha/2$ percentile. For example, for n=5 and α=0.05, we are looking for t with 4 degrees of freedom and the 0.975 percentile (will be a value around 2).

X^2 distribution:

- Starts at zero, and is not symmetric
- Is the square of a normally distributed variable e.g. sample variances have a X^2 distribution if the variable is normally distributed
- Need the degrees of freedom and the percentile as with the t-distribution



F-distribution:

- Is the ratio of 2 variables that each have a X^2 distribution eg. The ratio of 2 sample variances for variables that are each normally distributed.
- Need the percentile, and two degrees of freedom (one for the numerator and one for the denominator)

Central Limit Theorem: As n increases, the distribution of sample means will approach a normal distribution, even if the distribution is something else (e.g. could be non-symmetric)

Tables in the Textbook:
Some tables give the values for probability distribution for the degrees of freedom, and for the percentile. Others, give this for the degrees of freedom and for the alpha level (or sometimes alpha/2). Must be careful in reading probability tables.

Confidence Intervals for a single mean:

- Collect data and get point estimates:
  - The sample mean, $\bar{y}$ to estimate of the population mean μ ---- Will be unbiased
  - The sample mean, s^2 to estimate of the population mean σ^2 ---- Will be unbiased
- Can calculate interval estimates of each point estimate e.g. 95% confidence interval for the true mean
  - If the y's are normally distributed OR
  - The sample size is large enough that the Central Limit Theorem holds -- $\bar{y}$ will be normally distributed

n items measured out of N possible items
(sometimes N is infinite)

$$\bar{y} = \frac{\sum_{i=1}^{n} y_i}{n} \quad \text{where} \quad \sum_{i=1}^{n} y_i \quad (\text{sum over all } n \text{ items})$$

$$\sum_{i=1}^{n} {y_i}^2 \,(\text{square each value and then add them})$$

$$s_y{}^2 = \frac{\sum {y_i}^2 - \left(\sum y_i\right)^2 / n}{n-1}$$

$$s_{\bar{y}}{}^2 = \frac{s_y{}^2}{n}\left(\frac{N-n}{N}\right) \text{ without replacement;}$$

$$s_{\bar{y}}{}^2 = \frac{s_y{}^2}{n} \text{ with replacement or}$$

when N is very large

$$\text{Coefficient of Variation} = CV = \frac{s_y}{\bar{y}} \times 100$$

95% Confidence Intervals for the true mean of the population :

$$\bar{y} +/- \; t_{n-1,1-\alpha/2} \times s_{\bar{y}}$$

Examples:

n is: 4

Plot	volume	ba/ha	ave. dbh
1	200	34	50
2	150	20	40
3	300	40	55
4	0	0	0

mean:	162.50	23.50	36.25
variance:	15625.00	315.67	622.92
std.dev.:	125.00	17.77	24.96
std.dev. of mean:	62.50	8.88	12.48
t should be:	3.182		
Actual 95% CI (+/-):	198.88	28.27	39.71

NOTE: EXCEL: 95%(+/-)	**122.50**	**17.41**	**24.46**
t:	**1.96**	**1.96**	**1.96**
		not correct!!!	

Hypothesis Tests:

- Can hypothesize what the true value of any population parameter might be, and state this as null hypothesis (H0:)
- We also state an alternate hypothesis (H1: or Ha:) that it is a) not equal to this value; b) greater than this value; or c) less than this value
- Collect sample data to test this hypothesis
- From the sample data, we calculate a sample statistic as a point estimate of this population parameter and an estimated variance of the sample statistic.
- We calculate a "test-statistic" using the sample estimates
- Under H0, this test-statistic will follow a known distribution.
- If the test-statistic is very unusual, compared to the tabular values for the known distribution, then the H0 is very unlikely and we conclude H1:

Example for a single mean:

We believe that the average weight of ravens in Yukon is 1 kg.

H0:

H1:

A sample of 10 birds is taken (HOW??) and each bird is weighed and released. The average bird weight is 0.8 kg, and the standard deviation was 0.02 kg. Assuming the bird weights follow a normal distribution, we can use a t-test (why not a z-test?)

Mean:

Variance:

Standard Error of the Mean:

Aside: What is the CV?

Test statistic: t-distribution

t=

Under H0: this will follow a t-distribution with df = n-1.

Find value from t-table and compare:

Conclude?

The p-value:

Is the probability that we would get a value outside of the sample test statistic.

NOTE: In EXCEL use: =tdist(x,df,tails)

Example: Comparing two means:

We believe that the average weight of male ravens differs from female ravens

H0: $\mu_1 = \mu_2$ or $\mu_1 - \mu_2 = 0$

H1: $\mu_1 \neq \mu_2$ or $\mu_1 - \mu_2 \neq 0$

A sample of 20 birds is taken and each bird is weighed and released. 12 birds were males with an average weight of 1.2 kg and a standard deviation of 0.02 kg. 8 birds were females with an average weight of 0.8 and a standard deviation of 0.01 kg.

Means?

Sample Variances?

Test statistic:

$$t = \frac{\left(\bar{y}_1 - \bar{y}_2\right) - 0}{s_{\bar{y}_1 - \bar{y}_2}} = \frac{\bar{y}_1 - \bar{y}_2}{\sqrt{\frac{(n_1 - 1)s_1^{\;2} + (n_2 - 1)s_2^{\;2}}{n_1 + n_2 - 2}}}$$

t =

Under H0: this will follow a t-distribution with df = (n1+n2-2).

Find t-value from tables and compare, or use the p-value:

Conclude?

Errors for Hypothesis Tests

	H0 True	H0 False
Accept	1-α	β (Type II error)
Reject	α (Type I error)	1-β

Type I Error: Reject H0 when it was true. Probability of this happening is α

Type II Error: Accept H0 when it is false. Probability of this happening is β

Power of the test: Reject H0 when it is false. Probability of this is 1-β

What increases power?

- Increase sample sizes, resulting in lower standard errors
- A larger difference between mean for H0 and for H1
- Increase alpha. Will decrease beta.

Fitting Equations

REF:

<u>Idea is</u> :

- variable of interest (dependent variable) y_i ; hard to measure

- "easy to measure" variables (predictor/ independent) that are related to the variable of interest, labeled x_{1i} , $x_{2i}, \ldots x_{mi}$

- measure y_i, $x_{1i}, \ldots x_{mi}$ for a sample of n items

- use this sample to estimate an equation that relates y_i (dependent variable) to $x_{1i}, \ldots x_{mi}$ (independent or predictor variables)

- once equation is fitted, one can then just measure the x's, and get an estimate of y without measuring it

-- also can examine relationships between variables

Examples:

1. Percent decay = y_i ; x_i = logten (dbh)
2. Logten (volume) = y_i ; x_{1i} = logten(dbh),
   x_{2i} = logten(height)
3. Branch length = y_i ; x_{1i} = relative height above ground, x_{2i} = dbh, x_{3i} = height

Types of Equations

Simple Linear Equation:

$$y_i = \beta_o + \beta_1 x_i + \varepsilon_i$$

Multiple Linear Equation:

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_m x_{mi} + \varepsilon_i$$

Nonlinear Equation: takes many forms, for example:

$$y_i = \beta_0 + \beta_1 x_{1i}^{\beta_2} x_{2i}^{\beta_3} + \varepsilon_i$$

Objective:

Find estimates of $\beta_0, \beta_1, \beta_2 \ldots \beta_m$ such that the sum of squared differences between measured y_i and predicted y_i (usually labeled as $\hat{y}_i$, values on the line or surface) is the smallest (*minimize* the sum of squared errors, called least squared error).

OR

Find estimates of $\beta_0, \beta_1, \beta_2 \ldots \beta_m$ such that the likelihood (probability) of getting these y values is the largest (*maximize* the likelihood).

Finding the minimum of sum of squared errors is often easier. In some cases, they lead to the same estimates of parameters.

Simple Linear Regression (SLR)

Population: $y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$ $\mu_Y \mid x = \beta_0 + \beta_1 x_i$

Sample: $y_i = b_0 + b_1 x_i + e_i$ $\hat{y}_i = b_0 + b_1 x_i$ $e_i = y_i - \hat{y}_i$

b_0 is an estimate of β_0 [intercept]

b_1 is an estimate of β_1 [slope]

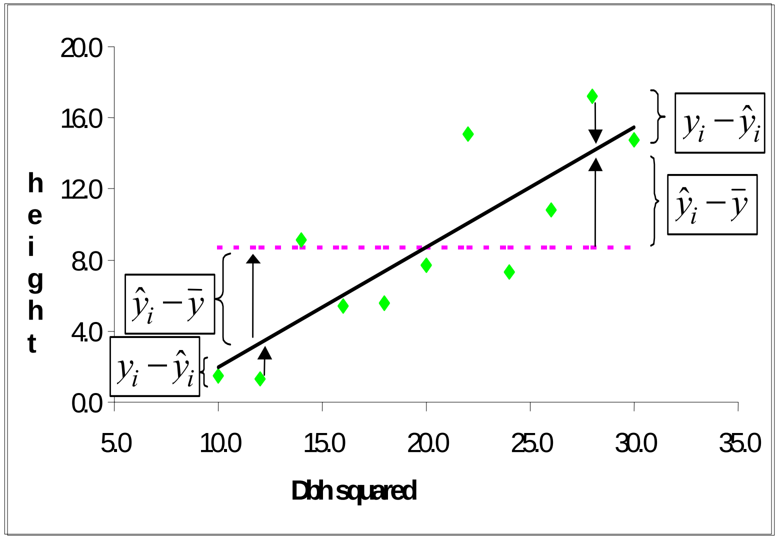
$\hat{y}_i$ is the predicted *y*; an estimate of the average for *y* for a particular x value

e_i is an estimate of ε_i, called the error or the residual; represents the variation in the dependent variable (the *y*) which is not accounted for by predictor variable (the *x*).

Find b_o (intercept; y_i when $x_i = 0$) and b_1 (slope) so that SSE=Σe_i^2 (sum of squared errors over all n sample observations) is the smallest (least squares solution)

- The variables do not have to be in the same units. Coefficients will change with different units of measure.
- Given estimates of b_o and b_1, we can get an estimate of the dependent variable (the *y*) for ANY value of the *x*, within the ranges of *x*'s represented in the original data.

Example: Tree Height (m) – hard to measure; Dbh (diameter at 1.3 m above ground in cm) – easy to measure – use Dbh squared for a linear equation



$y_i - \bar{y}$ Difference between measured y and the mean of *y*

$y_i - \hat{y}_i$ Difference between measured *y* and predicted *y*

$\hat{y}_i - \bar{y} = (y_i - \bar{y}) - (y_i - \hat{y}_i)$ Difference between predicted *y* and mean of *y*

Least Squares Solution: Finding the Set of Coefficients that Minimizes the Sum of Squared Errors

To find the estimated coefficients that minimizes SSE for a particular set of sample data and a particular equation (form and variables):

1. Define the sum of squared errors (SSE) in terms of the measured minus the predicted y's (the errors);
2. Take partial derivatives of the SSE equation with respect to each coefficient
3. Set these equal to zero (for the minimum) and solve for all of the equations (solve the set of equations using algebra or linear algebra).

For linear models (simple or multiple linear), there will be one solution. We can mathematically solve the set of partial derivative equations.

- WILL ALWAYS GO THROUGH THE POINT DEFINED BY $(\bar{x}, \bar{y})$.
- Will always result in $\sum e_i=0$

For nonlinear models, this is not possible and we must search to find a solution (covered in FRST 530).

If we used the criterion of finding the maximum likelihood (probability) rather than the minimum SSE, we would need to search for a solution, even for linear models (covered FRST 530).

Least Squares Solution for SLR:

Find the set of estimated parameters (coefficients) that minimize sum of squared errors

$$\min(SSE) = \min\left(\sum_{i=1}^{n} e_i^2\right) = \min\left(\sum_{i=1}^{n}\left(y_i - (b_0 + b_1 x_i)\right)^2\right)$$

Take partial derivatives with respect to b_0 and b_1, set them equal to zero and solve.

$$\frac{\partial SSE}{\partial b_0} = -2\sum_{i=1}^{n}\left(y_i - (b_0 + b_1 x_i)\right)$$

$$0 = \sum_{i=1}^{n} y_i - \sum_{i=1}^{n} b_0 - b_1 \sum_{i=1}^{n} x_i$$

$$0 = \sum_{i=1}^{n} y_i - n b_0 - b_1 \sum_{i=1}^{n} x_i$$

$$b_0 = \frac{1}{n}\sum_{i=1}^{n} y_i - b_1 \frac{1}{n}\sum_{i=1}^{n} x_i$$

$$\boxed{b_0 = \bar{y} - b_1 \bar{x}}$$

$$\frac{\partial SSE}{\partial b_1} = -2\sum_{i=1}^{n} x_i\left(y_i - (b_0 + b_1 x_i)\right)$$

$$0 = \sum_{i=1}^{n} y_i x_i - \sum_{i=1}^{n} b_0 x_i - b_1 \sum_{i=1}^{n} x_i^2$$

$$b_1 \sum_{i=1}^{n} x_i^2 = \sum_{i=1}^{n} y_i x_i - \sum_{i=1}^{n} b_0 x_i$$

$$b_1 = \frac{\sum_{i=1}^{n} y_i x_i - \sum_{i=1}^{n} b_0 x_i}{\sum_{i=1}^{n} x_i^2}$$

$$b_1 = \frac{\sum_{i=1}^{n} y_i x_i - \sum_{i=1}^{n} (\bar{y} - b_1 \bar{x}) x_i}{\sum_{i=1}^{n} x_i^2}$$

With some further manipulations:

$$\boxed{b_1 = \frac{\sum_{i=1}^{n}(y_i - \bar{y})(x_i - \bar{x})}{\sum_{i=1}^{n}(x_i - \bar{x})^2} = \frac{s^2{}_{xy}(n-1)}{s_x{}^2(n-1)} = \frac{SPxy}{SSx}}$$

Where *SPxy* refers to the corrected sum of cross products for *x* and *y*; *SSx* refers to the corrected sum of squares for *x* [Class example]

Properties of b_0 and b_1

b_0 and b_1 are least squares estimates of β_0 and β_1. **Under assumptions** concerning the error term and sampling/ measurements, these are:

- Unbiased estimates; given many estimates of the slope and intercept for all possible samples, the average of the sample estimates will equal the true values

- The variability of these estimates from sample to sample can be estimated from the single sample; these estimated variances will be unbiased estimates of the true variances (and standard errors)

- The estimated intercept and slope will be the most precise (most efficient with the lowest variances) estimates possible (called "Best")

- These will also be the maximum likelihood estimates of the intercept and slope

Assumptions of SLR

Once coefficients are obtained, we must **check the assumptions of** SLR. Assumptions must be met to:

- obtain the desired characteristics
- assess goodness of fit (i.e., how well the regression line fits the sample data)
- test significance of the regression and other hypotheses
- calculate confidence intervals and test hypothesis for the true coefficients (population)
- calculate confidence intervals for mean predicted y value given a set of x value (i.e. for the predicted y given a particular value of the x)

Need good estimates (unbiased or at least consistent) of the standard errors of coefficients and a known probability distribution to test hypotheses and calculate confidence intervals.

Checking assumptions using residual Plots

Assumptions of :

1. a linear relationship between the *y* and the *x*;
2. equal variance of errors; and
3. independence of errors (independent observations)

can be visually checked by using **RESIDUAL PLOTS**

A residual plot shows the residual (i.e., $y_i - \hat{y}_i$) as the y-axis and the predicted value ($\hat{y}_i$) as the x-axis.

Residual plots can also indicate unusual points (<u>outliers</u>) that may be measurement errors, transcription errors, etc.

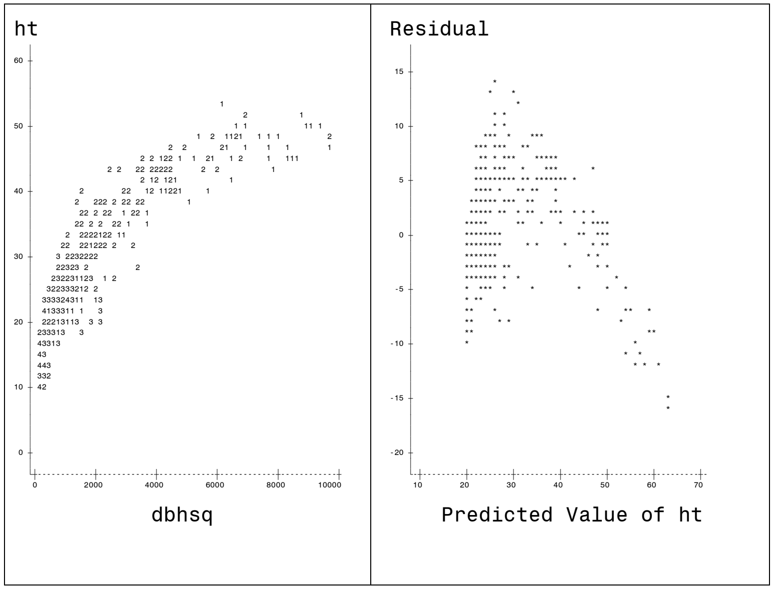
Residual plot that meets the assumptions of a linear relationship, and equal variance of the observations:

The data points are evenly distributed about zero and there are no outliers (very unusual points that may be a measurement or entry error).

For independence:

Examples of Residual Plots Indicating Failures to Meet Assumptions:

1. *The relationship between the x's and y is linear*. If not met, the residual plot and the plot of y vs. x will show a curved line:



Result: If this assumption is not met: the regression line does not fit the data well; biased estimates of coefficients and standard errors of the coefficients will occur

---

2. *The variance of the y values must be the same for every one of the x values.* If not met, the spread around the line will not be even.

Result: If this assumption is not met, the estimated coefficients (slopes and intercept) will be unbiased, but the estimates of the standard deviation of these coefficients will be biased.

∴ we cannot calculate CI nor test the significance of the x variable. However, estimates of the coefficients of the regression line and goodness of fit are still unbiased

3. *Each observation (i.e., x_i and y_i) must be independent of all other observations.* In this case, we produce a different residual plot, where the residuals are on the y-axis as before, but the x-axis is the variable that is thought to produce the dependencies (e.g., time). If not met, this revised residual plot will show a trend, indicating the residuals are not independent.

Result: If this assumption is not met, the <u>estimated coefficients (slopes and intercept) will be unbiased</u>, but the <u>estimates of the standard deviation of these coefficients will be biased.</u>

∴ we cannot calculate CI nor test the significance of the x variable. However, estimates of the coefficients of the regression line and goodness of fit are still unbiased

Normality Histogram or Plot

A fourth assumption of the SLR is:

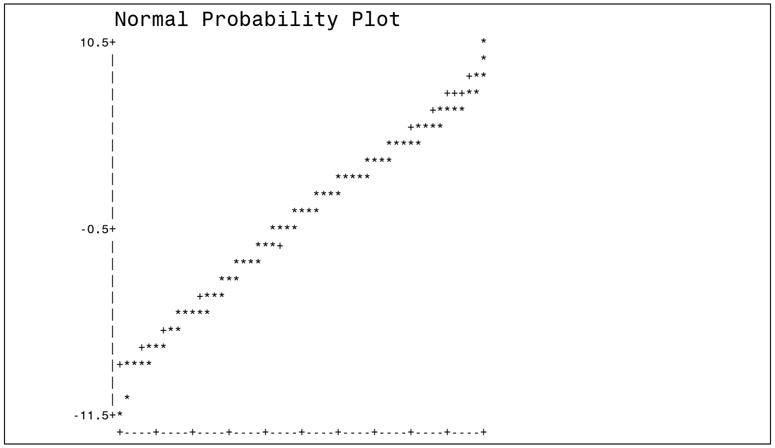
4. *The y values must be normally distributed for each of the x values.* A histogram of the errors, and/or a normality plot can be used to check this, as well as tests of normality

```
        Histogram                       #      Boxplot
 10.5+*                                 1         0
     .*                                 1         |
     .*                                 2         |
     .*                                 2         |
     .****                              8         |
     .*******                          14         |
     .**************                   27         |
     .********************             40         |
     .*****************************    57      +-----+
     .**************************       51      |     |
     .******************************   60      *--+--*
 -0.5+*****************************    58      |     |
     .*************************        49      |     |
     .*****************                33      +-----+
     .**************                   28         |
     .************                     24         |
     .***********                      22         |
     .****                              7         |
     .****                              7         |
     .***                               5         |
     .
     .*                                 1         0
-11.5+**                                3         0
      ----+----+----+----+----+----+
```

HO: data are normal H1: data are not normal

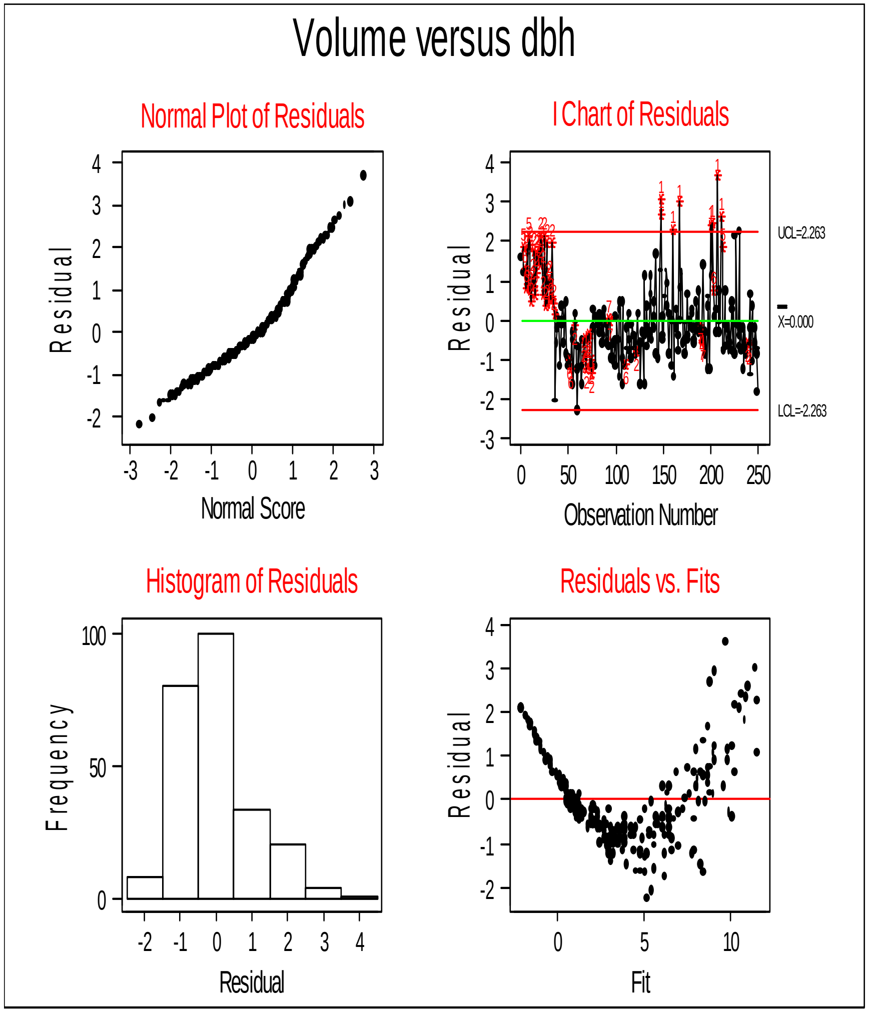
`Tests for Normality`

```
Test                  --Statistic---     -----p Value------
Shapiro-Wilk          W      0.991021    Pr < W       0.0039
Kolmogorov-Smirnov    D      0.039181    Pr > D       0.0617
Cramer-von Mises      W-Sq    0.19362    Pr > W-Sq    0.0066
Anderson-Darling      A-Sq   1.193086    Pr > A-Sq   <0.0050
```



Result: We cannot calculate CI nor test the significance of the x variable, since we do not know what probabilities to use. Also, estimated coefficients are no longer equal to the maximum likelihood solution.

Example:



Measurements and Sampling Assumptions

The remaining assumptions are based on the measurements and collection of the sampling data.

5. *The x values are measured without error (i.e., the x values are fixed).*

This can only be known if the process of collecting the data is known. For example, if tree diameters are very precisely measured, there will be little error. If this assumption is not met, the estimated coefficients (slopes and intercept) and their variances will be biased, since the x values are varying.

6. *The y values are randomly selected for value of the x variables (i.e., for each x value, a list of all possible y values is made, and some are randomly selected).*

For many biological problems, the observations will be gathered using simple random sampling or systematic sampling (grid across the land area). This does not strictly meet this assumption. Also, more complex sampling design such as multistage sampling (sampling large units and sampling smaller units within the large units), this assumption is not met. If the equation is "correct", then this does not cause problems. If not, the estimated equation will be biased.

Transformations

Common Transformations

- Powers x^3, $x^{0.5}$, etc. for relationships that look nonlinear
- log10, loge also for relationships that look nonlinear, or when the variances of y are not equal around the line
- Sin-1 [arcsine] when the dependent variable is a proportion.
- Rank transformation: for non-normal data
  - Sort the y variable
  - Assign a rank to each variable from 1 to n
  - Transform the rank to normal (e.g., Blom Transformation)

  PROBLEM: loose some of the information in the original data
- Try to transform x first and leave y_i = variable of interest; however, this is not always possible.

Use graphs to help choose transformations

Outliers: Unusual Points

Check for points that are quite different from the others on:

- Graph of y versus x
- Residual plot

Do not delete the point as it MAY BE VALID! Check:

- Is this a measurement error? E.g., a tree height of 100 m is very unlikely
- Is a transcription error? E.g. for adult person, a weight of 20 lbs was entered rather than 200 lbs.
- Is there something very unusual about this point? e.g., a bird has a short beak, because it was damaged.

Try to fix the observation. If it is very different than the others, or you know there is a measurement error that cannot be fixed, then **delete it and indicate this in your research report**.

On the residual plot, an outlier CAN occur if the model is not correct – may need a transformation of the variable(s), or an important variable is missing

Other methods, than SLR (and Multiple Linear Regression), when transformations do not work (some covered in FRST 530):

Nonlinear least squares: Least squares solution for nonlinear models; uses a search algorithm to find estimated coefficients; has good properties for large datasets; still assumes normality, equal variances, and independent observations

Weighted least squares: for unequal variances. Estimate the variances and use these in weighting the least squares fit of the regression; assumes normality and independent observations

General linear model: used for distributions other than normal (e.g., binomial, Poisson, etc.), but with no correlation between observations; uses maximum likelihood

Generalized least Squares and Mixed Models: use maximum likelihood for fitting models with unequal variances, correlations over space, correlations over time, but normally distributed errors

General linear mixed models: Allows for unequal variances, correlations over space and/or time, and non-normal distributions; uses maximum likelihood

Measures of Goodness of Fit

How well does the regression fit the sample data?

- For simple linear regression, a graph of the original data with the fitted line marked on the graph indicates how well the line fits the data [not possible with MLR]
- Two measures commonly used: coefficient of determination (r^2) and standard error of the estimate(SE_E).

To calculate r^2 and SE_E, first, calculate the SSE (this is what was minimized):

$$SSE = \sum_{i=1}^{n} e_i^2 = \sum_{i=1}^{n} \left(y_i - \hat{y}_i\right)^2 = \sum_{i=1}^{n} \left(y_i - (b_0 + b_1 x_i)\right)^2$$

The sum of squared differences between the measured and estimated *y*'s.

Calculate the sum of squares for *y*:

$$SSy = \sum_{i=1}^{n} \left(y_i - \bar{y}\right)^2 = \sum_{i=1}^{n} y_i^{\,2} - \left(\sum_{i=1}^{n} y_i^{\,2}\right) \Big/ n = s_y^{\,2}(n-1)$$

The sum of squared difference between the measured y and the mean of y-measures. NOTE: In some texts, this is called the <u>sum of squares total</u>.

Calculate the sum of squares regression:

$$SSreg = \sum_{i=1}^{n} \left(\bar{y} - \hat{y}_i\right)^2 = b_1 SPxy = SSy - SSE$$

The sum of squared differences between the mean of y-measures and the predicted *y*'s from the fitted equation. Also, is the sum of squares for *y* – the sum of squared errors.

Then: $$r^2 = \frac{SSy - SSE}{SSy} = 1 - \frac{SSE}{SSy} = \frac{SSreg}{SSy}$$

- SSE, SSY are based on *y*'s used in the equation – will not be in original units if *y* was transformed
- r^2 = coefficient of determination; proportion of variance of *y*, accounted for by the regression using *x*
- Is the square of the correlation between *x* and *y*
- O (very poor – horizontal surface representing no relationship between y and x's) to 1 (perfect fit – surface passes through the data)

And: $$SE_E = \sqrt{\frac{SSE}{n-2}}$$

- SSE is based on *y*'s used in the equation – will not be in original units if *y* was transformed
- SE_E - standard error of the estimate; in same units as y
- Under normality of the errors:
  - ±1 $SE_E \cong$ 68% of sample observations
  - ±2 $SE_E \cong$ 95% of sample observations
  - Want low SEE

y-variable was transformed: Can calculate estimates of these for the original y-variable unit, called I^2 (Fit Index) and estimated standard error of the estimate (SE_E'), in order to compare to r^2 and SE_E of other equations where the *y* was not transformed.

$$I^2 = 1 - SSE/SSY$$

- where SSE, SSY are in original units. NOTE must "back-transform" the predicted *y*'s to calculate the SSE in original units.
- Does not have the same properties as r^2, however:
  - it can be less than 0
  - it is not the square of the correlation between the y (in original units) and the *x* used in the equation.

Estimated standard error of the estimate (SE_E') , when the dependent variable, *y*, has been transformed:

$$SE_E' = \sqrt{\frac{SSE(original\ units)}{n-2}}$$

- SE_E' - standard error of the estimate ; in same units as original units for the dependent variable
- want low SE_E' [Class example]

Estimated Variances, Confidence Intervals and Hypothesis Tests

Testing Whether the Regression is Significant

Does knowledge of x improve the estimate of the mean of y? Or is it a flat surface, which means we should just use the mean of y as an estimate of mean y for any x?

SSE/ (n-2):

- Called the Mean squared error, as would be the average of the squared error if we divided by *n*.
- Instead, we divide by n-2. Why? The degrees of freedom are n-2; *n* observations with two statistics estimated from these, b_0 and b_1
- Under the assumptions of SLR, is an unbiased estimated of the true variance of the error terms (error variance)

SSR/1:

- Called the Mean Square Regression
- Degrees of Freedom=1: 1 *x*-variable
- Under the assumptions of SLR, this is an estimate the error variance PLUS a term of variance explained by the regression using *x*.

H0: Regression is not significant

H1: Regression is significant

Same as:

H0: $\beta_1 = 0$ [true slope is zero meaning no relationship with x]

H1: $\beta_1 \neq 0$ [slope is positive or negative, not zero]

This can be tested using an F-test, as it is the ratio of two variances, or with a t-test since we are only testing one coefficient (more on this later)

Using an F test statistic:

$$F = \frac{SSreg/1}{SSE/(n-2)} = \frac{MSreg}{MSE}$$

- Under H0, this follows an F distribution for a 1- $\alpha/2$ percentile with 1 and n-2 degrees of freedom.
- If the F for the fitted equation is larger than the F from the table, we reject H0 (not likely true). The regression is significant, in that the true slope is likely not equal to zero.

Information for the F-test is often shown as an Analysis of Variance Table:

Source	df	SS	MS	F	p-value
Regression	*1*	*SSreg*	*MSreg*= *SSreg*/1	*F*= *MSreg*/*MSE*	Prob F> $F_{(1,n-2,1-\alpha)}$
Residual	*n*-2	*SSE*	*MSE*= *SSE*/(*n*-2)		
Total	*n*-1	*SSy*			

[Class example and explanation of the p-value]

Estimated Standard Errors for the Slope and Intercept

Under the assumptions, we can obtain an unbiased estimated of the standard errors for the slope and for the intercept [measure of how these would vary among different sample sets], using the one set of sample data.

$$s_{b_0} = \sqrt{MSE\left(\frac{1}{n} + \frac{\bar{x}^2}{SSx}\right)} = \sqrt{\frac{MSE \times \sum_{i=1}^{n} x_i^{\,2}}{n \times SSx}}$$

$$s_{b_1} = \sqrt{\frac{MSE}{SSx}}$$

Confidence Intervals for the True Slope and Intercept

Under the assumptions, confidence intervals can be calculated as:

For β_o: $b_0 \pm t_{1-\alpha/2, n-2} \times s_{b_0}$

For β_1: $b_1 \pm t_{1-\alpha/2, n-2} \times s_{b_1}$

[class example]

Hypothesis Tests for the True Slope and Intercept

H0: $\beta_1 = c$ [true slope is equal to the constant, c]

H1: $\beta_1 \neq c$ [true slope differs from the constant c]

Test statistic:

$$t = \frac{b_1 - c}{s_{b_1}}$$

Under H0, this is distributed as a t value of $t_c = t_{n-2,\, 1-\alpha/2}$.

Reject H_o if $|t| > t_c$.

- The procedure is similar for testing the true intercept for a particular value
- It is possible to do one-sided hypotheses also, where the alternative is that the true parameter (slope or intercept) is greater than (or less than) a specified constant c. MUST be careful with the t_c as this is different.

[class example]

Confidence Interval for the True Mean of y given a particular x value

For the mean of all possible y-values given a particular value of x ($\mu_y|x_h$):

$$\hat{y} \mid x_h \pm t_{n-2,1-\alpha/2} \times s_{\hat{y}|x_h}$$

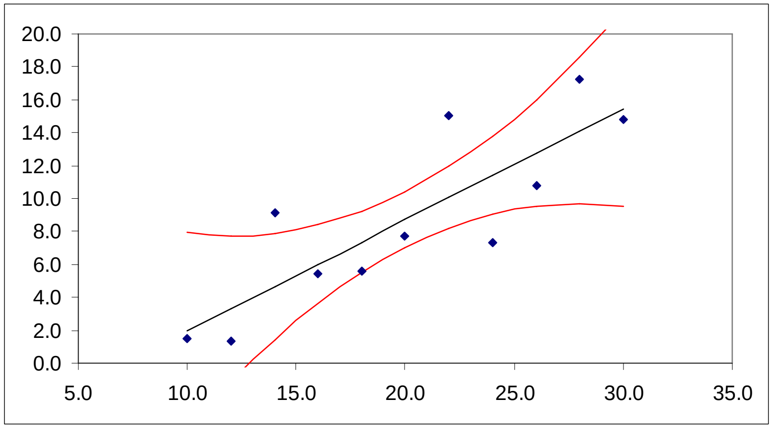
where

$$\hat{y} \mid x_h = b_0 + b_1 x_h$$

$$s_{\hat{y}|x_h} = \sqrt{MSE\left(\frac{1}{n} + \frac{(x_h - \bar{x})^2}{SSx}\right)}$$

Confidence Bands

Plot of the confidence intervals for the mean of y for several x-values. Will appear as:



Confidence Interval for 1 or more y-values given a particular x value

For one possible new y-value given a particular value of x:

$$\hat{y}_{(new)} \mid x_h \pm t_{n-2,1-\alpha/2} \times s_{\hat{y}(new)|x_h}$$

Where

$$\hat{y}_{(new)} \mid x_h = b_0 + b_1 x_h$$

$$s_{\hat{y}(new)|x_h} = \sqrt{MSE\left(1 + \frac{1}{n} + \frac{(x_h - \bar{x})^2}{SSx}\right)}$$

For the average of *g* new possible y-values given a particular value of x:

$$\hat{y}_{(new)} \mid x_h \pm t_{n-2,1-\alpha/2} \times s_{\hat{y}(newg)|x_h}$$

where

$$\hat{y}_{(new)} \mid x_h = b_0 + b_1 x_h$$

$$s_{\hat{y}(new\,g)|x_h} = \sqrt{MSE\left(\frac{1}{g} + \frac{1}{n} + \frac{(x_h - \bar{x})^2}{SSx}\right)}$$

[class example]

Selecting Among Alternative Models

Process to Fit an Equation using Least Squares

Steps:

1. Sample data are needed, on which the dependent variable and all explanatory (independent) variables are measured.
2. Make any transformations that are needed to meet the most critical assumption: The relationship between *y* and *x* is linear.

   Example: volume = $\beta_0 + \beta_1$ dbh^2 may be linear whereas volume versus dbh is not. Use y_i = volume , x_i = dbh^2.
3. Fit the equation to minimize the sum of squared error.

4. Check Assumptions. If not met, go back to Step 2.

5. If assumptions are met, then interpret the results.
   - Is the regression significant?
   - What is the r^2? What is the SE_E?
   - Plot the fitted equation over the plot of *y* versus *x*.

For a number of models, select based on:

1. Meeting assumptions: If an equation does not meet the assumption of a linear relationship, it is not a candidate model
2. Compare the fit statistics. Select higher r^2 (or I^2), and lower SE_E (or SE_E')
3. Reject any models where the regression is not significant, since this model is no better than just using the mean of *y* as the predicted value.
4. Select a model that is biologically tractable. A simpler model is generally preferred, unless there are practical/biological reasons to select the more complex model
5. Consider the cost of using the model

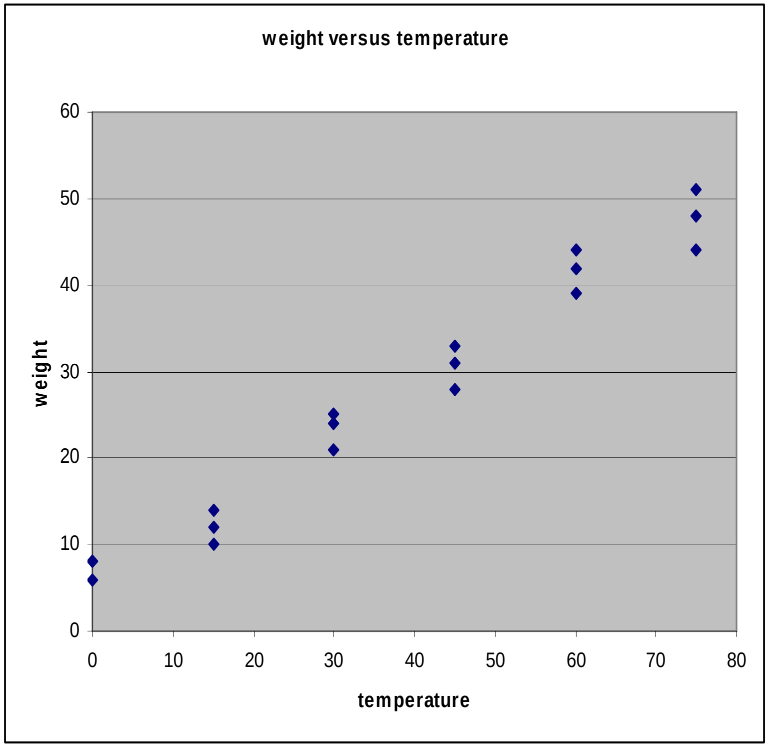
[class example]

Simple Linear Regression Example

Temperature (x)	Weight (y)	Weight (y)	Weight (y)
0	8	6	8
15	12	10	14
30	25	21	24
45	31	33	28
60	44	39	42
75	48	51	44

Observation	temp	weight
1	0	8
2	0	6
3	0	8
4	15	12
5	15	10
6	15	14
7	30	25
8	30	21

Et cetera…



Obs.	temp	weight	x-diff	x-diff. sq.
1	0	8	-37.50	1406.25
2	0	6	-37.50	1406.25
3	0	8	-37.50	1406.25
4	15	12	-22.50	506.25

Et cetera

mean	37.5	27.11

SSX=11,812.5 SSY=3,911.8 SPXY=6,705.0

$$b_1 = \frac{SPxy}{SSx} \qquad b_0 = \bar{y} - b_1 \times \bar{x}$$

b1:	0.567619
b0:	5.825397

NOTE: calculate b1 first, since this is needed to calculate b0.

From these, the residuals (errors) for the equation, and the sum of squared error (SSE) were calculated:

Obs.	weight	y-pred	residual	residual sq.
1	8	5.83	2.17	4.73
2	6	5.83	0.17	0.03
3	8	5.83	2.17	4.73
4	12	14.34	-2.34	5.47

Et cetera

SSE:	105.89

And SSR=SSY-SSE=3805.89

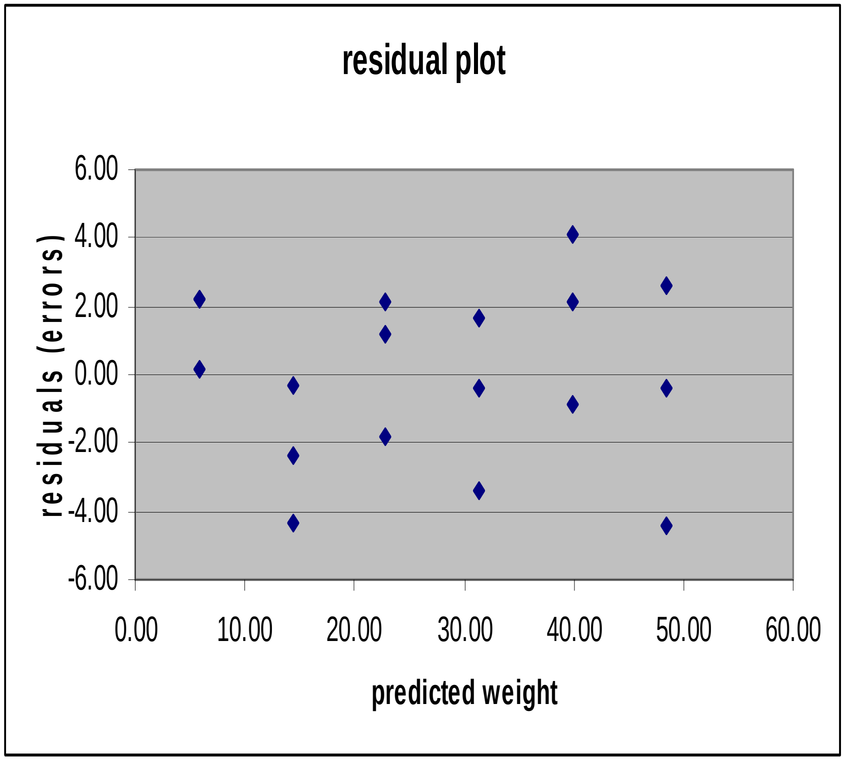
```
ANOVA

Source        df       SS       MS
Model          1  3805.89  3805.89
Error    18-2=16   105.89     6.62
Total    18-1=17  3911.78
```

F=575.06   with p=0.00 (very small)

In excel use: = fdist(x,df1,df2) to obtain a "p-value"

r^2:	0.97
Root MSE Or SE_E **:**	2.57

BUT: Before interpreting the ANOVA table, Are assumptions met?



Linear?

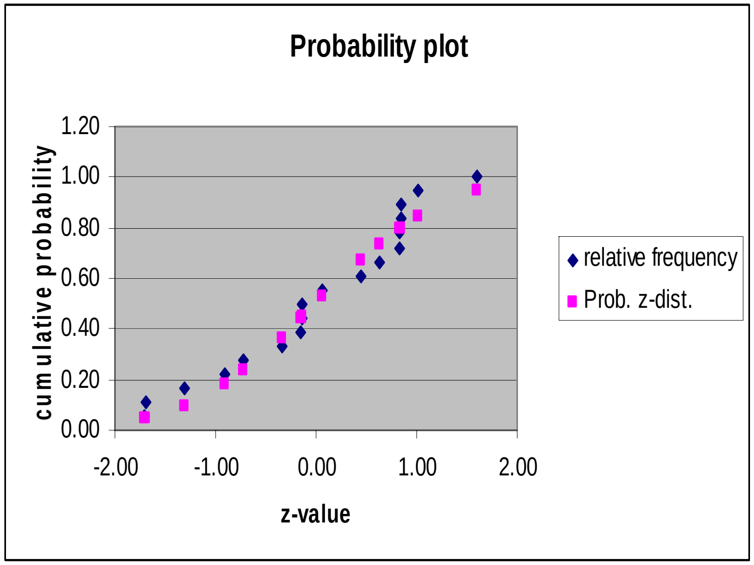
Equal variance?

Independent observations?

Normality plot:

Obs.	sorted resids	Stand. resids	Rel. Freq.	Prob. z-dist.
1	-4.40	-1.71	0.06	0.04
2	-4.34	-1.69	0.11	0.05
3	-3.37	-1.31	0.17	0.10
4	-2.34	-0.91	0.22	0.18
5	-1.85	-0.72	0.28	0.24
6	-0.88	-0.34	0.33	0.37
7	-0.40	-0.15	0.39	0.44
8	-0.37	-0.14	0.44	0.44
9	-0.34	-0.13	0.50	0.45

Etc.



Questions:

1. Are the assumptions of simple linear regression met? Evidence?

2. If so, interpret if this is a good equation based on goodness of it measures.

3. Is the regression significant?

For 95% confidence intervals for b0 and b1, would also need estimated standard errors:

$$s_{b_0} = \sqrt{MSE\left(\frac{1}{n} + \frac{\bar{x}^2}{SSx}\right)} = \sqrt{6.62 \times \left(\frac{1}{18} + \frac{37.5^2}{11812.50}\right)} = 1.075$$

$$s_{b_1} = \sqrt{\frac{MSE}{SSx}} = \sqrt{\frac{6.62}{11812.50}} = 0.0237$$

The t-value for 16 degrees of freedom and the 0.975 percentile is 2.12 (=tinv(0.05,16) in EXCEL)

$$b_0 \pm t_{1-\alpha/2,n-2} \times s_{b_0}$$

For β_o: $$5.825 \pm 2.120 \times 1.075$$

$$b_1 \pm t_{1-\alpha/2,n-2} \times s_{b_1}$$

For β_1: $$0.568 \pm 2.120 \times 0.0237$$

	Est. Coeff	**St. Error**
For b0:	5.825396825	1.074973559
For b1:	0.567619048	0.023670139

CI:	**b0**	**b1**
t(0.975,16)	2.12	2.12
lower	3.54645288	0.517438353
upper	8.104340771	0.617799742

Question: Could the real intercept be equal to 0?

Given a temperature of 22, what is the estimated average weight (predicted value) and a 95% confidence interval for this estimate?

$$\hat{y} \mid x_h = b_0 + b_1 x_h$$
$$\hat{y} \mid (x_h = 22) = 5.825 + 0.568 \times 22 = 18.313$$

$$s_{\hat{y}|x_h} = \sqrt{MSE\left(\frac{1}{n} + \frac{(x_h - \bar{x})^2}{SSx}\right)}$$
$$s_{\hat{y}|x_h} = \sqrt{6.62 \times \left(\frac{1}{18} + \frac{(22 - 37.5)^2}{11812.50}\right)} = 0.709$$

$$\hat{y} \mid x_h \pm t_{n-2,1-\alpha/2} \times s_{\hat{y}|x_h}$$
$$18.313 - 2.12 \times 0.709 = 16.810$$
$$18.313 + 2.12 \times 0.709 = 19.816$$

Given a temperature of 22, what is the estimated weight for any new observation, and a 95% confidence interval for this estimate?

$$\hat{y} \mid x_h = b_0 + b_1 x_h$$

$$\hat{y} \mid (x_h = 22) = 5.825 + 0.568 \times 22 = 18.313$$

$$s_{\hat{y}|x_h} = \sqrt{MSE\left(1 + \frac{1}{n} + \frac{(x_h - \bar{x})^2}{SSx}\right)}$$

$$s_{\hat{y}|x_h} = \sqrt{6.62 \times \left(1 + \frac{1}{18} + \frac{(22 - 37.5)^2}{11812.50}\right)} = 2.669$$

$$\hat{y} \mid x_h \pm t_{n-2,1-\alpha/2} \times s_{\hat{y}|x_h}$$

$$18.313 - 2.12 \times 2.669 = 12.66$$

$$18.313 + 2.12 \times 2.669 = 23.97$$

If assumptions were not met, we would have to make some transformations and start over again!

SAS code:

```
* wttemp.sas-------------------------------------;
options ls=70 ps=50;    run;
DATA regdata;    input temp weight;   cards;
 0   8
 0   6
 0   8
15  12
15  10
15  14
30  25
30  21
30  24
45  31
45  33
45  28
60  44
60  39
60  42
75  48
75  51
75  44
 run;
```

```
DATA regdata2;
set regdata;
  tempsq=temp**2;
  tempcub=temp**3;
  logtemp=log(temp);
run;
Proc plot data=regdata2;
plot weight*(temp tempsq logtemp)='*';
run;
*----------------------------------------------;
PROC REG data=regdata2 simple;
 model weight=temp;
 output out=out1 p=yhat1 r=resid1;
run;
*-------------------------------------------------;
PROC PLOT DATA=out1;
 plot resid1*yhat1;
run;
*----------------------------------------------;
PROC univariate data=out1 plot normal;
Var resid1;
Run;
```

SAS outputs:

1) Graphs – which appears more linear?
2) How many observations were there?
3) What is the mean weight?

```
The REG Procedure
                 Model: MODEL1
             Dependent Variable: weight

        Number of Observations Read          18
        Number of Observations Used          18


                Analysis of Variance

                  Sum of      Mean
 Source      DF   Squares     Square     F Value
 Model        1   3805.88571  3805.88571  575.06
 Error       16    105.89206   6.61825
 Corr. Total 17   3911.77778

 Source               F Value         Pr > F
 Model                575.06          <.0001
 Error
 Corrected Total


 Root MSE             2.57260    R-Square   0.9729
 Dependent Mean      27.11111    Adj R-Sq   0.9712
 Coeff Var            9.48909
```

```
Parameter Estimates
                 Parameter      Standard
Variable   DF    Estimate       Error       t Value
 Intercept  1    5.82540        1.07497       5.42
 temp       1    0.56762        0.02367      23.98

 Variable      t Value     Pr > |t|
 Intercept      5.42       <.0001
 temp          23.98       <.0001
```

```
Plot of resid1*yhat1.  Legend: A = 1 obs, B = 2 obs, etc.

     ,
   6 ^
     ,
     ,
     ,
     ,
     ,
   4 ^                                                 A
     ,
     ,
     ,
     ,                                                             A
     , B
   2 ^                         A                       A
     ,                                     A
R    ,
e    ,                         A
s    ,
i    , A
d  0 ^
u    ,             A                       A                       A
a    ,
l    ,                                                 A
     ,
     ,
  -2 ^                         A
     ,             A
     ,
     ,
     ,                                     A
     ,
  -4 ^
     ,             A                                               A
     ,
     ,
     ,
     ,
  -6 ^
       ----------------------------------------------------
     5.825      14.340      22.854      31.368      39.883      48.397

                      Predicted Value of weight
```

```
                 Tests for Normality

Test                  --Statistic---    --p Value---
Shapiro-Wilk          W      0.94352    Pr<W     0.3325
Kolmogorov-Smirnov    D      0.13523    Pr>D    >0.1500
Cramer-von Mises      W-Sq  0.061918    Pr>W-Sq >0.2500
Anderson-Darling      A-Sq  0.407571    Pr>A-Sq >0.2500

                 The UNIVARIATE Procedure
                 Variable:  resid1  (Residual)

                    Normal Probability Plot


 4.5+                                          +*++
    |                                      ++++
    |                              * **++++*
 1.5+                           * *++++
    |                         +*+++
    |                    **+**
-1.5+                 +*++
    |             ++++*
    |         ++++ *
-4.5+     ++*+   *
     +----+----+----+----+----+----+----+----+----+----+
         -2        -1         0        +1        +2
```

Multiple Linear Regression (MLR)

Population: $y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_p x_{mi} + \varepsilon_i$

Sample: $y_i = b_0 + b_1 x_{1i} + b_2 x_{2i} + \ldots + b_p x_{mi} + e_i$

$\hat{y}_i = b_0 + b_1 x_{1i} + b_2 x_{2i} + \ldots + b_m x_{mi}$ $\qquad e_i = y_i - \hat{y}_i$

β_o is the y intercept parameter

$\beta_1, \beta_2, \beta_3, \ldots, \beta_m$ are slope parameters

$x_{1i}, x_{2i}, x_{3i} \ldots x_{mi}$ independent variables

ε_i - is the error term or residual

- is the variation in the dependent variable (the y) which is not accounted for by the independent variables (the x's).

For any fitted equation (we have the estimated parameters), we can get the *estimated average for the dependent variable,* for any set of x's. This will be the "predicted" value for y, which is the estimated average of y, given the particular values for the x variables. NOTE: In text by Neter et al. $p=m+1$. This is not be confused with the p-value indicating significance in hypothesis tests.

For example:

Predicted log10(vol) = - 4.2 + 2.1 X log10(dbh) + 1.1 X log10(height)

where b_o= -4.2; b_1= 2.1 ; b_1= 1.1 estimated by finding the least squared error solution.

Using this equation for dbh =30 cm, height=28m, logten(dbh) =1.48, logten(height) =1.45; logten(vol) = 0.503. $\therefore$ **volume (m^3) = 3.184**. This represents the estimated average volume for trees with dbh=30 cm and height=28 m.

Note: This equation is originally a nonlinear equation:

$$vol = a \times dbh^b \times ht^c \varepsilon$$

Which was transformed to a linear equation using logarithms:

$$\log 10(vol) = \log 10(a) + b \log 10(dbh) + c \log 10(ht) + \log 10 \varepsilon$$

And this was fitted using multiple linear regression

For the observations in the sample data used to fit the regression, we can also get an estimate of the error (we have measured volume).

If the measured volume for this tree was 3.000 **m^3,** or 0.477 in log10 units:

$$error = y_i - \hat{y}_i = 0.477 - 0.503 = -0.026$$

For the fitted equation using log10 units. In original units, the estimated error is 3.000-3.184= - 0.184
NOTE: This is not simply the antilog of -0.026.

Finding the Set of Coefficients that Minimizes the Sum of Squared Errors

- Same process as for SLR: Find the set of coefficients that results in the minimum SSE, just that there are more parameters, therefore more partial derivative equations and more equations
    - E.g., with 3 x-variables, there will be 4 coefficients (intercept plus 3 slopes) so four equations
- For linear models, there will be one unique mathematical solution.
- For nonlinear models, this is not possible and we must search to find a solution

Using the criterion of finding the maximum likelihood (probability) rather than the minimum SSE, we would need to search for a solution, even for linear models (covered in other courses, e.g., FRST 530).

Least Squares Method for MLR:

Find the set of estimated parameters (coefficients) that minimize sum of squared errors

$$\min(SSE) = \min(\sum_{i=1}^{n} e_i^2)$$
$$= \min\left(\sum_{i=1}^{n} \left(y_i - (b_0 + b_1 x_{1_i} + b_2 x_{2_i} + \ldots + b_p x_{m_i}) \right)^2 \right)$$

Take partial derivatives with respect to each of the variables, set them equal to zero and solve.

For three x-variables we obtain:

$$b_0 = \bar{y} - b_1\bar{x}_1 - b_2\bar{x}_2 - b_3\bar{x}_3$$

$$b_1 = \frac{SPx_1y}{SSx_1} - b_2\frac{SPx_1x_2}{SSx_1} - b_3\frac{SPx_1x_3}{SSx_1}$$

$$b_2 = \frac{SPx_2y}{SSx_2} - b_1\frac{SPx_1x_2}{SSx_2} - b_3\frac{SPx_2x_3}{SSx_2}$$

$$b_3 = \frac{SPx_3y}{SSx_3} - b_1\frac{SPx_1x_3}{SSx_3} - b_2\frac{SPx_2x_3}{SSx_3}$$

Where SP= indicates sum of products between two variables, for example for y with x_1:

$$SPx_1y = \sum_{i=1}^{n}(y_i - \bar{y})(x_{1i} - \bar{x}_1)$$
$$= \sum_{i=1}^{n} y_i x_{1i} - \frac{\left(\sum_{i=1}^{n} x_{1i}\right)\left(\sum_{i=1}^{n} y_i\right)}{n} = s^2{}_{x_1y}(n-1)$$

And SS indicates sums of squares for one variable, for example for x_1:

$$SSx_1 = \sum_{i=1}^{n}(x_{1i} - \bar{x}_1)^2 = \sum_{i=1}^{n} x_{1i}{}^2 - \frac{\left(\sum_{i=1}^{n} x_{1i}\right)^2}{n} = s^2{}_{x_1}(n-1)$$

Properties of a least squares regression "surface":

1. Always passes through $(\bar{x}_1, \bar{x}_2, \bar{x}_3, \ldots, \bar{x}_m, \bar{y})$
2. Sum of residuals is zero, i.e., $\Sigma e_i = 0$
3. SSE the least possible (least squares)
4. The slope for a particular x-variable is AFFECTED by correlation with other x-variables: CANNOT interpret the slope for a particular x-variable, UNLESS it has zero correlation with all other x-variables (or nearly zero if correlation is estimated from a sample).

[class example]

Meeting Assumptions of MLR

Once coefficients are obtained, we must **check the assumptions of MLR** before we can:

- assess goodness of fit (i.e., how well the regression line fits the sample data)
- test significance of the regression
- calculate confidence intervals and test hypothesis

For these test to be valid, **assumptions of MLR concerning the observations and the errors (residuals) must be met.**

Residual Plots

Assumptions of:

1. The relationship between the x's and y is linear VERY IMPORTANT!
2. The variances of the y values must be the same for every combination of the x values.
3. Each observation (i.e., x_i's and y_i) must be independent of all other observations.

can be visually checked by using **RESIDUAL PLOTS**

A residual plot shows the residual (i.e., $y_i - \hat{y}_i$) as the y-axis and the predicted value ($\hat{y}_i$) as the x-axis.

THIS IS THE SAME as for SLR. Look for problems as with SLR. The effects of failing to meet a particular assumption are the same as for SLR

What is different? Since there are many x variables, it will be harder to decide what to do to fix any problems.

Normality Histogram or Plot

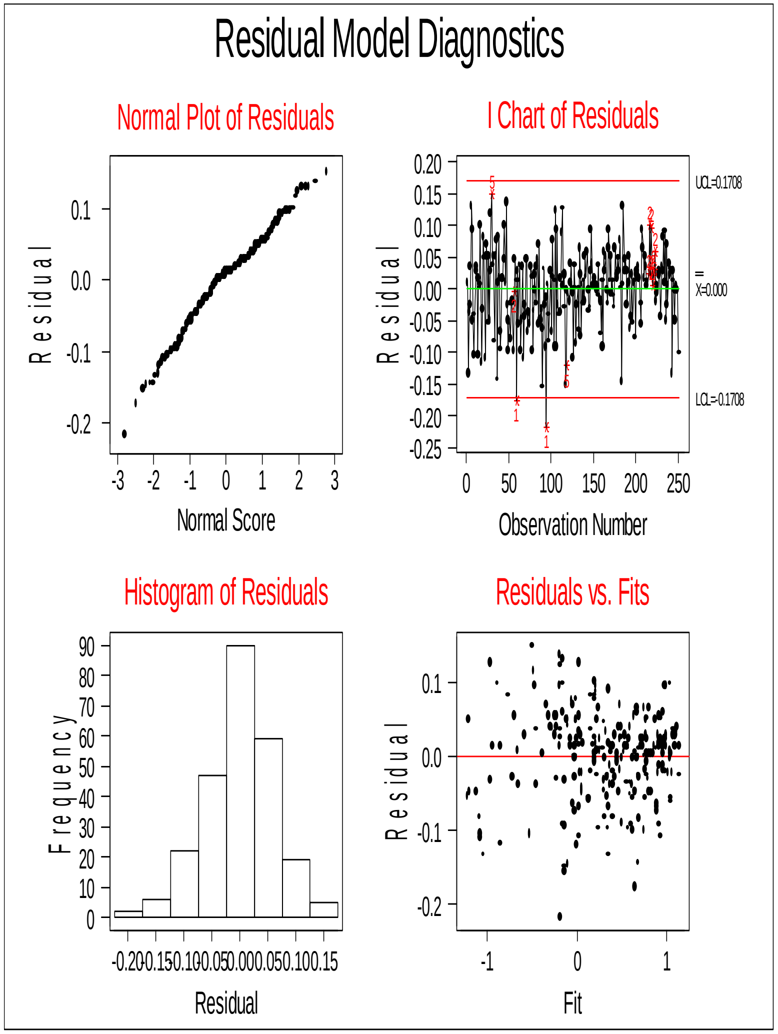
A fourth assumption of the MLR is:

4. The y values must be normally distributed <u>for each combination of x values.</u>

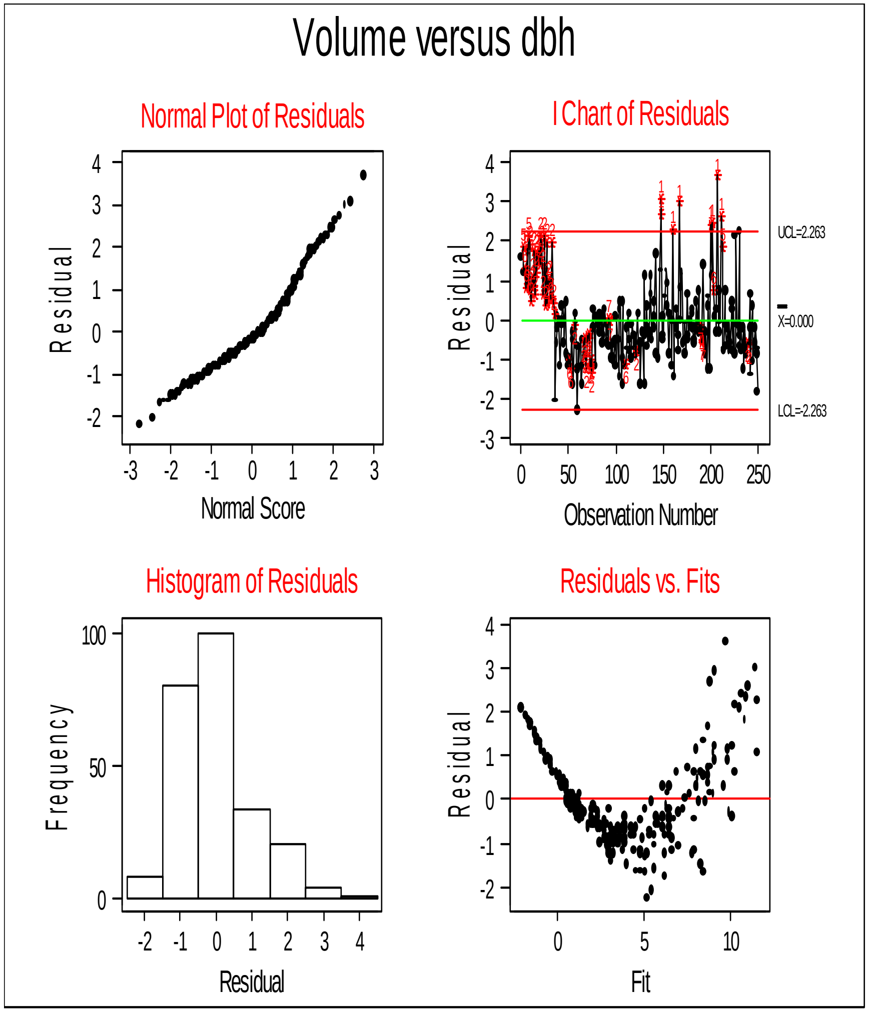
A histogram of the errors, and/or a normality plot can be used to check this, as well as tests of normality as with SLR. Failure to meet these assumptions will result in same problems as with SLR.

Example: Linear relationship met, equal variance, no evidence of trend with observation number (independence may be met). Also, normal distribution met.

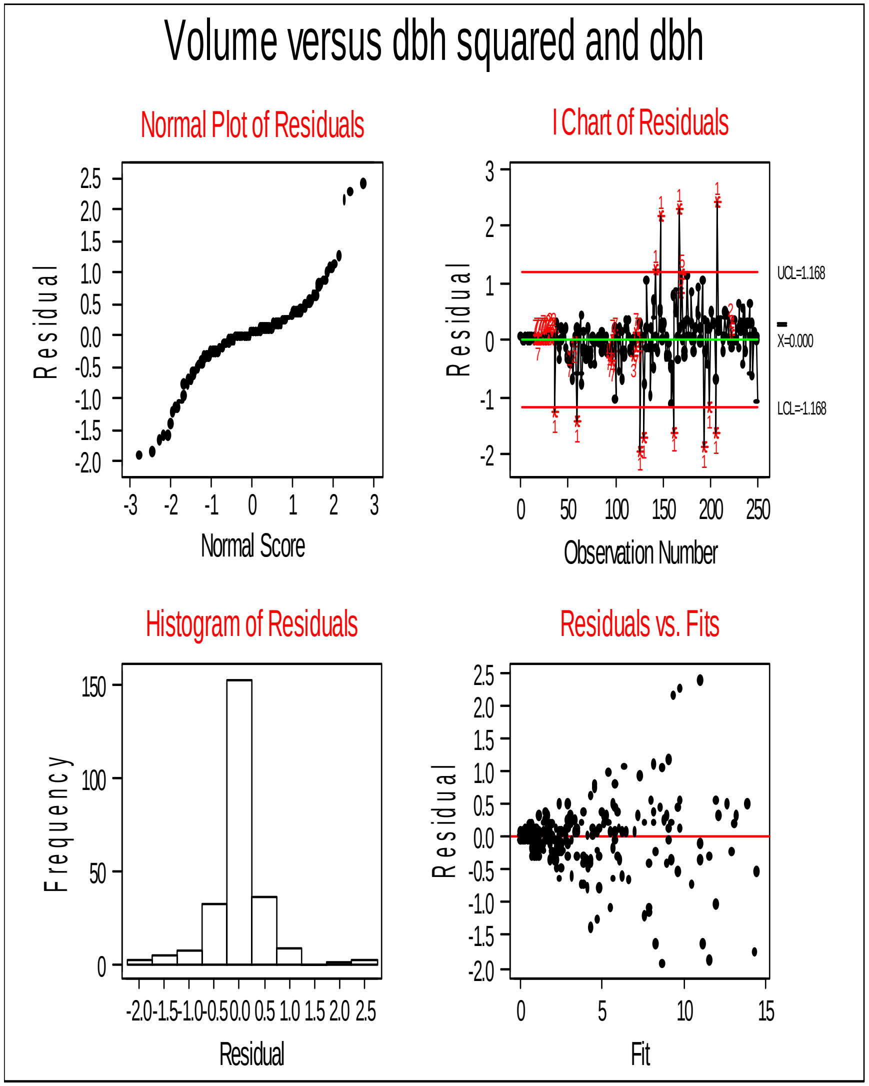
Logvol=f(dbh,logdbh)



Linear relationship assumption not met



Variances are not equal



Measurements and Sampling Assumptions

The remaining assumptions of MLR are based on the measurements and collection of the sampling data, as with SLR

5. The x values are measured without error (i.e., the x values are fixed).

6. The y values are randomly selected for each given set of the x variables (i.e., for each fixed set of x values, a list of all possible y values is made).

As with SLR, often observations will be gathered using simple random sampling or systematic sampling (grid across the land area). This does not strictly meet this assumption [much more difficult to meet with many x-variables!] <u>If the equation is “correct”, then this does not cause problems.</u> If not, the estimated equation will be biased.

Transformations

- Same as for SLR – except that there are more x variables; can also add variables e.g. use dbh and dbh^2 as x1 and x2.
- Try to transform *x's* first and leave y = variable of interest; not always possible.
- Use graphs to help choose transformations
- Will result in an "iterative" process:
    1. Fit the equation
    2. Check the assumptions [and check for outliers]
    3. Make any transformations based on the residual plot, and plots of *y* versus each *x*
    4. Also, check any very unusual points to see if these are measurement/transcription errors; ONLY remove the observation if there is a very good reason to do so
    5. Fit the equation again, and check the assumptions
    6. Continue until the assumptions are met [or nearly met]

Measures of Goodness of Fit

How well does the regression fit the sample data?

- For multiple linear regression, a graph of the the predicted versus measured *y* values indicates how well the line fits the data
- Two measures commonly used: coefficient of multiple determination (R^2) and standard error of the estimate(SE$_E$), similar to SLR

To calculate R^2 and SE$_{E,}$ first, calculate the SSE (this is what was minimized, as with SLR):

$$SSE = \sum_{i=1}^{n} e_i^2 = \sum_{i=1}^{n} \left(y_i - \hat{y}_i\right)^2$$
$$= \sum_{i=1}^{n} \left(y_i - (b_0 + b_1 x_{1i} + b_2 x_{2i} + \ldots b_m x_{mi})\right)^2$$

The sum of squared differences between the measured and estimated *y*'s. This is the same as for SLR, but there are more slopes and <u>more *x* (predictor) variables</u>.

Calculate the sum of squares for *y*:

$$SSy = \sum_{i=1}^{n} \left(y_i - \bar{y}\right)^2 = \sum_{i=1}^{n} {y_i}^2 - \left(\sum_{i=1}^{n} {y_i}^2 \right) \Big/ n = {s_y}^2 (n-1)$$

The sum of squared difference between the measured *y* and the mean of *y*-measures.

Calculate the sum of squares regression:

$$SSreg = \sum_{i=1}^{n} \left(\bar{y} - \hat{y}_i\right)^2 = b_1 SPx_1 y + b_2 SPx_2 y + \ldots + b_3 SPx_3 y$$

$$= SSy - SSE$$

The sum of squared differences between the mean of y-measures and the predicted *y*'s from the fitted equation. Also, is the sum of squares for *y* – the sum of squared errors.

Then: $$R^2 = \frac{SSy - SSE}{SSy} = 1 - \frac{SSE}{SSy} = \frac{SSreg}{SSy}$$

- SSE, SSY are based on *y*'s used in the equation – will not be in original units if *y* was transformed
- R^2 = coefficient of multiple determination; proportion of variance of *y*, accounted for by the regression using *x's*
- O (very poor – horizontal surface representing no relationship between *y* and *x*'s) to 1 (perfect fit – surface passes through the data)
- SSE falls as *m* (number of independent variable) increases, so R^2 rises as more explanatory (independent or predictor) variables are added.

A similar measure is called the Adjusted R^2 value. A penalty is added as you add x-variables to the equation:

$$R_a^{\,2} = 1 - \left(\frac{n-1}{n-(m+1)} \right) \frac{SSE}{SSy}$$

And: $$SE_E = \sqrt{\frac{SSE}{n-m-1}}$$

- SSE is based on *y*'s used in the equation – will not be in original units if *y* was transformed
- *n*-*m*-1 is the degrees of freedom for the error; is the number of observations minus the number of fitted coefficients
- SE_E - standard error of the estimate; in same units as *y*
- Under normality of the errors:
  - ○ ±1 $SE_E \cong$ 68% of sample observations
  - ○ ±2 $SE_E \cong$ 95% of sample observations
- Want low SE_E
- SE_E falls as the number of predictor variables increases and SSE falls, but then rises, since *n*-*m* -1 is getting smaller

y-variable was transformed: Can calculate estimates of these for the original y-variable unit, I^2 (Fit Index) and estimated standard error of the estimate (SE_E'), in order to compare to R^2 and SE_E of other equations where the *y* was not transformed, similar to SLR.

$I^2 = 1 - SSE/SSY$

- where SSE, SSY are in original units. NOTE must "back-transform" the predicted *y*'s to calculate the SSE in original units.
- Does not have the same properties as R^2, however it can be less than 0

Estimated standard error of the estimate (SE_E') , when the dependent variable, *y*, has been transformed:

$$SE_E' = \sqrt{\frac{SSE(original\ units)}{n-m-1}}$$

- SEE' - standard error of the estimate ; in same units as original units for the dependent variable
- want low SEE'

Estimated Variances, Confidence Intervals and Hypothesis Tests

Testing Whether the Regression is Significant

Does knowledge of *x*'s improve the estimate of the mean of *y*? Or is it a flat surface, which means we should just use the mean of *y* as an estimate of mean *y* for any set of *x* values?

SSE/ (*n*-*m*-1):

- Mean squared error.
  - The degrees of freedom are *n*-*m*-1 (same as *n*-(*m*+1)
  - *n* observations with (*m*+1) statistics estimated from these: $b_0, b_1, b_2, \ldots b_m$
- Under the assumptions of MLR, is an unbiased estimated of the true variance of the error terms (error variance)

SSR/*m*:

- Called the Mean Square Regression
- Degrees of Freedom=*m*: *m* *x*-variables
- Under the assumptions of SLR, this is an estimate the error variance PLUS a term of variance explained by the regression using *x's*.

H0: Regression is not significant

H1: Regression is significant

Same as:

H0: $\beta_1 = \beta_2 = \beta_3 = \ldots = \beta_m = 0$ [all slopes are zero meaning no relationship with x's]

H1: not all slopes =0 [some or all slopes are not equal to zero]

If H0 is true, then the equation is:

$$y_i = \beta_0 + 0\,x_{1i} + 0\,x_{2i} + \ldots + 0\,x_{mi} + \varepsilon_i$$

$$y_i = \beta_0 + \varepsilon_i \qquad \hat{y}_i = \beta_0$$

Where the *x*-variables have no influence over y; they do not help to better estimate *y*.

As with SLR, we can use an F-test, as it is the ratio of two variances; unlike SLR we cannot use a t-test since we are only testing several slope coefficients.

Using an F test statistic:

$$F = \frac{SSreg/m}{SSE/(n-m-1)} = \frac{MSreg}{MSE}$$

- Under H0, this follows an F distribution for a 1- α percentile with 1 and *n*-*m*-1 degrees of freedom.
- If the F for the fitted equation is larger than the F from the table, we reject H0 (not likely true). The regression is significant, in that one or more of the the true slopes (the population slopes) are likely not equal to zero.

Information for the F-test in the Analysis of Variance Table:

Source	df	SS	MS	F	p-value
Regression	*m*	*SSreg*	*MSreg*= *SSreg*/m	*F*= *MSreg*/*MSE*	Prob F> $F_{(m,n\text{-}m\text{-}1,1\text{-}\alpha)}$
Error	*n*-*m*-1	*SSE*	*MSE*= *SSE*/(*n* *m*-1)		
Total	*n*-1	*SSy*			

[See example]

Estimated Standard Errors for the Slope and Intercept

Under the assumptions, we can obtain an unbiased estimated of the standard errors for the slope and for the intercept [measure of how these would vary among different sample sets], using the one set of sample data.

For multiple linear regression, these are more easily calculated using matrix algebra. If there are more than 2 x-variables, the calculations become difficult; we will rely on statistical packages to do these calculations.

Confidence Intervals for the True Slope and Intercept

Under the assumptions, confidence intervals can be calculated as:

For β_o: $b_0 \pm t_{1-\alpha/2,n-m-1} \times s_{b_0}$

For β_j: $b_j \pm t_{1-\alpha/2,n-m-1} \times s_{b_j}$ [for any of the slopes]

[See example]

Hypothesis Tests for one of the True Slopes or Intercept

H0: $\beta_j = c$ [the parameter (true intercept or true slope is equal to the constant, c, given that the other x-variables are in the equation]

H1: $\beta_j \neq c$ [true intercept or slope differs from the constant c; given that the other x-variables are in the equation]

Test statistic:

$$t = \frac{b_j - c}{s_{b_j}}$$

Under H0, this is distributed as a t value of $t_c = t_{n-m-1,\, 1-\alpha/2}$.

Reject H_o if $|t| > t_c$.

- It is possible to do one-sided hypotheses also, where the alternative is that the true parameter (slope or intercept) is greater than (or less than) a specified constant c. MUST be careful with the t_c as this is different.

[See example]

The regression is significant, but which x-variables should we retain?

With MLR, we are particularly interested in which x-variables to retain. We then test: Is variable x_j significant given the other x variables? e.g. diameter, height - do we need both?

H0: $\beta_j = 0$, given other x-variables (i.e., variable not significant)

H1: $\beta_j \neq 0$, given other x-variables.

A t-test for that variable can be used to test this.

Another test, the partial F-test can be used to test one x-variable (as t-test) or to test a group of x-variables, given the other x-variables in the equation.

- Get regression analysis results for all x-variables [full model]
- Get regression analysis results for all but the x-variables to be tested [reduced model]

$$partial\ F = \frac{\left(SSreg(full) - SSreg(reduced)\right)/r}{SSE/(n-m-1)(full)}$$

OR

$$partial\ F = \frac{\left(SSE(reduced) - SSE(full)\right)/r}{SSE/(n-m-1)(full)}$$

$$= \frac{(SS\text{ due to dropped variable(s)})/r}{MSE(full)}$$

Where r is the number of x-variables that were dropped (also equals: (1)the regression degrees of freedom for the full model minus the regression degrees of freedom for the reduced model, OR (2) the error degrees of freedom for the reduced model, minus the error degrees of freedom for the full model)

- Under H0, this follows an F distribution for a 1- α/2 percentile with *r* and *n*-*m*-1 (full model) degrees of freedom.
- If the F for the fitted equation is larger than the F from the table, we reject H0 (not likely true). The regression is significant, in that the variable(s) that were dropped are significant (account for variance of the y-variable), given that the other x-variables are in the model.

[See example with the use of class variables, but can be for any subset of x-variables]

Confidence Interval for the True Mean of y given a particular set of x values

For the mean of all possible y-values given a particular value set of x-values ($\mu_y|\mathbf{x}_h$):

$$\hat{y} \mid \mathbf{x}_h \pm t_{n-m-1,1-\alpha/2} \times s_{\hat{y}|\mathbf{x}_h}$$

where

$$\hat{y} \mid \mathbf{x}_h = b_0 + b_1 x_{1h} + b_2 x_{2h} + \cdots + b_m x_{mh}$$

$$s_{\hat{y}|\mathbf{x}_h} = \text{from statistical package output}$$

Confidence Bands

Plot of the confidence intervals for the mean of y for several sets x-values is not possible with MLR

Confidence Interval for 1 or more y-values given a particular set of x values

For one possible new y-value given a particular set of x values:

$$\hat{y}_{(new)} \mid \mathbf{x}_h \pm t_{n-m-1,1-\alpha/2} \times s_{\hat{y}(new)|\mathbf{x}_h}$$

Where

$$\hat{y} \mid \mathbf{x}_h = b_0 + b_1 x_{1h} + b_2 x_{2h} + \cdots + b_m x_{mh}$$

$$s_{\hat{y}(new)|\mathbf{x}_h} = \text{from statistical package output}$$

For the average of *g* new possible y-values given a particular value of x:

$$\hat{y}_{(new)} \mid \mathbf{x}_h \pm t_{n-m-1,1-\alpha/2} \times s_{\hat{y}(newg)|\mathbf{x}_h}$$

where

$$\hat{y} \mid \mathbf{x}_h = b_0 + b_1 x_{1h} + b_2 x_{2h} + \cdots + b_m x_{mh}$$

$$s_{\hat{y}(newg)|\mathbf{x}_h} = \text{from statistical package output}$$

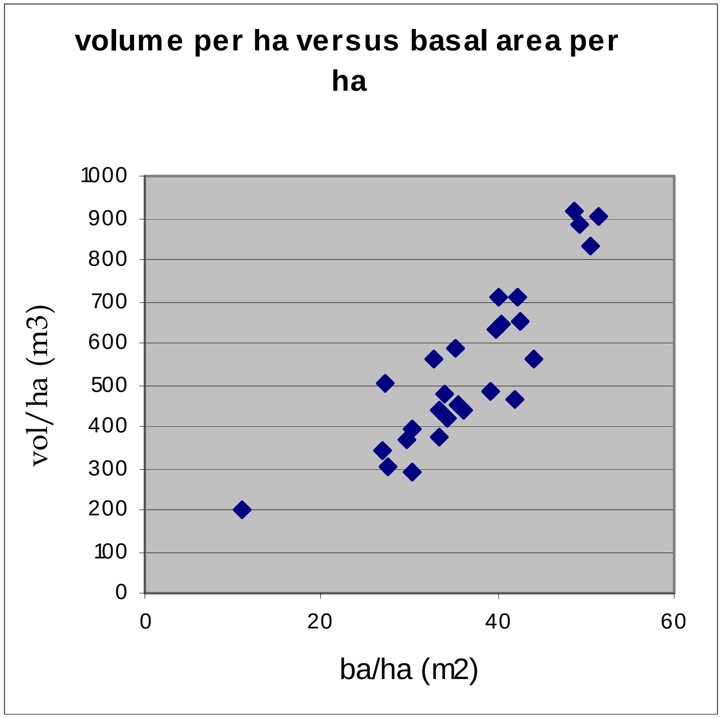
[See example]

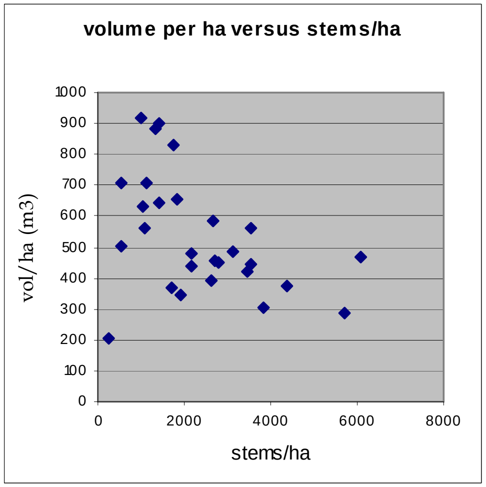
Multiple Linear Regression Example

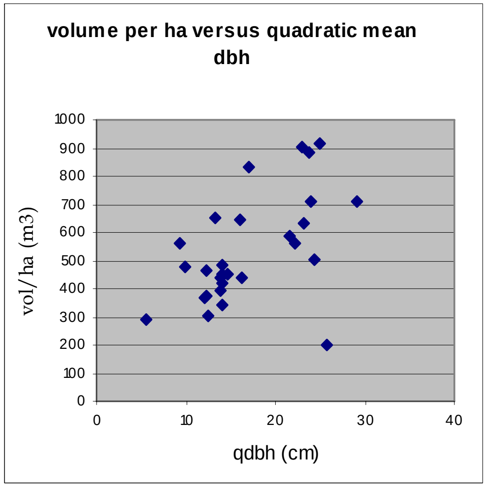
n=28 stands y=vol/ha (m3)

volume/ha m^3	Age years	Site Index	Basal area/ha m^2	Stems /ha	Top height m	Qdbh cm
559.3	82	14.6	32.8	1071	22.4	22.2
559	107	9.4	44.2	3528	17	9.3
831.9	104	12.8	50.5	1764	21.5	17
365.7	62	12.5	29.6	1728	16.4	12.1
454.3	52	14.6	35.4	2712	18.9	14.1
486	58	13.9	39.1	3144	17.5	14
441.6	34	18.5	36.2	3552	17.4	13.8
375.8	35	17	33.4	4368	15.6	12.2
451.4	33	19.1	35.4	2808	16.8	14.7
419.8	23	23.4	34.4	3444	17.3	14
467	33	17.7	42	6096	16.4	12.2
288.1	33	15	30.3	5712	13.8	5.6
306	32	18.2	27.4	3816	16.7	12.5
437.1	68	13.8	33.3	2160	19.1	16.2
633.2	126	11.4	39.9	1026	21	23.2
707.2	125	13.2	40.1	552	23.3	29.2
203	117	13.7	11	252	22.1	25.8
915.6	112	13.9	48.7	1017	24.2	25
903.5	110	13.9	51.5	1416	23.2	23
883.4	106	14.7	49.4	1341	24.3	23.7
586.5	124	12.8	35.2	2680	22.6	21.5
500.1	60	18.4	27.3	528	22.7	24.4
343.5	63	14	26.9	1935	17.6	14.1
478.6	60	15.2	34	2160	19.4	9.9
652.2	62	15.9	42.5	1843	20.5	13.2
644.7	63	16.2	40.4	1431	21	16.1
390.8	57	14.8	30.4	2616	18.3	13.9
709.8	87	14.3	42.3	1116	22.6	23.9

Objective: obtain an equation for estimating volume per ha from some of the easy to measure variables such as basal area /ha (only need dbh on each tree), qdbh (need dbh on each tree and stems/ha), and stems/ha







Then, we would need: SSY, SSX_1, SSX_2, SSX_3, SPX_1Y, SPX_2Y, SPX_3Y, SPX_1X_2, SPX_1X_3, SPX_2X_3, and insert these into the four equations and solve:

$$b_0 = \bar{y} - b_1\bar{x}_1 - b_2\bar{x}_2 - b_3\bar{x}_3$$

$$b_1 = \frac{SPx_1y}{SSx_1} - b_2\frac{SPx_1x_2}{SSx_1} - b_3\frac{SPx_1x_3}{SSx_1}$$

$$b_2 = \frac{SPx_2y}{SSx_2} - b_1\frac{SPx_1x_2}{SSx_2} - b_3\frac{SPx_2x_3}{SSx_2}$$

$$b_3 = \frac{SPx_3y}{SSx_3} - b_1\frac{SPx_1x_3}{SSx_3} - b_2\frac{SPx_2x_3}{SSx_3}$$

And then check assumptions, make any necessary transformations, and start over!

SAS code

```
*  MLR.sas  example for 430 and 533 classes;

PROC IMPORT OUT= WORK.voldata
DATAFILE="E:\frst430\lemay\examples\MLR.XLS"
     DBMS=EXCEL REPLACE; SHEET="data$";
     GETNAMES=YES; MIXED=NO;  SCANTEXT=YES;
     USEDATE=YES; SCANTIME=YES;
RUN;
options ls=70 ps=50;
run;
DATA voldata2;
set voldata;
  qdbhsq=qdbh**2;
run;
Proc plot data=voldata2;
plot volha*(baha stemsha qdbh)='*';
run;
*------------------------------------------;
PROC REG data=voldata2 simple outsscp=sscp;
 model volha=baha stemsha qdbh;
 output out=out1 p=yhat1 r=resid1;
run;
*------------------------------------------;
PROC PLOT DATA=out1;
 plot resid1*yhat1;
run;
*-----------------------------------------;
PROC univariate data=out1 plot normal;
Var resid1;
Run;

PROC PRINT data=sscp;
run;
```

SAS Outputs:

1) plots (as per EXCEL plots)
2) Simple statistics
3) Regression results
4) Residual plot
5) Normality tests and plot
6) SSCP (sums of squares and cross products)

```
                                The REG Procedure

                     Number of Observations Read          28
                     Number of Observations Used          28


                           Descriptive Statistics

                                    Uncorrected
Variable          Sum        Mean      SS        Variance

Intercept   28.00000    1.00000   28.00000           0
baha      1023.60000   36.55714      39443    74.93884
stemsha        65816 2350.57143  213051770     2160984
qdbh       476.80000   17.02857 9084.32000    35.74434
volha          14995  535.53929    9011680       36341

                           Descriptive Statistics

                                    Standard
                Variable           Deviation    Label

                Intercept                  0    Intercept
                baha                 8.65672    baha
                stemsha           1470.02848    stemsha
                qdbh                 5.97866    qdbh
                volha              190.63388    volha
```

```
                 Analysis of Variance

                  Sum of    Mean
 Source DF   Squares   Square    F Value Pr > F

 Model   3   954389     318130 284.62  <.0001
 Error  24    26826 1117.73481
 Corr.  27   981214
 Total

Root MSE         33.43254    R-Square 0.9727
Dependent Mean  535.53929    Adj R-Sq 0.9692
Coeff Var         6.24278


                 Parameter Estimates

                              Parameter Standard
Variable    Label      DF   Estimate     Error
Intercept   Intercept   1 -198.17649 47.89264
baha        baha        1   18.56615  0.75637
stemsha     stemsha     1   -0.03124  0.00702
qdbh        qdbh        1    7.54214  1.73965

                 Parameter Estimates


Variable    t Value   Pr > |t|

Intercept     -4.14    0.0004
baha          24.55    <.0001
stemsha       -4.45    0.0002
qdbh           4.34    0.0002
```

```
Plot of resid1*yhat1.
Legend: A = 1 obs, B = 2 obs, etc.

Residual
     ,
  60 ^               A
     ,
     ,                                 A                   A
     ,
     ,
     ,
  40 ^                           A
     ,
     ,
     ,
     ,                                                    A
     ,                              A
  20 ^                  A                    A          A
     ,                                       A              A
     ,                                  A
     ,             A
     ,
     ,
   0 ^                        A
     ,                      A A
     ,
     ,
     ,
     ,                              A
 -20 ^                           A
     ,                        A           A        A
     ,                             AA
     ,                              A
     ,
     ,                             A
 -40 ^
     ,                                              A
     ,
     ,                                 A
     ,                                          A
     ,
 -60 ^
     ,
     Š-^-----------^-----------^-----------^-----------^-----------^-
         0          200         400         600         800         1000

                    Predicted Value of volha
```

```
                     Tests for Normality

Test    --Statistic---      ----p Value-----
Shapiro-Wilk   W  0.960589  Pr < W    0.3600

Kolmogorov
-Smirnov       D  0.124393  Pr > D   >0.1500

Cramer-von
Mises       W-Sq 0.068064  Pr > W-Sq 0.2500

Anderson
-Darling    A-Sq 0.395352 Pr > A-Sq  0.2500

                   Normal Probability Plot

 65+                                            +++
   |                                     *  *+++*
   |                                     +++
   |                                  +*+
   |                               **+*
   |                         ******
  5+                        *+++
   |                     ++**
   |                  +++**
   |               +*****
   |            +**
   |        *++*
-55+    *++++
   +----+----+----+----+----+----+----+----+----+----+
       -2        -1         0        +1        +2
```

```
                       I
                       n
                       t                      s
  _    _               e                      t
  T    N               r                      e                     v
  Y    A               c          b           m         q           o
O P    M               e          a           s         d           l
b E    E               p          h           h         b           h
s _    _               t          a           a         h           a

1 SSCP Intercept    28.0    1023.60     65816.0    476.80    14995.10
2 SSCP baha       1023.6   39443.24   2399831.7  17612.44   587310.56
3 SSCP stemsha   65816.0 2399831.70 213051770.0 936359.90 31917995.70
4 SSCP qdbh        476.8   17612.44    936359.9   9084.32   271764.15
5 SSCP volha     14995.1  587310.56  31917995.7 271764.15  9011679.63
6 N                 28.0      28.00        28.0     28.00       28.00
```

```
                           s
                           t
                           e                    v
              b            m        q           o
              a            s        d           l
              h            h        b           h
              a            a        h           a

baha     39443.24   2399831.7  17612.44  587310.56
stemsh 2399831.70 213051770.0 936359.90 31917995.70
qdbh     17612.44    936359.9   9084.32  271764.15
volha   587310.56  31917995.7 271764.15  011679.63
```

Questions:

1. Are the assumptions of MLR met?

2. If they are met, what is the multiple coefficient of determination? The Adjusted R square? How are they different? What is the root MSE (SEE)? Units?

3. Is the regression significant?

4. If the equation is significant, are all of the variables needed, given the other variables in the equation?

5. Given stems/ha=300, qdbh=20 cm, and ba/ha=20 m2/ha, what is the estimated volume per ha? How would you get a CI for this estimate? What does it mean?

Selecting and Comparing Alternative Models

Process to Fit an Equation using Least Squares

Steps (same as for SLR):

3. Sample data are needed, on which the dependent variable and all explanatory (independent) variables are measured.
4. Make any transformations that are needed to meet the most critical assumption: The relationship between *y* and *x's* is linear.

   Example: volume = $\beta_0 + \beta_1$ dbh $+\beta_2$ dbh^2 may be linear whereas volume versus dbh is not. Need both variables.

3. Fit the equation to minimize the sum of squared error.
4. Check Assumptions. If not met, go back to Step 2.
5. If assumptions are met, then check if the regression is significant. If it is not, then it is not a candidate model (need other x-variables). If yes, then go through further steps for MLR.

6. Are all variables needed? If there are x-variables that are not significant, given the other variables:

- drop the least significant one (highest p-value, lowest F, or lowest absolute value of t)
- refit the regression and check assumptions.
- if assumptions are met, then repeat steps 5 and 6

continue until all variables in the regression are significant given the other x-variables also in the model

Methods to aid in selecting predictor (x) variables

Methods have been developed to help in choosing which x-variables to include in the equation. These include:

1. R^2 (or Adjusted R^2). The equation is fitted for a number of combinations of the x-variables to predict y. The ones with the highest R^2 are reported. CAUTION: You must check the assumptions of these fitted equations by fitting the equation with variables given. If assumptions are NOT met, these are NOT candidate models EVEN with a high R^2. ALSO, consider costs of measuring the x-variables, significance of the x-variables (given the other varables) etc. <u>This only gives some ideas of models to try</u>.

2. Stepwise.

1) The most important variable is added to the model (highest partial F-value or absolute value of t; has lowest p-value).
2) Each of the other variables are added; the next most important variable is added to the model
3) Repeat Step 2)
4) At any time, a variable already entered in, may become not significant. Drop it, and continue with Step 2.
5) Continue until all variables in the regression are significant, and the ones that are not in the equation are not significant, given the ones that are in the equation.

NOTES:

- This just gives candidate models. You must check whether the assumptions are met and do a full assessment of the regression results

3. Backwards Stepwise:

1) All x-variables are added to the model

2) Check to see if variables are not significant given the other variables in the equation (use partial F-test or t-test)

3) If all x-variables are significant given the other variables, stop. Otherwise, drop the variable with the lowest partial F-value (highest p-value)

4) Repeat step 2, until all variables in the equation are significant, given the other variables that are in the equation

NOTES:

- This again just gives candidate models. You must check whether the assumptions are met and do a full assessment of the regression results
- Unlike “stepwise”, once a variable is dropped, it cannot come back in, even if it might be significant with a different set of x-variables than when it was dropped.

4. Forward Stepwise: This is the same as Stepwise, EXCEPT, that once a x-variable is added to the model, it is not removed, even if it becomes non-significant at a particular step in the process.

NOTES:

- This again just gives candidate models. You must check whether the assumptions are met and do a full assessment of the regression results

[See example]

Steps for Forward Stepwise, for example:

To fit this “by hand”, you would need to do the following steps:

1. Fit a simple linear regression for vol/ha with each of the explanatory (x) variables.
2. Of the equations that are significant (assumptions met?), select the one with the highest F-value.
3. Fit a MLR with vol/ha using the selected variable, plus each of the explanatory variables (2 x-variables in each equations). Check to see if the “new” variable is significant given the original variable (which may now be not significant, but forward stepwise does not drop variables). Of the ones that are significant (given the original variable is also in the equation), pick the one with the largest partial-F (for the new variable).
4. Repeat step 3, bringing in varables until i) there are no more variables or ii) the remaining variables are not significant given the other variables.

SAS code

```
*MLR_stepwise.sas  example for 430 and
533 classes ;
* NOTE:  Must run a full regression on
your selected models once after using
these tools to help you choose a few
candidates;

PROC IMPORT OUT= WORK.voldata
     DATAFILE=
"E:\frst430\lemay\examples\MLR.XLS"
     DBMS=EXCEL REPLACE;
SHEET="data$";
     GETNAMES=YES; MIXED=NO;
SCANTEXT=YES;  USEDATE=YES;
     SCANTIME=YES;
RUN;
options ls=70 ps=50 pageno=1;
run;
*------forward stepwise-------------;
title 'forward stepwise';
PROC REG data=voldata simple;
 model volha=baha stemsha qdbh age si
topht/selection=forward;
 output out=out1 p=yhat1 r=resid1;
run;
```

```
* keep first 3 variables, then forward
stepwise;
title 'first 3 then forward';
PROC REG data=voldata;
 forward3: model volha=baha stemsha
qdbh age si topht/selection=forward
include=3;
 output out=out2 p=yhat2 r=resid2;
run;
*----------------------------------;
*  backward stepwise;
title 'backward';
PROC REG data=voldata;
 model volha=baha stemsha qdbh age si
topht/selection=backward;
 output out=out3 p=yhat3 r=resid3;
run;
*------------------------------------;
* stepwise –bring variables in or out;
title 'stepwise – can bring variables
in or out';
PROC REG data=voldata;
 model volha=baha stemsha qdbh age si
topht/selection=stepwise;
 output out=out4 p=yhat4 r=resid4;
run;
```

```
*--------------------------------------;

*  use rsquare to get a number of
regressions ;
title 'rsquare';
PROC REG data=voldata;
 model volha=baha stemsha qdbh age si
topht/selection=rsquare;
run;
```

SAS Outputs:

forward stepwise

```
                The REG Procedure

           Number of Observations Read          28
           Number of Observations Used          28

                    Descriptive Statistics

                                 Uncorrected
Variable    Sum       Mean           SS
Variance
Intercept 28.00000    1.00000    28.00000          0
baha    1023.60000   36.55714       39443   74.93884
stemsha      65816 2350.57143   213051770    2160984
qdbh    476.80000   17.02857  9084.32000    5.74434
age    2028.00000   72.42857      176972    4.32804
si      422.90000   15.10357  6594.19000    7.66258
topht   549.60000   19.62857       11022    8.66878
volha       14995  535.53929     9011680      36341

                 Descriptive Statistics

               Standard
Variable       Deviation    Label
Intercept              0    Intercept
baha             8.65672    baha
stemsha       1470.02848    stemsha
qdbh             5.97866    qdbh
age             33.38155    age
si               2.76814    si
topht            2.94428    topht
volha          190.63388    volha
```

```
                    The REG Procedure
                      Model: MODEL1
             Dependent Variable: volha volha

        Number of Observations Read          28
        Number of Observations Used          28

                 Forward Selection: Step 1

Variable baha Entered: R-Square = 0.7713 and C(p) =
387.3512

                  Analysis of Variance

                    Sum of      Mean
Source      DF  Squares     Square   F Value  Pr > F

Model        1  756843       756843   87.70  <.0001
Error       26  224372  8629.69076
Corrected
  Total     27  981214

           Parameter Standard  Type II   F
Variable   Estimate  Error       SS    Value  Pr>F
Intercept -171.49367 77.51211  42243    4.90  .0359
baha       19.34049   2.06520 756843   87.70 <.0001

    Bounds on condition number: 1, 1
```

```
            Forward Selection: Step 2

Variable topht Entered: R-Square = 0.9852 and C(p)
= 4.5439

              Analysis of Variance

                 Sum of       Mean
Source     DF   Squares     Square  F Value   Pr > F

Model       2    966736     483368   834.64  <.0001
Error      25     14478  579.13628
Corrected
   Total   27    981214

           Parameter  Standard   Type   F
Variable   Estimate    Error    II SS  Value Pr> F

Intercept -663.29189 32.71936  238002 410.9  <.0001
baha        15.73874  0.56747  445489 769.23 <.0001
topht       31.76327  1.66846  209894 362.43 <.0001

      Bounds on condition number: 1.1251, 4.5002
```

```
       Forward Selection: Step 3

Variable stemsha Entered: R-Square = 0.9879 and
C(p) = 1.6949


               Analysis of Variance

                 Sum of     Mean
Source    DF    Squares    Square   F Value  Pr > F

Model      3   969381       323127  655.35  <.0001
Error     24    11834    493.06283
Corrected
   Total  27   981214


         Parameter  Standard    Type
Variable Estimate    Error     II SS  F Value Pr> F

Intercept-537.86686 62.00085   37107   75.26 <.0001
baha      16.37897  0.59209  377309 765.24  <.0001
stemsha   -0.01319  0.00569 2644.90  5.36   0.0294
topht     25.76009  3.01468   36001 73.02   <.0001

    Bounds on condition number: 4.3142, 28.766
--------------------------------------------------

No other variable met the 0.5000 significance level
for entry into the model.
```

```
                 Summary of Forward Selection

Step      Number  Partial   Model
        Vars In R-Square R-Square   C(p)    F Value
1  baha    1     0.7713   0.7713   387.351    87.70
2  topht   2     0.2139   0.9852    4.5439   362.43
3  stemsha 3     0.0027   0.9879    1.6949     5.36

                   Summary of Forward Selection

                       Step Pr > F
                         1  <.0001
                         2  <.0001
                         3  0.0294
```

rsquare

```
                  The REG Procedure
                   Model: MODEL1
              Dependent Variable: volha
              R-Square Selection Method

           Number of Observations Read          28
           Number of Observations Used          28

Number in
 Model    R-Square  Variables in Model
   1       0.7713    baha
   1       0.5312    topht
   1       0.3624    age
   1       0.2847    qdbh
   1       0.1936    stemsha
   1       0.0833    si
   -------------------------------------------
   2       0.9852    baha topht
   2       0.9512    baha stemsha
   2       0.9501    baha qdbh
   2       0.8946    baha age
                           . . .

   5       0.9883    baha stemsha age si topht
   5       0.9881    baha stemsha qdbh si topht
   5       0.9880    baha stemsha qdbh age topht
   5       0.9854    baha qdbh age si topht
   5       0.9764    baha stemsha qdbh age si
   5       0.6568    stemsha qdbh age si topht
 --------------------------------------------------
   6       0.9883    baha stemsha qdbh age si topht
```

Questions:

1. What was the final equation for each of the types of stepwise (or R square) methods?

2. Which equations would you choose to fit based on these tools to select variables? (full regression output would be needed in order examination of the residual plot and normality plot, R^2 and SE_E, significance of the regression, significance of the variables, cost/biology of the model)

For a number of models, select based on:

1. Meeting assumptions: If an equation does not meet the assumption of a linear relationship, it is not a candidate model
2. Compare the fit statistics. Select higher R^2 (or I^2), and lower SE_E (or SE_E')
3. Reject any models where the regression is not significant, since this model is no better than just using the mean of y as the predicted value.
4. Select a model that is biologically tractable. A simpler model is generally preferred, unless there are practical/biological reasons to select the more complex model
5. Consider the cost of using the model

Adding class variables as predictors

(class variables as the dependent variable – covered in FRST 530; under generalized linear model – see also Chapter 14 in the textbook).

Want to add a class variable. Examples:

1. Add species to an equation to estimate tree height.
2. Add gender (male/female) to an equation to estimate weight of adult tailed frogs.
3. Add machine type to an equation that predicts lumber output.

How is this done?

- Use "dummy" or "indicator variables to represent the class variable

  e.g. have 3 species. Set up X1 and X2 as dummy variables:

Species	X1	X2
Cedar	1	0
Hemlock	0	1
Douglas fir	0	0

  - Only need two dummy variables to represent the three species.
  - **The two dummy variables as a group represent the species.**
- Add the dummy variables to the equation – this will alter the intercept

- To alter the slopes, add an interaction between dummy variables and continuous variable(s) e.g. have 3 species, and a continuous variable, dbh

Species	X1	X2	X3=dbh	X4=X1 * dbh	X5=X2*dbh
Cedar	1	0	10	10	0
Hemlock	0	1	22	0	22
Douglas fir	0	0	15	0	0

NOTE: There would be more than one line of data (sample) for each species.

  - **The two dummy variables, and the interactions with the continuous variable as a group represent the species.**

How does this work?

$$y_i = b_0 + \underbrace{b_1 x_{1i} + b_2 x_{2i}}_{\text{dummy variables}} + \underbrace{b_3 x_{3i}}_{\text{dbh}} + \underbrace{b_4 x_{41i} + b_5 x_{5i}}_{i\text{interactions}} + e_i$$

For Cedar (CW):

For Hemlock (HW):

For Douglas fir (FD):

Therefore: fit one equation using all data, but get different equations for different species. Also, can test for differences among species, using **a partial-F test.**

```
*  class_variables.sas ---------------;

options ls=70 ps=50 pageno=1;

PROC IMPORT OUT= WORK.trees
DATAFILE=
 "E:\frst430\lemay\examples\diversity_plots.xls"
     DBMS=EXCEL REPLACE;
     SHEET="Data$";
     GETNAMES=YES;
     MIXED=NO;
     SCANTEXT=YES;
     USEDATE=YES;
     SCANTIME=YES;
RUN;

data trees2;
set trees;
 if (tree_cls eq 'D') then delete;
 if ((species ne 'FD') and (species ne 'CW') and
   (species ne 'HW')) then delete;

* two dummies for 3 species;
x1=0;
x2=0;
if species eq 'CW ' then x1=1;
if species eq 'HW' then x2=1;
* all dummies are zero for Douglas-fir;

x3=log10(dbh);
x4=dbh;
y=log(ht);

 x5=x1*x3;
```

```
x6=x2*x3;
x7=x1*x4;
x8=x2*x4;
run;
proc sort data=trees2;
by species;
run;

proc plot data=trees2;
  plot ht*dbh=species;
run;

proc plot data=trees2;
  plot ht*dbh=species;
  by species;
run;

*-------------------------------------------
;
* full model with intercept and slope
varying by species;
proc reg;
  Full: model y=x1-x8;
  output out=out1 p=yhat1 r=resid1;
run;

PROC PLOT DATA=out1;
 plot resid1*yhat1=species;
run;

PROC univariate data=out1 plot;
Var resid1;
Run;
```

```
*-------------------------------------------
;
* reduced model with one common equation
regardless of species;
proc reg;
  Common: model y=x3 x4;
  output out=out2 p=yhat2 r=resid2;
run;

PROC PLOT DATA=out2;
 plot resid2*yhat2=species;
run;

PROC univariate data=out2 plot;
Var resid2;
Run;

*-------------------------------------------
;
* reduced model with common slopes for all
species, but different intercepts;
proc reg;
  INTONLY:model y=x1-x4;
  output out=out3 p=yhat3 r=resid3;
  run;

proc plot data=out3;
 plot resid3*yhat3=species;
run;

PROC univariate data=out3 plot;
Var resid3;
Run;
```

```
Plot of ht*dbh.  Symbol is value of species.

     ,
     ,
  70 ^
     ,
     ,
F
     ,                                  F
     ,
  60 ^                            FF            F            F  F
F
     ,
     ,                          F     F             F F   F
F
     ,                        F        F F      F F FF
     ,              HHHHHHH HH  H F F FF
  50 ^          H HHHHHHHHH  HH         FF             C
     ,        HHHHHHHHHHH HH      H  H F
     ,      H   HHHHHHH  HFCH      F F
     ,     HH HHHHHHHCFHHFHC  FHFFCF F F  C
     ,     HHHH HH H HFFHCFHH FFFCFC         C         C
  40 ^      HHHH HHH HHHHCFFFFFF C FC F                     C
h    ,    H  HHHHHHH FFFFFFFCFFFH FF       CCC   C
t    ,   HHHHHHHFF CFHCCFFFFCCH F HHC    C       C   C      C
     ,    HHHHH  FCFFFCCFFCHCCFFFCH    CCCC
     ,     HHHHHFCCCFCFCCFCCCCCCCCCC        C
  30 ^   HHHHHHHHHCHCFCCCFCCCCF CC
     ,   HHHH HCHCCFCCCCCCCCCCCF       C
     ,  HHHHHF CCCCCCCCCC CC  CC      F
     ,  HHHHHFCCFCCCCCCCCCC
     ,   HHHCCCCCCCCCCC     C
  20 ^   HCHFCCCCCFC    C
     ,  HHHCFCCCC C F C
     ,  HHFCCCCC HC FFH
     ,  HHFCCCCCFCF
     ,  HFCCCCC      C
  10 ^  HFCCCC C
     ,  FCCC F
     , FCCCH C
     , CCF F
     , CC
   0 ^

     ,
     Š^--------^--------^--------^--------^--------^--------^----
----^
     0.0      26.1      52.2      78.3      104.4    130.5
156.6  182.7

                                       dbh
NOTE: 1284 obs hidden.
```

```
---------     species=CW -------------------
-

Plot of ht*dbh.  Symbol is value of species.

        ,
     50 ˆ
        ,                                    C
        ,
        ,                 C
        ,                     C     C
        ,             C   C           C      C
        ,               C     CCC     C
     40 ˆ               C     C                 C
        ,                  C         CC
        ,                 C           C  C
        ,           C CC   C    C   C    C  C   C
        ,           C CC  CC  C   CCC
        ,          C   CCCCCCCCC     C
        ,           C CCCCCCCCC
     30 ˆ          CCCCCCCCC CC
        ,          C CCCCCCCC
   h    ,         CC CCCCCCCC     C
   t    ,        CCCCCCCCC  C
        ,        CCCCCCCCC
        ,      CCCCCCCC C
        ,        CCCCCC C C
     20 ˆ       CCCCC   C
        ,     C CCC   C
        ,      CCC C
        ,      CCC C
        ,      CCC C
        ,     CCC
        ,     CCC    C
     10 ˆ     CCCC
        ,    CC
        ,    CCC
        ,   CC  C
        ,   C
        ,   C
        ,
      0 ˆ
        Š--ˆ-----------ˆ-----------ˆ-----------ˆ-----------ˆ--
           0          50          100         150         200

                                  dbh

NOTE: 411 obs hidden.
```

```
---------------species=FD ------------------

Plot of ht*dbh.  Symbol is value of species.

        ,
     70 ˆ
        ,
        ,                                             F
        ,                          F
        ,
     60 ˆ                      F        F        F  FF
        ,
        ,                    F    F        FF  F    F
        ,                   F     FF    F FF
        ,                       FFFF
     50 ˆ                          FF
        ,                         F
        ,                F     FFF
        ,             F F   FF F FF
        ,             FFFF  FFF
     40 ˆ                FFFFF F F
   h    ,            FFFFFFFFFFF
   t    ,         FF FFFFFF  F
        ,          FFFFFFF  FFF
        ,         F  FFFFF F
     30 ˆ            FFFF F F
        ,        F FFF  F F F
        ,       FFFFF  F         F
        ,       FFFFFF
        ,        FFFF F
     20 ˆ      FFFFF
        ,      FFFFF F
        ,     FFFF   F
        ,     FFF FF
        ,    FFFFF
     10 ˆ    FF F
        ,   FFF F
        ,   FFF
        ,  FFFF
        ,  FF
      0 ˆ
        Š--ˆ-----------ˆ-----------ˆ-----------ˆ-----------ˆ--
           0          50          100         150         200

                                  dbh

NOTE: 319 obs hidden.
```

```
------ species=HW --------------------------

Plot of ht*dbh.  Symbol is value of species.

  60 ^
     ,
     ,
     ,
     ,
     ,                         H HHHH HHHH HHH H H H   HH
  50 ^                      HHHHHHHHHH H  H H     HHH
     ,                HHHHHHHHHHHHHHHHH   H  HHH            H
H
     ,               H   HHHHHHHH  HHHH H H
     ,           H   HH HH H HH  HH H H H       H     H
     ,         HHH   H  HHH  HHHHH           H
     ,         H  H HH     HH     H  H HHH    HH HH    H
  40 ^          HH H  HH  HHH  H     HHH H   H   H
     ,        H   H H HHHH  H H    H H HH HH  H         H
     ,     H HH H   HHHHH  H  H HHHHHHHHHHHHHH H   H H       H
     ,        HH H HHHH           HHH HH    H H             HH
     ,        H   H H H    H  H H     H     H     H
h    ,         HH HHHH HH H HHH  H     H     H      H
t 30 ^      H  H HH H  H HH HHHH    HH   HH
     ,       HHHHHH  H HHH HHHHHHHH   HH H     H
     ,    HH   HHHH H H HHHHHHHHHHH   HH
     ,    H   HHH  H  HH   H HH H    HH
     ,    HH H H  H HHH  HHHHHHHH
     ,     HHHH       H H H
  20 ^     H           H HHH H
     ,    HHHH HH HH H H H
     ,   HH H   H HHH     H
     ,   HHHHHH H HH                H
     ,    HHH HHHHHHHH
     ,   HH HHHHH HH
  10 ^   HHHHHHHH
     ,   H HHHH H
     ,  HHHHH H
     , HHHHH
     , HHH
     , HH
   0 ^
     Š-^---------^---------^---------^---------^---------^-------
--^--
       2        17        32        47        62        77
92

                                    dbh
```

```
                     The REG Procedure
                        Model: Full
                  Dependent Variable: y

        Number of Observations Read        1725
        Number of Observations Used        1725

                    Analysis of Variance

                          Sum of         Mean
 Source       DF       Squares       Square  F Value  Pr > F

 Model         8     688.80495     86.10062  1274.68  <.0001
 Error      1716     115.91051      0.06755
 Corrected
    Total   1724     804.71546

Root MSE              0.25990    R-Square     0.8560
Dependent Mean        3.09332    Adj R-Sq     0.8553
Coeff Var             8.40191


                     Parameter Estimates

                   Parameter Standard
Variable   DF    Estimate   Error         t Value     Pr >
|t|

Intercept  1     0.52420   0.05782         9.07      <.0001
x1         1    -0.37609   0.09275        -4.05      <.0001
x2         1    -0.37207     0.08463      -4.40      <.0001
x3         1     1.80625     0.05491      32.89      <.0001
x4         1    -0.00239   0.00070334     -3.40      0.0007
x5         1     0.29106     0.08800       3.31      0.0010
x6         1     0.98797     0.08989      10.99      <.0001
x7         1    -0.00524     0.00117      -4.46      <.0001
x8         1    -0.02160     0.00158     -13.67      <.0001
```

```
                    The REG Procedure
                      Model: Common
                   Dependent Variable: y

           Number of Observations Read        1725
           Number of Observations Used        1725

                   Analysis of Variance

                        Sum of        Mean
 Source       DF    Squares      Square    F Value  Pr > F

 Model         2    606.66176  303.33088  2637.34  <.0001
 Error      1722    198.05370    0.11501
 Corrected
     Total  1724    804.71546


Root MSE              0.33914    R-Square     0.7539
Dependent Mean        3.09332    Adj R-Sq     0.7536
Coeff Var            10.96352


                      Parameter Estimates

                  Parameter   Standard
 Variable   DF   Estimate       Error    t Value    Pr > |t|

 Intercept  1   0.45235    0.04517      10.01      <.0001
 x3         1   2.05848    0.04409      46.69      <.0001
 x4         1  -0.00825  0.00064234    -12.84      <.0001
```

Summary:

Assumptions met?

Full:
Common:
Intercept Only:

R Square and SE^E

Full:
Common:
Intercept Only:

Df, SSR, SSE:

Model	df model	SSR	df error	SSE
Full				
Common				
Int. Only				

Full versus Common

HO: Equations are the same for all species
H1: Equations differ

Partial F:

$$partial\ F = \frac{\left(SSreg(full) - SSreg(reduced)\right)/r}{SSE/(n-m-1)(full)}$$

Compare to:

F distribution for a 1- α percentile with *r* and *n*-*m*-1 (full model) degrees of freedom.

Decision:

If equations differ – could we use the same slope, just different intercepts?

Full versus Intercepts only models

HO: Slopes are the same for all species
H1: Slopes differ

Partial F:

Compare to:

Decision:

Modifications:

More than 3 species:

More than 1 continuous variable:

Experimental Design

Sampling versus experiments

- similar to sampling and inventory design in that information about forest variables is gathered and analyzed
- experiments presuppose intervention through applying a *treatment* (an action or absence of an action) to a unit, called the *experimental unit*. The experimental unit is an item on which the treatment is applied.
- The goal is to obtain results that indicate cause and effect.

Definitions of terms and examples

- For each experimental unit, measures of the *variables of interest* (i.e., *response* or *dependent variables*) are used to indicate treatment impacts.
- Treatments are randomly assigned to the experimental units.
- *Replication* is the observation of two or more experimental units under identical experimental conditions.
- A *factor* is a grouping of related treatments.

Examples:

1. 1,000 seedlings in a field. Half of the seedlings get a "tea bag" of nutrients, others do not, *randomly* assigned.

   Experimental unit: the seedling.

   Treatments are: no tea bag, and tea bag.

   Factor: only one – fertilizer (none, tea bag)

   Replications: 500 seedlings get each treatment

2. 300 plant pots in a greenhouse: Each plant gets either 1) standard genetic stock; 2) genetic stock from another location; 3) improved genetic stock.

   Treatments:

   Experimental Unit:

   Factor(s):

   Replications:

3. The number of tailed frogs in different forest types is of interest. There are six areas. Three are cut and the other three are not cut.

Treatments:

Experimental Unit:

Factor(s):

Replications:

4. Two forest types are identified, Coastal western hemlock and interior Douglas fir. For each, a number of samples are located, and the growth of each tree in each sample is measured.

Treatments:

Experimental Unit:

Factor(s):

Replications:

5. The effect of animal browsing on herbaceous plants is of interest. In each of two forest types, 10 areas are established at the beginning of the year. Five out of the 10 are fenced off, eliminating animal browsing. The rest are marked but left open to animals. The heights and coverages of plants are measured at the end of the year.

Treatments:

Experimental Unit:

Factor(s):

Replications:

Randomization?

What is *treatments are randomly assigned to experimental units*?

- Haphazard vs. random allocation
- Practical problems and implications

Other terms:

- The *null hypothesis* is that there are no differences among the treatment means. For more than one factor, there is more than one hypothesis
- The sum of squared differences (termed, *sum of squares*) between the average for the response variable by treatment versus the average over all experimental units represents the variation attributed to a factor.
- The *degrees of freedom*, associated with a factor, are the number of treatment levels within the factor minus one.

Example:

Factor A, fertilizer: none, medium, heavy (3 levels)

Factor B, species: spruce, pine (2 levels)

Number of possible treatments: 6 e..g, spruce, none is one treatment.

Experimental Unit: 0.001 ha plots

Replicates planned: 2 per treatment (cost constraint). How many experimental units do we need?

Variable of interest: Average 5-year height growth for trees in the plot

Null hypotheses:

There is no different between the 6 treatments. This can be broken into:

1) There is no interaction between species and fertilizer.
2) There is no difference between species.
3) There is no difference between fertilizers.

- *Experimental error* is the measure of variance due to chance causes, among experimental units that received the same treatment.
- The degrees of freedom for the experimental error relate to the number of experimental units and the number of treatment levels.
- The impacts of treatments on the response variables will be detectable only if the impacts are measurably larger than the variance due to chance causes.
- To reduce the variability due to causes other than those manipulated by the experimenter, relatively homogenous experimental units are carefully selected.

- Random allocation of a treatment to an experimental unit helps insure that the measured results are due to the treatment, and not to another cause.

Example: if we have applied the no fertilizer treatment to experimental units on north facing sites, whereas moderate and heavy fertilizer treatments are applied only to south facing sites, we would not know if differences in average height growth were due to the application of fertilization, the orientation of the sites, or both. The results would be *confounded* and very difficult to interpret.

Variations in experimental design

Introduction of More Than One Factor:

- Interested in the interaction among factors, and the effect of each factor.
- A treatment represents a particular combination of levels from each of the factors.
- When all factor levels of one factor are given for all levels of each of the other factors, this is a *crossed experiment*. Example: two species and three fertilization levels = six treatments using a crossed experiment.

Fixed, Random, or Mixed Effects:

- *Fixed factors*: the experimenter would like to know the change that is due to the particular treatments applied; only interested in the treatment levels that are in the experiment (e.g., difference in growth between two particular genetic stocks) [*fixed effects*]
- *Random factors*: the variance due to the factor is of interest, not particular levels (e.g., variance due to different genetic stocks—randomly select different stock to use as the treatment) [*random effects*]
- Mixture of factor types: Commonly, experiments in forestry include a mixture of factors, some random and some fixed [*mixed effect*].

Restricted Randomization Through Blocking: Randomized Block (RCB), Latin Square, and Incomplete Blocks Designs:

- Randomize treatments with blocks of experimental units
- Reduces the variance by taking away variance due to the item used in blocking (e.g., high, medium and low site productivity
- Results in more homogeneous experimental units within each block.

Restricted Randomization Through Splitting Experimental Units:

- Called “split plot”
- An experimental unit is split. Another factor is randomly applied to the split.

Example: The factor fertilizer is applied to 0.001 ha plots. Each of the 0.001 ha plot is then split into two, and two different species are planted in each. Fertilizer is applied to the whole plot, and species is applied to the split plot. Species is therefore randomly assigned to the split plot, not to the whole experimental unit.

Nesting of Factors

- Treatment levels for one factor may be particular to the level of another factor, resulting in nesting of treatments.

Example, for the first level of fertilizer, we might use medium and heavy thinning, whereas, for the second level of fertilizer, we might use no thinning and light thinning.

Hierarchical Designs and Sub-Sampling:

- Commonly in forestry experiments, the experimental unit represents a group of items that we measure. E.g. several pots in a greenhouse, each with several plants germinating from seeds.
- Treatments are randomly assigned to the larger unit (e.g, to each plot not to each seedling). The experimental unit is the larger sized unit.
- May want variance due to the experimental unit (pots in the example) and to units within (plants in the example). These are 1) nested in the treatment; 2) random effects; and 3) hierarchical
- A common variation on hierarchical designs is measuring a sample of items, instead of measuring all items in an experimental unit.

Introduction of Covariates

- The initial conditions for an experiment may not be the same for all experimental units, even if blocking is used to group the units.
- Site measures such as soil moisture and temperature, and starting conditions for individuals such as starting height, are then measured (called covariates) along with the response variable
- These covariates are used to reduce the experimental error.
- Covariates are usually interval or ratio scale (continuous).

Designs in use

- The most simple design is one fixed-effects factor, with random allocation of treatments to each experimental unit, with no 1) blocking; 2) sub-sampling; 4) splits; or 5) covariates
- Most designs use combinations of the different variations. For example, one fixed-effects factor, one mixed-effects factor, blocked into three sites, with trees measured within plots within experimental units (sub-sampling/hierarchical), and measures taken at the beginning of the experiment are used as covariates (e.g., initial heights of trees.

Why?

- Want to look at interactions among factors and/or is cheaper to use more than one factor in one experiment than do two experiments.
- Experiments and measurements are expensive – use sampling within experimental units to reduce costs
- Finding homogeneous units is quite difficult: blocking is needed

BUT can end up with problems:

- some elements are not measured,
- random allocation is not possible, or
- measures are correlated in time and/or space.

In this course, start with the simple designs and add complexity.

Main questions in experiments

Do the treatments affect the variable of interest?

For fixed effects: Is there a different between the treatment means of the variable of interest? Which means differ? What are the means by treatment and confidence intervals on these means?

For random effects: Do the treatments account for some of the variance of the variables of interest? How much?

Completely Randomized Design (CRD)

- Homogeneous experimental units are located
- Treatments are randomly assigned to treatment units
- No blocking is used
- We measure a variable of interest for each experimental unit

CRD: One Factor Experiment, Fixed Effects

REF: Ch. 16, 17, 18 of Neter et al.

Main questions of interest

Are the treatment means different?

Which means are different?

What are the estimated means and confidence intervals for these estimates?

Notation:

Population: $y_{ij} = \mu + \tau_j + \varepsilon_{ij}$ OR $y_{ij} = \mu_j + \varepsilon_{ij}$

y_{ij} = response variable measured on experimental unit *i* and treatment *j*

j=1 to *J* treatments

μ = the grand or overall mean regardless of treatment

μ_j = the mean of all measures possible for treatment *j*

τ_j = the difference between the overall mean of all measures possible from all treatments and the mean of all possible measures for treatment *j*, called the *treatment effect*

ε_{ij} = the difference between a particular measure for an experimental unit *i*, and the mean for the treatment *j* that was applied to it

$$\varepsilon_{ij} = y_{ij} - \mu_j$$

For the experiment:

$$y_{ij} = \bar{y}_{\bullet\bullet} + \hat{\tau}_j + e_{ij} \quad \text{OR} \quad y_{ij} = \bar{y}_{\bullet j} + e_{ij}$$

$\bar{y}_{\bullet\bullet}$ = the grand or overall mean of all measures from the experiment regardless of treatment; under the assumptions for the error terms, this will be an unbiased estimate of μ

$\bar{y}_{\bullet j}$ = the mean of all measures for treatment *j*; under the assumptions for the error terms, this will be an unbiased estimate of μ_j

$\hat{\tau}_j$ = the difference between the mean of experiment measures for treatment *j* and the overall mean of measures from all treatments; under the error term assumptions, will be an unbiased estimate of τ_j

e_{ij} = the difference between a particular measure for an experimental unit *i*, and the mean for the treatment *j* that was applied to it

$$e_{ij} = y_{ij} - \bar{y}_{\bullet j}$$

n_j = the number of experimental units measured in treatment *j*

n_T = the number of experimental units measured over all treatments = $\sum_{j=1}^{J} n_j$

Example: Fertilization Trial

A forester would like to test whether different site preparation methods result in difference in heights. Fifteen areas each 0.02 ha in size are laid our over a fairly homogeneous area. Five site preparation treatments are randomly applied to 25 plots. One hundred trees are planted (same genetic stock and same age) in each area. At the end of 5 years, the heights of seedlings in each plot were measured, and averaged for the plot.

i = a particular 0.02 ha area in treatment *j*, from 1 to 5.

Response variable y_{ij}: 5-year height growth (one average for each experimental unit)

Number of treatments: *J*=5 site preparation methods

n_T = the number of experimental units measured over all treatments = $\sum_{j=1}^{5} n_j = 25$

$n_1 = n_2 = n_3 = n_4 = n_5 = 5$ experimental units measured each treatment

Schematic of Layout:

3	4	4	5	1
1	2	3	5	2
2	1	2	4	2
5	4	3	1	5
4	3	1	5	3

Data Organization and Preliminary Calculations

For easy calculations by hand, the data could be organized in a spreadsheet as:

Obs:	Treatment, j=1 to J					
i=1 to n_j	1	2	3	…	J	
1	y_{11}	y_{12}	y_{13}	…	y_{1J}	
2	y_{21}	y_{22}	y_{23}	…	y_{2J}	
3	y_{31}	y_{32}	y_{33}	…	y_{3J}	
…	…	…	…	…	…	
n	y_{n1}	y_{n2}	y_{n3}	…	y_{nJ}	
Sum	$y_{\cdot 1}$	$y_{\cdot 2}$	$y_{\cdot 3}$	…	$y_{\cdot J}$	y..
Averages	$\bar{y}_{\bullet 1}$	$\bar{y}_{\bullet 2}$	$\bar{y}_{\bullet 3}$		$\bar{y}_{\bullet J}$	$\bar{y}_{\bullet\bullet}$

$$y_{\bullet j} = \sum_{i=1}^{n_j} y_{ij} \qquad \bar{y}_{\bullet j} = \frac{y_{\bullet j}}{n_j} \qquad y_{\bullet\bullet} = \sum_{i=1}^{J}\sum_{i=1}^{n_j} y_{ij} \qquad \bar{y}_{\bullet\bullet} = \frac{y_{\bullet\bullet}}{n_T}$$

NOTE: may not be the same number of observations for each treatment.

Example:

J= 5 site preparation treatments randomly applied to n=25 plots.

Response Variable: Plot average seedling height after 5 years

Plot Average Heights (m)

	Treatments					Overall
Observation	**1**	**2**	**3**	**4**	**5**	
1	4.6	4.9	4.0	3.4	4.3	
2	4.3	4.3	3.7	4.0	3.7	
3	3.7	4.0	3.4	3.0	3.7	
4	4.0	4.6	3.7	3.7	3.0	
5	4.0	4.3	3.0	3.4	3.4	
SUMS	20.600	22.100	17.800	17.500	18.100	96.100
Means	4.120	4.420	3.560	3.500	3.620	3.844
n_j	5	5	5	5	5	25

Example Calculations:

$$\bar{y}_{\bullet 1} = \frac{\sum_{i=1}^{5} y_{ij}}{5} = (4.6 + 4.3 + 3.7 + 4.0 + 4.3)/5 = 4.12$$

$$\bar{y}_{\bullet\bullet} = \frac{\sum_{j=1}^{5}\sum_{i=1}^{n_j} y_{ij}}{\sum_{k=1}^{5} n_j} = (20.6 + 22.1 ... 17.8 + 17.5) = 96.1/25 = 3.844$$

We then calculate:

1) Sum of squared differences between the observed values

and the overall mean (*SSy*):

$$SSy = \sum_{j=1}^{J}\sum_{i=1}^{n_j}\left(y_{ij} - \bar{y}_{\bullet\bullet}\right)^2 \quad df = \sum_{j=1}^{J} n_j - 1$$

Also called, sum of squares total (same as in regression)

2) Sum of squared differences between the treatment

means, and the grand mean, weighted by the number of

experimental units in each treatment (SS_{TR})

$$SS_{TR} = \sum_{j=1}^{J}\sum_{i=1}^{n_j}\left(\bar{y}_{\bullet j} - \bar{y}_{\bullet\bullet}\right)^2 = \sum_{j=1}^{J} n_j\left(\bar{y}_{\bullet j} - \bar{y}_{\bullet\bullet}\right)^2 \quad df = J - 1$$

3) Sum of squared differences between the observed values for each experimental unit and the treatment means (*SSE*)

$$SSE = \sum_{j=1}^{J}\sum_{i=1}^{n_j}\left(y_{ij} - \bar{y}_{\bullet j}\right)^2 \quad df = n_T - J$$

$$SSy = SS_{TR} + SSE$$

Alternative formulae for the sums of squares that may be easier to calculate are:

$$SSy = \sum_{j=1}^{J}\sum_{i=1}^{n_j} y_{ij}^2 - \frac{y_{\bullet\bullet}^{\ 2}}{n_T}$$

$$SS_{TR} = \sum_{j=1}^{J} n_j \bar{y}_{\bullet j}^2 - \frac{y_{\bullet\bullet}^{\ 2}}{n_T}$$

$$SSE = SSy - SS_{TR}$$

For the example, differences from treatment means (m):

	Treatments					Overall
Obs.	**1**	**2**	**3**	**4**	**5**	
1	0.480	0.480	0.440	-0.100	0.680	
2	0.180	-0.120	0.140	0.500	0.080	
3	-0.420	-0.420	-0.160	-0.500	0.080	
4	-0.120	0.180	0.140	0.200	-0.620	
5	-0.120	-0.120	-0.560	-0.100	-0.220	
SUMS	0.000	0.000	0.000	0.000	0.000	0.000
Sum of Squares Error	0.468	0.468	0.572	0.560	0.908	2.976
n_j	5	5	5	5	5	25
s^2_j	0.117	0.117	0.143	0.140	0.227	

Example Calculations:

$$SSE \text{ for } treatment\ 1 = \sum_{j=1}^{5} \left(y_{1j} - \bar{y}_{\bullet 1}\right)^2$$

$$= (4.6-4.1)^2 + (4.3-4.1)^2 + (3.7-4.1)^2 + (4.0-4.1)^2 + (4.0-4.1)^2 = 0.468$$

$$s^2{}_1 = \frac{SSE \text{ for } treatment\ 1}{n_1 - 1} = \frac{0.468}{5-1} = 0.117$$

$$SSE = \sum_{j=1}^{J} \sum_{i=1}^{n_j} \left(y_{ij} - \bar{y}_{\bullet j}\right)^2$$

$$= SSE \text{ for } treatment\ 1 + \text{SSE for } treatment\ 2 + \ldots + \text{SSE for } treatment\ 5$$

$$= 0.468 + 0.468 + 0.572 + 0.560 + 0.908 = 2.976$$

Differences from grand mean (m)

	Treatments					Overall
Obs.	**1**	**2**	**3**	**4**	**5**	
1	0.756	1.056	0.156	-0.444	0.456	
2	0.456	0.456	-0.144	0.156	-0.144	
3	-0.144	0.156	-0.444	-0.844	-0.144	
4	0.156	0.756	-0.144	-0.144	-0.844	
5	0.156	0.456	-0.844	-0.444	-0.444	
SUMS	1.380	2.880	-1.420	-1.720	-1.120	0.000
Sum of Squares Total	0.849	2.127	0.975	1.152	1.159	6.262
n_j	5	5	5	5	5	25

$$SSy = \sum_{j=1}^{J} \sum_{i=1}^{n_j} \left(y_{ij} - \bar{y}_{\bullet\bullet}\right)^2$$

$$= SSy \text{ for } treatment\ 1 + \text{SSy for } treatment\ 2 + \ldots + \text{SSy for } treatment\ 5$$

$$= 0.849 + 02.127 + 0.975 + 1.152 + 1.159 = 6.262$$

Difference between treatment means and grand mean (m)

	Treatments					Overall
	1	**2**	**3**	**4**	**5**	
Mean	4.120	4.420	3.560	3.500	3.620	
Difference	0.276	0.576	-0.284	-0.344	-0.224	0.000
Sum of Squares						
Treatment	0.076	0.332	0.081	0.118	0.050	3.286
n_j	5	5	5	5	5	25

Example Calculations:

$$SS_{TR} = \sum_{j=1}^{J} n_j \left(\bar{y}_{\bullet j} - \bar{y}_{\bullet\bullet}\right)^2 = \left(5 \times (4.120 - 3.844)^2\right) + \left(5 \times (4.420 - 3.844)^2\right)$$

$$+ \left(5 \times (3.560 - 3.844)^2\right) + \left(5 \times (3.500 - 3.844)^2\right) + \left(5 \times (3.620 - 3.844)^2\right)$$

$$= 3.286$$

Test for differences among treatment means

The first main question is: Are the treatment means different?

H_0: $\mu_1 = \mu_2 = \ldots = \mu_J$

H_1: not all the same

OR:

H_0: $\tau_1 = \tau_2 = \cdots = \tau_J$

H_1: not all equal to 0

OR:

H_0: $(\phi_{TR} + \sigma^2_{\varepsilon}) / \sigma^2_{\varepsilon} = 1$

H_1: $(\phi_{TR} + \sigma^2_{\varepsilon}) / \sigma^2_{\varepsilon} > 1$

Where σ^2_{ε} is the variance of the error terms;

ϕ_{TR} is the effect of the fixed treatments (see page 234 for more details on what this is).

If the treatment does not account for any of the variance in the response variable, then treatment effects are likely all = 0, and all the treatment means are likely all the same.

Using an analysis of variance table:

Source	df	SS	MS	F	p-value
Treatment	J-1	SS_{TR}	MS_{TR}= $SS_{TR}/(J-1)$	F= MS_{TR}/MSE	Prob F> $F_{(J-1),(nT-J),(1-\alpha)}$
Error	n_T -J	SSE	MSE= $SSE/(n_T$-$J)$		
Total	n_T -1	SSy			

$$F = \frac{SS_{TR}/(J-1)}{SSE/\sum_{j=1}^{J}(n_j-1)} = \frac{SS_{TR}/(J-1)}{SSE/(n_T-J)} = \frac{MS_{TR}}{MSE}$$

Under H_0, and the assumptions of analysis of variance, this follows an F-distribution. If

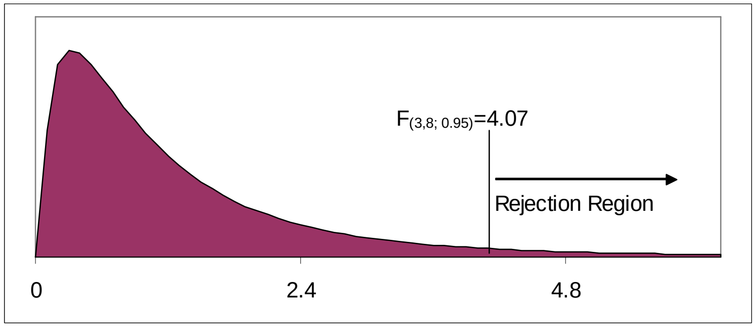
$$F > F_{(J-1, n_T-J, 1-\alpha)}$$

We reject H_0 and conclude that there is a difference between the treatment means.

Notice that this is a one-sided test, using 1-α

This is because we are testing if the ratio of variances is > 1.

For example, if we have 4 treatments, and 12 experimental units, and we want α=0.05:



If the calculated F is larger than 4.07, we reject H_0: The treatments means are likely different, unless a 5% error has occurred.

OR: We take our calculated F value from our experiment and plot it on this F curve. Then, find the area to the right of this value (p-value). We reject a hypothesis if the probability value (p-value) for the test is less than the specified significance level.

For the example:

If assumptions of ANOVA are met then interpret the F-value.

H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5$

H_1: not all equal

Analysis of Variance (ANOVA) Table:

Source	df	SS	MS	F	p-value
Treatment	5-1=4	3.286	0.821	5.51	0.004
Error	25-5=20	2.976	0.149		
Total	25-1=24	6.262			

If assumptions of ANOVA are met then interpret the F-value. NOTE: Fcritical for alpha=0.05, df treatment=4 and df error=20 is 2.87.

Since the p-value is very smaller (smaller than alpha=0.05), we reject H0 and conclude that there is a difference in the treatment means. BUT this is only a good test if the assumptions of analysis of variance have been met. Need to check these first (as with regression analysis).

Assumptions regarding the error term

For the estimated means for this experiment to be unbiased estimates of the means in the population, and the MSE to be an unbiased estimate of the variance within each experimental unit, the following assumptions must be met:

1. Observations are independent – not related in time nor in space [independent data]
2. There is normal distribution of the y-values [or the error terms] around each treatment mean [normally distributed]
3. The variances of the y's around each treatment mean [or the error terms] are the same (homogeneous) for all treatment means [equal variance]

Similar to regression:

- a normal probability plot for the error terms can be used to check the assumption of normality, and
- a residual plot can be used to visually check the assumption of equal variance.

OR, these can be tested using (1) normality tests (as with regression); (2) Bartlett's test for equal variances (for more than one factor or for other designs with blocking, etc. this becomes difficult).

Transformations to meet assumptions

Similar to regression:

- logarithmic transformations can be used to equalize variances
- arcsine transformation can be used to transform proportions into normally distributed variables
- rank transformation can be used when data are not normally distributed and other transformations do not "work" [nonparametric analysis of variance using ranks]

Unlike regression you must transform the y-variable

Process:

- do your analysis with the measured response variable
- if assumptions of the error term are not met, transform the y-variable
- do the analysis again and check the assumptions; if not me, try another transformation
- may have to switch to another method: generalized linear models, etc.

Expected values:

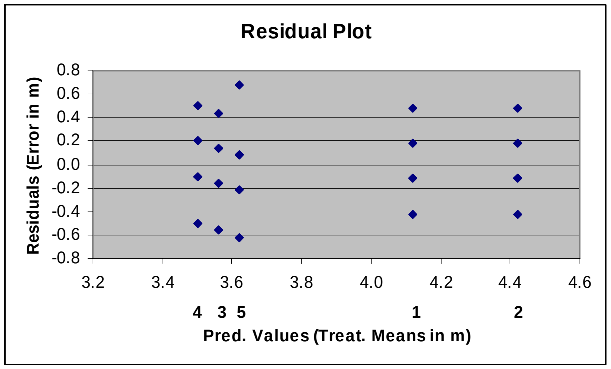
Under the assumptions of analysis of variance, MSE is an unbiased estimate of σ^2_ε and MS_{TR} is an unbiased estimate of $\phi_{TR}+\sigma^2_\varepsilon$. Therefore, this F-test will give the correct probabilities under the assumptions.

This is the same as saying that the expected value of MSE is σ^2_ε, and the expected value of MS_{TR} is $\phi_{TR}+\sigma^2_\varepsilon$.

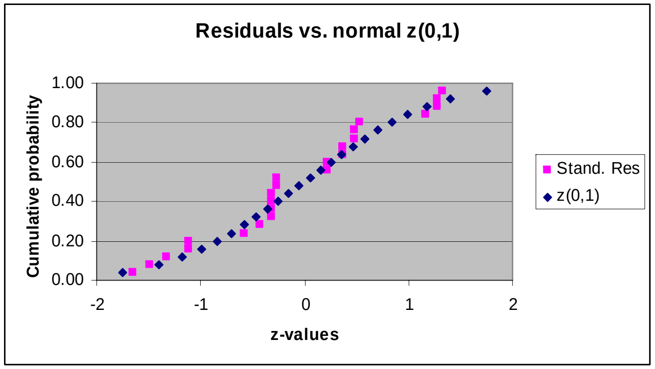
The F-test is then a measure of how much larger the value is when the treatment means are accounted for.

For the example, before interpreting the ANOVA table, we must check assumptions of ANOVA:

Is there equal variance across treatments? (estimated by MSE as 0.149 on our ANOVA table). Using a residual plot and EXCEL:



Are residuals normally distributed? Again using EXCEL:



Where standardized residuals are calculated by:

$$e_i\,(\text{standardized}) = \frac{e_i - 0}{\sqrt{MSE}}$$

Compare these to z-values for a standard normal distribution with a mean of zero and a variance of 1 (z(0,1))

Differences among particular treatment means

If there are differences among means detected, which means differ?

Can use:

- Orthogonal contrasts – see textbook
- Multiple comparisons

Multiple comparisons (or contrasts):

- Many different types, e.g.
  - T-test for every pair of means; must adjust the alpha level used by dividing by the number of pairs.
  - Scheffe's multiple comparisons
  - Bonferonni's adjustments

- Try to "preserve" the alpha level used to test all the means together (the F-test)

For the example, given that there is a difference among treatment means, which pairs of means differ?

t-test for pairs of means:

- determine the number of pairs possible

$$\binom{5}{2} = \frac{5!}{3!2!} = 10 \text{ possible pairs of means}$$

Comparing Treatments 2 (largest estimated mean) versus 4 (smallest estimated mean):

$$\mathrm{H}_0 : \mu_2 - \mu_4 = 0 \quad \text{OR} \quad \mathrm{H}_0 : \mu_2 = \mu_4$$

$$\mathrm{H}_1 : \mu_2 - \mu_4 \neq 0$$

$$t = \frac{(\bar{y}_{\bullet 2} - \bar{y}_{\bullet 4}) - 0}{\sqrt{MSE\left(\frac{1}{n_2} + \frac{1}{n_4}\right)}}$$

$$t = \frac{(4.4 - 3.5)}{\sqrt{0.149 \times \left(\frac{1}{5} + \frac{1}{5}\right)}} = 3.686$$

Under H_0: This follows:

$$t_{1-\alpha/2, n_T - J}$$

Using alpha=0.005 (0.05/10=0.005), for 5 treatments and 25 observations, the t-value is 3.153. Result?

Another way to assess this is to obtain the p-value for t=3.686, with 20 degrees of freedom (25-5).

This is 0.001464. Since this is less than 0.005, we reject H_0 and conclude that these two means differ.

Can test

- the other pairs of means.
- could test for any size of difference between two means, for example:

$$\mathrm{H0} : \mu_2 - \mu_4 = c$$

$$\mathrm{H1} : \mu_2 - \mu_4 \neq c$$

$$t = \frac{(\bar{y}_{\bullet 2} - \bar{y}_{\bullet 4}) - c}{\sqrt{MSE\left(\frac{1}{n_2} + \frac{1}{n_4}\right)}}$$

Scheffe's multiple comparison test – conservative

Can test

- any pair of means
- or other comparisons.

Testing whether the means for Treatments 2 and 4 differ:

$$\mathrm{H0}: 0\mu_1 + \frac{1}{2}\mu_2 + 0\mu_3 - \frac{1}{2}\mu_4 + 0\mu_5 = 0$$

$$\mathrm{H0}: \frac{1}{2}\mu_2 - \frac{1}{2}\mu_4 = 0 \qquad \mathrm{H0}: \mu_2 = \mu_4$$

The test statistic is:

$$S = \frac{\hat{L}}{s(\hat{L})} \qquad \hat{L} = \sum_{j=1}^{J} c_j \bar{y}_{\bullet j} \qquad s(\hat{L}) = \sqrt{MSE \times \left(\sum_{j=1}^{J} c_j^{\ 2} \times \frac{1}{n_j} \right)}$$

The sum of the c_j values must add up to zero.

For this example:

$$c_1 = 0 \quad c_2 = \frac{1}{2} \quad c_3 = 0 \quad c_4 = -\frac{1}{2} \quad c_5 = 0$$

$$\hat{L} = \frac{1}{2} \times 4.4 - \frac{1}{2} \times 3.5 = 0.45$$

$$s(\hat{L}) = \sqrt{0.149 \times \left(\left(\frac{1}{2}\right)^2 \times \frac{1}{5} + \left(-\frac{1}{2}\right)^2 \times \frac{1}{5} \right)} = 0.122$$

$$S = \frac{0.45}{0.122} = 3.686$$

Under H_0, this follows:

$$\sqrt{(J-1) F_{1-\alpha, J-1, n_T - J}}$$

For J=5, alpha=0.05, and n_T=25 observations:

$$\sqrt{(5-1) 2.87} = 3.38$$

Calculated S > 3.38, so we reject H_0, the treatment means differ. (NOTE: The means would have to be at least 0.826 apart to reject)

Scheffe’s can be used for many comparisons.

For example: Test if treatments 3, 4 and 5 differ from treatments 1 and 2:

$$\text{H0}: \frac{1}{2}\mu_1 + \frac{1}{2}\mu_2 - \frac{1}{3}\mu_3 - \frac{1}{3}\mu_4 - \frac{1}{3}\mu_5 = 0 \quad \text{OR}$$

$$\text{H0}: \frac{\mu_1 + \mu_2}{2} - \frac{\mu_3 + \mu_4 + \mu_5}{3} = 0$$

NOTE: c’s add up to 0.

$$c_1 = \frac{1}{2} \quad c_2 = \frac{1}{2} \quad c_3 = -\frac{1}{3} \quad c_4 = -\frac{1}{3} \quad c_5 = -\frac{1}{3}$$

$$\hat{L} = \frac{1}{2}\times 4.1 + \frac{1}{2}\times 4.4 - \frac{1}{3}\times 3.6 - \frac{1}{3}\times 3.5 - \frac{1}{3}\times 3.6 = 0.68$$

$$s(\hat{L}) = 0.158$$

$$S = \frac{0.68}{0.158} = 4.30$$

Result: Greater than the critical value of 3.38; do reject H_0.

$$s(\hat{L}) = \sqrt{0.149\times\left(\left(\frac{1}{2}\right)^2\times\frac{1}{5}+\left(\frac{1}{2}\right)^2\times\frac{1}{5}\left(-\frac{1}{3}\right)^2\times\frac{1}{5}+\left(-\frac{1}{3}\right)^2\times\frac{1}{5}+\left(-\frac{1}{3}\right)^2\times\frac{1}{5}\right)} = 0.158$$

Confidence limits for treatment means

Under the assumptions, confidence intervals for each treatment mean can be obtained by:

$$\bar{y}_{\bullet j} \pm t_{(n_T - J),1-\alpha/2}\sqrt{\frac{MSE}{n_j}}$$

Since MSE estimates the variance that is assumed to be equal, and the observations are normally distribution and independent.

For the example:

$$\bar{y}_{\bullet j} \pm t_{(n-k),1-\alpha/2}\sqrt{\frac{MSE}{n_j}}$$

$$\bar{y}_{\bullet 1} = 4.1 \quad \bar{y}_{\bullet 2} = 4.4 \quad \bar{y}_{\bullet 3} = 3.6 \quad \bar{y}_{\bullet 4} = 3.5 \quad \bar{y}_{\bullet 5} = 3.6$$

$$\text{All } \sqrt{\frac{MSE}{n_j}} \text{ the same as } n_j \text{ are all equal } \sqrt{\frac{0.149}{5}} = 0.173$$

$$t_{20,0.975} = 2.09$$

For treatment 1:

$$4.1 \pm 2.09 \times 0.173 \qquad 4.1 \pm 0.36$$

$$(3.74, 4.46)$$

Using SAS:

For entry into statistical programs like SAS, the data should be organized as:

Treatment j=1 to J	Obs: i=1 to n_j	Response
1	1	y_{11}
1	2	y_{21}
1	3	y_{31}
…	…	...
1	n_1	$y_{(n1)\ 1}$
2	1	y_{12}
2	2	y_{22}
2	3	y_{32}
…	…	...
2	n_2	$Y_{(n2)\ 2}$
…	...	...
J	1	y_{1J}
J	2	y_{2J}
J	3	y_{3J}
…	…	...
J	n_J	$y_{(nJ)\ 3}$

For the example, we can put the data into an EXCEL file:

Treatment	Observation	AveHt
1	1	4.6
1	2	4.3
1	3	3.7
1	4	4.0
1	5	4.0
2	1	4.9
2	2	4.3
2	3	4.0
2	4	4.6
2	5	4.3
3	1	4.0
3	2	3.7
3	3	3.4
3	4	3.7
3	5	3.0
4	1	3.4
4	2	4.0
4	3	3.0
4	4	3.7
4	5	3.4
5	1	4.3
5	2	3.7
5	3	3.7
5	4	3.0
5	5	3.4

```
*  CRD.sas  example for 430 and 533 classes
;
PROC IMPORT OUT= WORK.htdata
    DATAFILE= "E:\frst430\lemay\examples\
CRD_one_factor_no_sampling.XLS"
    DBMS=EXCEL REPLACE;
     SHEET="rawdata$";
     GETNAMES=YES;
     MIXED=NO;
     SCANTEXT=YES;
     USEDATE=YES;
     SCANTIME=YES;
RUN;

options ls=70 ps=50 pageno=1;
run;

PROC GLM data=htdata;
CLASS Treatment;
MODEL aveht=treatment;
MEANS treatment/scheffe hovtest=bartlett;
estimate '1 VS others' treatment 4 -1 -1 -1
-1/divisor=4;
OUTPUT OUT=GLMOUT PREDICTED=PREDICT
RESIDUAL=RESID;
RUN;

PROC PLOT DATA=GLMOUT;
PLOT RESID*PREDICT='*';
RUN;

PROC UNIVARIATE DATA=GLMOUT PLOT NORMAL;
VAR RESID;
RUN;
```

```
                    The GLM Procedure

                 Class Level Information

               Class          Levels    Values
               Treatment           5    1 2 3 4 5

           Number of Observations Read          25
           Number of Observations Used          25

                     The GLM Procedure

Dependent Variable: AveHt   AveHt

                          Sum of     Mean
Source      DF      Squares    Square       F Value

Model        4     3.28560000  0.82140000    5.52
Error       20     2.97600000  0.14880000
Corrected
    Total   24     6.26160000

            Source                 Pr > F
             Model                  0.0037
             Error
             Corrected Total

R-Square   Coeff Var   Root MSE    AveHt Mean

0.524722   10.03502    0.385746    3.844000
```

```
Source     DF    Type I SS   Mean         F Value
                             Square
Treatment   4    3.28560000  0.82140000  5.52

            Source                 Pr > F
            Treatment              0.0037


Source     DF   Type III SS   Mean Square   F Value

Treatment   4    3.28560000   0.82140000      5.52

               Source                 Pr > F
               Treatment              0.0037


              The GLM Procedure

Bartlett's Test for Homogeneity of AveHt Variance

Source      DF    Chi-Square    Pr > ChiSq

Treatment    4        0.5790        0.9654
```

```
                 The GLM Procedure

                Scheffe's Test for AveHt

NOTE: This test controls the Type I experimentwise
error rate.


Alpha                                  0.05
Error Degrees of Freedom                 20
Error Mean Square                    0.1488
Critical Value of F                 2.86608
Minimum Significant Difference        0.826

Means with the same letter are not significantly
different.


Scheffe
Grouping          Mean       N    Treatment

   A            4.4200      5       2
   A
 B    A         4.1200      5       1
 B    A
 B    A         3.6200      5       5
   B
   B            3.5600      5       3
   B
   B            3.5000      5       4

                   The GLM Procedure

Dependent Variable: AveHt   AveHt

                         Standard
Parameter     Estimate   Error      t Value  Pr >
|t|

1 VS others  0.34500000 0.19287302   1.79    0.0888
```

```
             Plot of RESID*PREDICT.  Symbol used is '*'.

RESID ,
      ,
  0.8 ^
      ,
      ,            *
      ,
  0.6 ^
      ,
      ,      *                              *              *
      ,         *
  0.4 ^
      ,
      ,
      ,
  0.2 ^      *                              *              *
      ,         *
      ,            *
      ,
  0.0 ^
      ,
      ,      *                              *              *
      ,         *
 -0.2 ^            *
      ,
      ,
      ,
 -0.4 ^                                     *              *
      ,
      ,      *
      ,         *
 -0.6 ^            *
      ,
      ,
      ,
 -0.8 ^
      ,
      Š-^---------^---------^---------^---------^---------^---------^-
       3.4       3.6       3.8       4.0       4.2       4.4       4.6

                                   PREDICT
```

NOTE: 5 obs hidden.

```
                  The SAS System

            The UNIVARIATE Procedure
               Variable:  RESID

                    Moments

N                       25  Sum Weights                25
Mean                     0  Sum Observations            0
Std Deviation 0.35213634  Variance             0.124
Skewness       0.0634775  Kurtosis       -0.6323427
Uncorrected SS     2.976  Corrected SS         2.976
Coeff Variation        .  Std Error Mean 0.07042727


            Basic Statistical Measures

    Location                    Variability

Mean      0.00000     Std Deviation         0.35214
Median   -0.10000     Variance              0.12400
Mode     -0.12000     Range                 1.30000
Interquartile Range      0.34000


               Tests for Location: Mu0=0

Test           -Statistic-    -----p Value------

Student's t    t         0    Pr > |t|    1.0000
Sign           M      -0.5    Pr >= |M|   1.0000
Signed Rank    S         2    Pr >= |S|   0.9584
```

```
          Tests for Normality

Test               --Statistic---   --p Value----

Shapiro-Wilk       W     0.962795  Pr < W  0.4729
Kolmogorov-Smirnov D     0.131787  Pr > D >0.1500
Cramer-von Mises   W-Sq  0.059919  Pr > W-Sq>0.2500
Anderson-Darling   A-Sq  0.370893  Pr > A-Sq
>0.2500


            The UNIVARIATE Procedure
            Variable:  RESID

          Quantiles (Definition 5)

           Quantile      Estimate
           100% Max          0.68
            99%               0.68
            95%               0.50
            90%               0.48
            75% Q3            0.18
            50% Median       -0.10
            25% Q1           -0.16
            10%              -0.50
             5%               -0.56
             1%               -0.62
             0% Min           -0.62

            Extreme Observations

     ----Lowest----        ----Highest---

   Value      Obs        Value      Obs
   -0.62       24         0.44       11
   -0.56       15         0.48        1
   -0.50       18         0.48        6
   -0.42        8         0.50       17
   -0.42        3         0.68       21
```

```
Stem Leaf                     #             Boxplot
 6 8                         1               |
 4 4880                      4               |
 2 0                         1               |
 0 884488                    6             +--+--+
-0 6222200                   7             *-----*
-2 2                         1               |
-4 6022                      4               |
-6 2                         1               |
                ----+----+----+----+
            Multiply Stem.Leaf by 10**-1


             The UNIVARIATE Procedure
                Variable:  RESID

           Normal Probability Plot
 0.7+                                         ++*++
    |                                   * *+++*++
    |                                ++*+++
    |                          +***+**
    |                    **+*+*
    |               +++*++
    |         ++*+*+*
-0.7+   ++*++
    +----+----+----+----+----+----+----+----+----+----+
    -2        -1         0        +1        +2
```

Power of the Test:

A Type I error rate (α, significance level), the chance of rejecting a null hypothesis when it is true (you reject when the means are actually the same) must be selected. Given:

- a particular number of experimental units
- sizes of the differences between true population means, and
- variation within the experimental units

this will set the Type II error rate (β), the chance of accepting a null hypothesis when it is false (you fail to reject when the means are actually different)

The power of the test is 1- β, the probability you will reject the null hypothesis and conclude that there is a difference in means, when there IS a difference between population means.

If the difference between population means (real treatment means) is very large, than a small number of experimental units will result in rejection of the null hypothesis.

If the number of experimental units is very large, then even a small difference between population means will be detected.

If the variation within experimental units is very small, then the difference will be detected, even with a small difference between population means, and even with only a few treatment units.

Statistical Significance is not the same as differences of Practical importance! UNLESS you:

- have some idea of within experimental unit variation from a previous study with the same conditions (e.g., MSE from a previous study)
- know the size of the difference that you wish to detect
- have selected the α level

Then:

You can calculate the number of experimental units per treatment that will result in rejection of H_0: when the differences are that large or greater.

Alternatively:

You can calculate the power of the test for an experiment you have already completed.

Power of the test for the example:

Have:

J=5 treatments, and df treatment is 5-1=4
n=5 observations in each treatment, and df error is 25-5=20
MS_{TR}=0.821
MSE=0.149 as an estimate of σ_ε^2
Fcritical is F(0.95,4,20)=2.87

Also, $E[MS_{TR}]=\varphi_{TR}+\sigma_\varepsilon^2$ and $E[MS_{TR}]=\sigma_\varepsilon^2$.

$$\phi_{TR} = \frac{n\sum_{j=1}^{J}\tau_j^2}{J-1}$$

$$\textit{where}$$

$$\tau_j = \mu_{\bullet j} - \mu$$

$$\textit{then}$$

$$\sum_{j=1}^{J}\hat{\tau}_j^2 = \frac{J-1}{n}(MS_{TR} - MSE)$$

$$\sum_{j=1}^{J}\hat{\tau}_j^2 = \frac{5-1}{5}(0.821 - 0.149) = 0.538$$

Power is then Prob(F>Fcritical | Noncentral) where Noncentral is the noncentrality parameter, and for when H1 is true.

$$\delta = noncentral = \frac{n\sum_{j=1}^{J}\tau_j^{\,2}}{\sigma_\varepsilon^{\,2}}$$

$$\hat{\delta} = noncentral = \frac{5\times 0.538}{0.149} = 18.04$$

Then use SAS:

```
Data power;
*  Power=1-probf(Fcritical,df Treatment, df Error,
Noncentral);
Power=1-probf(2.87,4,20,18.04);
Run;
```

The temporary file will have the result in it, which is 0.87. Often try to get power between 0.80 and 0.95.

Can do power analysis for a planned experiment using:

1. A estimate of the of the variance of the error. This could be from a previous, similar experiment.
2. The differences between treatment means that are the minimum required to be of practical importance.

Can then test for how many observations are needed so that statistical differences also mean differences of practical importance [See SAS code called **One_way_anova_power_using_min_differences.sas**]

Methods based on maximum likelihood rather than least squares

ML methods can be used when:

- Treatments are random rather than fixed (more on this later)
- Transformations do not result in assumptions being met
- Your dependent variable is a count, or it is a binary variable (e.g., yes or no; dead or alive; present or absent)

[See text for a little on this, also FRST 530]

CRD: Two Factor Factorial Experiment, Fixed Effects

REF: Neter et al., Ch 19 and 20

Introduction

- Treatments can be combinations of more than one factor
- For 2-factor experiment, have several levels of Factor A and of Factor B
- All levels of Factor A occur for Factor B and vice versa (called a *Factorial Experiment*, or *crossed* treatments)

Example:

- Factor A, (three levels of fertilization: A1, A2, and A3)
- Factor B (four species: B1, B2, B3 and B4)
- Crossed: 12 treatments
- Four replications per treatment for a total of 48 experimental units
- Measured Responses: height growth in mm

Schematic and Measured Response for the Example:

A1B1=10	A3B2=25	A3B4=35	A2B2=23	A1B2=14	A2B3=24
A1B4=24	A2B2=22	A1B2=15	A2B4=28	A3B3=32	A3B2=25
A3B2=27	A1B4=23	A3B3=29	A3B2=26	A1B3=17	A1B1=11
A3B4=35	A1B2=13	A1B4=22	A1B1=11	A2B3=24	A3B3=30
A1B3=19	A2B1=18	A2B4=30	A3B3=31	A2B3=23	A1B4=22
A3B1=22	A2B4=29	A3B1=23	A2B1=18	A1B2=15	A3B1=23
A2B2=25	A3B4=37	A1B1=9	A3B1=24	A3B4=36	A2B4=28
A1B3=17	A2B1=18	A2B2=20	A2B1=18	A2B3=26	A1B3=18

A1B1=10 indicates that the response variable was 10 for this experimental unit that received Factor A, level 1 and Factor B, level 1. Treatments randomly assigned to the 48 experimental units.

Organization of data for analysis using a statistics package:

A	**B**	**result**
1	1	10
1	1	11
1	1	9
1	1	11
1	2	15
1	2	15
1	2	13
1	2	14
1	3	17
1	3	18
1	3	17
1	3	19
1	4	22
1	4	23
1	4	24
1	4	22
2	1	18
2	1	18
2	1	18
2	1	18
2	2	20
. . .		
3	3	32
3	4	35
3	4	36
3	4	37
3	4	35

Main questions

1. Is there an interaction between Factor A and Factor B (fertilizer and species in the example)? Or do the means by Factor A remain the same regardless of Factor B and vice versa?
2. If there is no interaction, is there a difference
   a. Between Factor A means?
   b. Between Factor B means?
3. If there are differences:
   a. If there is an interactions, which treatment means differ?
   b. If there is no interaction, then which levels of Factor A means differ? Factor B means?

Notation, Assumptions, and Transformations

Models

Population: $y_{ijk} = \mu + \tau_{A\,j} + \tau_{Bk} + \tau_{AB\,jk} + \varepsilon_{ijk}$

y_{ijk} = response variable measured on experimental unit *i* and factor A level *j*, factor B level *k*

j=1 to *J* levels for Factor A; *k*=1 to *K* levels for Factor B

μ = the grand or overall mean regardless of treatment

τ_{Aj} = the *treatment effect* for Factor A, level *j*

τ_{Bk} = the *treatment effect* for Factor B, level *k*

τ_{ABjk} = the *interaction* for Factor A, level *j* and Factor B, level *k*

ε_{ijk} = the difference between a particular measure for an experimental unit *i*, and the mean for a treatment:

$$\varepsilon_{ijk} = y_{ijk} - (\mu + \tau_{A\,j} + \tau_{Bk} + \tau_{AB\,ij})$$

For the experiment:

$$y_{ijk} = \bar{y}_{\bullet\bullet\bullet} + \hat{\tau}_{Aj} + \hat{\tau}_{Bk} + \hat{\tau}_{AB\,jk} + e_{ijk}$$

$\bar{y}_{\bullet\bullet\bullet}$ = the grand or overall mean of all measures from the experiment regardless of treatment; under the assumptions for the error terms, this will be an unbiased estimate of μ

$\bar{y}_{\bullet jk}$ = the mean of all measures from the experiment for a particular treatment *jk*

$\bar{y}_{\bullet j\bullet}$ = the mean of all measures from the experiment for a particular level *j* of Factor A (includes all data for all levels of Factor B)

$\bar{y}_{\bullet\bullet k}$ = the mean of all measures from the experiment for a particular level *k* of Factor B (includes all data for all levels of Factor A)

$\hat{\tau}_{Aj}, \hat{\tau}_{Bk}, \hat{\tau}_{ABjk}$ = under the error term assumptions, will be unbiased estimates of corresponding treatment effects for the population

e_{ijk} = the difference between a particular measure for an experimental unit *i*, and the mean for the treatment *jk* that was applied to it

$$e_{ijk} = y_{ijk} - \bar{y}_{\bullet jk}$$

n_{jk} = the number of experimental units measured in treatment *jk*

n_T = the number of experimental units measured over all treatments = $\sum_{k-1}^{K}\sum_{j=1}^{J} n_{jk}$

Means for the example:

Factor A: 16 observations per level

A1=16.25, A2=23.38, A3=28.75

Factor B: 12 observations per level

B1=17.08, B2=20.83, B3=24.17, B4=29.08

Treatments (A X B): 4 observations per treatment

Sums of Squares:

$SSy = SS_{TR} + SSE$ as with CRD: One Factor. BUT

SS_{TR} is now divided into:

$$SS_{TR} = \quad SSA \quad + \quad SSB \quad + \quad SSAB$$

SSy: The sum of squared differences between the observations and the grand mean:

$$SSy = \sum_{k=1}^{K}\sum_{j=1}^{J}\sum_{i=1}^{n_{jk}}\left(y_{ijk} - \bar{y}_{\bullet\bullet\bullet}\right)^2 \quad df = n_T - 1$$

SSA: Sum of squared differences between the level means for factor A and the grand mean, weighted by the number of experimental units for each treatment:

$$SSA = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\left(\bar{y}_{\bullet j \bullet} - \bar{y}_{\bullet\bullet\bullet}\right)^2 \quad df = J - 1$$

SSB: Sum of squared differences between the level means for factor B and the grand mean, weighted by the number of experimental units for each treatment:

$$SSB = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\left(\bar{y}_{\bullet\bullet k} - \bar{y}_{\bullet\bullet\bullet}\right)^2 \quad df = K - 1$$

SSAB: Sum of squared differences between treatment means for *jk* and the grand mean, minus the factor level differences, all weighted by the number of experimental units for each treatment:

$$SSAB = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\left(\left(\bar{y}_{\bullet jk} - \bar{y}_{\bullet\bullet\bullet}\right) - \left(\bar{y}_{\bullet\bullet k} - \bar{y}_{\bullet\bullet\bullet}\right) - \left(\bar{y}_{\bullet j \bullet} - \bar{y}_{\bullet\bullet\bullet}\right)\right)^2$$

Since some of the estimated grand means cancel out we obtain:

$$SSAB = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\left(\bar{y}_{\bullet jk} - \bar{y}_{\bullet\bullet k} - \bar{y}_{\bullet j \bullet} + \bar{y}_{\bullet\bullet\bullet}\right)^2$$

SSE: Sum of squared differences between the observed values for each experimental unit and the treatment means:

$$SSE = \sum_{k=1}^{K}\sum_{j=1}^{J}\sum_{i=1}^{n_{jk}}\left(y_{ijk} - \bar{y}_{\bullet jk}\right)^2 \qquad df = n_T - JK$$

Alternative computational formulae:

$$SSy = \sum_{k=1}^{K}\sum_{j=1}^{J}\sum_{i=1}^{n_{jk}} y_{ijk}^2 - \frac{\bar{y}_{\bullet\bullet\bullet}^{\;2}}{n_T} \qquad SSA = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\bar{y}_{\bullet j\bullet}^2 - \frac{\bar{y}_{\bullet\bullet\bullet}^{\;2}}{n_T}$$

$$SS_{TR} = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\bar{y}_{\bullet jk}^2 - \frac{\bar{y}_{\bullet\bullet\bullet}^{\;2}}{n_T} \qquad SSB = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\bar{y}_{\bullet\bullet k}^2 - \frac{\bar{y}_{\bullet\bullet\bullet}^{\;2}}{n_T}$$

$$SSAB = SS_{TR} - SSA - SSB \qquad SSE = SSy - SS_{TR}$$

[See Excel Spreadsheet for the Example]

Assumptions and Transformations:

Assumptions regarding the error term

- Must meet assumptions to obtain unbiased estimates of population means, and an unbiased estimate of the variance of the error term (same as CRD: One Factor)
  - o independent observations (not time or space related)
  - o normality of the errors,
  - o equal variance for each treatment.
- Use residual plot and a plot of the standardized errors against the expected errors for a normal distribution to check these assumptions.

Transformations:

As with CRD: One Factor, you must transform the y-variable

Process:

- do your analysis with the measured response variable
- if assumptions of the error term are not met, transform the y-variable
- do the analysis again and check the assumptions; if not me, try another transformation
- may have to switch to another method: generalized linear models, etc.

Test for Interactions and Main Effects

The first main question is: Is there an interaction between the two factors?

H_0: No interaction
H_1: Interaction
OR:

$$H_0: (\phi_{AB}+\sigma^2_{\varepsilon})/\sigma^2_{\varepsilon} = 1$$
$$H_1: (\phi_{AB}+\sigma^2_{\varepsilon})/\sigma^2_{\varepsilon} > 1$$

Where σ^2_{ε} is the variance of the error terms;

ϕ_{AB} is the interaction effect of the fixed treatments.

Using an analysis of variance table:

Source	df	SS	MS	F	p-value
A	J-1	SSA	MSA= $SSA/(J$-1)	F= MSA/MSE	Prob F> $F_{(J\text{-}1),(\text{dfE}),\,1\text{-}\,\alpha}$
B	K-1	SSB	MSB= $SSB/(K$-1)	F= MSB/MSE	Prob F> $F_{(K\text{-}1),(\text{dfE}),1\text{-}\,\alpha}$
A X B	(J-1)(K-1)	$SSAB$	$MSAB$= $SSAB/$ (J-1)(K-1)	F= $MSAB/MSE$	Prob F> $F_{dfAB,dfE,,1\text{-}\,\alpha}$
Error	n_T-JK	SSE	MSE= $SSE/(n_T$-$J)$		
Total	n_T-1	SSy			

Source	df	MS	E[MS]
A	J-1	MSA	$\sigma_{\varepsilon}^{2}+\phi_{A}$
B	K-1	MSB	$\sigma_{\varepsilon}^{2}+\phi_{B}$
A X B	(J-1)(K-1)	MSB	$\sigma_{\varepsilon}^{2}+\phi_{AB}$
Error	n_T-JK	MSE	σ_{ε}^{2}
Total	n_T-1		

See Neter et al., page 826, Table 19.8 for details on expected mean squares; ϕ is used here to represent fixed effects.

For the interactions:

$$F = \frac{SSAB/(J-1)(K-1)}{SSE/(n_T - JK)} = \frac{MSAB}{MSE}$$

- Under H_0, this follows $F_{\text{df1,df2, 1-}\alpha}$ where df1 is from the numerator (J-1)(K-1), and df2 is from the denominator (n_T-JK)
- If the F calculated is greater than the tabular F, or if the p-value for F calculated is less than α, reject H_0.
    - The means of Factor A are influenced by the levels of Factor B and the two factors cannot be interpreted separately.
    - Graph the means of all treatments
    - Conduct multiple comparisons all treatments (rather then on means of each Factor, separately
    - Not as much power (reject H_0 when it is false), if this occurs.

If there are no interactions between the factors, we can look at each factor separately – fewer means, less complicated.

Factor A:

$$H_0\text{: } \mu_1 = \mu_2 = \ldots = \mu_J$$

OR:

$$H_0\text{: } (\phi_{A+}\sigma^2_{\varepsilon}))/\sigma^2_{\varepsilon} = 1$$
$$H_1\text{: } (\phi_{A+}\sigma^2_{\varepsilon})/\sigma^2_{\varepsilon} > 1$$

Where σ^2_{ε} is the variance of the error terms;

ϕ_A is fixed effect for Factor A.

From the ANOVA table:

$$F = \frac{SSA/(J-1)}{SSE/(n_T - JK)} = \frac{MSA}{MSE}$$

- Under H_0, this follows $F_{\text{df1,df2, 1-}\alpha}$ where df1 is from the numerator (J-1) and df2 is from the denominator (n_T-JK)
- If the F calculated is greater than the tabular F, or if the p-value for F calculated is less than α, reject H_0.
    - The means of Factor A in the population are likely not all the same
    - Graph the means of Factor A levels
    - Conduct multiple comparisons between means for the J levels of Factor A, separately

The analysis and conclusions would follow the same pattern for Factor B.

Analysis of Variance Table Results for the Example

Source	Degrees of Freedom	Sum of Squares	Mean Squares	F	p
A	2	1258.17	629.08	514.70	<0.0001
B	3	934.75	311.58	254.93	<0.0001
A X B	6	17.00	2.836	2.32	0.0539
Error	36	44.00	1.22		
Total	47	2253.92			

If assumptions met, (residuals are independent, are normally distributed, and have equal variances among treatments), we can interpret the results.

Interpretation using $\alpha = 0.05$:

- No significant interaction (p=0.0539); we can examine species and fertilizer effects separately.
- Are significant differences between the three fertilizer levels of Factor A (p<0.0001), and between the four species of Factor B (p<0.0001).
- The mean values based on these data are:

  A1=16.25, A2=23.38, A3=28.75

  B1=17.08, B2=20.83, B3=24.17, B4=29.08

Did not have to calculate these for each of the 12 treatments since there is no interaction.

Further analyses, for each Factor separately:

- Scheffé's test for multiple comparisons, could then be used to compare and contrast Factor level means.
  - The number of observations in each factor level are: 16 for Factor A, and 12 for Factor B
  - Use the MSE for both Factor A and for Factor B (denominator of their F-tests)
- t-tests for each pair of means could be used instead.
  - Again, use MSE, and 16 observations for Factor A versus 12 for Factor B
  - Must split alpha level used in the F-tests by the number of pairs

Factor A: t-tests for pairs of means

Determine the number of pairs possible

$$\binom{3}{2} = \frac{3!}{1!2!} = 3 \text{ possible pairs of means}$$

Use a significance level of 0.05/3 pairs=0.017 for each t-test

Comparing Factor Levels 1 and 2: A1 vs. A2

$$\text{H0} : \mu_{1\bullet} - \mu_{2\bullet} = 0 \qquad \text{H1} : \mu_{1\bullet} - \mu_{2\bullet} \neq 0$$

$$t = \frac{(\bar{y}_{\bullet 1} - \bar{y}_{\bullet 2}) - 0}{\sqrt{MSE\left(\frac{1}{\sum_{k=1}^{K} n_{1k}} + \frac{1}{\sum_{k=1}^{K} n_{4k}}\right)}}$$

$$t = \frac{(16.25 - 23.38)}{\sqrt{1.22 \times \left(\frac{1}{16} + \frac{1}{16}\right)}} = -18.258$$

Critical t value from a probability table for:

- df(error) = 36 based on ($n_T - JK$), and 0.017 significance level (For α =0.05 use 0.05/3 pairs for each t-test), 2-sided test
- Using an EXCEL function: =tinv(0.017,36), returns the value of 2.50 (this assumes a 2-sided test).
- Since the absolute value of the calculated t is greater than 2.50 we reject H0.

OR

- enter your t-value, df (error), and 2 (for 2-sided) into the EXCEL function =tdist(18.258,36,2)
- Returns a p-value of <0.000. (NOTE that you must enter the positive value, and the p-value is for the two "ends" (area greater than 18.258 plus area less than -18.258)
- Since p<0.017, we reject H0

The mean of treatment A1 differs from the mean of A2.

For Factor B

- Recalculate the number of possible pairs for 4 factor levels (will be 6 pairs; divide alpha by this for each test)
- The observations per factor level is 12, rather than 16
- Df(error) and MSE are the same as for Factor A.

A Different Interpretation using α =0.10:

- There is a significant interaction (p=0.0539) using α =0.10; cannot interpret main effects (A and B) separately.
- The mean values based on these data are: [Excel]

  A1B1=10.25 A1B2=14.25 A1B3= 17.75 A1B4= 22.75
  A2B1=18.00 A2B2=22.50 A2B3= 24.25 A2B4=28.75
  A3B1= 23.00 A3B2=25.75 A3B3=30.50 A3B4=35.75

12 mean values as there is a significant interaction

Further analyses:

- Scheffé's test for multiple comparisons (or others), could then be used to compare and contrast treatment means (pairs or other groupings of means). The number of observations in each treatment are 4 [lower power than if there was no interaction], and use the MSE.

- Using t-tests for pairs of means, the number of observations are 4 for each *jk* treatment, use the MSE, and recalculate the number of possible pairs out of 12 treatments (will be 66 pairs! Retaining α =0.10, we would use 0.10/66 = 0.0015 for each t-test)

Confidence limits for factor level and treatment means

Treatment means:

$$\bar{y}_{\bullet jk} \pm t_{(n-JK),1-\alpha/2}\sqrt{\frac{MSE}{n_{jk}}}$$

Factor A means:

$$\bar{y}_{\bullet j\bullet} \pm t_{(n-JK),1-\alpha/2}\sqrt{\frac{MSE}{\sum_{k=1}^{K} n_{jk}}}$$

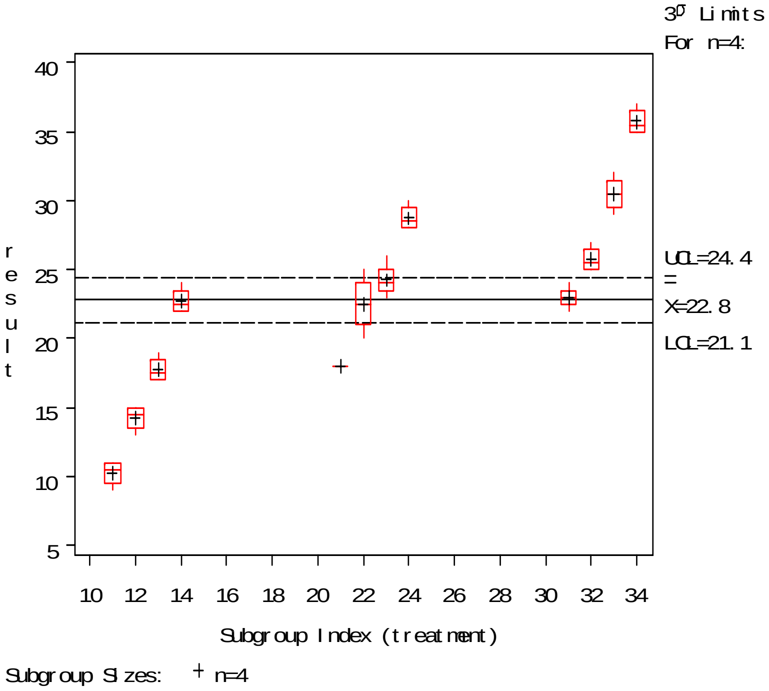
Factor B means:

$$\bar{y}_{\bullet\bullet k} \pm t_{(n-JK),1-\alpha/2}\sqrt{\frac{MSE}{\sum_{j=1}^{J} n_{jk}}}$$

SAS code and Results:

```
PROC IMPORT OUT= WORK.twofactor
    DATAFILE=“E:\frst430\lemay\examples\encyl_examples.xls"
         DBMS=EXCEL REPLACE;
    SHEET="crd$";
    GETNAMES=YES;
    MIXED=NO;
    SCANTEXT=YES;
    USEDATE=YES;
    SCANTIME=YES;
RUN;
options ls=70 ps=50 pageno=1;

data twofactor;
set twofactor;
*set up a label for each treatment, with factor a and factor b, for
example, treatment of 11 is factor A of 1,and factor b of 1;
treatment=(a*10)+b;
run;

proc print data=twofactor;
run;

proc shewhart data=twofactor;
     boxchart result*treatment;
run;

proc sort data=twofactor;
by a b;
run;
```

```
Proc means data=twofactor;
var result;
by a b;
run;

PROC GLM  data=twofactor;
class a b;
model result=a b a*b;
output out=glmout r=resid p=predict;
lsmeans a b a*b/pdiff tdiff;
run;

proc plot data=glmout;
plot resid*predict='*';
run;

PROC univariate data=glmout plot normal;
Var resid;
Run;
```



Crosses indicate mean value
Centre of the box is the median (50%)
Boxes indicate third and first quartile (25% and 75%)
“Whiskers” indicate Maximum and Minimum values

```
                 The SAS System                 1

               Obs   A    B    result    treatment
               1     1    1      10          11
               2     1    1      11          11
               3     1    1       9          11
               4     1    1      11          11
               5     1    2      15          12

                          . . .
--------------------- A=1 B=1 -----------------------------
                          The MEANS Procedure

                Analysis Variable : result result

N        Mean         Std Dev     Minimum         Maximum
  ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ
4      10.2500000    0.9574271    9.0000000      11.0000000
  ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ

---------------------------- A=1 B=2 ----------------------
                Analysis Variable : result result
N        Mean         Std Dev     Minimum         Maximum
  ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ
4      14.2500000    0.9574271   13.0000000      15.0000000
  ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ ヤ

                            . . .
```

```
                    The GLM Procedure

                 Class Level Information
                   Class         Levels    Values
                     A                3    1 2 3
                     B                4    1 2 3 4

             Number of Observations Read          48
             Number of Observations Used          48

                The GLM Procedure

Dependent Variable: result   result

                                          Sum of
Source       DF        Squares    Mean Square   F Value
Model        11    2209.916667     200.901515    164.37
Error        36      44.000000       1.222222
Corrected
    Total     47    2253.916667

                    Source                Pr > F
                    Model                 <.0001
                    Error
                    Corrected Total

R-Square     Coeff Var      Root MSE    result Mean
0.980478      4.850640      1.105542       22.79167
```

```
Source   DF      Type I SS    Mean Square   F Value
A         2    1258.166667     629.083333    514.70
B         3     934.750000     311.583333    254.93
A*B       6      17.000000       2.833333      2.32

                    Source                  Pr > F
                    A                       <.0001
                    B                       <.0001
                    A*B                     0.0539


Source       DF    Type III SS    Mean Square   F Value
A             2    1258.166667     629.083333    514.70
B             3     934.750000     311.583333    254.93
A*B           6      17.000000       2.833333      2.32

Dependent Variable: result   result

                    Source                  Pr > F
                    A                       <.0001
                    B                       <.0001
                    A*B                     0.0539

                     The GLM Procedure
                    Least Squares Means

                          result      LSMEAN
                A         LSMEAN      Number
                1     16.2500000           1
                2     23.3750000           2
                3     28.7500000           3
```

```
              Least Squares Means for Effect A
          t for H0: LSMean(i)=LSMean(j) / Pr > |t|

                Dependent Variable: result

  i/j              1                2              3

     1                        -18.2287       -31.9801
                                 <.0001         <.0001
     2      18.22866                         -13.7514
              <.0001                            <.0001
     3      31.98011    13.75145
              <.0001      <.0001


NOTE: To ensure overall protection level, only probabilities
      associated with pre-planned comparisons should be used.


                    result      LSMEAN
                  B         LSMEAN      Number
                  1     17.0833333           1
                  2     20.8333333           2
                  3     24.1666667           3
                  4     29.0833333           4
                Least Squares Means for Effect B
             t for H0: LSMean(i)=LSMean(j) / Pr > |t|

                   Dependent Variable: result

 i/j           1              2              3              4

   1                 -8.30868      -15.6942      -26.5878
                      <.0001         <.0001       <.0001
   2      8.308676                  -7.38549      -18.2791
           <.0001                    <.0001       <.0001
   3      15.69417     7.385489                      -10.8936
           <.0001       <.0001                            <.0001
   4      26.58776    18.27909      10.8936
           <.0001       <.0001         <.0001


NOTE: To ensure overall protection level, only probabilities
      associated with pre-planned comparisons should be used.

                              result      LSMEAN
                A    B        LSMEAN      Number
                1    1      10.2500000           1
                1    2      14.2500000           2
                1    3      17.7500000           3
                1    4      22.7500000           4
                2    1      18.0000000           5
                2    2      22.5000000           6
                2    3      24.2500000           7
                2    4      28.7500000           8
                3    1      23.0000000           9
                3    2      25.7500000          10
                3    3      30.5000000          11
                3    4      35.7500000          12
```

```
                  Least Squares Means for Effect A*B
                t for H0: LSMean(i)=LSMean(j) / Pr > |t|

                       Dependent Variable: result

i/j          1          2          3          4          5          6

  1             -5.11682   -9.59403   -15.9901   -9.91383   -15.6703
                  <.0001     <.0001     <.0001     <.0001     <.0001
  2   5.116817             -4.47722   -10.8732   -4.79702   -10.5534
        <.0001               <.0001     <.0001     <.0001     <.0001
  3   9.594032   4.477215             -6.39602    -0.3198   -6.07622
        <.0001     <.0001               <.0001     0.7510     <.0001
  4   15.99005   10.87324   6.396021               6.07622   0.319801
        <.0001     <.0001     <.0001                <.0001     0.7510
  5   9.913833   4.797016   0.319801   -6.07622              -5.75642
        <.0001     <.0001     0.7510     <.0001                <.0001
  6   15.67025   10.55344    6.07622    -0.3198   5.756419
        <.0001     <.0001     <.0001     0.7510     <.0001
  7   17.90886   12.79204   8.314828   1.918806   7.995027   2.238608
        <.0001     <.0001     <.0001     0.0630     <.0001     0.0315
  8   23.66528   18.54846   14.07125   7.675226   13.75145   7.995027
        <.0001     <.0001     <.0001     <.0001     <.0001     <.0001
  9   16.30985   11.19304   6.715823   0.319801   6.396021   0.639602
        <.0001     <.0001     <.0001     0.7510     <.0001     0.5265
 10   19.82767   14.71085   10.23363   3.837613   9.913833   4.157414
        <.0001     <.0001     <.0001     0.0005     <.0001     0.0002
 11   25.90389   20.78707   16.30985   9.913833   15.99005   10.23363
        <.0001     <.0001     <.0001     <.0001     <.0001     <.0001
 12   32.61971   27.50289   23.02568   16.62966   22.70588   16.94946
        <.0001     <.0001     <.0001     <.0001     <.0001     <.0001
```

```
                Least Squares Means for Effect A*B
               t for H0: LSMean(i)=LSMean(j) / Pr > |t|

                      Dependent Variable: result

i/j           7         8         9        10        11        12

   1  -17.9089  -23.6653  -16.3099  -19.8277  -25.9039  -32.6197
        <.0001    <.0001    <.0001    <.0001    <.0001    <.0001
   2   -12.792  -18.5485   -11.193  -14.7108  -20.7871  -27.5029
        <.0001    <.0001    <.0001    <.0001    <.0001    <.0001
   3  -8.31483  -14.0712  -6.71582  -10.2336  -16.3099  -23.0257
        <.0001    <.0001    <.0001    <.0001    <.0001    <.0001
   4  -1.91881  -7.67523   -0.3198  -3.83761  -9.91383  -16.6297
        0.0630    <.0001    0.7510    0.0005    <.0001    <.0001
   5  -7.99503  -13.7514  -6.39602  -9.91383  -15.9901  -22.7059
        <.0001    <.0001    <.0001    <.0001    <.0001    <.0001
   6  -2.23861  -7.99503   -0.6396  -4.15741  -10.2336  -16.9495
        0.0315    <.0001    0.5265    0.0002    <.0001    <.0001
   7            -5.75642  1.599005  -1.91881  -7.99503  -14.7108
                  <.0001    0.1186    0.0630    <.0001    <.0001
   8  5.756419            7.355425  3.837613  -2.23861  -8.95443
        <.0001              <.0001    0.0005    0.0315    <.0001
   9  -1.59901  -7.35542            -3.51781  -9.59403  -16.3099
        0.1186    <.0001              0.0012    <.0001    <.0001
  10  1.918806  -3.83761  3.517812            -6.07622   -12.792
        0.0630    0.0005    0.0012              <.0001    <.0001
  11  7.995027  2.238608  9.594032   6.07622            -6.71582
        <.0001    0.0315    <.0001    <.0001              <.0001
  12  14.71085   8.95443  16.30985  12.79204  6.715823
        <.0001    <.0001    <.0001    <.0001    <.0001


NOTE: To ensure overall protection level, only probabilities
      associated with pre-planned comparisons should be used.
```

```
              Plot of resid*predict.  Symbol used is '*'.

resid ·
      ·
 2.50 ·                          *
 2.25 ·
 2.00 ·
 1.75 ·                              *
 1.50 ·                                          *
 1.25 ·                 *         *     *     *             *
 1.00 ·                           *
 0.75 ·  *       *
 0.50 ·                          *               *
 0.25 ·                 *         *     *     *             *
 0.00 ·                 *         *
-0.25 ·  *       *                   *
-0.50 ·                          *               *
-0.75 ·                 *         *     *     *             *
-1.00 ·                           *
-1.25 ·  *       *                   *
-1.50 ·                                          *
-1.75 ·
-2.00 ·
-2.25 ·
-2.50 ·                          *
      ·
      -· --------· --------· --------· --------· --------· --------·
      10        15        20        25        30        35        40

                                   predict

NOTE: 12 obs hidden.
```

```
                       The UNIVARIATE Procedure
                           Variable:  resid

                               Moments

N                          48    Sum Weights                 48
Mean                        0    Sum Observations             0
Std Deviation      0.96755889    Variance            0.93617021
Skewness           0.16544631    Kurtosis            0.21553629
Uncorrected SS             44    Corrected SS                44
Coeff Variation             .    Std Error Mean       0.1396551

                              . . .

                         Tests for Normality

      Test                  --Statistic---    -----p Value------

      Shapiro-Wilk          W     0.977162    Pr < W      0.4666
      Kolmogorov-Smirnov    D     0.114207    Pr > D      0.1169
      Cramer-von Mises      W-Sq  0.082279    Pr > W-Sq   0.1963
      Anderson-Darling      A-Sq  0.513709    Pr > A-Sq   0.1926

                           Normal Probability Plot
        2.75+                                               *
            |                                              +++++
            |                                         *+*++
            |                                  ***+***+
            |                              **+*++
            |                        *****+*
            |                    +****+
            |             **+**+**
            |       * *+++*++
            |     +++++
            |+++*+
       -2.75+
             +----+----+----+----+----+----+----+----+----+----+
                 -2        -1         0        +1        +2
```

CRD: Random and Mixed Effects

REF: Neter et al., Ch 24 (in newer edition with white cover, Chapter 25)

Factors in experiments can be:

- Fixed: all levels of interest are included in the experiment; we are mostly interested in testing differences and estimating means for factor levels
- Random: levels are randomly selected; not all levels of interest are included; we are mostly interested in the variance of the response variable that is DUE TO the factor
- Mixed: When there is more than one factor, there may be a mixture, with some factors that are fixed-effects and others that are mixed-effects
- Often, it is difficult to make the distinction!

Examples:

We are interested in height growth for different families (genetic stock). We select 4 families from all possible families, and include these in the experiment. Then, we get an estimate of the variance in the height growth due to changes in genetics. [One random-effect factor – family]

We are interested in seedling success depending on species and soil moisture. We select 3 species out of 12 possible species, and include moisture levels of low, medium, and high. The <u>species are considered random-effects</u> (we are interested estimating the variance in seedling success due to species). The <u>moisture levels are fixed-effects</u> (we are only interested in these specific levels that we might apply in a greenhouse to generate seedlings).

- This will effect
    - the expected values of the Mean squares, and then, the F-tests that are used
    - Tests that are done following the overall F-test
    - The conclusions that are made

For J levels of Factor A and K levels of Factor B, we have the following model:

$$y_{ijk} = \bar{y}_{\bullet\bullet\bullet} + \hat{\tau}_{A\,j} + \hat{\tau}_{Bk} + \hat{\tau}_{AB\,jk} + e_{ijk}$$

Possibilities:

- Both are fixed (covered already)
- Both are random
- One is fixed and one is random

Expected Mean Square Values Comparison:

Mean Square	Model I Both A and B are Fixed	Model II Both A and B are Random	Model III A is Fixed B is Random
A (MSA)	$\sigma_\varepsilon^2 + \phi_A{}^*$	$\sigma_\varepsilon^2 + nK\sigma_A^2 + n\sigma_{AB}^2$	$\sigma_\varepsilon^2 + \phi_A + n\sigma_{AB}^2$
B (MSB)	$\sigma_\varepsilon^2 + \phi_B$	$\sigma_\varepsilon^2 + nJ\sigma_B^2 + n\sigma_{AB}^2$	$\sigma_\varepsilon^2 + nJ\sigma_B^2$
A X B (MSAB)	$\sigma_\varepsilon^2 + \phi_{AB}$	$\sigma_\varepsilon^2 + n\sigma_{AB}^2$	$\sigma_\varepsilon^2 + n\sigma_{AB}^2$
Error (MSE)	σ_ε^2	σ_ε^2	σ_ε^2

$* \sigma_\varepsilon^2 + \phi_A = \sigma_\varepsilon^2 + nK \frac{\sum_{j=1}^{J} \tau_{Aj}}{J-1}$ when the number of observations (n) are all equal.

F-tests

- Sums of squares, means squares, etc are calculated the same for all three types of models
- Assumptions: Same are for fixed-effects models
- Change the F-test, so that the numerator differs from the denominator ONLY in the item that you are testing
- For means tests, use the same denominator as used for the F-test (e.g., instead of MSE for Model III, use MSAB when testing for differences in Factor A means)
- Not really relevant to test for differences among means of a Random-effects factor as we are interested in the variance due to that factor

Example Using SAS:

Example from before for two Factors:

- Factor A, (three levels of fertilization: A1, A2, and A3)
- Factor B (four species: B1, B2, B3 and B4)
- Crossed: 12 treatments
- Four replications per treatment for a total of 48 experimental units
- Measured Responses: height growth in mm
- We assumed both Factors were fixed – wanted to compare mean height growth between species and between fertilizers.

Now, we will assume that **species is random** -- these are a few of the species that we are interested in and we wish to look at the variance in height growth that is due to species.

SAS CODE:

```
PROC IMPORT OUT= WORK.twofactor
     DATAFILE=
"E:\frst430\lemay\examples\encyl_examples.xls"
     DBMS=EXCEL REPLACE;
     SHEET="crd$";
     GETNAMES=YES;
     MIXED=NO;
     SCANTEXT=YES;
     USEDATE=YES;
     SCANTIME=YES;
RUN;

options ls=70 ps=50 pageno=1;

*  Using the same data as for fixed two-factor
experiment, but
assuming that factor b, species, is random;

PROC GLM  data=twofactor;
class a b;
model result=a b a*b;
random b/test;
test h=a e=a*b;
lsmeans a /e=a*b pdiff tdiff;
output out=glmout r=resid p=predict;
run;

proc plot data=glmout;
plot resid*predict='*';
run;

proc univariate data=glmout normal plot;
var resid;
run;
```

Maximum Likelihood as an Alternative for Random-Effects and Mixed-Effects Models

- For mixed models, maximum likelihood may be a better approach than least squares methods.
- Why? Better estimates of the variances than least squares methods.

Details: See text – a bit on this.

Example: Using SAS, use PROC MIXED instead of GLM for the same example. [added to the SAS code for comparison]

```
PROC IMPORT OUT= WORK.twofactor
     DATAFILE=
"E:\frst430\lemay\examples\encyl_examples.xls"
     DBMS=EXCEL REPLACE;
     SHEET="crd$";
     GETNAMES=YES;
     MIXED=NO;
     SCANTEXT=YES;
     USEDATE=YES;
     SCANTIME=YES;
RUN;

options ls=70 ps=50 pageno=1;

*  Using the same data as for fixed two-factor
experiment, but
assuming that factor b is random;
PROC GLM  data=twofactor;
class a b;
model result=a b a*b;
random b/test;
test h=a e=a*b;
lsmeans a /e=a*b pdiff tdiff;
output out=glmout r=resid p=predict;
run;

proc plot data=glmout;
plot resid*predict='*';
run;

proc univariate data=glmout normal plot;
var resid;
run;

PROC MIXED data=twofactor;
class a b;
model result=a;
lsmeans a/pdiff;
random b a*b;
run;
```

```
                The SAS System                    1

               The GLM Procedure

           Class Level Information

        Class         Levels    Values

        A                  3    1 2 3
        B                  4    1 2 3 4

     Number of Observations Read          48
     Number of Observations Used          48

               The SAS System                     2

             The GLM Procedure

Dependent Variable: result   result

                    Sum of
Source      DF      Squares     Mean Square F Value

Model       11    2209.916667   200.901515  164.37
Error       36      44.000000     1.222222
Corrected
   Total    47    2253.916667

           Source                 Pr > F

           Model                  <.0001
           Error
           Corrected Total

R-Square  Coeff Var   Root MSE    result Mean

0.980478  4.850640     1.105542     22.79167
```

```
Source   DF      Type I SS    Mean Square   F Value

A         2    1258.166667     629.083333    514.70
B         3     934.750000     311.583333    254.93
A*B       6      17.000000       2.833333      2.32

             Source                 Pr > F

             A                      <.0001
             B                      <.0001
             A*B                    0.0539


Source   DF    Type III SS    Mean Square   F Value

A         2    1258.166667     629.083333    514.70
B         3     934.750000     311.583333    254.93
A*B       6      17.000000       2.833333      2.32

                 The SAS System                    3

                The GLM Procedure

Dependent Variable: result   result

              Source                 Pr > F

              A                      <.0001
              B                      <.0001
              A*B                    0.0539
```

```
                The SAS System                  4

               The GLM Procedure

Source         Type III Expected Mean Square

A              Var(Error) + Q(A,A*B)
B              Var(Error) + 12 Var(B) + Q(A*B)
A*B            Var(Error) + Q(A*B)

               The SAS System                   5

             The GLM Procedure

Tests of Hypotheses for Mixed Model Analysis of
Variance

Dependent Variable: result   result

Source     DF   Type III SS   Mean Square  F Value

 *  A      2   1258.166667    629.083333   514.70
    B      3    934.750000    311.583333   254.93
    A*B    6     17.000000      2.833333     2.32

Error:
MS(Error) 36     44.000000      1.222222

* This test assumes one or more other fixed effects
are zero.

          Source                Pr > F

          *  A                     <.0001
             B                     <.0001
             A*B                   0.0539

Error: MS(Error)
* This test assumes one or more other fixed effects
are zero.
```

```
                                         The SAS System              6

                                 Least Squares Means
                     Standard Errors and Probabilities Calculated Using
                     the Type III MS for A*B as an Error Term

                                              result      LSMEAN
                                 A            LSMEAN      Number
                                 1        16.2500000           1
                                 2        23.3750000           2
                                 3        28.7500000           3


                             Least Squares Means for Effect A
                           t for H0: LSMean(i)=LSMean(j) / Pr > |t|

                                 Dependent Variable: result

                     i/j         1             2           3

                     1                  -11.9724      -21.0042
                                          <.0001        <.0001
                     2      11.97239                  -9.03181
                              <.0001                    0.0001
                     3       21.0042    9.031807
                              <.0001      0.0001


                     NOTE: To ensure overall protection level, only
                     probabilities associated with pre-planned
                     comparisons should be used.
```

```
                 The SAS System                    7

Dependent Variable: result   result

Tests of Hypotheses Using the Type III MS for A*B
as an Error Term

Source   DF    Type III SS    Mean Square   F Value
A        2    1258.166667     629.083333    222.03

Tests of Hypotheses Using the Type III MS for A*B
as an Error Term

              Source                 Pr > F
               A                     <.0001

               The SAS System                    8

       Plot of resid*predict.  Symbol used is '*'.

resid ,
      ,
 2.50 ^                          *
 2.25 ^
 2.00 ^
 1.75 ^                              *
 1.50 ^                                          *
 1.25 ^                 *         *     *     *             *
 1.00 ^                           *
 0.75 ^  *       *
 0.50 ^                          *               *
 0.25 ^                 *         *     *     *             *
 0.00 ^                 *         *
-0.25 ^  *       *                   *
-0.50 ^                          *               *
-0.75 ^                 *         *     *     *             *
-1.00 ^                           *
-1.25 ^  *       *                   *
-1.50 ^                                          *
-1.75 ^
-2.00 ^
-2.25 ^
-2.50 ^                          *
      ,
      Š-^---------^---------^---------^---------^---------^---------^-
       10        15        20        25        30        35        40

                                  predict
NOTE: 12 obs hidden.
```

```
                 The SAS System                  9

            The UNIVARIATE Procedure
               Variable:  resid

               Moments

N                      48   Sum Weights           48
Mean                    0   Sum Observations       0
Std Deviation 0.96755889   Variance      0.93617021
Skewness      0.16544631   Kurtosis      0.21553629
Uncorrected                Corrected
         SS            44   SS                    44
Coeff Variation         .   Std Error Mean 0.1396551


          Basic Statistical Measures

Location           Variability

Mean      0.00000      Std Deviation       0.96756
Median   -0.00000      Variance            0.93617
Mode     -0.75000      Range               5.00000

              Interquartile Range      1.50000

            Tests for Location: Mu0=0

Test           -Statistic-    -----p Value------

Student's t    t         0    Pr > |t|    1.0000
Sign           M        -4    Pr >= |M|   0.3123
Signed Rank    S       -32    Pr >= |S|   0.7463
```

```
                  Tests for Normality

Test                  --Statistic--   --p Value----

Shapiro-Wilk       W     0.977162 Pr < W   0.4666
Kolmogorov-Smirnov D     0.114207 Pr > D   0.1169
Cramer-von Mises   W-Sq  0.082279 Pr >W-Sq 0.1963
Anderson-Darling   A-Sq  0.513709 Pr >A-Sq 0.1926


                The SAS System                   10

              The UNIVARIATE Procedure
                 Variable:  resid

          Quantiles (Definition 5)

          Quantile      Estimate

          100% Max          2.50
           99%               2.50
           95%               1.50
           90%               1.25
           75% Q3            0.75
           50% Median       -0.00
           25% Q1           -0.75
           10%              -1.25
            5%               -1.25
            1%               -2.50
            0% Min           -2.50
```

```
                  Extreme Observations

           ----Lowest----        ----Highest---

          Value      Obs        Value      Obs

          -2.50       21         1.25       40
          -1.50       41         1.25       47
          -1.25        7         1.50       44
          -1.25        3         1.75       27
          -1.25       25         2.50       23

               The SAS System                11

              The UNIVARIATE Procedure
                  Variable:  resid

Stem Leaf                     #             Boxplot
   2 5                        1                |
   2                                           |
   1 58                       2                |
   1 022222                   6                |
   0 558888                   6             +-----+
   0 00000022222             11             *--+--*
  -0 2222                     4             |     |
  -0 888888888855            12             +-----+
  -1 2220                     4                |
  -1 5                        1                |
  -2                                           |
  -2 5                        1                |
   ----+----+----+----+
           Normal Probability Plot
 2.75+                                               *
     |                                              +++++
     |                                         *+*++
     |                                  ***+**+
     |                              **+*++
     |                        *****+*
     |                    +****+
     |             **+**+**
     |       * *+++*++
     |     +++++
     |++++*+
-2.75+
      +----+----+----+----+----+----+----+----+----+----+
          -2        -1         0        +1        +2


                 The SAS System                          12

              The Mixed Procedure

                 Model Information

Data Set                     WORK.TWOFACTOR
Dependent Variable           result
Covariance Structure         Variance Components
Estimation Method            REML
Residual Variance Method     Profile
Fixed Effects SE Method      Model-Based
Degrees of Freedom Method    Containment


            Class Level Information

       Class    Levels    Values

       A             3    1 2 3
       B             4    1 2 3 4
```

```
                   Dimensions

         Covariance Parameters             3
         Columns in X                      4
         Columns in Z                     16
         Subjects                          1
         Max Obs Per Subject              48


              Number of Observations

        Number of Observations Read              48
        Number of Observations Used              48
        Number of Observations Not Used           0


                 Iteration History

 Iteration  Evaluations  -2 Res Log Like   Criterion

  0             1       275.37975211
  1             1       166.72010292     0.00000000

                      The SAS System               13

                    The Mixed Procedure

                 Convergence criteria met.


                   Covariance Parameter
                        Estimates

                  Cov Parm     Estimate

                   B            25.7292
                   A*B           0.4028
                   Residual      1.2222
                 Fit Statistics

        -2 Res Log Likelihood           166.7
        AIC (smaller is better)         172.7
        AICC (smaller is better)        173.3
        BIC (smaller is better)         170.9


         Type 3 Tests of Fixed Effects

                         Num      Den
 Effect         DF      DF    F Value    Pr > F

 A               2       6     222.03    <.0001


              Least Squares Means

                        Standard
Effect   A   Estimate   Error   DF  t Value   Pr>|t|
A        1   16.2500   2.5709   6    6.32    0.0007
A        2   23.3750   2.5709   6    9.09    <.0001
A        3   28.7500   2.5709   6   11.18    <.0001


                 The SAS System                  14

              The Mixed Procedure

         Differences of Least Squares Means

                       Standard
Effect  A  A  Estimate  Error    DF  t Value   Pr >
|t|

A       1  2  -7.1250   0.5951    6  -11.97 <.0001
A       1  3 -12.5000   0.5951    6  -21.00 <.0001
A       2  3  -5.3750   0.5951    6   -9.03 0.0001
```

Randomized Complete Block (RCB)

With One Fixed-Effects Factor

REF: Neter et al., Ch 19, 20; Freese Handbook, page 34.

Introduction and Example

- In RCB, treatments are assigned randomly, but only within blocks of treatments
- Restricting randomization of treatments to within blocks (often called sites or trials) is used when the experimental units can be grouped by another variable that may impact the results
- In field experiments with large experimental units, blocking is often very useful in reducing error variance with only a small reduction in error degrees of freedom
- Blocks are most often random effects (we are interested in the variance due to blocks)
- The interest with RCB is with the factor, not with the blocks; the blocks are simply used to reduce the variability among experimental units

Example: Randomized Block Design (RCB), with Factor A (six levels of fertilization: A1 to A6), and two sites.

Randomization of Factor A is restricted to within sites.

Site 1		Site 2	
A1 = 9	A6=21	A4=25	A3=19
A3=15	A2=12	A1=12	A5=27
A5=20	A4=17	A2=16	A6=29

Response variable: biomass of grasses and herbs (kg)

2 observations per treatment – 1 in each site

Organization of data for analysis using a statistics package:

Site	**Treatment**	**yjk**
1	A1	9
1	A2	12
1	A3	15
1	A4	17
1	A5	20
1	A6	21
2	A1	12
2	A2	16
2	A3	19
2	A4	25
2	A5	27
2	A6	29

Main questions of interest:

- Are the treatment means different?
- Which means are different?
- What are the estimated means and confidence intervals for these estimates?

As for CRD with one factor

The organization of the data is the same for CRD with **two** factors as with RCB, BUT the **interpretation** differs:

- It is assumed that there is no interaction between the blocks and the treatments. Not really appropriate to check this since the randomization of treatments is restricted to within blocks
- Blocks are usually considered random-effects; want to remove the effects of blocks from the analysis

Notation

Population: $y_{jk} = \mu + +\tau_{Bj} + \tau_{Ak} + \varepsilon_{jk}$

y_{jk} = response variable measured on block *j* and treatment *k*

j=1 to *J* blocks; *k*=1 to *K* treatments

μ = the grand or overall mean regardless of treatment or block

τ_{Ak} = the *treatment effect* for *k*

τ_{Bj} = the *block effect* for block *j*

ε_{jk} = is actually an interaction term between block and treatment, defined as:

$$\varepsilon_{jk} = y_{jk} - (\mu + \tau_{Ak} + \tau_{Bj})$$

For the experiment:

$$y_{jk} = \bar{y}_{\bullet\bullet} + \hat{\tau}_{Bj} + \hat{\tau}_{Ak} + e_{jk}$$

$\bar{y}_{\bullet\bullet}$ = the grand or overall mean of all measures from the experiment regardless of treatment; under the assumptions for the error terms, this will be an unbiased estimate of μ

$\bar{y}_{j\bullet}$ = the mean of all measures from the experiment for a particular block j (includes all data for all levels of the treatment)

$\bar{y}_{\bullet k}$ = the mean of all measures from the experiment for a particular treatment k over all blocks

$\hat{\tau}_{Ak}, \hat{\tau}_{Bj}$ = under the error term assumptions, will be unbiased estimates of corresponding treatment effects for the population

e_{jk} = is defined as:

$$\begin{aligned} e_{jk} &= (y_{jk} - \bar{y}_{\bullet\bullet}) - (\bar{y}_{j\bullet} - \bar{y}_{\bullet\bullet}) - (\bar{y}_{\bullet k} - \bar{y}_{\bullet\bullet}) \\ &= y_{jk} - \bar{y}_{j\bullet} - \bar{y}_{\bullet k} + \bar{y}_{\bullet\bullet} \end{aligned}$$

J= number of blocks and also the number of measures (experimental units) for treatment *k*

KJ = total number of experimental units on which the response was measured

Sums of Squares:

$$SSy = SS_{BLK} + SS_{TR} + SSE$$

SSy: The sum of squared differences between the observations and the grand mean:

$$SSy = \sum_{k=1}^{K}\sum_{j=1}^{J}\left(y_{jk} - \bar{y}_{\bullet\bullet}\right)^2 \qquad df = JK - 1$$

SS_{TR} : Sum of squared differences between the treatment means, and the grand mean, weighted by the number of blocks (experimental units in each treatment)

$$SS_{TR} = \sum_{k=1}^{K} J\left(\bar{y}_{\bullet k} - \bar{y}_{\bullet\bullet}\right)^2 \qquad df = K - 1$$

SS_{BLK} : Sum of squared differences between the block means, and the grand mean, weighted by the number of treatments (experimental units in each block)

$$SS_{BLK} = \sum_{j=1}^{J} K\left(\bar{y}_{j\bullet} - \bar{y}_{\bullet\bullet}\right)^2 \qquad df = J - 1$$

SSE: sum of squared differences between the observation and the grand mean plus the treatment and block effects.

$$SSE = SSy - SS_{TR} - SS_{BLK} \qquad df = (J-1)(K-1)$$

Alternative computational formulae:

$$SSy = \sum_{k=1}^{K}\sum_{j=1}^{J} y_{jk}^2 - \frac{{y_{\bullet\bullet}}^2}{JK}$$

$$SS_{TR} = J\sum_{k=1}^{K} \bar{y}_{\bullet k}^2 - \frac{{y_{\bullet\bullet}}^2}{JK} \qquad SS_{BLK} = K\sum_{j=1}^{J} \bar{y}_{j\bullet}^2 - \frac{{y_{\bullet\bullet}}^2}{JK}$$

$$SSE = SSy - SS_{TR} - SS_{BLK}$$

Assumptions and Transformations:

- Must meet assumptions for the error term to obtain unbiased estimates of population means, and an unbiased estimate of the variance of the error term
    - independent observations (not time or space related)
    - normality of the errors,
    - equal variance for each treatment.
- Use residual plot and a plot of the standardized errors against the expected errors for a normal distribution to check these assumptions.
- To meet assumptions you might have to transform the y-variable, as with other designs

Differences among treatment means

The main question is: Is there a difference between treatment means:

$$H_0: \mu_1 = \mu_2 = \ldots = \mu_K$$

OR:

$$H_0: (\phi_{TR}+\sigma^2_{\varepsilon}) / \sigma^2_{\varepsilon} = 1$$
$$H_1: (\phi_{TR}+\sigma^2_{\varepsilon}) / \sigma^2_{\varepsilon} > 1$$

Where σ^2_{ε} is the variance of the error terms;

ϕ_{TR} is fixed effect for the treatments.

Using an analysis of variance table:

Source	df	SS	MS	F	p-value
Block	J-1	SS_{BLK}	$MSA= SS_{BLK} / (J\text{-}1)$		
Treat.	K-1	SS_{TR}	$MS_{TR}= SS_{TR} / (K\text{-}1)$	$F= MS_{TR}/MSE$	Prob F> $F_{(K\text{-}1),(\text{dfE}),1-\alpha}$
Error	(J-1)(K-1)	SSE	$MSE= SSE/ (J\text{-}1)(K\text{-}1)$		
Total	JK-1	SSy			

Source	df	MS	E[MS]
Block	J-1	MS_{BLK}	$\sigma_{\varepsilon}^{2} + K\sigma_{BLK}^{2}$
Treat.	K-1	MS_{TR}	$\sigma_{\varepsilon}^{2} + \phi_{TR}$
Error	(J-1)(K-1)	MSE	σ_{ε}^{2}
Total	n_T-1		

NOTE: Neter et al., assume blocks are fixed rather than random

ϕ is used here to represent fixed effects and σ^{2} is used to represent random effects.

From the ANOVA table:

$$F = \frac{SS_{TR}/(K-1)}{SSE/(J-1)(K-1)} = \frac{MS_{TR}}{MSE}$$

- Under H_0, this follows $F_{\text{df1,df2, 1-}\alpha}$ where df1 is from the numerator (K-1) and df2 is from the denominator (J-1)(K-1)
- If the F calculated is greater than the tabular F, or if the p-value for F calculated is less than α, reject H_0, the means of treatments in the population are likely not all the same

Further analyses:

Can conduct multiple comparisons between means for the K treatments:

- using MSE and using J (number of blocks) as the number of observations per treatment.

Can use t-tests of pairs of means -- must divide alpha by the number of possible pairs

Confidence limits for treatment means

Treatment means:

$$\bar{y}_{\bullet k} \pm t_{(dfE),1-\alpha/2}\sqrt{\frac{MSE}{J}}$$

As each block has a measure for each treatment.

SAS code and Results for the Example

```
PROC IMPORT OUT= WORK.biomass
     DATAFILE=
"E:\frst430\lemay\examples\RCB_examples.xls"
     DBMS=EXCEL REPLACE;
     SHEET="'no reps$'";
     GETNAMES=YES;
     MIXED=NO;
     SCANTEXT=YES;
     USEDATE=YES;
     SCANTIME=YES;
RUN;

options ls=70 ps=50 pageno=1 nodate;

data biomass2;
 set biomass;
 lnbiomass=log(yjk);
run;

PROC GLM  data=biomass2;
class site treatment;
model lnbiomass=site treatment;
random site;
lsmeans treatment/pdiff tdiff;
output out=glmout r=resid p=predict;
run;

proc plot data=glmout;
plot resid*predict='*';
run;

proc univariate data=glmout normal plot;
var resid;
run;
```

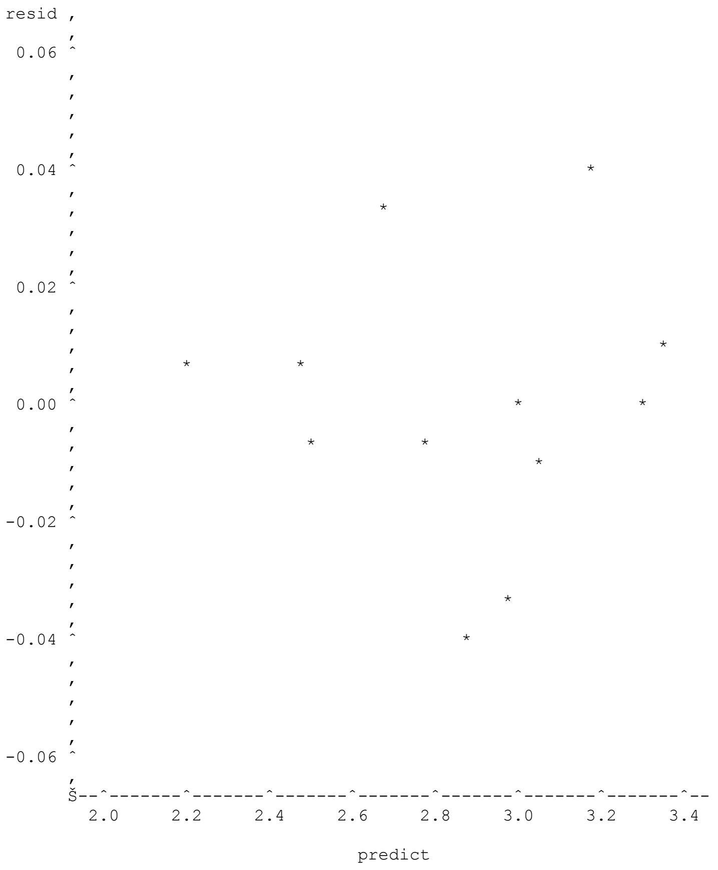
```
          The SAS System                 1

        The GLM Procedure

     Class Level Information

Class          Levels    Values

Site                2    1 2

Treatment           6    A1 A2 A3 A4 A5 A6


 Number of Observations Read          12
 Number of Observations Used          12
```

```
                The SAS System                    2

               The GLM Procedure

Dependent Variable: lnbiomass

                 Sum of
Source      DF   Squares      Mean Square   F Value

Model        6   1.38167231   0.23027872    189.72

Error        5   0.00606896   0.00121379

Corrected
   Total    11   1.38774127

               Source                 Pr > F

               Model                  <.0001

               Error

               Corrected Total


R-Square   Coeff Var    Root MSE    lnbiomass Mean

0.995627   1.217186      0.034840     2.862299
```

```
Source       DF    Type I SS   Mean Square  F Value

Site          1    0.27612234  0.27612234    227.49
Treatment     5    1.10554998  0.22111000    182.16

                Source            Pr > F

                Site              <.0001
                Treatment         <.0001


Source     DF   Type III SS    Mean Square  F Value

Site        1   0.27612234     0.27612234   227.49
Treatment   5   1.10554998     0.22111000    182.16

              Source                 Pr > F

              Site                   <.0001
              Treatment              <.0001

                   The SAS System                 3

                  The GLM Procedure

Source       Type III Expected Mean Square

Site         Var(Error) + 6 Var(Site)

Treatment    Var(Error) + Q(Treatment)
```

```
              The SAS System                    4

             The GLM Procedure
           Least Squares Means

                 lnbiomass      LSMEAN
         Treatment           LSMEAN      Number

           A1            2.34106561           1
           A2            2.62874769           2
           A3            2.82624459           3
           A4            3.02604458           4
           A5            3.14578457           5
           A6            3.20590913           6


          Least Squares Means for Effect Treatment
          t for H0: LSMean(i)=LSMean(j) / Pr > |t|

         Dependent Variable: lnbiomass

i/j    1       2        3       4        5          6

1          -8.25735 -13.9261  -19.661 -23.0979 -24.8236
             0.0004   <.0001   <.0001   <.0001   <.0001
2  8.257352         -5.66876 -11.4036 -14.8405 -16.5663
     0.0004           0.0024   <.0001   <.0001   <.0001
3 13.92612 5.668763          -5.73487 -9.17177 -10.8975
    <.0001   0.0024            0.0023   0.0003   0.0001
4 19.66098 11.40363 5.734869          -3.4369 -5.16266
    <.0001   <.0001   0.0023            0.0185   0.0036
5 23.09789 14.84053 9.171771 3.436902          -1.72576
    <.0001   <.0001   0.0003   0.0185            0.1450
6 24.82364 16.56629 10.89753 5.162661 1.725758
    <.0001   <.0001   0.0001   0.0036   0.1450


NOTE: To ensure overall protection level, only
probabilities associated with pre-planned
comparisons should be used.
```

```
              The SAS System                    5

     Plot of resid*predict.  Symbol used is '*'.
```



```
                 The SAS System                  6

               The UNIVARIATE Procedure
                  Variable:  resid

                     Moments

N                       12    Sum Weights        12
Mean                     0    Sum Observations    0
Std Deviation   0.02348879    Variance   0.00055172
Skewness                 0    Kurtosis   0.25289374
Uncorrected                   Corrected
     SS         0.00606896        SS     0.00606896
Coeff Variation          .    Std Error
                                 Mean    0.00678063


          Basic Statistical Measures

Location                    Variability

Mean      0.00000     Std Deviation         0.02349
Median    0.00000     Variance            0.0005517
Mode     -0.00785     Range                 0.08228
Interquartile Range      0.01755


             Tests for Location: Mu0=0

Test           -Statistic-    -----p Value------

Student's t    t         0    Pr > |t|    1.0000
Sign           M         0    Pr >= |M|   1.0000
Signed Rank    S         2    Pr >= |S|   0.8979
```

```
                 Tests for Normality

Test                  --Statistic---    --p Value------

Shapiro-Wilk          W     0.949629  Pr<W      0.6316
Kolmogorov-Smirnov D     0.173219  Pr>D     >0.1500
Cramer-von Mises      W-Sq  0.058634  Pr>W-Sq  >0.2500
Anderson-Darling      A-Sq  0.344788  Pr>A-Sq  >0.2500


            Quantiles (Definition 5)

            Quantile         Estimate

            100% Max       0.04114012
             99%            0.04114012

                 The SAS System                  7

             The UNIVARIATE Procedure
                Variable:  resid

             Quantiles (Definition 5)

             Quantile         Estimate

               95%            0.04114012
               90%            0.03349673
               75% Q3         0.00877283
               50% Median     0.00000000
               25% Q1        -0.00877283
               10%           -0.03349673
                5%            -0.04114012
                1%            -0.04114012
                0% Min        -0.04114012
```

```
          Extreme Observations

-------Lowest-------        -------Highest------

Value            Obs              Value      Obs

-0.04114012        4         0.00785008        1
-0.03349673        9         0.00785008        2
-0.00969558        6         0.00969558       12
-0.00785008        8         0.03349673        3
-0.00785008        7         0.04114012       10
```

```
Stem Leaf                     #             Boxplot
     4 1                        1                0
     3 3                        1                |
     2                                           |
     1 0                        1                |
     0 288                      3             +--+--+
    -0 882                      3             +-----+
    -1 0                        1                |
    -2                                           |
    -3 3                        1                |
    -4 1                        1                0
       ----+----+----+----+
   Multiply Stem.Leaf by 10**-2
```

```
            The SAS System                      8

        The UNIVARIATE Procedure
             Variable:  resid
           Normal Probability Plot
 0.045+                                         * ++++
      |                                    * +++++
      |                                  ++++
 0.015+                              ++++
      |                         +*+*+*  *
      |                 *  *++++*
-0.015+                 ++++
      |             ++++
      |        +++++ *
-0.045+    ++++ *
       +----+----+----+----+----+----+----+----+----+----+
           -2        -1         0        +1        +2
```

NOTE: Could use PROC MIXED instead of GLM (for interest only)

```
* note:  could use PROC MIXED instead of GLM for
this;
PROC IMPORT OUT= WORK.biomass
     DATAFILE=
"E:\frst430\lemay\examples\RCB_examples.xls"
     DBMS=EXCEL REPLACE;
     SHEET="'no reps$'";
     GETNAMES=YES;
     MIXED=NO;
     SCANTEXT=YES;
     USEDATE=YES;
     SCANTIME=YES;
RUN;

options ls=70 ps=50 pageno=1 nodate;

data biomass2;
 set biomass;
 lnbiomass=log(yjk);
run;

PROC MIXED data=biomass2;
class site treatment;
model lnbiomass=treatment;
lsmeans treatment/pdiff;
random site;
run;
```

```
               The SAS System                9

           The Mixed Procedure

           Model Information

 Data Set                     WORK.BIOMASS2
 Dependent Variable           lnbiomass
 Covariance Structure         Variance Components
 Estimation Method            REML
 Residual Variance Method     Profile
 Fixed Effects SE Method      Model-Based
 Degrees of Freedom Method    Containment

            Class Level Information

      Class        Levels    Values

      Site              2    1 2
      Treatment         6    A1 A2 A3 A4 A5 A6

             Dimensions
            Covariance Parameters             2
            Columns in X                      7
            Columns in Z                      2
            Subjects                          1
            Max Obs Per Subject              12


            Number of Observations
      Number of Observations Read             12
      Number of Observations Used             12
      Number of Observations Not Used          0

               Iteration History
Iteration  Evaluations  -2 Res Log Like  Criterion
 0              1         2.84456806
 1              1       -13.67079866    0.00000000
            Convergence criteria met.
```

```
         The SAS System                          10

         The Mixed Procedure

         Covariance Parameter
             Estimates

         Cov Parm     Estimate

         Site          0.04582
         Residual     0.001214


            Fit Statistics

-2 Res Log Likelihood           -13.7
AIC (smaller is better)          -9.7
AICC (smaller is better)         -5.7
BIC (smaller is better)         -12.3


           Type 3 Tests of Fixed Effects

                           Num     Den
Effect         DF      DF    F Value    Pr > F

Treatment       5       5     182.16    <.0001

               Least Squares Means

                          Standard
Effect   Treat Estimate  Error    DF t Value Pr>|t|

Treatment  A1  2.3411    0.1533    5  15.27  <.0001
Treatment  A2  2.6287    0.1533    5  17.14  <.0001
Treatment  A3  2.8262    0.1533    5  18.43  <.0001
Treatment  A4  3.0260    0.1533    5  19.73  <.0001
Treatment  A5  3.1458    0.1533    5  20.51  <.0001
Treatment  A6  3.2059    0.1533    5  20.91  <.0001
```

```
          Differences of Least Squares Means


                                   Standard
Effect    Treat Treat  Estimate  Error    DF  t
Value

Treatment  A1     A2   -0.2877   0.03484     5    -8.26
Treatment  A1     A3   -0.4852   0.03484     5   -13.93
Treatment  A1     A4   -0.6850   0.03484     5   -19.66
Treatment  A1     A5   -0.8047   0.03484     5   -23.10
Treatment  A1     A6   -0.8648   0.03484     5   -24.82
Treatment  A2     A3   -0.1975   0.03484     5    -5.67
Treatment  A2     A4   -0.3973   0.03484     5   -11.40
Treatment  A2     A5   -0.5170   0.03484     5   -14.84
Treatment  A2     A6   -0.5772   0.03484     5   -16.57
Treatment  A3     A4   -0.1998   0.03484     5    -5.73
Treatment  A3     A5   -0.3195   0.03484     5    -9.17
Treatment  A3     A6   -0.3797   0.03484     5   -10.90
Treatment  A4     A5   -0.1197   0.03484     5    -3.44
Treatment  A4     A6   -0.1799   0.03484     5    -5.16
Treatment  A5     A6  -0.06012   0.03484     5    -1.73

           Differences of Least Squares Means

Effect    Treatment  Treatment  Pr > |t|
Treatment  A1         A2          0.0004
Treatment  A1         A3          <.0001
Treatment  A1         A4          <.0001
Treatment  A1         A5          <.0001
Treatment  A1         A6          <.0001
Treatment  A2         A3          0.0024
Treatment  A2         A4          <.0001
Treatment  A2         A5          <.0001
Treatment  A2         A6          <.0001
Treatment  A3         A4          0.0023
Treatment  A3         A5          0.0003
Treatment  A3         A6          0.0001
Treatment  A4         A5          0.0185
Treatment  A4         A6          0.0036
Treatment  A5         A6          0.1450
```

Randomized Block Design with other experiments

RCB with Two Fixed Factors

- Within each block. treatments are randomly located to each experimental unit, but each treatment is a combination of two factors

Example: Randomized Block Design (RCB), with three types of food (Factor A: A1 to A3), two species of fish (Factor B) and two labs (blocks). Randomization of treatments (e.g., A1, B2) is restricted to within labs.

Lab 1		Lab 2	
A1B1 = 6	A1B2=5	A3B1=11	A3B2=12
A3B1=10	A2B2=8	A1B1=4	A2B2=9
A2B1=7	A3B2=12	A2B1=8	A1B2=5

Response variable: weight gain of fish (kg)

Experimental unit: one tank of fish; 6 tanks in each lab

Organization of data for analysis using a statistics package:

Site	A Food	B Species	yijk
1	A1	B1	6
1	A1	B2	5
1	A2	B1	8
1	A2	B2	7
1	A3	B1	10
1	A3	B2	12
2	A1	B1	4
2	A1	B2	5
2	A2	B1	9
2	A2	B2	8
2	A3	B1	11
2	A3	B2	12

Main questions of interest—same as for RCB:

- Is there an interaction between factors? If not, is there a difference between means for Factor A? Factor B? Which means are different? What are the estimated means and confidence intervals for these estimates?

- We are not really interested in the blocks – just used to reduce the amount of variation

Models

The model is a mixture between a single factor RCB and a 2-factor CRD; interpretation is more difficult

  - Blocks are usually random not fixed factors
  - Blocks are used to reduce variability within treatments; not of interest on their own

Population: $y_{jkl} = \mu + \tau_{BLK\,j} + \tau_{Ak} + \tau_{Bl} + \tau_{ABkl} + \varepsilon_{jkl}$

y_{jkl} = response variable measured on block *j* and treatment *kl*

j=1 to *J* blocks; *k*=1 to *K* levels for Factor A; *l*=1 to *L* levels for Factor B

Definition of terms follows other designs

Test for Interactions and Main Effects

H_0: No interaction between Factor A and Factor B

H_1: Interaction

OR:

$$H_0: (\phi_{A\text{ X}B}+\sigma^2_\varepsilon)/\sigma^2_\varepsilon = 1$$
$$H_1: (\phi_{A\text{ X }B}+\sigma^2_\varepsilon)/\sigma^2_\varepsilon > 1$$

Where σ^2_ε is the variance of the error terms;

$\sigma^2_{A\text{ X }B}$ is the interaction between Factor A and Factor B fixed-effect treatments

ANOVA: Blocks Random, Factor A and Factor B are Fixed

Source	df	SS	MS	F ??? correct?
BLK.	J-1	SS_{BLK}	$MS_{BLK}= SS_{BLK}/(J\text{-}1)$	$F= MS_{BLK}/MSE$
Factor A	K-1	SS_A	$MS_A= SS_A/(K\text{-}1)$	$F= MS_A/MS_{BXT}$
Factor B	L-1	SS_B	$MS_B= SS_B/(L\text{-}1)$	$F= MS_B/MS_{BXT}$
A X B	(K-1)(L-1)	SS_{AXB}	$MS_{AXB}=SS_{AXB}$ / (K-1)(L-1)	$F= MSAB/MSE$
Error	*(J-1)(KL-1)*	*SSE*	*MSE= SSE/ (J-1)(KL-1)*	
Total	n_T-1	SSy		

Source	df	MS	p-value	E[MS]
BLK.	J-1	MS_{BLK}	Prob F> $F_{(J\text{-}1),(\text{dfE}),\ 1-\alpha}$	$\sigma_\varepsilon^2 + KL\sigma_{BLK}^2$
A	K-1	MS_A	Prob F> $F_{(K\text{-}1),(\text{df}BXT),1-\alpha}$	$\sigma_\varepsilon^2 + \phi_A$
B	L-1	MS_B	Prob F> $F_{(\text{L-}1),(\text{df}BXT),1-\alpha}$	$\sigma_\varepsilon^2 + \phi_B$
AXB	(J-1)(L-1)	MS_{AXB}	Prob F> $F_{dfAXB,dfE,,1-\alpha}$	$\sigma_\varepsilon^2 + \phi_{A\times B}$
Error	*(J-1)(KL-1)*	*MSE*		σ_ε^2
Total	n_T-1			

ϕ is used here to represent fixed effects.

SAS code for example and output: Food and Species Fixed effects; Site is a Random Effect.

```
PROC IMPORT OUT= WORK.blocktwo
    DATAFILE=
"E:\frst430\lemay\examples\RCB_examples.xls"
     DBMS=EXCEL REPLACE;
     SHEET="'2-factors$'";
     GETNAMES=YES;
     MIXED=NO;
     SCANTEXT=YES;
     USEDATE=YES;
     SCANTIME=YES;
RUN;
options ls=70 ps=50 pageno=1 nodate;
data blocktwo2;
 set blocktwo;
lnfishwt=log(yijk);
run;

PROC GLM  data=blocktwo2;
class site food species;
model lnfishwt=site food species food*species;
random site;
lsmeans food/pdiff tdiff;
lsmeans species/pdiff tdiff;
lsmeans food*species/pdiff tdiff;
output out=glmout r=resid p=predict;
run;

proc plot data=glmout;
plot resid*predict='*';
run;
proc univariate data=glmout normal plot;
var resid;
run;
```

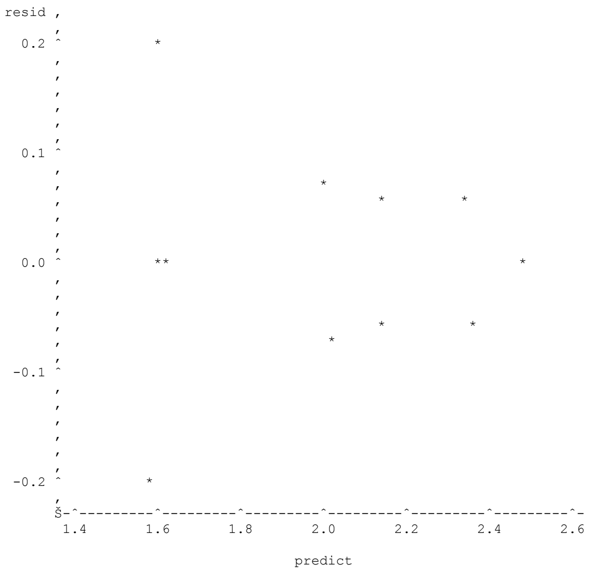
```
                    The SAS System                 1

                  The GLM Procedure

               Class Level Information

              Class          Levels    Values

              Site                2    1 2
              Food                3    A1 A2 A3
              Species             2    B1 B2

           Number of Observations Read           12
           Number of Observations Used           12

                 The SAS System                     2
               The GLM Procedure

Dependent Variable: lnfishwt

                           Sum of
Source         DF     Squares      Mean Square   F
Value

Model           6    1.38600089  0.23100015   11.29
Error           5    0.10230621  0.02046124
Corrected
   Total       11    1.48830710

              Source                   Pr > F

              Model                    0.0088
              Error
              Corrected Total

R-Square    Coeff Var   Root MSE   lnfishwt Mean

0.931260    7.043771    0.143043    2.030770
```

```
Source         DF     Type I SS  Mean Square FValue
Site            1     0.00028852  0.00028852   0.01
Food            2     1.35137097  0.67568548  33.02
Species         1     0.00028852  0.00028852   0.01
Food*Species    2     0.03405288  0.01702644   0.83

               Source                 Pr > F
               Site                   0.9101
               Food                   0.0013
               Species                0.9101
               Food*Species           0.4876


Source      DF     Type III SS  Mean Square F Value
Site         1     0.00028852   0.00028852     0.01
Food         2     1.35137097   0.67568548    33.02
Species      1     0.00028852   0.00028852     0.01
Food*Species 2     0.03405288   0.01702644     0.83

           Source                 Pr > F
           Site                   0.9101
           Food                   0.0013
           Species                0.9101
           Food*Species           0.4876
                  The SAS System                4

               The GLM Procedure

Source     Type III Expected Mean Square
Site          Var(Error) + 6 Var(Site)
Food          Var(Error) + Q(Food,Food*Species)
Species       Var(Error) + Q(Species,Food*Species)
Food*Species  Var(Error) + Q(Food*Species)
```

```
                 The SAS System                     5

                The GLM Procedure
               Least Squares Means

                 lnfishwt        LSMEAN
     Food         LSMEAN         Number
       A1       1.59923241          1
       A2       2.07550445          2
       A3       2.41757342          3

     Least Squares Means for Effect Food
     t for H0: LSMean(i)=LSMean(j) / Pr > |t|

        Dependent Variable: lnfishwt

i/j          1          2          3
 1                -4.70873      -8.09065
                    0.0053        0.0005

 2      4.708733                -3.38191
          0.0053                  0.0196

 3      8.090648   3.381915
          0.0005     0.0196
NOTE: To ensure overall protection level, only
probabilities associated with pre-planned
comparisons should be used.

                         The SAS System             6

                the GLM Procedure
                 Least Squares Means
                      lnfishwt
H0:LSMean1=LSMean2
Species          LSMEAN    t Value    Pr > |t|

 B1          2.02586672     -0.12      0.9101
 B2          2.03567347
```

```
                 The SAS System                  7

               The GLM Procedure
              Least Squares Means

                         lnfishwt      LSMEAN
Food    Species           LSMEAN       Number

 A1      B1          1.58902692           1
 A1      B2          1.60943791           2
 A2      B1          2.13833306           3
 A2      B2          2.01267585           4
 A3      B1          2.35024018           5
 A3      B2          2.48490665           6

Least Squares Means for Effect Food*Species
t for H0: LSMean(i)=LSMean(j) / Pr > |t|

          Dependent Variable: lnfishwt

i/j   1        2        3        4         5        6

1           -0.14269 -3.84015 -2.96169 -5.32158 -6.26302
              0.8921   0.0121   0.0315   0.0031   0.0015

2 0.142692          -3.69746   -2.819 -5.17889  -6.12033
    0.8921            0.0140   0.0372   0.0035    0.0017

3 3.840152 3.697461          0.878459 -1.48142  -2.42287
    0.0121   0.0140            0.4199   0.1986    0.0599

4 2.961693 2.819002 -0.87846          -2.35988  -3.30133
    0.0315   0.0372   0.4199            0.0648    0.0214

5 5.321577 5.178885 1.481425 2.359883           -0.94144
    0.0031   0.0035   0.1986   0.0648             0.3897

6 6.263019 6.120327 2.422866 3.301325 0.941442
    0.0015   0.0017   0.0599   0.0214   0.3897

NOTE: To ensure overall protection level, only
probabilities associated with pre-planned
comparisons should be used.
```

```
                 The SAS System                          8

     Plot of resid*predict.  Symbol used is '*'.
```



```
NOTE: 1 obs hidden.
```

```
                     The SAS System                 9

                The UNIVARIATE Procedure
                    Variable:  resid

                             Moments

N                     12    Sum Weights          12
Mean                   0    Sum Observations      0
Std Deviation   0.096439    Variance     0.00930056
Skewness               0    Kurtosis     1.73130021
Uncorrected SS  0.10230621  Corrected SS 0.10230621
Coeff Variation        .    Std Error
                               Mean      0.02783967
```

(some outputs on basic stats for residuals trimmed off)

```
               Tests for Normality

Test           --Statistic---      -----p Value---

Shapiro-Wilk       W     0.95208    Pr < W   0.6676
Kolmogorov-Smirnov D     0.146392   Pr > D  >0.1500
Cramer-von Mises   W-Sq  0.056429   Pr>W-Sq >0.2500
Anderson-Darling   A-Sq  0.357776   Pr>A-Sq >0.2500


             Quantiles (Definition 5)
             Quantile        Estimate
             100% Max       0.1978292
              99%            0.1978292
              95%            0.1978292
              90%            0.0716691
              75% Q3         0.0581767
              50% Median     0.0000000
              25% Q1        -0.0581767
              10%           -0.0716691
               5%            -0.1978292
               1%            -0.1978292
               0% Min        -0.1978292
```

```
                  Extreme Observations

------Lowest-------        -------Highest------

Value      Obs              Value      Obs

-0.19782918        7         0.00490338       12
-0.07166907        4         0.05255846       11
-0.06379489        3         0.06379489        9
-0.05255846        5         0.07166907       10
-0.00490338        6         0.19782918        1

 Stem Leaf                     #             Boxplot
   2 0                         1                |
   1                                            |
   1                                            |
   0 567                       3             +-----+
   0 00                        2             *--+--*
  -0 00                        2             |     |
  -0 765                       3             +-----+
  -1                                            |
  -1                                            |
  -2 0                         1                |
               ----+----+----+----+
           Multiply Stem.Leaf by 10**-1


               The UNIVARIATE Procedure
                   Variable:  resid

                     Normal Probability Plot
 0.225+                                              +++++
      |                                         *++++
      |                                    +++++
 0.075+                              *++*++*
      |                         +*+*++
      |                    ++*+*
-0.075+              *++*++*
      |          +++++
      |     ++++*
-0.225++++++
       +----+----+----+----+----+----+----+----+----+----+
           -2        -1         0        +1        +2
```

RCB with One fixed, one random factor

- Within each block treatments are randomly located to each experimental unit, but each treatment is a combination of two factors
- For one factor, we are interested in comparing treatment means
- For the other factor, we are interested in obtaining an estimate of the variance of the response variable that is due to that factor

Example: Randomized Block Design (RCB), with three types of fertilizer (Factor A: A1 to A3), two genetic families of pine trees (Factor B) and two sites (blocks).

- Randomization of treatments (e.g., A1, B2) is restricted to within sites.
- Blocks are random; factor B is random (random selection of possible families)

- Interpretation will differ from RCB with two factors; F-tests will vary also, as Expected Mean Squares will be different
- If there is no interaction among the two factors, we can interpret the factors separately
- For Factor A: use multiple comparisons to compare factor level means
- For Factor B: obtain an estimate of the variance due to this factor.
- NOTE: we could use least squares analysis of variance for this analysis. HOWEVER: using MIXED models with Maximum Likelihood is considered a better approach for mixed-effects (one random, one fixed effects factor)

Incomplete Block Design

- Like RCB, BUT there are not enough experimental units in each block to have every treatment in each block – incomplete
- For example:

We have 2 sites. There are 4 experimental units in each site. However, we have 5 treatments! There are not enough experimental units in site 1 to have all 5 treatments, nor is there enough experimental units in site 2 to have all 5. (REF: Chapter 28 of textbook)

RCB with replicates in each block

- Within each block there are several replicates of each treatment
- Sometimes called "Generalized RCB"

Example: Randomized Block Design (RCB), with Factor A (three types of food: A1 to A3), and two labs (blocks).

Randomization of Factor A is restricted to within labs.

Lab 1		Lab 2	
A1 = 6	A1=5	A3=11	A3=12
A3=10	A2=8	A1=4	A2=9
A2=7	A3=12	A2=8	A1=5

Response variable: weight gain of fish (kg)

Experimental unit: one tank of fish; 6 tanks in each lab

Organization of data for analysis using a statistics package:

Site	Treatment	Replicate	yijk
1	A1	1	6
1	A1	2	5
1	A2	1	8
1	A2	2	7
1	A3	1	10
1	A3	2	12
2	A1	1	4
2	A1	2	5
2	A2	1	9
2	A2	2	8
2	A3	1	11
2	A3	2	12

Main questions of interest—same as for RCB:

- Are the treatment means different? Which means are different? What are the estimated means and confidence intervals for these estimates?

Models

Population: $y_{ijk} = \mu + \tau_{BLK\ j} + \tau_{TR\ k} + \tau_{BLK \times TR\ jk} + \varepsilon_{ijk}$

y_{ijk} = response variable measured on experimental unit *I* in block *j* and treatment *k*

j=1 to *J* blocks; *k*=1 to *K* treatments; *i*=1 to *n* replicates

μ = the grand or overall mean regardless of treatment or block

$\tau_{BLK\ j}$ = the *block effect* for *j*

τ_{TRk} = the *treatment effect* for block *k*

$\tau_{BLK \times TR\ jk}$ = the *interaction effect* between block *j* and treatment *k*

ε_{ijk} = is error term, specific to observation *i*

For the experiment:

$$y_{ijk} = \bar{y}_{\bullet\bullet\bullet} + \hat{\tau}_{BLK\,j} + \hat{\tau}_{TR\,k} + \hat{\tau}_{BLK\times TR\,jk} + e_{ijk}$$

$\bar{y}_{\bullet\bullet\bullet}$ = the grand or overall mean of all measures from the experiment regardless of treatment or block; under the assumptions for the error terms, this will be an unbiased estimate of μ

$\bar{y}_{\bullet jk}$ = the mean of all measures from the experiment for a particular block *j* and experiment *k*

$\bar{y}_{\bullet j \bullet}$ = the mean of all measures from the experiment for a particular block *j* (includes all data for all levels of the treatments)

$\bar{y}_{\bullet\bullet k}$ = the mean of all measures from the experiment for a particular level *k* of the Factor A (includes all data for all blocks)

$\hat{\tau}_{BLK\,j}, \hat{\tau}_{TR\,k}, \hat{\tau}_{BLK\times TR\,jk}$ = under the error term assumptions, will be unbiased estimates of corresponding treatment, block, and block by treatment for the population

e_{ijk} = the difference between a particular measure for an experimental unit *i*, and the mean for the block *j* and treatment *k* that was applied to it

$$e_{ijk} = y_{ijk} - \bar{y}_{\bullet jk}$$

n_{jk} = the number of experimental units measured in the block *j* and treatment *k*

n_T = the number of experimental units measured over all blocks and treatments = $\sum_{k-1}^{K}\sum_{j=1}^{J} n_{jk}$

Sums of Squares:

$$SSy = SS_{BLK} + SS_{TR} + SS_{TR\times BLK} + SSE$$

SSy: The sum of squared differences between the observations and the grand mean:

$$SSy = \sum_{k=1}^{K}\sum_{j=1}^{J}\sum_{i=1}^{n_{jk}} \left(y_{ijk} - \bar{y}_{\bullet\bullet\bullet}\right)^2 \quad df = n_T - 1$$

SS

SS_{BLK}: Sum of squared differences between the block means and the grand mean, weighted by the number of experimental units for each block:

$$SS_{BLK} = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\left(\bar{y}_{\bullet j\bullet} - \bar{y}_{\bullet\bullet\bullet}\right)^2 \quad df = J - 1$$

SS_{TR}: Sum of squared differences between the level means for factor A and the grand mean, weighted by the number of experimental units for each treatment:

$$SS_{TR} = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\left(\bar{y}_{\bullet\bullet k} - \bar{y}_{\bullet\bullet\bullet}\right)^2 \quad df = K - 1$$

$SS_{BLK \text{ X } TR}$: Sum of squared differences between means for block *j* and treatment *k* and the grand mean, minus the block and treatment level differences, all weighted by the number of experimental units for each block and treatment:

$$SS_{BLK \times TR} = \sum_{k=1}^{K} \sum_{j=1}^{J} n_{jk} ((\bar{y}_{\bullet jk} - \bar{y}_{\bullet\bullet\bullet}) - (\bar{y}_{\bullet\bullet k} - \bar{y}_{\bullet\bullet\bullet}) - (\bar{y}_{\bullet j \bullet} - \bar{y}_{\bullet\bullet\bullet}))^2$$

Since some of the terms cancel out we obtain:

$$SS_{BLK \times TR} = \sum_{k=1}^{K} \sum_{j=1}^{J} n_{jk} (\bar{y}_{\bullet jk} - \bar{y}_{\bullet\bullet k} - \bar{y}_{\bullet j \bullet} + \bar{y}_{\bullet\bullet\bullet})^2$$

SSE: Sum of squared differences between the observed values for each experimental unit and the treatment means:

$$SSE = \sum_{k=1}^{K} \sum_{j=1}^{J} \sum_{i=1}^{n_{jk}} \left(y_{ijk} - \bar{y}_{\bullet jk}\right)^2 \qquad df = n_T - JK$$

Assumptions regarding the error term

- Must meet assumptions to obtain unbiased estimates of population means, and an unbiased estimate of the variance of the error term as with other designs

Process:

- do your analysis with the measured response variable
- Check the residual plot and normal plot to see if assumptions are met
- if assumptions of the error term are not met, transform the y-variable
- do the analysis again and check the assumptions; if not me, try another transformation
- may have to switch to another method: generalized linear models, etc.

Test for Interactions and Main Effects

Although an interaction between treatments and blocks would result in a difficult interpretation of results, this can be tested first.

H_0: No interaction
H_1: Interaction
OR:

$$H_0: (\sigma^2_{B \text{ X } T}+\sigma^2_{\varepsilon})/\sigma^2_{\varepsilon} = 1$$
$$H_1: (\sigma^2_{B \text{ X } T}+\sigma^2_{\varepsilon})/\sigma^2_{\varepsilon} > 1$$

Where σ^2_{ε} is the variance of the error terms;

σ^2_{BXT} is the interaction between blocks and fixed treatments; since blocks are random, the interaction between blocks and treatments is also random.

Using an analysis of variance table: Blocks Random,

Treatments Fixed

Source	df	SS	MS	F
BLK.	J-1	SS_{BLK}	$MS_{BLK}= SS_{BLK}/(J\text{-}1)$	$F= MS_{BLK}/MSE$
TR.	K-1	SS_{TR}	$MS_{TR}= SS_{TR}/(K\text{-}1)$	$F= MS_{TR}/MS_{BXT}$
BLK X TR	$(J$-1$)(K$-1$)$	SS_{BXT}	$MS_{BXT}= SS_{BXT}\,/\,(J\text{-}1)(K\text{-}1)$	$F= MSBT/MSE$
Error	n_T-JK	SSE	$MSE= SSE/(n_T\text{-}JK)$	
Total	n_T-1	SSy		

Source	df	MS	p-value	E[MS]
BLK.	J-1	MS_{BLK}	Prob F> $F_{(J\text{-}1),(\text{dfE}),\ 1\text{-}\ \alpha}$	$\sigma_{\varepsilon}^{2} + Kn\sigma_{BLK}^{2}$
TR.	K-1	MS_{TR}	Prob F> $F_{(K\text{-}1),(\text{df}BXT),1\text{-}\ \alpha}$	$\sigma_{\varepsilon}^{2} + n\sigma^{2}_{B\times T} + \phi_{TR}$
BLK X TR	$(J$-1$)(K$-1$)$	MS_{BXT}	Prob F> $F_{dfBXT,dfE,,1\text{-}\ \alpha}$	$\sigma_{\varepsilon}^{2} + n\sigma^{2}_{B\times T}$
Error	n_T-JK	MSE		σ_{ε}^{2}
Total	n_T-1			

ϕ is used here to represent fixed effects.
Assuming all n are equal (same number of replicates in each block and treatment combination)

For the interactions:

$$F = \frac{SS_{B\times T}/(J-1)(K-1)}{SSE/(n_T - JK)} = \frac{MS_{B\times T}}{MSE}$$

- Under H_0, this follows $F_{\text{df1,df2, 1-}\alpha}$ where df1 is from the numerator (J-1)(K-1), and df2 is from the denominator (n_T-JK)
- If the F calculated is greater than the tabular F, or if the p-value for F calculated is less than α, reject H_0.
    - The means of Factor A are influenced by the levels of the blocks; the design should have been a completely randomized design for ease of interpretation
    - Graph the means of all treatments by block and try to interpret results

If there are no interactions (hopefully the case) we can look at the impact of the treatments

Factor A:

$$H_0\text{: } \mu_1 = \mu_2 = \ldots = \mu_J$$

$$OR:$$

$$H_0\text{: } (\phi_A + n\sigma^2_{B \text{ X } T} + \sigma^2_{\varepsilon})\ /(n\sigma^2_{B \text{ X } T} + \sigma^2_{\varepsilon}\ ) = 1$$
$$H_1\text{: } (\phi_A + n\ \sigma^2_{B \text{ X } T} + \sigma^2_{\varepsilon})\ /(n\sigma^2_{B \text{ X } T} + \sigma^2_{\ \varepsilon}\ ) > 1$$

Where σ^2_{ε} is the variance of the error terms; $\sigma^2_{\ B \text{ X } T}$ is the variance for the interaction between blocks and treatments; ϕ_A is fixed effect for Factor A.

From the ANOVA table:

$$F = \frac{SS_{TR}/(K-1)}{SS_{B\times T}/(J-1)(K-1)} = \frac{MS_{TR}}{MS_{B\times T}}$$

- Under H_0, this follows $F_{\text{df1,df2, 1-}\alpha}$ where df1 is from the numerator (K-1) and df2 is from the denominator (J-1)(K-1)
- If the F calculated is greater than the tabular F, or if the p-value for F calculated is less than α, reject H_0.
    - The true means of the treatment in the population are likely not all the same
    - Graph the means of treatment levels
    - Conduct multiple comparisons between means for the K levels of the treatment

SAS code and Results for example:

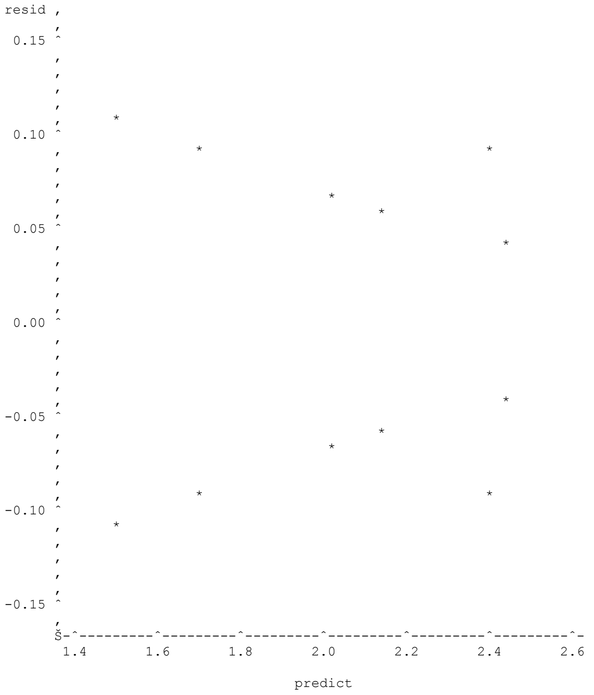
```
PROC IMPORT OUT= WORK.fishweight
DATAFILE=
     "E:\frst430\lemay\examples\RCB_examples.xls"
     DBMS=EXCEL REPLACE;
     SHEET="'reps$'";   GETNAMES=YES;
     MIXED=NO;    SCANTEXT=YES;
     USEDATE=YES;  SCANTIME=YES;
RUN;
options ls=70 ps=50 pageno=1 nodate;
data fishweight2;
 set fishweight;
lnfishwt=log(yijk);
run;

PROC GLM  data=fishweight2;
class site treatment;
model lnfishwt=site treatment site*treatment;
random site site*treatment;
test h=treatment e=site*treatment;
lsmeans treatment/e=site*treatment pdiff tdiff;
output out=glmout r=resid p=predict;
run;
proc plot data=glmout;
plot resid*predict='*';
run;
proc univariate data=glmout normal plot;
var resid;
run;

* note:  could use PROC MIXED instead of GLM for
this – for interest only;
PROC MIXED data=fishweight2;
class site treatment;
model lnfishwt=treatment;
lsmeans treatment/pdiff;
random site site*treatment;
run;
```

```
                 The SAS System                  1
              The GLM Procedure

            Class Level Information

          Class          Levels    Values

          Site                2    1 2
          Treatment           3    A1 A2 A3


        Number of Observations Read          12
        Number of Observations Used          12
                 The SAS System                  2
                  The GLM Procedure

Dependent Variable: lnfishwt

                  Sum of
Source     DF    Squares     Mean Square   F Value

Model       5   1.41053220   0.28210644    21.76

Error       6   0.07777490   0.01296248

Corrected
   Total   11   1.48830710
            Source                 Pr > F

            Model                  0.0009

            Error

                   Corrected Total

R-Square   Coeff Var   Root MSE    lnfishwt Mean
0.947743   5.606391    0.113853      2.030770
```

```
Source        DF   Type I SS  Mean Square   F Value

Site           1   0.00028852 0.00028852      0.02
Treatment      2   1.35137097 0.67568548     52.13
Site*Treatment 2   0.05887271 0.02943636      2.27

                Source                 Pr > F

                Site                   0.8863
                Treatment              0.0002
                Site*Treatment         0.1844


Source        DF  Type III SS  Mean Square  F Value

Site           1  0.00028852   0.00028852    0.02
Treatment      2  1.35137097   0.67568548   52.13
Site*Treatment 2  0.05887271   0.02943636    2.27

                Source             Pr > F

                Site               0.8863
                Treatment          0.0002
                Site*Treatment     0.1844

              The SAS System                     4

              The GLM Procedure

Source     Type III Expected Mean Square

Site       Var(Error) + 2 Var(Site*Treatment)
           + 6 Var(Site)

Treatment  Var(Error) + 2 Var(Site*Treatment)
           +Q(Treatment)

Site*Treatment  Var(Error) + 2 Var(Site*Treatment)
```

```
                 The SAS System             5

              The GLM Procedure
             Least Squares Means
Standard Errors and Probabilities Calculated Using
the Type III MS for Site*Treatment as an Error Term

              lnfishwt      LSMEANS

Treatment           LSMEAN      Number

A1             1.59923241           1
A2             2.07550445           2
A3             2.41757342           3

    Least Squares Means for Effect Treatment
  t for H0: LSMean(i)=LSMean(j) / Pr > |t|

         Dependent Variable: lnfishwt

 i/j         1        2        3

  1                -3.9258  -6.74539
                    0.0592   0.0213

  2      3.925799           -2.81959
         0.0592              0.1061

  3      6.745393   2.819594
         0.0213     0.1061


NOTE: To ensure overall protection level, only
probabilities associated with pre-planned
comparisons should be used.
```

```
                 The SAS System             6
               The GLM Procedure

         Dependent Variable: lnfishwt
       Tests of Hypotheses Using the Type III
       MS for Site*Treatment as an Error Term

Source      DF    Type III SS  Mean Square  F Value
Treatment    2    1.35137097   0.67568548     22.95

           Source                 Pr > F
           Treatment              0.0417

                 The SAS System             7
     Plot of resid*predict.  Symbol used is '*'.
```



```
                 The SAS System                 8

               The UNIVARIATE Procedure
                 Variable:  resid

                      Moments

N                     12  Sum Weights           12
Mean                   0  Sum Observations       0
Std Deviation 0.08408594  Variance      0.00707045
Skewness               0  Kurtosis      -1.9620284
Uncorrected
         SS   0.0777749   Corrected SS   0.0777749
Coeff Variation       .   Std Error Mean 0.02427352


              Basic Statistical Measures

     Location               Variability

Mean                0  Std Deviation     0.08409
Median   2.22E-16      Variance          0.00707
Mode            .      Range             0.22314
Interquartile Range      0.15793


          Tests for Location: Mu0=0

Test           -Statistic-    -----p Value------

Student's t    t         0    Pr > |t|    1.0000
Sign           M         0    Pr >= |M|   1.0000
Signed Rank    S         0    Pr >= |S|   1.0000
```

```
Tests for Normality
Test                  --Statistic---    ---p Value----

Shapiro-Wilk       W     0.871142  Pr<W      0.0676
Kolmogorov-Smirnov D      0.19756  Pr>D     >0.1500
Cramer-von Mises   W-Sq  0.1182    Pr>W-Sq   0.0563
Anderson-Darling   A-Sq  0.672686  Pr>A-Sq   0.0611


            Quantiles (Definition 5)

            Quantile        Estimate
            100% Max       0.1115718
            99%            0.1115718

                 The SAS System                 9

              The UNIVARIATE Procedure
              Variable:  resid

              Quantiles (Definition 5)

              Quantile        Estimate

              95%            0.1115718
              90%            0.0911608
              75% Q3         0.0789632
              50% Median     0.0000000
              25% Q1        -0.0789632
              10%           -0.0911608
               5%            -0.1115718
               1%            -0.1115718
               0% Min        -0.1115718
```

```
             Extreme Observations

    -------Lowest------         ------Highest------

    Value      Obs              Value      Obs

    -0.1115718        7          0.0588915        9
    -0.0911608        2          0.0667657        3
    -0.0911608        5          0.0911608        1
    -0.0667657        4          0.0911608        6
    -0.0588915       10          0.1115718        8

 Stem Leaf                     #             Boxplot
  1 1                          1                |
  0 6799                       4             +-----+
  0 4                          1             *--+--*
 -0 4                          1             |     |
 -0 9976                       4             +-----+
 -1 1                          1                |
           ----+----+----+----+
      Multiply Stem.Leaf by 10**-1


               The SAS System                 10

           The UNIVARIATE Procedure
              Variable:  resid

                  Normal Probability Plot
  0.125+                                    ++++*+
      |                            * *++*++*
      |                         +*++++
      |                    ++++*
      |              *++*++* *
 -0.125+       +*++++
       +----+----+----+----+----+----+----+----+----+----+
          -2        -1         0        +1        +2
```

OPTIONAL – FOR INTEREST ONLY

```
             The SAS System                      11

           The Mixed Procedure

          Model Information

Data Set                     WORK.FISHWEIGHT2
Dependent Variable           lnfishwt
Covariance Structure         Variance Components
Estimation Method            REML
Residual Variance Method     Profile
Fixed Effects SE Method      Model-Based
Degrees of Freedom Method    Containment


             Class Level Information

        Class        Levels    Values

        Site              2    1 2
        Treatment         3    A1 A2 A3


                Dimensions

            Covariance Parameters             3
            Columns in X                      4
            Columns in Z                      8
            Subjects                          1
            Max Obs Per Subject              12

            Number of Observations

        Number of Observations Read          12
        Number of Observations Used          12
        Number of Observations Not Used       0
```

```
             Iteration History

Iteration    Evaluations    -2Res LogLike Criterion

   0              1        -7.96941039
   1              3        -8.14751521
0.00045738
   2              2        -8.15260197
0.00000806
   3              1        -8.15270255
0.00000000

                  The SAS System                 12

                The Mixed Procedure

                Convergence criteria met.


               Covariance Parameter
                     Estimates
           Cov Parm           Estimate

           Site                      0
           Site*Treatment     0.003378
           Residual            0.01296


              Fit Statistics

         -2 Res Log Likelihood           -8.2
         AIC (smaller is better)         -4.2
         AICC (smaller is better)        -2.2
         BIC (smaller is better)         -6.8
```

```
          Type 3 Tests of Fixed Effects

              Num     Den
Effect         DF      DF    F Value    Pr > F

Treatment       2       2      34.27    0.0284


               Least Squares Means

                     Standard
Treatment   Estimate  Error    DF  t Value Pr > |t|

Treatment A1  1.5992   0.07021   2    22.78   0.0019
Treatment A2  2.0755   0.07021   2  29.56    0.0011
Treatment A3  2.4176   0.07021   2  34.43    0.0008


        Differences of Least Squares Means

                             Standard
Effect   Treatments  Estimate  Error    DF  t Value

Treatment  A1  A2   -0.4763   0.09929    2    -4.80
Treatment  A1  A3   -0.8183   0.09929    2    -8.24
Treatment  A2  A3   -0.3421   0.09929    2    -3.45

          Differences of Least Squares Means

Effect     Treatments            Pr > |t|

Treatment  A1         A2          0.0408
Treatment  A1         A3          0.0144
Treatment  A2         A3          0.0749
```

Latin Square (LS) With One Fixed-Effects Factor

REF: Neter et al., Chapter 26 (White-newest edition) or Chapter 28 (Blue – older edition in the library)

Introduction and Example

- In RCB, treatments are assigned randomly, but only within blocks of treatments; blocking is in “one” direction
- The Latin Square Design extends grouping of experimental units to two variables. For example, two sites may represent north versus south facing stands, and there might be a moisture gradient within sites
- Treatments are randomly assigned in two directions; treatment appears once in every row and every column

Example:

Response variable: average 5-year height growth in each experimental unit (plot) in cm

Treatments: four different species, A1 to A4

Nutrient Gradient from East to West; *Moisture Gradient* from North to South

					Means
	A2=40	A1=35	A4=53	A3=47	43.75
	A4=48	A3=46	A2=39	A1=34	41.75
	A1=27	A4=53	A3=45	A2=41	41.50
	A3=44	A2=39	A1=31	A4=52	41.50
Means	39.75	43.25	42.00	43.50	42.125

Treatment Means:

A1: 31.75 A2: 39.75 A3: 45.50 A4: 51.50

16 experimental units

Comparison of Degrees of Freedom for CRD, RCB, LS for 16 experimental units, 4 treatments, J=K=L=4 blocks (rows/columns)

Source	*CRD*
Treatment	3
Error	**12**
Total	15

Source	*RCB*
Treatment	3
Block	3
Error	**9**
Total	15

Source	*LS*
Treatment	3
Row	3
Column	3
Error	**6**
Total	15

- Lose degrees of freedom for the error with blocking, and even more with latin square
- Therefore, only block (one or two directions), if this will reduce the variance of the error term
- Analysis is similar to a 3-factor experiment, for the Main Effects, only – no interactions
- Rows and Columns are considered “nuisance variables” to reduce variation in the response variable – not really of interest.

Notation, Assumptions, and Transformations

Models

Population: $y_{jkl} = \mu + \tau_{Ak} + \tau_{Rj} + \tau_{Cl} + \varepsilon_{jkl}$

y_{jkl} = response variable measured on Row j , Column l and treatment k

k=1 to K treatments; j=1 to J rows; l=1 to L columns; J=K=L

μ = the grand or overall mean regardless of treatment or blocking

τ_{Ak} = the *treatment effect* for k

τ_{Rj} = the *row effect* for row j

τ_{Cl} = the *column effect* for column l

ε_{jkl} = is defined as:

$$\varepsilon_{jkl} = y_{jkl} - (\mu + \tau_{Ak} + \tau_{Rj} + \tau_{Cl})$$

Same as for a 3-factor crossed experiment, BUT all interactions are assumed to be zero.

For the experiment:

$$y_{jkl} = \bar{y}_{\bullet\bullet\bullet} + \hat{\tau}_{Ak} + \hat{\tau}_{Rj} + \hat{\tau}_{Cl} + e_{jkl}$$

$\bar{y}_{\bullet\bullet\bullet}$ = the grand or overall mean of all measures from the experiment regardless of treatment; under the assumptions for the error terms, this will be an unbiased estimate of μ

$\bar{y}_{\bullet k\bullet}$ = the mean of all measures for a particular treatment *k*

$\bar{y}_{j\bullet\bullet}$ = the mean of all measures from the experiment for a particular row *j*

$\bar{y}_{\bullet\bullet l}$ = the mean of all measures from the experiment for a particular column *l*

$\hat{\tau}_{Ak}, \hat{\tau}_{Rj}, \hat{\tau}_{Cl}$ = under the error term assumptions, will be unbiased estimates of corresponding treatment effect or row and column effects for the population

e_{jkl} = is defined as:

$$\begin{aligned} e_{jkl} &= (y_{jkl} - \bar{y}_{\bullet\bullet\bullet}) - (\bar{y}_{j\bullet\bullet} - \bar{y}_{\bullet\bullet\bullet}) - (\bar{y}_{\bullet k\bullet} - \bar{y}_{\bullet\bullet\bullet}) \\ &\quad - (\bar{y}_{\bullet\bullet l} - \bar{y}_{\bullet\bullet\bullet}) \\ &= y_{jkl} - \bar{y}_{j\bullet\bullet} - \bar{y}_{\bullet k\bullet} - \bar{y}_{\bullet\bullet l} + \bar{y}_{\bullet\bullet\bullet} \end{aligned}$$

$n_T = K^2 = JL$

Partition the total variation in y:

$$SS_y = SS_T = \sum_{all\,units} (y_{jkl} - \bar{y}_{\bullet\bullet\bullet})^2 = J\sum_{k=1}^{K} (\bar{y}_{\bullet k\bullet} - \bar{y}_{\bullet\bullet\bullet})^2$$

$$+ K\sum_{j=1}^{J} (\bar{y}_{j\bullet\bullet} - \bar{y}_{\bullet\bullet\bullet})^2 + J\sum_{l=1}^{L} (\bar{y}_{\bullet\bullet l} - \bar{y}_{\bullet\bullet\bullet})^2$$

$$+ \sum_{all\ units} (y_{jkl} - \bar{y}_{j\bullet\bullet} - \bar{y}_{\bullet k\bullet} - \bar{y}_{\bullet\bullet l} + 2\bar{y}_{\bullet\bullet\bullet})^2$$

$$SS_y = \quad SS_{TR} \quad + \quad SS_R \quad + \quad SS_C \quad + \quad SSE$$

Analysis of Variance Table: Assuming that <u>all are fixed-effects.</u>

Source	*Df*	*SS*	*MS*	*F*
Treatment	*K*-1	SS_{TR}	MS_{TR}	MS_{TR}/MSE
Row	*J*-1	SS_R	MS_R	MS_R/MSE
Column	*L*-1	SS_C	MS_C	MS_C/MSE
Error	(*K*-1)(*J*-2)	*SSE*	*MSE*	
Total	*JK*-1	SS_y		

NOTE: May be more reasonable to consider Rows and Columns as random-effects, and Treatment as fixed-effects. For Latin Square, we assume that all interactions are 0. Therefore, the F-tests would be the same as for all fixed-effects.

Hypotheses and Tests:

Treatment: H0: $\mu_{\bullet 1 \bullet} = \mu_{\bullet 2 \bullet} = \mu_{\bullet 3 \bullet} \cdots = \mu_{\bullet K \bullet}$

(all treatment means are the same and all treatment effects equal zero)

H1: treatment means are not all equal

Test: $F_{K\text{-}1,\ \mathrm{df(error)}} = MS_{TR}/MSE$

Can test Row effects and Column effects, but these are really not of interest.

If there are differences among treatment means:

- you might wish to test which means differ using t-tests for pairs of treatments (must divide α by the no. of pairs) or a multiple comparison test (like Scheffé's test).
- Use the MSE from the ANOVA table for each of these.

Confidence intervals for treatment means (also use the MSE from the ANOVA):

$$\bar{y}_{\bullet k \bullet} \pm t_{1-\alpha/2, df(error)} \sqrt{\frac{MSE}{J}}$$

Example, SAS code, and Results

Data Organization for Analysis within SAS:

Row	Column	Treatment	Response
1	1	2	40
1	2	1	35
1	3	4	53
1	4	3	47
2	1	4	48
2	2	3	46
2	3	2	39
2	4	1	34
3	1	1	27
3	2	4	53
3	3	3	45
3	4	2	41
4	1	3	44
4	2	2	39
4	3	1	31
4	4	4	52

SAS Code:

```
PROC IMPORT OUT= WORK.htgrowth
     DATAFILE=
"E:\frst430\lemay\examples\latin_square.xls"
     DBMS=EXCEL REPLACE;   SHEET="'data$'";
     GETNAMES=YES;       MIXED=NO;
     SCANTEXT=YES;       USEDATE=YES;
     SCANTIME=YES;
RUN;
options ls=70 ps=50 pageno=1 nodate;

* can get simple means by sorting and then using
proc means;
proc sort data=htgrowth;
by row;
run;

proc means data=htgrowth mean;
var response;
by row;
run;

proc sort data=htgrowth;
by column;
run;

proc means data=htgrowth mean;
var response;
by column;
run;

proc sort data=htgrowth;
by treatment;
run;

proc means data=htgrowth mean;
var response;
by treatment;
run;
```

```
* note using ht growth results in some unequal
variance.  Using logarithm of height
growth to fix this.  Need to calculate it;

data htgrowth2;
 set htgrowth;
lnhtgrowth=log(response);
run;

PROC GLM  data=htgrowth2;
class row column treatment;
model lnhtgrowth=row column treatment;
random row column;
lsmeans treatment/pdiff tdiff;
output out=glmout r=resid p=predict;
run;

proc plot data=glmout;
plot resid*predict='*';
run;

proc univariate data=glmout normal plot;
var resid;
run;
```

```
                The SAS System               13

-------------------- Row=1 --------------------
               The MEANS Procedure
           Analysis Variable : Response Response

                        Mean
                     ------------
                      43.7500000
                    ------------

-------------------- Row=2 --------------------

        Analysis Variable : Response Response

                        Mean
                    ------------
                     41.7500000
                    ------------

------------------- Row=3 ------------------------

         Analysis Variable : Response Response

                       Mean
                   ------------
                    41.5000000
                   ------------

-------------------- Row=4 ------------------------

        Analysis Variable : Response Response

                       Mean
                   ------------
                     41.5000000
                  ------------
                The SAS System                   14
```

```
---------------------- Column=1 -------------------

                   The MEANS Procedure

               Analysis Variable : Response Response

                          Mean
                       ------------
                        39.7500000
                      ------------

--------------------- Column=2 -------------------

               Analysis Variable : Response Response

                           Mean
                       ------------
                        43.2500000
                      ------------

-------------------- Column=3 ---------------------

               Analysis Variable : Response Response

                          Mean
                      ------------
                       42.0000000
                      ------------

---------------------- Column=4 -------------------

           Analysis Variable : Response Response

                         Mean
                     ------------
                      43.5000000
                     ------------
```

```
                 The SAS System                15
------------------- Treatment=1 -------------------

              The MEANS Procedure

           Analysis Variable : Response Response

                     Mean
                 ------------
                  31.7500000
                 ------------

------------------ Treatment=2 -------------------

          Analysis Variable : Response Response

                     Mean
                  ------------
                   39.7500000
                  ------------

------------------ Treatment=3 --------------------

          Analysis Variable : Response Response

                     Mean
                  ------------
                   45.5000000
                 ------------

------------------- Treatment=4 -------------------

         Analysis Variable : Response Response

                      Mean
                  ------------
                   51.5000000
                  ------------
              The SAS System                    1
```

```
               The SAS System                   4
             The GLM Procedure

            Class Level Information

            Class          Levels    Values

            Row                 4    1 2 3 4
            Column              4    1 2 3 4
            Treatment           4    1 2 3 4


        Number of Observations Read          16
        Number of Observations Used          16

             The SAS System                     5
             The GLM Procedure
```

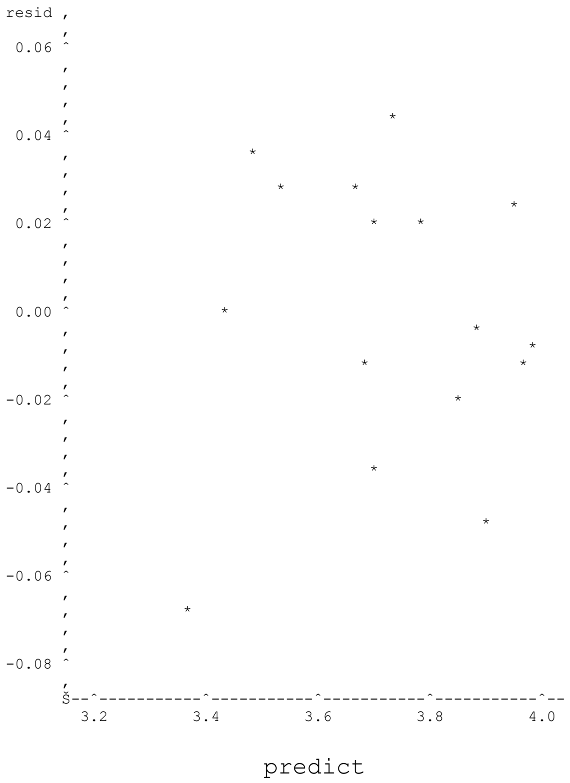
Dependent Variable: lnhtgrowth **NOTE: logarithm of height growth was used.**

```
                    Sum of
Source     DF      Squares    Mean Square   F Value

Model       9   0.56035540     0.06226171     24.63
Error       6   0.01516796     0.00252799
Corrected
   Total   15   0.57552336

              Source                 Pr > F

               Model                  0.0005
               Error
               Corrected Total

R-Square   Coeff Var    Root MSE  lnhtgrowth Mean

0.973645   1.350370     0.050279       3.723361
```

```
Source     DF    Type I SS    Mean Square   F Value

Row        3     0.01111319   0.00370440      1.47
Column     3     0.02547050   0.00849017      3.36
Treatment  3     0.52377171   0.17459057     69.06

           Source                 Pr > F

           Row                    0.3152
           Column                 0.0964
           Treatment              <.0001


Source    DF    Type III SS  Mean Square   F Value

Row        3     0.01111319  0.00370440      1.47
Column     3     0.02547050  0.00849017      3.36
Treatment  3     0.52377171  0.17459057     69.06


       Source                 Pr > F
       Row                    0.3152
       Column                 0.0964
       Treatment              <.0001
                    The SAS System               7

                  The GLM Procedure

Source               Type III Expected Mean Square

Row                  Var(Error) + 4 Var(Row)
Column               Var(Error) + 4 Var(Column)
Treatment            Var(Error) + Q(Treatment)
```

```
               The SAS System              8

              The GLM Procedure
              Least Squares Means

              lnhtgrowth    LSMEAN
Treatment       LSMEAN      Number

  1           3.45288316       1
  2           3.68239370       2
  3           3.81741028       3
  4           3.94075714       4


         Least Squares Means for Effect Treatment
        t for H0: LSMean(i)=LSMean(j) / Pr > |t|

         Dependent Variable: lnhtgrowth

i/j        1          2          3            4

 1                 -6.4555    -10.2531     -13.7225
                    0.0007      <.0001       <.0001

 2      6.455497              -3.79764     -7.26705
          0.0007                0.0090       0.0003

 3      10.25314  3.797643                 -3.46941
          <.0001    0.0090                   0.0133

 4      13.72255  7.267049    3.469406
          <.0001    0.0003      0.0133


NOTE: To ensure overall protection level, only
probabilities associated with pre-planned
comparisons should be used.
```

```
          The SAS System                   9

Plot of resid*predict.  Symbol used is '*'.
```



```
                    The SAS System                    10
                The UNIVARIATE Procedure
                   Variable:  resid

Moments

N                     16    Sum Weights             16
Mean                   0    Sum Observations         0
Std Deviation  0.03179933 Variance           0.0010112
Skewness       -0.5578556 Kurtosis          -0.3222064
Uncorrected SS 0.01516796 Corrected SS      0.01516796
Coeff Variation         . Std Error Mean    0.00794983
```

NOTE: some outputs on basic statistics for residuals was removed.

```
               Tests for Normality

Test               --Statistic---    -----p Value---

Shapiro-Wilk       W    0.950408  Pr < W     0.4962
Kolmogorov-Smirnov D    0.180548  Pr > D    >0.1500
Cramer-von Mises   W-Sq 0.053763  Pr > W-Sq >0.2500
Anderson-Darling   A-Sq  0.33663  Pr > A-Sq >0.2500

                Quantiles (Definition 5)

              Quantile         Estimate
              100% Max       0.04522920
               99%            0.04522920
               95%            0.04522920
               90%            0.03742738
               75% Q3         0.02610986
               50% Median    -0.00217353
               25% Q1        -0.01606276
               10%           -0.04703827
                5%            -0.06694173
                1%            -0.06694173
                0% Min        -0.06694173
               Extreme Observations

-------Lowest------         ------Highest------

Value           Obs          Value          Obs

-0.0669417        1          0.0252053       14
-0.0470383       12          0.0270144        5
-0.0348162        6          0.0285595        2
-0.0189486       10          0.0374274        4
-0.0131769        7          0.0452292        9


Stem Leaf                   #             Boxplot
 4 5                        1                |
 2 115797                   6             +-----+
 0 1                        1             |  +  |
-0 93195                    5             *-----*
-2 5                        1                |
-4 7                        1                |
-6 7                        1                |
 ----+----+----+----+
            Multiply Stem.Leaf by 10**-2

                  The SAS System                  12
                The UNIVARIATE Procedure
                    Variable:  resid

                   Normal Probability Plot
   0.05+                                      +++++*
       |                           * * *+*+*++*
       |                         +*+++++
  -0.01+                 * *+*+**
       |             ++*+++
       |       +++++*
  -0.07++++++++*
        +----+----+----+----+----+----+----+----+----+----+
            -2        -1         0        +1        +2
```

Split-Plot Experiments

REF: Neter et al., Ch 27.6 (white book, newest edition); or Chapter 29.6 (blue book); Freese pp. 45 to 50.

Introduction

- As with factorial experiments, treatments can be combinations of more than one factor
- In a split-plot experiment, the experimental unit (called the "whole-plot" for one factor is subdivided, and the second factor is applied to the subdivided experimental unit (called the "split" plot).
- Can be a CRD or RCB
- Split-split plot experiment: one Factor is applied to the whole experimental unit, the second Factor is applied to a sub-divided experimental unit (split-plot), and for the third factor, the split-plot is divided once more. For more on this, see "Fundamental concepts in the design of experiments" by Charles R. Hicks.

Example from Freese: Randomized Block Design, with two factors, but using a split-plot for the second factor

Four plantation areas of each 12 acres (imperial units) each were selected (blocks; I, II, III and IV). Each was divided into two areas (whole plot of 6 acres each), and a burning treatment (A or B) was randomly assigned to the 2 areas in each block. Each experimental unit was then sub-divided into six areas (split-plot, 1 acre each), and planting date (a,b,c,d,e,f) was randomly assigned to each split-plot In each split-plot, 1 pound of seeds were sown. At the end of the first growing season, the number of seeds were counted. (see schematic on page 45 of the Freese book).

Main questions:

4. Is there an interaction between Factors?
5. If there is an interaction, look at treatment means for differences.
6. If there is no interaction:
   a. Are there differences between levels for Factor A?
   b. Are there differences between levels for Factor B?

Model for a 2-factor RCB, split-plot

The model is a like a 2-factor RCB except that we will divide the effects into whole plot versus split plot.

Population:

$$y_{jkl} = \mu_{\bullet\bullet\bullet} + \tau_{BLK\,j} + \tau_{A\,k} + \tau_{BLK\times A\,jk} + \tau_{Bl} + \tau_{A\,Bkl} + \varepsilon_{jkl}$$

y_{jkl} = response variable measured on block j and subunit kl

j=1 to J blocks; k=1 to K levels for Factor A (whole plot); l=1 to L levels for Factor B (split-plot)

Definition of terms follows other designs, except that:

$\tau_{BLK\times A\,jk}$ is considered "Error 1", the whole plot error; and

ε_{jkl} is considered "Error 2", the subunit (i.e., split-plot) error.

Partition SS_y:

$$SS_y = \underbrace{SS_{BLK} + SS_A + SS_{E1}}_{\text{whole plot}} + \underbrace{SS_B + SS_{AXB} + SS_{E2}}_{\text{split or sub-plot}}$$

Block x main plot interaction

Block x subunit interaction (nested in main plot)

Two error terms for Factors A and B both fixed:

- whole plot error (Error 1) to test Factor A, and
- split-plot error (Error 2) to test interaction between A and B and to test B.

$$\sum_{j=1}^{J}\sum_{k=1}^{K}\sum_{l=1}^{L}(y_{jkl} - \bar{y}_{\bullet\bullet\bullet})^2 = KL\sum_{j=1}^{J}(\bar{y}_{j\bullet\bullet} - \bar{y}_{\bullet\bullet\bullet})^2$$

$$+ JL\sum_{k=1}^{K}(\bar{y}_{\bullet k\bullet} - \bar{y}_{\bullet\bullet\bullet})^2 + L\sum_{k=1}^{K}\sum_{J=1}^{J}(\bar{y}_{jk\bullet} - \bar{y}_{j\bullet\bullet} - \bar{y}_{\bullet k\bullet} + \bar{y}_{\bullet\bullet\bullet})^2$$

$$+ JK\sum_{l=1}^{L}(\bar{y}_{\bullet\bullet l} - \bar{y}_{\bullet\bullet\bullet})^2 + J\sum_{j=1}^{J}\sum_{k=1}^{K}(\bar{y}_{\bullet kl} - \bar{y}_{\bullet k\bullet} - \bar{y}_{\bullet\bullet l} + \bar{y}_{\bullet\bullet\bullet})^2$$

$$+ \sum_{j=1}^{J}\sum_{k=1}^{K}\sum_{l=1}^{L}(y_{jkl} - \bar{y}_{jk\bullet} - \bar{y}_{\bullet kl} + \bar{y}_{\bullet k\bullet})^2$$

[There are also "working formulae" for easier hand calculations in many textbooks]

Degrees of Freedom:

$$\left.\begin{array}{ll} SS_{BLK} & J-1 \\ SS_{A} & K-1 \\ SS_{E1} & (J-1)(K-1) \end{array}\right\} \text{whole plot}$$

$\text{NOTE: Whole plots together have } JK-1$ degrees of freedom

$$\left.\begin{array}{ll} SS_{B} & (L-1) \\ SS_{AXB} & (K-1)(L-1) \\ SS_{E2} & K(J-1)(L-1) \end{array}\right\} \text{split plot}$$

$\text{NOTE: Split plots together have } JK(L-1)$ degrees of freedom

$SS_{y} \quad JKL-1$

Analysis of Variance Table (for Split-Plot RCB)

Source	*df*	*SS*	*MS*
Block	J-1	SS_{BLK}	MS_{BLK}
Factor A	K-1	SS_{A}	MS_{A}
Exp. Err. #1	(J-1)(K-1)	SS_{E1}	MS_{E1}
Factor B	L-1	SS_{B}	MS_{B}
A x B	(K-1)(L-1)	SS_{AXB}	MS_{AXB}
Exp. Err. #2	K(J-1)(L-1)	SS_{E2}	MS_{E2}
Total	JKL-1		

What are the appropriate F-tests?

- Depends upon which are fixed and which are random-effects.
- Then, need the expected means squares in order to decide this.

Expected Mean Square Values for Model for a 2-factor RCB, split-plot:

Mean Square	Both A and B are Fixed; Blocks are Random	Both A and B are Random; Blocks are Random
Blocks (MS_{BLK})	$KL\sigma_{BLK}^2$	$\sigma_{\varepsilon 2}^2 + L\sigma_{\varepsilon 1}^2 + KL\sigma_{BLK}^2$
A (MS_A)	$L\sigma_{\varepsilon 1}^2 + \phi_A{}^*$	$\sigma_{\varepsilon 2}^2 + L\sigma_{\varepsilon 1}^2 + JL\sigma_A^2 + J\sigma_{A\times B}^2$
Error 1(MS_{E1})	$L\sigma_{\varepsilon 1}^2$	$\sigma_{\varepsilon 2}^2 + L\sigma_{\varepsilon 1}^2$
B (MS_B)	$\sigma_{\varepsilon 2}^2 + \phi_B$	$\sigma_{\varepsilon 2}^2 + JK\sigma_B^2 + J\sigma_{A\times B}^2$
A X B (MS_{AB})	$\sigma_{\varepsilon 2}^2 + \phi_{A\times B}$	$\sigma_{\varepsilon 2}^2 + J\sigma_{A\times B}^2$
Error 2 (MSE_{E2})	$\sigma_{\varepsilon 2}^2$	$\sigma_{\varepsilon 2}^2$

$* \sigma_{\varepsilon}^2 + \phi_A = \sigma_{\varepsilon}^2 + JL\frac{\sum_{k=1}^{K}\tau_{Aj}}{K-1}$ when the number of observations (n) are all equal. Similar values for other fixed effects.

Organization of Example Data for Analysis using a Statistics Package:

Block	Burn_Type	Date	yjkl
I	A	a	900
I	A	b	880
I	A	c	1530
I	A	d	1970
I	A	e	1960
I	A	f	830
I	B	a	880
I	B	b	1050
I	B	c	1140
I	B	d	1360
I	B	e	1270
I	B	f	150
II	A	a	810
II	A	b	1170
II	A	c	1160
II	A	d	1890
II	A	e	1670
II	A	f	420
II	B	a	1100
II	B	b	1240
II	B	c	1270
II	B	d	1510
II	B	e	1380
II	B	f	380
III	A	a	760
III	A	b	1060
III	A	c	1390
III	A	d	1820
III	A	e	1310
III	A	f	570
III	B	a	960

III	B	b	1110
III	B	c	1320
III	B	d	1490
III	B	e	1500
III	B	f	420
IV	A	a	1040
IV	A	b	910
IV	A	c	1540
IV	A	d	2140
IV	A	e	1480
IV	A	f	760
IV	B	a	1040
IV	B	b	1120
IV	B	c	1080
IV	B	d	1270
IV	B	e	1450
IV	B	f	270

SAS code for Freese example:

```
PROC IMPORT OUT= WORK.seedlings
   DATAFILE= "E:\frst430\lemay\examples\split-plot.XLS"
   DBMS=EXCEL REPLACE;
   SHEET="data$";      GETNAMES=YES;
   MIXED=NO;      SCANTEXT=YES;
   USEDATE=YES;      SCANTIME=YES;
RUN;

options ls=70 ps=50 nodate pageno=1;
run;

PROC GLM data=seedlings;
TITLE 'split plot, blocks random, treatments fixed';
CLASS block burn_type date;
MODEL yjkl=block burn_type block*burn_type date
date*burn_type;
Test h=burn_type e=block*burn_type;
LSMEANS burn_type/e=block*burn_type tdiff pdiff;
LSMEANS date burn_type*date/tdiff pdiff;
OUTPUT OUT=GLMOUT PREDICTED=PREDICT
RESIDUAL=RESID;
RUN;

PROC PLOT DATA=GLMOUT;
PLOT RESID*PREDICT='*';
RUN;

PROC UNIVARIATE DATA=GLMOUT PLOT NORMAL;
VAR RESID;
RUN;
```

SAS output for Freese Example:

```
      split plot, blocks random, treatments fixed

                   The GLM Procedure

                Class Level Information

          Class          Levels    Values

          Block               4    I II III IV
          Burn_Type           2    A B
          Date                6    a b c d e f


        Number of Observations Read          48
        Number of Observations Used          48

     split plot, blocks random, treatments fixed

                  The GLM Procedure

Dependent Variable: yjkl   yjkl

                          Sum of
Source      DF         Squares    Mean Square   F Value

Model       17    8833968.750     519645.221     30.83
Error       30     505679.167      16855.972

Corrected
   Total    47    9339647.917

                    Source                 Pr > F

                    Model                  <.0001
                    Error

                    Corrected Total

 R-Square     Coeff Var      Root MSE     yjkl Mean
 0.945857      11.18225      129.8306      1161.042
```

```
Source          DF   Type I SS    Mean Square   F Value

Block            3    6856.250       2285.417      0.14
Burn_Type        1  369252.083     369252.083     21.91
Block*Burn_Type  3  271389.583      90463.194      5.37
Date             5 7500085.417    1500017.083     88.99
Burn_Type*Date   5  686385.417     137277.083      8.14

                    Source                 Pr > F

                    Block                  0.9380
                    Burn_Type              <.0001
                    Block*Burn_Type        0.0044
                    Date                   <.0001
                    Burn_Type*Date         <.0001

   split plot, blocks random, treatments fixed

                   The GLM Procedure

Dependent Variable: yjkl   yjkl

Source          DF    Type III SS  Mean Square   F Value

Block            3       6856.250     2285.417      0.14
Burn_Type        1     369252.083   369252.083     21.91
Block*Burn_Type  3     271389.583    90463.194      5.37
Date             5    7500085.417  1500017.083     88.99
Burn_Type*Date   5     686385.417   137277.083      8.14

                    Source                 Pr > F

                    Block                  0.9380
                    Burn_Type              <.0001
                    Block*Burn_Type        0.0044
                    Date                   <.0001
                    Burn_Type*Date         <.0001
```

```
        Tests of Hypotheses Using the Type III
        MS for Block*Burn_Type as an Error Term

Source     DF    Type III SS    Mean Square   F Value

Burn_Type    1    369252.0833    369252.0833      4.08

Tests of Hypotheses Using the Type III MS for
Block*Burn_Type as an Error Term

                    Source                 Pr > F

                    Burn_Type              0.1366
```

```
          split plot, blocks random, treatments fixed

                  The GLM Procedure
                  Least Squares Means
 Standard Errors and Probabilities Calculated Using the
Type III MS for Block*Burn_Type as an Error Term
                   H0:LSMean1=LSMean2

Burn_Type     yjkl LSMEAN    t Value    Pr > |t|

A              1248.75000       2.02      0.1366
B              1073.33333
```

```
                   The GLM Procedure
                 Least Squares Means

                                        LSMEAN
              Date     yjkl LSMEAN      Number

              a          936.25000           1
              b         1067.50000           2
              c         1303.75000           3
              d         1681.25000           4
              e         1502.50000           5
              f          475.00000           6


           Least Squares Means for Effect Date
           t for H0: LSMean(i)=LSMean(j) / Pr > |t|

                 Dependent Variable: yjkl

i/j      1         2          3          4          5
6

1            -2.02187  -5.66123  -11.4765 -8.72291  .105415
               0.0522   <.0001    <.0001   <.0001   <.0001

2   2.021866           -3.63936  -9.45463 -6.70104 9.127282
      0.0522             0.0010    <.0001   <.0001   <.0001

3   5.661225 3.639359            -5.81527 -3.06168 12.76664
      <.0001   0.0010              <.0001   0.0046   <.0001

4    11.4765 9.454631  5.815272           2.753589 18.58191
      <.0001   <.0001    <.0001             0.0099   <.0001

5   8.722908 6.701042 3.061683   -2.75359          15.82832
      <.0001   <.0001   0.0046     0.0099            <.0001

6   -7.10542 -9.12728 -12.7666   -18.5819 -15.8283
     <.0001   <.0001  <.0001     <.0001  <.0001


NOTE: To ensure overall protection level, only
probabilities associated with pre-planned comparisons
should be used.
```

```
                                             LSMEAN
Burn_Type    Date     yjkl LSMEAN            Number

A            a          877.50000                 1
A            b         1005.00000                 2
A            c         1405.00000                 3
A            d         1955.00000                 4
A            e         1605.00000                 5
A            f          645.00000                 6
B            a          995.00000                 7
B            b         1130.00000                 8
B            c         1202.50000                 9
B            d         1407.50000                10
B            e         1400.00000                11
B            f          305.00000                12

       Least Squares Means for Effect Burn_Type*Date
        t for H0: LSMean(i)=LSMean(j) / Pr > |t|

                 Dependent Variable: yjkl

i/j            1           2           3           4           5           6

   1                -1.38883    -5.74593     -11.737    -7.92449    2.532568
                      0.1751      <.0001      <.0001      <.0001      0.0168
   2    1.388827                -4.35711    -10.3481    -6.53566    3.921395
          0.1751                  0.0001      <.0001      <.0001      0.0005
   3    5.745933    4.357106                -5.99102    -2.17855    8.278501
          <.0001      0.0001                  <.0001      0.0374      <.0001
   4    11.73695    10.34813     5.99102                3.812467    14.26952
          <.0001      <.0001      <.0001                  0.0006      <.0001
   5    7.924486    6.535658    2.178553    -3.81247                10.45705
          <.0001      <.0001      0.0374      0.0006                  <.0001
   6    -2.53257     -3.9214     -8.2785    -14.2695    -10.4571
          0.0168      0.0005      <.0001      <.0001      <.0001
   7      1.2799    -0.10893    -4.46603    -10.4571    -6.64459    3.812467
          0.2104      0.9140      0.0001      <.0001      <.0001      0.0006
   8    2.750423    1.361595    -2.99551    -8.98653    -5.17406    5.282991
          0.0100      0.1835      0.0055      <.0001      <.0001      <.0001
   9    3.540148    2.151321    -2.20578     -8.1968    -4.38434    6.072716
          0.0013      0.0396      0.0352      <.0001      0.0001      <.0001
  10    5.773165    4.384338    0.027232    -5.96379    -2.15132    8.305733
          <.0001      0.0001      0.9785      <.0001      0.0396      <.0001
  11    5.691469    4.302642    -0.05446    -6.04548    -2.23302    8.224037
          <.0001      0.0002      0.9569      <.0001      0.0332      <.0001
  12    -6.23611    -7.62493     -11.982    -17.9731    -14.1606    -3.70354
          <.0001      <.0001      <.0001      <.0001      <.0001      0.0009
```

```
                         The GLM Procedure
                        Least Squares Means

            Least Squares Means for Effect Burn_Type*Date
               t for H0: LSMean(i)=LSMean(j) / Pr > |t|

                       Dependent Variable: yjkl

i/j            7           8           9          10          11          12

   1     -1.2799    -2.75042    -3.54015    -5.77316    -5.69147    6.236107
          0.2104      0.0100      0.0013      <.0001      <.0001      <.0001
   2    0.108928     -1.3616    -2.15132    -4.38434    -4.30264    7.624935
          0.9140      0.1835      0.0396      0.0001      0.0002      <.0001
   3    4.466033     2.99551    2.205785    -0.02723    0.054464    11.98204
          0.0001      0.0055      0.0352      0.9785      0.9569      <.0001
   4    10.45705     8.98653    8.196805    5.963788    6.045484    17.97306
          <.0001      <.0001      <.0001      <.0001      <.0001      <.0001
   5    6.644586    5.174063    4.384338    2.151321    2.233017    14.16059
          <.0001      <.0001      0.0001      0.0396      0.0332      <.0001
   6    -3.81247    -5.28299    -6.07272    -8.30573    -8.22404     3.70354
          0.0006      <.0001      <.0001      <.0001      <.0001      0.0009
   7                -1.47052    -2.26025    -4.49327    -4.41157    7.516007
                      0.1518      0.0312      <.0001      0.0001      <.0001
   8    1.470523                -0.78973    -3.02274    -2.94105     8.98653
          0.1518                  0.4359      0.0051      0.0062      <.0001
   9    2.260249    0.789725                -2.23302    -2.15132    9.776256
          0.0312      0.4359                  0.0332      0.0396      <.0001
  10    4.493265    3.022742    2.233017                0.081696    12.00927
          <.0001      0.0051      0.0332                  0.9354      <.0001
  11    4.411569    2.941046    2.151321     -0.0817                11.92758
          0.0001      0.0062      0.0396      0.9354                  <.0001
  12    -7.51601    -8.98653    -9.77626    -12.0093    -11.9276
          <.0001      <.0001      <.0001      <.0001      <.0001


NOTE: To ensure overall protection level, only
probabilities associated with pre-planned comparisons
should be used.
```

```
              split plot, blocks random, treatments fixed

           Plot of RESID*PREDICT.  Symbol used is '*'.

RESID ,
  300 ^
      ,
      ,                                          *
      ,
      ,                        *
      ,
  200 ^
      ,
      ,
      ,                       *
      ,                                      *
      ,                                                 *
  100 ^                        *
      ,                   *    *       * *
      ,                                    *
      ,          *       *            **
      ,                           ** *     **
      ,              *           *         *
    0 ^       *  *          *          *             *
      ,                    *  *
      ,                                *             *
      ,      *
      ,                        *
      ,                             **                   *
 -100 ^                          *       * *
      ,
      ,
      ,                           *
      ,               *
      ,                                 *       *
 -200 ^                                     *
      ,                           *
      ,
      ,
      ,
      ,
 -300 ^
      ,
      Š-^-----------^-----------^-----------^-----------^-----------^-
        0          500        1000        1500        2000        2500

                                   PREDICT

NOTE: 2 obs hidden.
```

```
          split plot, blocks random, treatments fixed
                The UNIVARIATE Procedure
                   Variable:  RESID

                        Moments

N                         48    Sum Weights             48
Mean                       0    Sum Observations         0
Std Deviation     103.726232    Variance        10759.1312
Skewness          -0.0730794    Kurtosis        0.26668103
Uncorrected
         SS       505679.167    Corrected SS    505679.167
Coeff Variation            .    Std Error Mean   14.971592
```

NOTE: some outputs removed

```
              Tests for Normality

Test                  --Statistic---    -----p Value---
---

Shapiro-Wilk       W     0.973694    Pr < W      0.3503
Kolmogorov-Smirnov D     0.102576    Pr > D     >0.1500
Cramer-von Mises   W-Sq  0.087186    Pr > W-Sq   0.1671
Anderson-Darling   A-Sq  0.518069    Pr > A-Sq   0.1877


                       The UNIVARIATE Procedure
                           Variable:  RESID

                       Quantiles (Definition 5)
                       Quantile       Estimate
                       100% Max       258.7500
                       99%            258.7500
                       95%            152.0833
                       90%            122.0833
                       75% Q3          56.2500
                       50% Median      20.2083
                       25% Q1         -76.8750
                       10%           -162.9167
                       5%            -187.9167
                       1%            -221.2500
                       0% Min        -221.2500
```

```
                    Extreme Observations

------Lowest-----        -----Highest-----

 Value        Obs         Value        Obs

-221.250        2         122.083       40
-197.917       29         127.083       17
-187.917       41         152.083       26
-182.917       15         227.083       14
-162.917       18         258.750        5
```

```
Stem Leaf                     #             Boxplot
   2 6                        1                0
   2 3                        1                |
   1 5                        1                |
   1 023                      3                |
   0 556678889                9             +-----+
   0 002222333444            12             *--+--*
  -0 4322110                  7             |     |
  -0 998876                   6             +-----+
  -1 00                       2                |
  -1 9866                     4                |
  -2 20                       2                |
     ----+----+----+----+
 Multiply Stem.Leaf by 10**+2
```

```
              The UNIVARIATE Procedure
                  Variable:  RESID

                   Normal Probability Plot
 275+                                               *  +
    |                                          * +++++
    |                                       +*+++
    |                                  +++**
    |                             ********
  25+                       *******
    |                   ****+
    |              *****+
    |          +++*+
    |     +*+*+***
-225+ ++*++
     +----+----+----+----+----+----+----+----+----+----+
         -2        -1         0        +1        +2
```

CRD: Two Factor Experiment, Both Fixed Effects, with Second Factor Nested in the First Factor

REF: Neter et al., 4th edition, chapter 28.1; not in the Freese Handbook

Introduction and Example

- In a CRD with two factors, a crossed design shows that all levels of Factor A are crossed with all levels in Factor B. Example:
    - Response is weight gain
    - Factor A: Salmon or Trout
    - Factor B: no warming; warmed 1 degree C; warmed 2 degrees C.
    - Treatments: 6 treatments; all combinations of Factor A crossed with Factor B.

- A nested design is when Factor B has different levels, depending on which level of Factor A.
    - Response: Weight gain
    - Factor A: Salmon or Trout
    - Factor B:
        - For Salmon: No warming; warmed 2 degree C
        - For Trout: No warming; warmed 1 degrees C
- Both CRD and nested designs have "No warming", but the levels of warming differ by Factor A (species) for the nested design.
- Sometimes it is difficult to decide if the experiment is crossed or nested. For example:
    - For the experiment, could evaluate this as Factor A, Salmon or Trout crossed with Factor B, Not warmed or warmed, where the level of warming differs slightly by species.

Main questions

7. Is there a difference
    a. Between Factor A means?
    b. Between Factor B means, within Factor A?
    c. Not able to look at the interaction between Factors as there is nesting of B within A.
8. If there are differences:
    a. Which levels of Factor A means differ?
    b. Which levels of Factor B within Factor A differ?

Notation, Assumptions, and Transformations

Models

If this were a *crossed* experiment (Factorial), for two factors, we would have:

Population: $y_{ijk} = \mu + \tau_{A\,j} + \tau_{Bk} + \tau_{AB\,jk} + \varepsilon_{ijk}$

However, for a *nested* experiment, we have:

Population: $y_{ijk} = \mu + \tau_{A\,j} + \tau_{Bk(j)} + \varepsilon_{ijk}$

We cannot separate get the interaction between Factor A and B, since we do not have all levels of B for every level of A (nested, not crossed).

y_{ijk} = response variable measured on experimental unit *i* and Factor A level *j*. and Factor B level *k*

j=1 to *J* levels for Factor A; *k*=1 to *K* levels for Factor B (nested in Factor A)

μ = the grand or overall mean regardless of treatment

τ_{Aj} = the *treatment effect* for Factor A, level *j*

$\tau_{Bk(j)}$ = the *treatment effect* for Factor B, level *k*, nested in Factor A.

ε_{ijk} = the difference between a particular measure for an experimental unit *i*, and the mean for a treatment:

$$\varepsilon_{ijk} = y_{ijk} - (\mu + \tau_{A\,j} + \tau_{Bk(j)})$$

For the experiment:

$$y_{ijk} = \bar{y}_{\bullet\bullet\bullet} + \hat{\tau}_{A\,j} + \hat{\tau}_{Bk(j)} + e_{ijk}$$

$\bar{y}_{\bullet\bullet\bullet}$ = the grand or overall mean of all measures from the experiment regardless of treatment; under the assumptions for the error terms, this will be an unbiased estimate of μ

$\bar{y}_{\bullet jk}$ = the mean of all measures from the experiment for a particular treatment *jk*

$\bar{y}_{\bullet j\bullet}$ = the mean of all measures from the experiment for a particular level *j* of Factor A (includes all data for all levels of Factor B)

$\bar{y}_{\bullet\bullet k}$ = the mean of all measures from the experiment for a particular level *k* of Factor B (includes all data for all levels of Factor A)

$\hat{\tau}_{Aj}, \hat{\tau}_{Bk(j)}$ = under the error term assumptions, will be unbiased estimates of corresponding treatment effects for the population

e_{ijk} = the difference between a particular measure for an experimental unit *i*, and the mean for the treatment *jk* that was applied to it

$$e_{ijk} = y_{ijk} - \bar{y}_{\bullet jk}$$

n_{jk} = the number of experimental units measured in treatment *jk*

n_T = the number of experimental units measured over all treatments = $\sum_{k-1}^{K} \sum_{j=1}^{J} n_{jk}$

Assumptions and Transformations:

As with other designs, we need to meet the assumptions that i) the observations are independent; ii) the variances by treatments are all equal (residual plot); and iii) the errors are normally distributed (normality plot and normality tests).

If these are not met, we would transform the response variable and check the assumptions for the transformed y-variable. Interpretation of all hypothesis tests and calculation of confidence intervals would be based on the analysis where the assumptions were met.

In a crossed experiment,

$$SSy = SS_{TR} + SSE$$

And for two-factors, SS_{TR} is divided into:

$$SS_{TR} = SSA + SSB + SSAB$$

For a nested experiment with two factors, where Factor B is nested in Factor A:

$$SS_{TR} = SSA + SSB(\mathrm{A})$$

Sums of Squares

SSy: The sum of squared differences between the observations and the grand mean (same as two-factor crossed experiment)

$$SSy = \sum_{k=1}^{K}\sum_{j=1}^{J}\sum_{i=1}^{n_{jk}}\left(y_{ijk} - \bar{y}_{\bullet\bullet\bullet}\right)^2 \quad df = n_T - 1$$

SSA: Sum of squared differences between the level means for factor A and the grand mean, weighted by the number of experimental units for each treatment (same as for the crossed experiment):

$$SSA = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\left(\bar{y}_{\bullet j\bullet} - \bar{y}_{\bullet\bullet\bullet}\right)^2 \quad df = J - 1$$

SSB(A): Sum of squared differences between the level means for Factor B with each level of Factor A, and the mean and mean of all observations for that level of Factor

A, weighted by the number of experimental units for each treatment:

$$SSB(A) = \sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}\left(\bar{y}_{\bullet jk} - \bar{y}_{\bullet j\bullet}\right)^2 \quad df = J(K-1)$$

SSE: Sum of squared differences between the observed values for each experimental unit and the treatment means (same as for crossed experiments):

$$SSE = \sum_{k=1}^{K}\sum_{j=1}^{J}\sum_{i=1}^{n_{jk}}\left(y_{ijk} - \bar{y}_{\bullet jk}\right)^2 \qquad df = n_T - JK$$

Expected Mean Squares and F-tests for Nested Design, Both Factors Fixed:

Source	SS	MS	EMS	F
A	SSA	$MSA = \frac{SSA}{J-1}$	$\sigma_\varepsilon^2 + \phi_A$ *	F=MSA/MSE
B (A)	SSB(A)	$MSB(A) = \frac{SSB(A)}{J(K-1)}$	$\sigma_\varepsilon^2 + \phi_{B(A)}$ **	F=MSB(A)/MSE
Error	SSE	$MSE = \frac{SSE}{n_T - JK}$	σ_ε^2	

$*\sigma_\varepsilon^2 + \phi_A = \sigma_\varepsilon^2 + nK\frac{\sum_{j=1}^{J}\tau_{Aj}}{J-1}$ when the number of observations (n) are all equal.

$**\sigma_\varepsilon^2 + \phi_{B(A)} = \sigma_\varepsilon^2 + n\frac{\sum_{k=1}^{K}\sum_{j=1}^{J}\tau_{Bk(Aj)}}{J(K-1)}$ when the number of observations (n) are all equal.

Comparison of Factorial (Crossed) versus Nested experiments, with J=3, K=3 and n_{jk}=4 observations per treatment

Factorial Exp.	
Source	DoF
Treatment	8
Factor A	2
Factor B	2
A x B	4
Error	27
Total	35

Nested Exp.	
Source	DoF
Treatment	8
Factor A	2
Factor B(A)	6
Error	27
Total	35

Example:

A1B1 = 10	A1B1 = 11	A1B2= 13	A2B4 = 23
A1B2 = 15	A2B3 = 18	A2B4= 25	A1B1 = 11
A2B4 = 20	A2B3 = 18	A1B1= 9	A2B3 = 18
A2B4 = 22	A1B2 = 15	A2B3 = 18	A1B2 = 14

Nested design with two factors, where the second factor is nested in the first factor, with four replications per treatment.

Data:

A	**B**	**result**
1	1	10.00
1	1	11.00
1	1	9.00
1	1	11.00
1	2	15.00
1	2	15.00
1	2	13.00
1	2	14.00
2	3	18.00
2	3	19.00
2	3	17.00
2	3	18.00
2	4	20.00
2	4	22.00
2	4	25.00
2	4	23.00

SAS:

```
PROC IMPORT OUT= WORK.nested
    DATAFILE= “E:\frst430\lemay\examples\encyl_examples.xls"
    DBMS=EXCEL REPLACE;
    SHEET="nested$";        GETNAMES=YES;
    MIXED=NO;               SCANTEXT=YES;
    USEDATE=YES;            SCANTIME=YES;
RUN;
options ls=70 ps=50 pageno=1;

data nested2;
set nested;
*set up a label for each treatment, with factor a and factor b, for
example,
treatment of 11 is factor A of 1,and factor b of 1;
treatment=(a*10)+b;
lnresult=log(result);
run;

proc print data=nested2;
run;

proc shewhart data=nested2;
     boxchart result*treatment;
run;

PROC GLM  data=nested2;
class a b;
model result=a b(a);
output out=glmout r=resid p=predict;
lsmeans a b(a)/pdiff tdiff;
run;
```

```
proc plot data=glmout;
plot resid*predict='*';
run;

PROC univariate data=glmout plot normal;
Var resid;
Run;
PROC GLM  data=nested2;
class a b;
model lnresult=a b(a);
output out=glmout2 r=resid2 p=predict2;
lsmeans a b(a)/pdiff tdiff;
run;

proc plot data=glmout2;
plot resid2*predict2='*';
run;

PROC univariate data=glmout2 plot normal;
Var resid2;
Run;
```

Selected SAS Output:

```
                   The SAS System          1

Obs  A    B    result    treatment  lnresult

1    1    1      10          11      2.30259
2    1    1      11          11      2.39790
3    1    1       9          11      2.19722
4    1    1      11          11      2.39790
5    1    2      15          12      2.70805
6    1    2      15          12      2.70805
7    1    2      13          12      2.56495
8    1    2      14          12      2.63906
9    2    3      18          23      2.89037
10   2    3      19          23      2.94444
11   2    3      17          23      2.83321
12   2    3      18          23      2.89037
13   2    4      20          24      2.99573
14   2    4      22          24      3.09104
15   2    4      25          24      3.21888
16   2    4      23          24      3.13549
```

```
                 The SAS System            2

                The GLM Procedure

             Class Level Information

Class         Levels    Values
A                  2    1 2
B                  4    1 2 3 4

Number of Observations Read          16
Number of Observations Used          16

                 The SAS System            3
                  The GLM Procedure

Dependent Variable: result   result

                 Sum of
Source    DF    Squares  Mean Square F Value
Model      3 328.5000000 109.5000000 64.10
Error     12  20.5000000   1.7083333
Corrected
   Total  15 349.0000000

           Source                 Pr > F
           Model                  <.0001
           Error
           Corrected Total


R-Square   Coeff Var   Root MSE  result Mean
0.941261    8.043275   1.307032     16.25000
```

(Type I SS not shown)

```
Source   DF  Type III SS Mean Square  F Value
A         1  256.0000000 256.0000000   149.85
B(A)      2   72.5000000  36.2500000    21.22

              Source          Pr > F
                A             <.0001
                B(A)          0.0001

                The SAS System
               The GLM Procedure
              Least Squares Means

           result     H0:LSMean1=LSMean2
A          LSMEAN    t Value    Pr > |t|

1      12.2500000     -12.24      <.0001
2      20.2500000


                result      LSMEAN
B    A          LSMEAN      Number
1    1      10.2500000           1
2    1      14.2500000           2
3    2      18.0000000           3
4    2      22.5000000           4
```

```
Least Squares Means for Effect B(A)
t for H0: LSMean(i)=LSMean(j) / Pr > |t|

        Dependent Variable: result

i/j        1         2         3          4
1              -4.32801  -8.38553   -13.2545
                 0.0010    <.0001     <.0001

2    4.328014            -4.05751   -8.92653
       0.0010              0.0016     <.0001

3    8.385528  4.057513             -4.86902
       <.0001    0.0016               0.0004

4    13.25454  8.926529  4.869016
       <.0001    <.0001    0.0004

NOTE: To ensure overall protection level,
only probabilities associated with pre-
planned comparisons should be used.
```

```
             Plot of resid*predict.  Symbol used is '*'.

resid ,
      ,
 2.50 ^                                                             *
 2.25 ^
 2.00 ^
 1.75 ^
 1.50 ^
 1.25 ^
 1.00 ^                                       *
 0.75 ^  *                  *
 0.50 ^                                                             *
 0.25 ^
 0.00 ^                                       *
-0.25 ^  *                  *
-0.50 ^                                                             *
-0.75 ^
-1.00 ^                                       *
-1.25 ^  *                  *
-1.50 ^
-1.75 ^
-2.00 ^
-2.25 ^
-2.50 ^                                                             *
      ,
      Š-^-----------^-----------^-----------^-----------^-----------^-
      10.0        12.5        15.0        17.5        20.0        22.5

                                   predict

NOTE: 3 obs hidden.
```

The SAS System
The UNIVARIATE Procedure
Variable: resid

Some outputs removed

```
          Tests for Normality

Test             --Statistic---   --p value--
Shapiro-Wilk       W    0.960624  Pr<W   0.6731
Kolmogorov-Smirnov D    0.135583  Pr>D  >0.1500
Cramer-von Mises W-Sq   0.054347  Pr>W-Sq>0.2500
Anderson-Darling A-Sq   0.353872  Pr>A-Sq>0.2500
```

```
Stem Leaf                     #            Boxplot
   2 5                        1               |
   1 0                        1               |
   0 0058888                  7            +--+--+
  -0 522                      3            +-----+
  -1 220                      3               |
  -2 5                        1               |
     ----+----+----+----+
```

Variable: resid

```
                   Normal Probability Plot
 2.5+                                           *+++++++
    |                                  ++++*++++
    |                        *+**+*+++*
    |                 *+*+*+++
    |        ++++*++*+
-2.5++++++++*
     +----+----+----+----+----+----+----+----+----+----+
         -2        -1         0        +1        +2
```

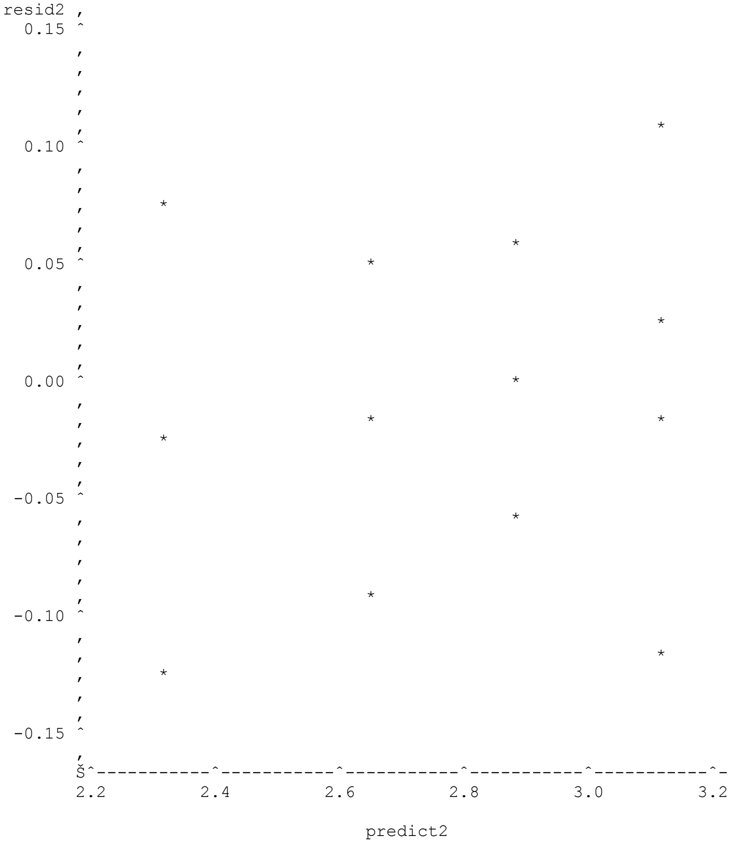
```
                The SAS System            10

              The GLM Procedure

            Class Level Information

Class         Levels    Values
 A               2      1 2
 B               4      1 2 3 4

Number of Observations Read          16
Number of Observations Used          16

                  The SAS System
                  The GLM Procedure

Dependent Variable: lnresult

               Sum of
Source   DF    Squares    Mean Square   F
Value

Model     3  1.35905142   0.45301714   73.91
Error    12  0.07355155   0.00612930
Corrected
  Total  15  1.43260297

             Source                 Pr > F
             Model                  <.0001
             Error
             Corrected Total

R-Square   Coeff Var  Root MSE lnresult Mean
0.948659    2.852397  0.078290      2.744703
```

(Type I SS not shown)

```
Source  DF  Type III SS  Mean Square F Value
A        1   1.04235590   1.04235590  170.06
B(A)     2   0.31669552   0.15834776   25.83

    Source                 Pr > F
    A                      <.0001
    B(A)                   <.0001

              The GLM Procedure
            Least Squares Means

        lnresult    H0:LSMean1=LSMean2
A         LSMEAN    t Value    Pr > |t|
1     2.48946341     -13.04      <.0001
2     2.99994258


             lnresult      LSMEAN
B    A         LSMEAN      Number

1    1     2.32390005           1
2    1     2.65502677           2
3    2     2.88959896           3
4    2     3.11028619           4
```

```
Least Squares Means for Effect B(A)
t for H0: LSMean(i)=LSMean(j) / Pr > |t|

      Dependent Variable: lnresult

i/j          1         2         3         4

1               -5.98141  -10.2187  -14.2051
                  <.0001    <.0001    <.0001

2     5.981415            -4.23727  -8.22373
        <.0001              0.0012    <.0001

3     10.21869 4.237271             -3.98646
        <.0001   0.0012               0.0018

4     14.20514 8.223726   3.986455
        <.0001   <.0001     0.0018


NOTE: To ensure overall protection level,
only probabilities associated with pre-
planned comparisons should be used.
```

Plot of resid2*predict2. Symbol used is '*'.



NOTE: 3 obs hidden.

```
              The UNIVARIATE Procedure
                 Variable:  resid2
```

(Some outputs deleted)

```
             Tests for Normality

Test                  -Statistic---    --p Value--

Shapiro-Wilk        W     0.950268  Pr<W  0.4939
Kolmogorov-Smirnov  D     0.150539  Pr>D >0.1500
Cramer-von Mises    W-Sq  0.047813  Pr>W-Sq
                                         >0.2500
Anderson-Darling    A-Sq  0.321185  Pr>A-Sq
                                         >0.2500
```

```
Stem Leaf                      #             Boxplot
   1 1                         1                |
   0 55577                     5             +-----+
   0 003                       3             *--+--*
  -0 222                       3             +-----+
  -0 96                        2                |
  -1 31                        2                |
     ----+----+----+----+
 Multiply Stem.Leaf by 10**-1
```

```
                     Normal Probability Plot
 0.125+                                        +++*+++
      |                             * * *+*++++
      |                        *+**+++++
      |                  +*+*+*+
      |           ++++*+*
-0.125+    +++*+++ *
       +----+----+----+----+----+----+----+----+----+----+
           -2        -1         0        +1        +2
```

CRD: One Factor Experiment, Fixed Effects with subsampling [26.7 of textbook (White)]

Example: Site Preparation

A forester would like to test whether different site preparation methods result in difference in heights. Fifteen areas each 0.02 ha in size are laid our over a fairly homogeneous area. Five site preparation treatments are randomly applied to 15 plots. One hundred trees are planted (same genetic stock and same age) in each area. At the end of 5 years, the heights of EACH seedling in each plot were measured.

We have three hierarchical levels:

- Treatments
- Experimental units within treatments – level at which the treatment is applied
- Trees within experimental units – are “nested” in experimental units; different trees in different experimental units

We have variation:

- Between treatments
- Between experimental units within each treatment
- Between trees within each experimental unit in each treatment

Notation

Population: $y_{ijl} = \mu + \tau_{TRj} + \varepsilon_{EUij} + \varepsilon_{SUijl}$

y_{ijl} = response variable measured on sample l of experimental unit i and treatment j

j=1 to J treatments

μ = the grand or overall mean regardless of treatment

τ_{TRj} = the treatment effect

μ_j = the mean for treatment j; grand mean plus the treatment effect

The difference between a particular measure for a sample l, an experimental unit i, and the mean for the treatment j that was applied to it is now two parts:

$$\varepsilon_{EUij} + \varepsilon_{SUijl} = y_{ijl} - \mu_j$$

The error for the experimental unit and the error for the sample unit in the experimental unit.

For the experiment:

$y_{ijl} = \bar{y}_{\bullet\bullet\bullet} + \hat{\tau}_{TRj} + e_{EUij} + e_{SUijl}$

$\bar{y}_{\bullet\bullet\bullet}$ = the grand or overall mean of all measures from the experiment regardless of treatment

$\bar{y}_{\bullet j \bullet}$ = the mean of all measures for treatment j ; under error variance assumptions, will be an unbiased estimate of μ_j

$\hat{\tau}_{TRj}$ = the difference between the mean of experiment measures for treatment j and the overall mean of measures from all treatments

n_j = the number of experimental units measured in treatment j; = n if these are all equal.

n_T = the number of experimental units measured over all treatments = $\sum_{j=1}^{J} n_j$; = J X n if these are all equal.

m_{ij} = the number of samples measured in experimental unit i of treatment j ; $m_{ij} = m$ if these are all equal

$m_T = \sum_{j=1}^{J}\sum_{i=1}^{n_j} m_{ij}$ the number of samples measured in experimental unit i of treatment j ; $m_T = J$ X n X $m = Jnm$ if these are all equal

Analysis Methods

Possible ways to analyze this experiment are:

1. Simplify this by calculating averages for each experimental unit and use these in the analysis of variance (would then be Completely Randomized Design: one factor, already covered)

2. Keep each sample observation, and use least squares to calculate as per CRD: one factor, but also estimate the within experimental unit variance (will cover this now)

3. Keep each sample observation, and use a mixed model and maximum likelihood, with the two "error terms" as random-effects (e.g., PROC MIXED in SAS).

Option 1 is simpler; Options 2 and 3 allow us to look at the variability within experimental unit.

Another option you will see but NOT CORRECT!!

- Keep each sample observation and treat this as one experimental unit as if this was a CRD: one factor experiment.

Since the treatment was NOT applied at this level, this **analysis would not be correct**. Treatments are randomly assigned to the experimental unit level. **The degrees of freedom and the estimated error variance used in the F-test would not be correct. In some literature, the samples are termed "pseudo-replications".**

We then calculate:

1) Sum of squared differences between the observed values and the overall mean (SSy):

$$SSy = \sum_{j=1}^{J}\sum_{i=1}^{n_j}\sum_{l=1}^{m_{ij}}\left(y_{ijl} - \bar{y}_{\bullet\bullet\bullet}\right)^2$$

$$df = \sum_{j=1}^{J}\sum_{i=1}^{n_j} m_{ij} - 1 = m_T - 1$$

2) Sum of squared differences between the treatment means, and the grand mean, weighted by the number of experimental units in each treatment (SS_{TR})

$$SS_{TR} = \sum_{j=1}^{J}\sum_{i}^{n_j} m_{ij}\left(\bar{y}_{\bullet j\bullet} - \bar{y}_{\bullet\bullet\bullet}\right) \quad df = J - 1$$

If the number of samples per experimental unit are all the same (m) and the number of experimental units per treatment are all the same (n), this becomes:

$$SS_{TR} = nm\sum_{j=1}^{J}\left(\bar{y}_{\bullet j\bullet} - \bar{y}_{\bullet\bullet\bullet}\right) \quad df = J - 1$$

3) Sum of squared differences between the means values for each experimental unit and the treatment means

$$SS_{EE} = \sum_{j=1}^{J} \sum_{i=1}^{n_j} m_{ij} \left(\bar{y}_{ij\bullet} - \bar{y}_{\bullet j\bullet} \right)^2$$

$$df = n_T - J = \sum_{j=1}^{J} (n_j - 1)$$

If the number of samples per experimental unit are all the same (m) and the number of experimental units per treatment are all the same (n), this becomes:

$$SS_{EE} = m \sum_{j=1}^{J} \sum_{i=1}^{n} \left(\bar{y}_{ij\bullet} - \bar{y}_{\bullet j\bullet} \right)^2$$

$$df = n_T - J = J(n-1)$$

This is then experimental units nested in treatments.

4) Sum of squared differences between the observed values for each experimental unit and the treatment means

$$SS_{SE} = \sum_{j=1}^{J} \sum_{i=1}^{n_j} \sum_{l=1}^{m_{ij}} \left(y_{ijl} - \bar{y}_{ij\bullet} \right)^2 \quad df = \sum_{j=1}^{J} \sum_{i=1}^{n_j} (m_{ij} - 1)$$

If the number of samples per experimental unit are all the same (m) and the number of experimental units per treatment are all the same (n), this becomes:

$$SS_{SE} = \sum_{j=1}^{J} \sum_{i=1}^{n} \sum_{l=1}^{m} \left(y_{ijl} - \bar{y}_{ij\bullet} \right)^2 \quad df = Jn(m-1)$$

This is then sample units nested in experimental units and treatments.

AND:

$$SSy = SS_{TR} + SS_{EE} + SS_{SE}$$

Test for differences among treatment means

The main question is: Are the treatment means different?

H_0: $\mu_1 = \mu_2 = \ldots = \mu_J$

H_1: not all the same

OR:

What is the appropriate F-test? Need to look at the expected mean squares.

Expected Mean Square: Treatments Fixed, and assuming the number of experimental units per treatment, and samples per experimental unit are all equal

Source	df	SS	MS	Expected Mean Squares
Treatment	J-1	SS_{TR}	MS_{TR}	$\sigma_{SE}^2 + m\sigma_{EE}^2 + \phi_A$
Exp. Error	$J(n$-1)	SS_{EE}	MS_{EE}	$\sigma_{SE}^2 + m\sigma_{EE}^2$
Sampling Error	$Jn(m$-1)	SS_{SE}	MS_{SE}	σ_{SE}^2
Total	Jmn -1	SSy		

Expected Mean Square: Treatments Random, and assuming the number of experimental units per treatment, and samples per experimental unit are all equal

Source	df	SS	MS	Expected Mean Squares
Treatment	J-1	SS_{TR}	MS_{TR}	$\sigma_{SE}^2 + m\sigma_{EE}^2 + nm\sigma_{TR}^2$
Exp. Error	$J(n$-1)	SS_{EE}	MS_{EE}	$\sigma_{SE}^2 + m\sigma_{EE}^2$
Sampling Error	$Jn(m$-1)	SS_{SE}	MS_{SE}	σ_{SE}^2
Total	Jmn -1	SSy		

F-test is the same for Fixed-effects or Random Effects Treatments:

Source	MS	F	p-value
Treatment	MS_{TR}	$F= MS_{TR}/MS_{EE}$	Prob F> $F_{(J\text{-}1),(\ nT\ \text{-}J),1\text{-}\alpha}$
Exp. Error	MS_{EE}		
Sampling Error	MS_{SE}		
Total			

If $F > F_{(J-1, n_T - J, 1-\alpha)}$ we reject H_0 and conclude that there is a difference between the treatment means.

Assumptions: Check residuals as other experiments. NOTE: There are also assumptions on the experimental error – could also be checked.

Tests for pairs of Means: Use experimental error as the error term rather than the default which is the sampling error.

Confidence Intervals:

$$\bar{y}_{\bullet j \bullet} \pm t_{(dfEE),1-\alpha/2} \sqrt{\frac{MS_{EE}}{\sum_{i=1}^{n_j} m_{ij}}}$$

e.g., use the mean square used for the denominator of the F-test (MS_{EE}), and divide by the number of observations (samples) for that treatment. Degrees of freedom for the *t* corresponds to the df for the mean square (*dfEE*).

Example from Textbook:

- Have three temperatures: low, medium, and high (*J*=3)
- For each, we have two experimental units (batches) (n=2)
- Randomly assign temperatures to each batch
- For each batch, we have three loaves of bread (m=2)
- The response variable is crustiness of bread.

Data:

temp	**batch**	**observation**	**yijl**
low	1	1	4
low	1	2	7
low	1	3	5
low	2	1	12
low	2	2	8
low	2	3	10
medium	1	1	14
medium	1	2	13
medium	1	3	11
medium	2	1	9
medium	2	2	10
medium	2	3	12
high	1	1	14
high	1	2	17
high	1	3	15
high	2	1	16
high	2	2	19
high	2	3	18

SAS code: Three options presented

1. Using PROC GLM and the sample observations. **Model yijk= treat batch(treat);**
2. Using the averages for each experimental unit and PROC GLM. **Model yijk=treat;**
3. Using PROC MIXED, and the sample observations. **Model yijk=treat; Random batch(treat);**

```
PROC IMPORT OUT= WORK.onesub
     DATAFILE= "E:\frst430\lemay\examples\
            subsampling_neter_newest_p1109.xls"
     DBMS=EXCEL REPLACE;       SHEET="data$";
     GETNAMES=YES;    MIXED=NO;   SCANTEXT=YES;
     USEDATE=YES;       SCANTIME=YES;
RUN;

options ls=70 ps=50 pageno=1;

* Analysis 1. first, use GLM and bring in the
Experimental error and the Sampling error into
the design;
PROC GLM data=onesub;
class temp batch;
model yijl=temp batch(temp);
random batch(temp)/test;
test h=temp e=batch(temp);
lsmeans temp /e=batch(temp) pdiff tdiff;
output out=glmout r=resid p=predict;
run;

proc plot data=glmout;
plot resid*predict='*';
run;
proc univariate data=glmout normal plot;
var resid;
run;
```

```
*Analysis 2.  This is least squares but using
the mean of all samples in each experimental
unit;
proc sort data=onesub;
by temp batch;
run;

proc means data=onesub;
var yijl;
by temp batch;
output out=meany mean=ybars;
run;

PROC GLM  data=meany;
class temp;
model ybars=temp;
lsmeans temp /pdiff tdiff;
output out=glmout2 r=resid2 p=predict2;
run;

proc plot data=glmout2;
plot resid2*predict2='*';
run;
proc univariate data=glmout2 normal plot;
var resid2;
run;

* Analysis 3: this is using maximum likelihood
for a mixed model to estimate variances and get
correct F-tests;

PROC MIXED data=onesub;
class temp batch;
model yijl=temp;
lsmeans temp/pdiff;
random batch(temp);
run;
```

Analysis 1: GLM using samples with experimental error given as batch(treat), and sampling error as the Error term.

```
                  The SAS System            1

                  The GLM Procedure

               Class Level Information

         Class         Levels    Values
         temp               3    high low medium
         batch              2    1 2

    Number of Observations Read          18
    Number of Observations Used          18

                The SAS System

               The GLM Procedure

Dependent Variable: yijl   yijl

                        Sum of
Source      DF         Squares  Mean Square   F Value

Model        5    284.4444444  56.8888889     21.79
Error       12     31.3333333   2.6111111
Corrected
   Total    17    315.7777778

                 Source                 Pr > F
                 Model                  <.0001
                 Error
                 Corrected Total


R-Square     Coeff Var      Root MSE     yijl Mean

0.900774      13.59163      1.615893      11.88889
```

(**NOTE: Type I SS removed)**

```
Source      DF     Type III SS  Mean Square   F Value
temp         2    235.4444444  117.7222222     45.09
batch(temp)  3     49.0000000   16.3333333      6.26

                 Source                 Pr > F
                 temp                   <.0001
                 batch(temp)            0.0084
```

NOTE: Variance components and GLM Mixed model analysis given by SAS removed – often not correct.

```
                 Least Squares Means
Standard Errors and Probabilities Calculated Using
the Type III MS for batch(temp) as an Error Term


                                  LSMEAN
temp        yijl LSMEAN      Number
high         16.5000000           1
low           7.6666667           2
medium       11.5000000           3

     Least Squares Means for Effect temp
    t for H0: LSMean(i)=LSMean(j) / Pr > |t|

    Dependent Variable: yijl

i/j           1             2             3
1                    3.785714      2.142857
                       0.0323        0.1215
2      -3.78571                    -1.64286
         0.0323                      0.1990
3      -2.14286      1.642857
         0.1215        0.1990

NOTE: To ensure overall protection level, only
probabilities associated with pre-planned
comparisons should be used.
```

```
Dependent Variable: yijl   yijl

  Tests of Hypotheses Using the Type III
     MS for batch(temp) as an Error Term

Source      DF   Type III SS  Mean Square   F Value
temp         2   235.4444444  117.7222222      7.21

                Source                 Pr > F
                temp                   0.0715
```

```
     Plot of resid*predict.  Symbol used is '*'.

 resid ,
 2.000 ˆ                    *
       ,
       ,
 1.667 ˆ *                   *                   *
       ,
       ,
 1.333 ˆ                               *                   *
       ,
       ,
 1.000 ˆ
       ,
       ,
 0.667 ˆ
       ,
       ,
 0.333 ˆ                               *                   *
       ,
       ,
 0.000 ˆ                    *
       ,
       ,
-0.333 ˆ *                   *                   *
       ,
       ,
-0.667 ˆ
       ,
       ,
-1.000 ˆ
       ,
       ,
-1.333 ˆ *                   *                   *
       ,
       ,
-1.667 ˆ                               *                   *
       ,
       ,
-2.000 ˆ                    *
       ,
       Šˆ---------ˆ---------ˆ---------ˆ---------ˆ---------ˆ---------ˆ-
       5.0       7.5      10.0      12.5      15.0      17.5      20.0

                                  predict
```

```
              The UNIVARIATE Procedure
                 Variable:  resid
```

NOTE: All outputs removed except for Normality tests and box plot and normality plot

```
              Tests for Normality

Test                  --Statistic---    -p Value------

Shapiro-Wilk          W     0.908031    Pr<W      0.0794
Kolmogorov-Smirnov    D      0.17031    Pr>D     >0.1500
Cramer-von Mises      W-Sq  0.084708    Pr>W-Sq   0.1732
Anderson-Darling      A-Sq  0.605378    Pr>A-Sq   0.0984
```

```
Stem Leaf                           #             Boxplot
   2 0                              1                |
   1 777                            3                |
   1 33                             2             +-----+
   0                                              |     |
   0 033                            3             |  +  |
  -0 333                            3             *-----*
  -0                                              |     |
  -1 333                            3             +-----+
  -1 77                             2                |
  -2 0                              1                |
     ----+----+----+----+
```

```
               The UNIVARIATE Procedure
                  Variable:  resid

                    Normal Probability Plot
 2.25+                                        +++*
     |                                 *  *+*+
     |                              * *++++
 0.75+                             ++++
     |                         +**+*
     |                     *+**
-0.75+                  ++++
     |              +++** *
     |       *   +*+*
-2.25+       ++++
      +----+----+----+----+----+----+----+----+----+----+
          -2        -1         0        +1        +2
```

Analysis 2: GLM using averages for each sample unit experimental error is now the Error term.

```
               The SAS System
               The MEANS Procedure

-------------- temp=high batch=1 ------------------

            Analysis Variable : yijl yijl

N      Mean       Std Dev      Minimum      Maximum
-------------------------------------------------
3  15.3333333    1.5275252   14.0000000  17.0000000
-------------------------------------------------

--------------- temp=high batch=2 -------

          Analysis Variable : yijl yijl

   N     Mean       Std Dev     Minimum     Maximum
-------------------------------------------------
3     17.6666667    1.5275252  16.0000000 9.0000000
-------------------------------------------------

--------------------- temp=low batch=1 -------

          Analysis Variable : yijl yijl

   N     Mean       Std Dev     Minimum     Maximum
-------------------------------------------------
 3     5.3333333   1.5275252    4.0000000 7.0000000
---------------------------------------------------
```

```
----------------- temp=low batch=2 -------

            Analysis Variable : yijl yijl

   N     Mean       Std Dev     Minimum     Maximum
-------------------------------------------------
3      10.0000000   2.0000000  8.0000000 12.0000000
---------------------------------------------------

--------------------- temp=medium batch=1 ---------

               Analysis Variable : yijl yijl
   N     Mean       Std Dev     Minimum     Maximum
-------------------------------------------------
  3    12.6666667  1.5275252  11.0000000 14.0000000
-------------------------------------------------


----------------- temp=medium batch=2 -------------

               Analysis Variable : yijl yijl

   N     Mean       Std Dev     Minimum   Maximum
-------------------------------------------------
   3   10.3333333  1.5275252   9.0000000 12.0000000
---------------------------------------------------
```

```
                 The SAS System

              The GLM Procedure

              Class Level Information

          Class         Levels    Values
          temp               3    high low medium
          batch              2    1 2


          Number of Observations Read           6
          Number of Observations Used           6
                    The GLM Procedure

Dependent Variable: ybars   yijl

                          Sum of
Source        DF         Squares    Mean Square   F Value
Model          2     78.48148148    39.24074074      7.21
Error          3     16.33333333     5.44444444
Corrected
   Total       5     94.81481481

              Source                 Pr > F
               Model                 0.0715
               Error
               Corrected Total


R-Square     Coeff Var      Root MSE    ybars Mean

0.827734      19.62617      2.333333      11.88889
```

NOTE: Type I SS removed from the SAS outputs.

```
Source    DF     Type III SS     Mean Square   F Value
temp       2     78.48148148     39.24074074      7.21

                  Source                 Pr > F
                  temp                   0.0715

                 The SAS System

                             LSMEAN
temp      ybars LSMEAN      Number

high        16.5000000           1
low          7.6666667           2
medium      11.5000000           3


            Least Squares Means for Effect temp
          t for H0: LSMean(i)=LSMean(j) / Pr > |t|

               Dependent Variable: ybars

i/j          1             2             3

1                     3.785714      2.142857
                        0.0323        0.1215
2     -3.78571                     -1.64286
        0.0323                        0.1990
3     -2.14286        1.642857
        0.1215          0.1990


NOTE: To ensure overall protection level, only
probabilities associated with pre-planned
comparisons should be used.
```

```
                   The SAS System

       Plot of resid2*predict2.  Symbol used is '*'.

resid2 ,
       ,
 2.333 ˆ        *
       ,
       ,
       ,
       ,
       ,
       ,
 1.167 ˆ                            *                        *
       ,
       ,
       ,
       ,
       ,
       ,
 0.000 ˆ
       ,
       ,
       ,
       ,
       ,
       ,
-1.167 ˆ                            *                        *
       ,
       ,
       ,
       ,
       ,
       ,
-2.333 ˆ        *
       ,
       Šˆ---------ˆ---------ˆ---------ˆ---------ˆ---------ˆ---------ˆ-
        6         8         10        12        14        16        18

                                   predict2
```

```
                  The UNIVARIATE Procedure
                   Variable:  resid2
```

NOTE: removed all but the normality tests and normality plots.

```
              Tests for Normality

Test              --Statistic---    --p Value------
Shapiro-Wilk       W    0.912907    Pr<W     0.4558
Kolmogorov-Smirnov D    0.240697    Pr>D    >0.1500
Cramer-von Mises  W-Sq   0.06404    Pr>W-Sq >0.2500
Anderson-Darling  A-Sq  0.352911    Pr>A-Sq >0.2500
```

```
                       The UNIVARIATE Procedure
                          Variable:  resid2

                         Normal Probability Plot
      2.5+                                        +*+++
         |                             *   *+++++
         |                           ++++++
         |                     +++++
         |               +++++*   *
     -2.5+         +++*+
          +----+----+----+----+----+----+----+----+----+----+----+
             -2         -1          0        +1         +2
```

Analysis 3: MIXED using each sample unit value.

```
                    The SAS System
                 The Mixed Procedure

            Model Information
Data Set                     WORK.ONESUB
Dependent Variable           yijl
Covariance Structure         Variance
                             Components
Estimation Method            REML
Residual Variance Method     Profile
Fixed Effects SE Method      Model-Based
Degrees of Freedom Method    Containment
             Class Level Information

          Class    Levels    Values
          temp          3    high low medium
          batch         2    1 2

                  Dimensions
     Covariance Parameters               2
     Columns in X                        4
     Columns in Z                        6
     Subjects                            1
     Max Obs Per Subject                18

          Number of Observations
 Number of Observations Read                18
 Number of Observations Used                18
 Number of Observations Not Used             0
```

```
              Iteration History

Iteration Evaluations -2 Res Log Like Criterion
0             1        73.11545106
1             1        67.84036856    0.00000000

            Convergence criteria met.

              Covariance Parameter
              Estimates
        Cov Parm        Estimate
        batch(temp)       4.5741
        Residual          2.6111

              Fit Statistics
       -2 Res Log Likelihood              67.8
       AIC (smaller is better)            71.8
       AICC (smaller is better)           72.8
       BIC (smaller is better)            71.4

          Type 3 Tests of Fixed Effects
         Num    Den
Effect    DF     DF     F Value     Pr > F
temp       2      3        7.21     0.0715

                  Least Squares Means

                         Standard
Effect temp   Estimate   Error    DF   t Value Pr>|t|
temp   high    16.5000   1.6499    3     10.00 0.0021
temp   low      7.6667   1.6499    3      4.65 0.0188
temp   medium 11.5000   1.6499    3      6.97 0.0061
```

```
Differences of Least Squares Means

                        Standard
Effect temp temp Estimate Error DF t Value Pr>|t|
temp high  low    8.8333  2.3333 3  3.79   0.0323
temp high medium  5.0000  2.3333 3  2.14   0.1215
temp low  medium -3.8333  2.3333 3 -1.64   0.1990
```

RCB: One Factor Experiment, Fixed Effects with subsampling

- Blocked (random or fixed-effect, usually random)
- Fixed-effect factor A (we will label this as TR for treatment)
- Experimental units – level at which the block with factor A combinations are applied; may be one experimental unit or more than one (generalized RCB or RCB with replicates)
- Sampling units – number of items measured within each experimental unit.

<u>Notation for a Generalized RCB with subsampling:</u>

Population:

$$y_{ijl} = \mu + \tau_{BLKj} + \tau_{TRk} + \tau_{BLK\times TRjk} + \varepsilon_{EUijk} + \varepsilon_{SUijkl}$$

y_{ijkl} = response variable measured on sample *l* of experimental unit *i,* block *j,* and treatment *k*

The difference between a particular measure for a sample *l*, an experimental unit *i*, and the mean for the block *j* and treatment *k* combination that was applied to it is now two parts:

$$\varepsilon_{EUijk} + \varepsilon_{SUijkl}$$

The error for the experimental unit and the error for the sample unit in the experimental unit.

For the experiment:

$$y_{ijkl} = \bar{y}_{\bullet\bullet\bullet\bullet} + \hat{\tau}_{BLKj} + \hat{\tau}_{TRk} + \hat{\tau}_{BLK\times TRjk} + e_{EUijk} + e_{SUijkl}$$

$\bar{y}_{\bullet\bullet\bullet\bullet}$ = the grand or overall mean of all measures from the experiment regardless of treatment

$\bar{y}_{\bullet jk\bullet}$ = the mean of all measures for block j and treatment k ; under error variance assumptions, will be an unbiased estimate of μ_{jk}

$\bar{y}_{\bullet j\bullet\bullet}$ = the mean of all measures for block j will be an unbiased estimate of μ_j

$\bar{y}_{\bullet\bullet k\bullet}$ = the mean of all measures for treatment k will be an unbiased estimate of μ_k

n_{jk} = the number of experimental units measured in each combination of block by treatment; $= n$ if these are all equal.

n_T = the number of experimental units measured over all treatments = $\sum_{k=1}^{K}\sum_{j=1}^{J} n_{jk}$; $= J$ X K X n if these are all equal.

m_{ijk} = the number of samples measured in experimental unit i of treatment and block jk ; $m_{ijk} = m$ if these are all equal

$m_T = \sum_{k=1}^{K}\sum_{j=1}^{J}\sum_{i=1}^{n_j} m_{ijk}$ the number of samples measured in experimental unit i of treatment j ; $m_T = J$ X K X n X m = $JKnm$ if these are all equal

Analysis Methods

Possible ways to analyze this experiment are:

4. Simplify this by calculating averages for each experimental unit and use these in the analysis of variance (would then be Generalized Randomized Complete Block Design: one factor, already covered)

5. Keep each sample observation, and use least squares or to calculate as per Generalized Random Complete Block: one factor, but also estimate the within experimental unit variance (will cover this now)

6. Keep each sample observation, and use a mixed model and maximum likelihood, with the two "error terms" as random-effects (e.g., PROC MIXED in SAS).

Option 1 is simpler; Options 2 and 3 allow us to look at the variability within experimental unit.

Another option you will see but NOT CORRECT!!

- Keep each sample observation and treat this as one experimental unit
- Since the treatment was NOT applied at this level, this **analysis would not be correct**. Treatments are randomly assigned to the experimental unit level. **The degrees of freedom and the estimated error variance used in the F-test would not be correct. In some literature, the samples are termed "pseudo-replications".**

We then calculate:

$$SSy = SS_{BLK} + SS_{TR} + SS_{BLK \times TR} + SS_{EE} + SS_{SE}$$

For a Generalized Randomized Complete Block design with one-factor, and subsampling of the experimental units.

Main Questions:

1. For the generalized RCB, we can look at interactions between blocks and the treatment (cannot, if there is only one experimental unit per treatment and block combination with the more simpler RCB, since the interaction <u>is</u> the exp. unit error.). Test this first.
2. Then, if no interaction, test if there is a difference among the Factor A levels (the treatment).
3. Not really interested in the blocks.

What is the appropriate F-test? Need to look at the expected mean squares.

Expected Mean Square: Treatments and Blocks BOTH Fixed, and assuming the number of experimental units per treatment, and samples per experimental unit are all equal

Source	df	SS	MS	Expected Mean Squares
Block	J-1	SS_{BLK}	MS_{BLK}	$\phi_{BLK} + m\sigma_{EE}^2 + \sigma_{SE}^2$
Treatment	K-1	SS_{TR}	MS_{TR}	$\phi_{TR} + m\sigma_{EE}^2 + \sigma_{SE}^2$
Block X Treatment	(J-1)(K-1)	$SS_{BLK\ X\ TR}$	$MS_{BLK\ X\ TR}$	$\phi_{BLK \times TR} + m\sigma_{EE}^2 + \sigma_{SE}^2$
Exp. Error	$JK(n$-1)	SS_{EE}	MS_{EE}	$\sigma_{SE}^2 + m\sigma_{EE}^2$
Sampling Error	$JKn(m$-1)	SS_{SE}	MS_{SE}	σ_{SE}^2
Total	$JKnm$ -1	SSy		

Expected Mean Square: Treatments Fixed, but Blocks are Random, and assuming the number of experimental units per treatment, and samples per experimental unit are all equal

Source	df	SS	MS	Expected Mean Squares
Block	J-1	SS_{BLK}	MS_{BLK}	$Knm\sigma_{BLK}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$
Treatment	K-1	SS_{TR}	MS_{TR}	$\phi_{TR} + nm\sigma_{BLK\times TR}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$
Block X Treatment	(J-1)(K-1)	$SS_{BLK\ X\ TR}$	$MS_{BLK\ X\ TR}$	$nm\sigma_{BLK\times TR}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$
Exp. Error	$JK(n$-1)	SS_{EE}	MS_{EE}	$\sigma_{SE}^2 + m\sigma_{EE}^2$
Sampling Error	$JKn(m$-1)	SS_{SE}	MS_{SE}	σ_{SE}^2
Total	$JKnm$ -1	SSy		

Assumptions: Check residuals as other experiments. NOTE: There are also assumptions on the experimental error – could also be checked.

Tests for pairs of Means: Use experimental error as the error term rather than the default which is the sampling error.

Confidence Intervals: both Blocks and Treatments are fixed:

$$\bar{y}_{\bullet\bullet k\bullet} \pm t_{(dfEE),1-\alpha/2}\sqrt{\frac{MS_{EE}}{\sum_{j=1}^{J}\sum_{i=1}^{n_{jk}} m_{ijk}}}$$

e.g., use the mean square used for the denominator of the F-test (MSEE), and divide by the number of observations (samples) for that Factor level k. Degrees of freedom for the t corresponds to the df for the mean square (dfEE).

Confidence Intervals: Blocks Random and Treatments are fixed:

$$\bar{y}_{\bullet\bullet k\bullet} \pm t_{(dfBLK\times TR),1-\alpha/2}\sqrt{\frac{MS_{BLK\times TR}}{\sum_{j=1}^{J}\sum_{i=1}^{n_{jk}} m_{ijk}}}$$

Analysis of Covariance (ANCOVA)

For experimental designs covered so far:

- The response variable (y) is a continuous variable
- A number of class variables (x's) are used (effects) to explain the variation in the response variable, via a linear model
- We are interested in differences in means for each class variable (fixed-effects) or in the variance in the response variable that is due to the class variable (random-effects).

For example, for CRD: two factors, mixed, we were interested in:

- Whether there is an interaction between Factor A and Factor B.
- If there is no interaction
    - whether the means for levels of Factor A differ, and if so, which ones differ?
    - and whether Factor B accounts for some of the variability in the response variable, and if so, how much?

For linear regression analysis, covered in the beginning of the course:

- The dependent variable (y) is a continuous variable
- A number of continuous predictor variables (x's) are used to explain the variation in the dependent variable in a linear equation.
- We also introduced class variables (x's also) to help explain the variation in the dependent variable, represented by:
    - Dummy variables to alter the intercept
    - Interactions between dummy variables and continuous predictor variable to alter the slope.

Analysis of covariance is an experimental design, where we add continuous explanatory variables (called covariates) to help explain the variability in the response variable, for example:

- Record the initial weight of all fish prior to adding different foods. Use this initial weight as a covariate
- Record soil moisture of all plots in a field prior to applying different treatments. Use this soil moisture as a covariate.

The covariates help "even-out" conditions that we were not able to control in trying to obtain homogeneous treatment units, and explain some of the variation in the response variable.

Blocking does this in a similar fashion, but:

- Blocking restricts the randomization of treatments to experimental units (treatments assigned randomly within blocks)
- Blocks are class variables.

This is very similar to using continuous and class variables in regression analysis to explain the variation in the dependent variable, except:

- We have an experiment, and we are trying to assign cause and effect
- For analysis of covariance:
    - the slopes are considered the same over all treatments (common slope), in order to assess the impacts of different factors (called homogeneity of slopes)
    - This means that the treatment does not affect the relationship (linear trend) between y and x
    - This must be tested, as the slope of y versus x may vary by treatment
- We use these covariates to "adjust" the factor level means to a common value (usually the mean) of the covariate.

Example:

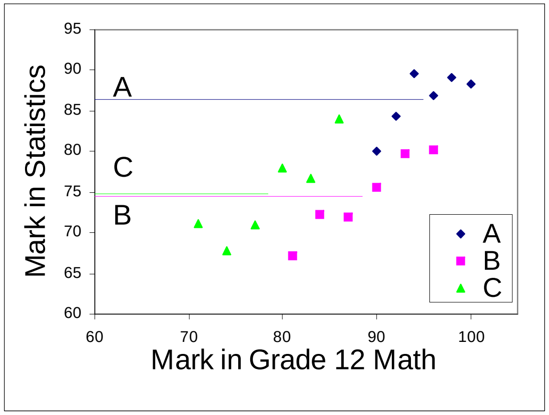
UBC would like to evaluate three ways of teaching basic statistics:
(A) stats dept. method (3 lectures),
(B) computer method (3 lectures plus lab using statistical software with no lab write-up),
(C) applied science method (3 lectures plus written lab).
"Success" is measured as a grade in a common examination for all students.

The response (exam grade) might be related to abilities before taking the course:

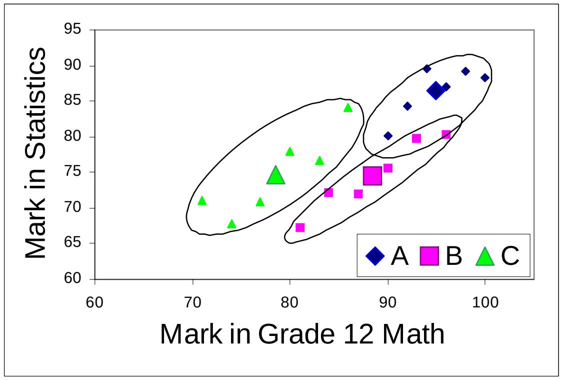
- Grade in Math 12 is used as a covariate (x variable) and obtained for each student.
- Then students are randomly assigned to one of the three class types.

The Math 12 grade is then used to "adjust" the grade in the common exam.

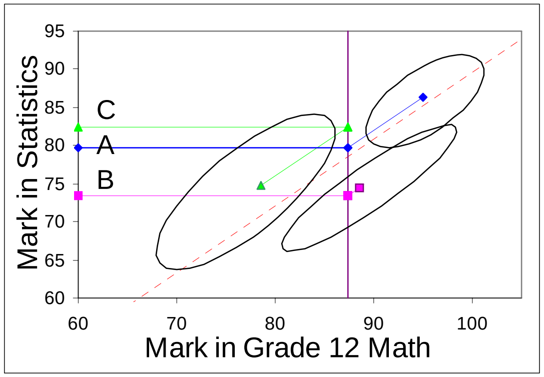
Looking at the trends, between Mark in Stats (y) versus Mark in Grade 12 math(x), the slopes appear to be similar.



Ignoring the Grade 12 March, the mark in Statistics is higher for A, and B and C are similar.



Using the covariate, and adjusting the means along the y vs x trend line to the average Mark in Grade 12 Math, C and A are similar, and B is different



If the Math grade was not used as a covariate, the conclusion would be much different.

Model:

We add a covariate to whichever experimental design we wish to use.

For example, using an RCB with two fixed-effect factors, we add in the covariate.

Population:

$$y_{jkl} = \mu + \beta(x_{jkl} - \bar{x}) + \tau_{BLK\,j} + \tau_{Ak} + \tau_{Bl} + \tau_{ABkl} + \varepsilon_{jkl}$$

y_{jkl} = response variable measured on block *j* and treatment *kl*

j=1 to *J* blocks; *k*=1 to *K* levels for Factor A; *l*=1 to *L* levels for Factor B; and definition of terms follows other designs.

x_{jkl} is a measurement of the covariate for a particular experimental unit, standardized around the mean of x over all observations, as this can be easier to interpret; β is the slope of the line between y and x.

The expected mean squares are the same as the design without the covariate.

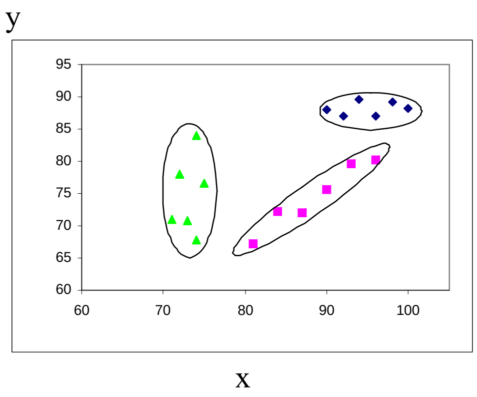
The covariate will take up one degree of freedom from the error term.

Variations in ANCOVA:

1. More than one covariate. Can add in more than one continuous variable.

- Must check for ANY interactions between continuous variables and each of the class variables (effects) in the experiment.
- Each covariate will have a df of 1 (like a continuous variable in regression), and this will be taken away from the error term df.

2. Slopes are not equal



Interactions between class variables and continuous variables are significant. Can test these using partial F-tests as we did for regression using dummy variables to represent classes.

- Get generalized linear models (GLM) results for all class variables (blocks, factors, interactions, etc.), all continuous x-variables (covariates) , and interactions between covariates and all class variables [full model]
    - Record the df(model) and df(error) [full]
    - Record the SSmodel (includes all class and continuous variables and interactions) and SSerror [full]
- Get generalized linear models results for all class variables (blocks, factors, interactions, etc.), all continuous x-variables (covariates) [reduced model]
    - Record the df(model) and df(error) [reduced]
    - Record the SSmodel and SSerror [reduced]

$$partial\ F = \frac{\left(SSreg(full) - SSreg(reduced)\right)/r}{SSE/(dferror)(full)}$$

OR

$$partial\ F = \frac{\left(SSE(reduced) - SSE(full)\right)/r}{SSE/(dferror)(full)}$$

$$= \frac{(SS \text{ due to dropped interaction variable(s)})/r}{MSE(full)}$$

Where *r* is the number of x-variables that were dropped. Equals: (1)the model degrees of freedom for the full model minus the model degrees of freedom for the reduced model, OR (2) the error degrees of freedom for the reduced model, minus the error degrees of freedom for the full model)

- Under H0, this follows an F distribution for a 1- α/2 percentile with *r* and *n*-*m*-1 (full model) degrees of freedom.
- If the F for the fitted equation is larger than the F from the table, we reject H0 (not likely true). There are different slopes (relationship between y and x) for different treatments (combinations of the class variable levels)

- Harder to interpret, as with any interaction
  - Use graphs to show relationships
  - Switch to a regression approach to finding equations using the continuous and class variables (represented as dummies) and interpret these results.

(Assignment 8 as the example during class)

Expected Mean Squares to get called components of variance

1. Get these from a book where they are already determined for your type of design. Must know which of your factors are fixed and which are random.
2. Use the EMS rules to determine these. Expected Means Squares "rules": Appendix D of text (white or blue editions)

Calculation of Expected Mean Squares Using an Example

Steps to Derive Expected Mean Squares.

1. Write up linear model. For example, RCB with more than one experiment unit for each treatment within a block (generalized RCB):

   $$y_{ijk} = \mu + \tau_{BLK\,j} + \tau_{TR\,k} + \tau_{BLK\times TR\,jk} + \varepsilon_{i(jk)}$$

   Note brackets added around *jk*

   for *j*=1 to *J*, *k*=1 to K, *i*=1 to *n*
   (blocks) (treatments) (replications)

   NOTE: will use instead:

   for *j*=1 to *b*, *k*=1 to *t*, *i*=1 to *n*
   (blocks) (treatments) (replications)

   Then *b* is taken from *B* possible blocks;
   t is taken from *T* possible treatments;
   n is taken from *N* possible replicates within each *jk*. Since the replicates are nested within each Treament /Block combination, we have added brackets to indicate this.

2. Generate table of indices and number of factor levels etc.

Effect	n i	b j	t k	
τ_{BLKj}				
τ_{TRk}				
$\tau_{BLK\ X\ TRjk}$				
$\varepsilon_{i(jk)}$				

3. Indicate which effects are fixed versus random and add a symbol for each component. Note that we will use the symbol for variance (random-effects) for all components, and change this to ϕ_{TR} for the fixed-effects treatment at the end.

Type: Effect	R n i	R b j	F t k	Symbol
τ_{BLKj}				σ^2_{BLK}
τ_{TRk}				σ^2_{TR}
$\tau_{BLK\ X\ TRjk}$				$\sigma^2_{BLK\times TR}$
$\varepsilon_{i(jk)}$				σ^2_{ε}

4. Fill in the table by:
   a. Put down a "1", where subscript is bracketed (nested)

Type:	R	R	F	
	n	b	t	
Effect	i	j	k	Symbol
τ_{BLKj}				σ^2_{BLK}
τ_{TRk}				σ^2_{TR}
$\tau_{BLK\ X\ TRjk}$				$\sigma^2_{BLK\times TR}$
$\varepsilon_{i(jk)}$		1	1	σ^2_{ε}

   b. For each effect, put down the end value (e.g., t for number of treatments in the experiment) for each subscript that does *not* appear for the effect

Type:	R	R	F	
	n	b	t	
Effect	i	j	k	Symbol
τ_{BLKj}	n		t	σ^2_{BLK}
τ_{TRk}	n	b		σ^2_{TR}
$\tau_{BLK\ X\ TRjk}$	n			$\sigma^2_{BLK\times TR}$
$\varepsilon_{i(jk)}$		1	1	σ^2_{ε}

c. Add the “finite population correction factor” for each of the other factors: e.g., for Blocks, this is $\left(\frac{B-b}{B}\right)=\left(1-\frac{b}{B}\right)$

Type:	R	R	F	
	n	b	t	
Effect	i	j	k	Symbol
τ_{BLKj}	n	$\left(1-\frac{b}{B}\right)$	t	σ_{BLK}^{2}
τ_{TRk}	n	b	$\left(1-\frac{t}{T}\right)$	σ_{TR}^{2}
$\tau_{BLK\ X\ TRjk}$	n	$\left(1-\frac{b}{B}\right)$	$\left(1-\frac{t}{T}\right)$	$\sigma_{BLK\times TR}^{2}$
$\varepsilon_{i(jk)}$	$\left(1-\frac{n}{N}\right)$	1	1	σ_{ε}^{2}

5. Change FPC values to either 1 or zero.
   a. If factors are random and there is a very large number of available levels, e.g., $N\approx\infty$, and $B\approx\infty$. Thus FPC→1
   b. If factors are fixed, then the number of available factors is the number of factors sampled, e.g., $T=t$. Thus, FPC→0
   c. If factors are random and there is a finite number of available factors, then no change is made (we will assume we have none of these).

Type:	R	R	F	
	n	b	t	
Effect	i	j	k	Symbol
τ_{BLKj}	n	1	t	σ_{BLK}^{2}
τ_{TRk}	n	b	0	σ_{TR}^{2}
$\tau_{BLK\ X\ TRjk}$	n	1	0	$\sigma_{BLK\times TR}^{2}$
$\varepsilon_{i(jk)}$	1	1	1	σ_{ε}^{2}

6. Write up components
   a. For each effect, select all the row(s) with effects that contain the same subscript(s)
   b. Ignore any columns with the heading for that (those) subscript(s). (i.e., select all columns that do not have the subscript.
   c. Add up the product of the remaining columns for the selected row(s)

For Blocks, the subscript is *j*:

Type:	*R*	*R*	*F*	
	n	*b*	*t*	
Effect	*i*	*j*	*k*	Symbol
τ_{BLKj}	*n*	1	*t*	σ_{BLK}^2
τ_{TRk}	*n*	*b*	*0*	σ_{TR}^2
$\tau_{BLK\ X\ TRjk}$	*n*	1	*0*	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	*1*	σ_{ε}^2

For Block, the E[MS$_{\mathrm{BLK}}$] is:

$$nt\sigma_{BLK}^2 + \sigma_{\varepsilon}^2$$

For Treatment, the subscript is *k*:

Type:	*R*	*R*	*F*	
	n	*b*	*t*	
Effect	*i*	*j*	*k*	Symbol
τ_{BLKj}	*n*	1	*t*	σ_{BLK}^2
τ_{TRk}	*n*	*b*	*0*	σ_{TR}^2
$\tau_{BLK\ X\ TRjk}$	*n*	1	*0*	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	**1**	1	*1*	σ_{ε}^2

For Treatment, the E[MS$_{\mathrm{TR}}$] is:

$$nb\sigma_{TR}^2 + n\sigma_{BLK\times TR}^2 + \sigma_{\varepsilon}^2$$

BUT Treatment is a fixed-effect (want to estimate the effects due to treatment, rather than the variance due to treatment). Using the ϕ_{TR} instead, the E[MS$_{\mathrm{TR}}$] is, therefore:

$$\phi_{TR} + n\sigma_{BLK\times TR}^2 + \sigma_{\varepsilon}^2$$

Note:The interaction remains Random with a variance symbol, as this is the interaction between blocks and treatments. Since one of these is a random-effect, this is random.

For Block X Treatment, the subscript is *jk*:

Type: Effect	R n i	R b j	F t k	Symbol
τ_{BLKj}	n	1	t	σ_{BLK}^{2}
τ_{TRk}	n	b	0	σ_{TR}^{2}
$\tau_{BLK\ X\ TRjk}$	n	1	0	$\sigma_{BLK\times TR}^{2}$
$\varepsilon_{i(jk)}$	1	1	1	σ_{ε}^{2}

For Block Treatment, the E[$MS_{\text{BLK X TR}}$] is:

$$n\sigma_{BLK\times TR}^{2}+\sigma_{\varepsilon}^{2}$$

For the error term, the subscript is *ijk*:

Type: Effect	R n i	R b j	F t k	Symbol
τ_{BLKj}	n	1	t	σ_{BLK}^{2}
τ_{TRk}	n	b	0	σ_{TR}^{2}
$\tau_{BLK\ X\ TRjk}$	n	1	0	$\sigma_{BLK\times TR}^{2}$
$\varepsilon_{i(jk)}$	1	1	1	σ_{ε}^{2}

The E[MSE] is simply: σ_{ε}^{2}

For the ANOVA table then: Using j=1 to J blocks; k=1 to K treatments; and assuming all n_{ij} are equal to n (as per the notes on Generalized RCB):

Source	df	MS	p-value	E[MS]
BLK	J-1	MS_{BLK}	Prob F> $F_{(J\text{-}1),(\text{dfE}),\ 1\text{-}\ \alpha}$	$\sigma_{\varepsilon}^{2}+Kn\sigma_{BLK}^{2}$
TR	K-1	MS_{TR}	Prob F> $F_{(K\text{-}1),(\text{df}BXT),1\text{-}\ \alpha}$	$\sigma_{\varepsilon}^{2}+n\sigma^{2}_{B\times T}+\phi_{TR}$
BLK X TR	(J-1) (K-1)	MS_{BXT}	Prob F> $F_{dfBXT,dfE,,1\text{-}\ \alpha}$	$\sigma_{\varepsilon}^{2}+n\sigma^{2}_{B\times T}$
Error	n_T-JK	MSE		σ_{ε}^{2}
Total	n_T-1			

More complex example: RCB, two-factors, split-plot. Factor B is in split-plots (subdivided experimental units):

1. Write up linear model.

$$y_{jkl} = \mu_{\bullet\bullet\bullet} + \tau_{BLK\,j} + \tau_{A\,k} + \tau_{BLK\times A\,jk} + \tau_{Bl} + \tau_{A\,Bkl} + \varepsilon_{k(jl)}$$

for j=1 to J, k=1 to K, l=1 to L
(blocks) (Factor A) (Factor B)

NOTE: will use instead:
for j=1 to b, k=1 to f_A , l=1 to f_B
(blocks) (Factor A) (Factor B)

Then b is taken from B possible blocks;
f_A is taken from F_A possible levels of Factor A;
f_B is taken from F_B possible levels of Factor B.

The other interactions
BLK X B
BLK X A X B
are combined in the error term in this model. We will separate these out to calculate the EMS:

$$\varepsilon_{jkl} = \tau_{BLK\times Bjl} + \tau_{BLK\times ABjkl}$$

Steps 2 and 3: Generate table of indices and number of factor levels etc. Indicate which factors are fixed versus random and add a symbol for each component. Note that we will use the symbol for variance (random-effects) for all components, and change this to ϕ_A, ϕ_B for the fixed-effects treatment at the end.

Type: Effect	R b j	F f_A k	F f_B l	Symbol
τ_{BLKj}				σ^2_{BLK}
τ_{Ak}				σ^2_{A}
$\tau_{BLK\ X\ Ajk}$				$\sigma^2_{BLK\times A}$
τ_{Bk}				σ^2_{B}
τ_{ABkl}				σ^2_{AB}
$\tau_{BLK\ X\ Bjk}$				$\sigma^2_{BLK\times B}$
$\tau_{BLK\ X\ ABjkl}$				$\sigma^2_{BLK\times AB}$

4. Fill in the table by:
   a. Put down a "1", where subscript is bracketed (nested)
   b. For each effect, put down the end value (e.g., f_A for number of levels of Factor A) for each subscript that does *not* appear for the effect

Type:	R	F	F	
	b	f_A	f_B	
Effect	j	k	l	Symbol
τ_{BLKj}		f_A	f_B	σ_{BLK}^2
τ_{Ak}	b		f_B	σ_A^2
$\tau_{BLK\ X\ Ajk}$			f_B	$\sigma_{BLK\times A}^2$
τ_{Bk}	b	f_A		σ_B^2
τ_{ABkl}	b			σ_{AB}^2
$\tau_{BLK\ X\ Bjl}$		f_A		$\sigma_{BLK\times B}^2$
$\tau_{BLK\ X\ ABjkl}$				$\sigma_{BLK\times AB}^2$

---

c. Add the "finite population correction factor" for each of the other factors: e.g., for Blocks, this is $\left(\frac{B-b}{B}\right)=\left(1-\frac{b}{B}\right)$

Type:	R	F	F	
	b	f_A	f_B	
Effect	j	k	l	Symbol
τ_{BLKj}	$\left(1-\frac{b}{B}\right)$	f_A	f_B	σ_{BLK}^2
τ_{Ak}	b	$\left(1-\frac{f_A}{F_A}\right)$	f_B	σ_A^2
$\tau_{BLK\ X\ Ajk}$	$\left(1-\frac{b}{B}\right)$	$\left(1-\frac{f_A}{F_A}\right)$	f_B	$\sigma_{BLK\times A}^2$
τ_{Bk}	b	f_A	$\left(1-\frac{f_B}{F_B}\right)$	σ_B^2
τ_{ABkl}	b	$\left(1-\frac{f_A}{F_A}\right)$	$\left(1-\frac{f_B}{F_B}\right)$	σ_{AB}^2
$\tau_{BLK\ X\ Bjk}$	$\left(1-\frac{b}{B}\right)$	f_A	$\left(1-\frac{f_B}{F_B}\right)$	$\sigma_{BLK\times B}^2$
$\tau_{BLK\ X\ ABjkl}$	$\left(1-\frac{b}{B}\right)$	$\left(1-\frac{f_A}{F_A}\right)$	$\left(1-\frac{f_B}{F_B}\right)$	$\sigma_{BLK\times AB}^2$

5. Change FPC values to either 1 or zero.
    a. If factors are random and there is a very large number of available levels, e.g., $B \approx \infty$. Thus FPC→1
    b. If factors are fixed, then the number of available factors is the number of factors sampled, e.g., $f_A = F_A$. Thus, FPC→0
    c. If factors are random and there is a finite number of available factors, then no change is made (we will assume we have none of these).

Type: Effect	R b j	F f_A k	F f_B l	Symbol
τ_{BLKj}	1	f_A	f_B	σ^2_{BLK}
τ_{Ak}	b	0	f_B	σ^2_{A}
$\tau_{BLK\ X\ Ajk}$	1	0	f_B	$\sigma^2_{BLK \times A}$
τ_{Bk}	b	f_A	0	σ^2_{B}
τ_{ABkl}	b	0	0	σ^2_{AB}
$\tau_{BLK\ X\ Bjk}$	1	f_A	0	$\sigma^2_{BLK \times B}$
$\tau_{BLK\ X\ ABjkl}$	1	0	0	$\sigma^2_{BLK \times AB}$

6. Write up components
    a. For each effect, select all the row(s) with effects that contain the same subscript(s)
    b. Ignore any columns with the heading for that (those) subscript(s). (i.e., select all columns that do not have the subscript.
    c. Add up the product of the remaining columns for the selected row(s)

For Blocks, the subscript is *j*.

Type: Effect	R b j	F f_A k	F f_B l	Symbol
τ_{BLKj}	1	f_A	f_B	σ^2_{BLK}
τ_{Ak}	b	0	f_B	σ^2_{A}
$\tau_{BLK\ X\ Ajk}$	1	0	f_B	$\sigma^2_{BLK \times A}$
τ_{Bk}	b	f_A	0	σ^2_{B}
τ_{ABkl}	b	0	0	σ^2_{AB}
$\tau_{BLK\ X\ Bjk}$	1	f_A	0	$\sigma^2_{BLK \times B}$
$\tau_{BLK\ X\ ABjkl}$	1	0	0	$\sigma^2_{BLK \times AB}$

For Block, the $E[MS_{BLK}]$ is:

$$f_A f_B \sigma_{BLK}^2$$

For Factor A, the subscript is *k*:

Type: Effect	R b j	F f_A k	F f_B l	Symbol
τ_{BLKj}	1	f_A	f_B	σ_{BLK}^{2}
τ_{Ak}	b	0	f_B	σ_{A}^{2}
$\tau_{BLK\ X\ Ajk}$	1	0	f_B	$\sigma_{BLK\times A}^{2}$
τ_{Bk}	b	f_A	0	σ_{B}^{2}
τ_{ABkl}	b	0	0	σ_{AB}^{2}
$\tau_{BLK\ X\ Bjk}$	1	f_A	0	$\sigma_{BLK\times B}^{2}$
$\tau_{BLK\ X\ ABjkl}$	1	0	0	$\sigma_{BLK\times AB}^{2}$

For Factor A, the E[MS_A] is:

$$bf_B\sigma_A^2 + f_B\sigma_{BLK\times A}^2$$

Since Factor A is a fixed-effect, using the ϕ_A instead, the E[MS_A] is, therefore:

$$\phi_A + f_B\sigma_{BLK\times TR}^2$$

Note:The interaction remains Random with a variance symbol, as this is the interaction between blocks and treatments. Since one of these is a random-effect, this is also a random-effect.

For Block X Factor A, the subscript is *jk*:

Type: Effect	R b j	F f_A k	F f_B l	Symbol
τ_{BLKj}	1	f_A	f_B	σ_{BLK}^{2}
τ_{Ak}	b	0	f_B	σ_{A}^{2}
$\tau_{BLK\ X\ Ajk}$	1	0	f_B	$\sigma_{BLK\times A}^{2}$
τ_{Bk}	b	f_A	0	σ_{B}^{2}
τ_{ABkl}	b	0	0	σ_{AB}^{2}
$\tau_{BLK\ X\ Bjk}$	1	f_A	0	$\sigma_{BLK\times B}^{2}$
$\tau_{BLK\ X\ ABjkl}$	1	0	0	$\sigma_{BLK\times AB}^{2}$

For Block by Factor A, the E[$MS_{BLK\ X\ A}$] is:

$$f_B\sigma_{BLK\times TR}^2$$

This was simply called "Error 1" ($\sigma_{\varepsilon 1}^2$) on the notes for split plot.

For Factor B, the subscript is *l*:

Type:	R	F	F	
	b	f_A	f_B	
Effect	j	k	l	Symbol
τ_{BLKj}	1	f_A	f_B	σ_{BLK}^2
τ_{Ak}	b	0	f_B	σ_A^2
$\tau_{BLK\ X\ Ajk}$	1	0	f_B	$\sigma_{BLK\times A}^2$
τ_{Bk}	b	f_A	0	σ_B^2
τ_{ABkl}	b	0	0	σ_{AB}^2
$\tau_{BLK\ X\ Bjl}$	1	f_A	0	$\sigma_{BLK\times B}^2$
$\tau_{BLK\ X\ ABjkl}$	1	0	0	$\sigma_{BLK\times AB}^2$

For Factor B, the E[MS$_B$] is:

$$bf_A\sigma_B^2 + f_A\sigma_{BLK\times B}^2$$

Since Factor B is a fixed-effect, using the ϕ_B instead, the E[MS$_B$] is, therefore:

$$\phi_B + f_A\sigma_{BLK\times B}^2$$

For Factor A X Factor B, the subscript is *kl*:

Type:	R	F	F	
	b	f_A	f_B	
Effect	j	k	l	Symbol
τ_{BLKj}	1	f_A	f_B	σ_{BLK}^2
τ_{Ak}	b	0	f_B	σ_A^2
$\tau_{BLK\ X\ Ajk}$	1	0	f_B	$\sigma_{BLK\times A}^2$
τ_{Bk}	b	f_A	0	σ_B^2
τ_{ABkl}	b	0	0	σ_{AB}^2
$\tau_{BLK\ X\ Bjl}$	1	f_A	0	$\sigma_{BLK\times B}^2$
$\tau_{BLK\ X\ ABjkl}$	1	0	0	$\sigma_{BLK\times AB}^2$

For Factor A by Factor B, the E[MS$_{AB}$] is:

$$b\sigma_{AB}^2 + \sigma_{BLK\times AB}^2$$

Since Factor A and Factor B are both fixed-effects, using the $\phi_{A\times B}$ instead, the E[MS$_{AB}$] is, therefore:

$$\phi_{A\times B} + \sigma_{BLK\times AB}^2$$

For Block X Factor B, the subscript is *jl*:

Type:	R	F	F	
	b	f_A	f_B	
Effect	j	k	l	Symbol
τ_{BLKj}	1	f_A	f_B	σ_{BLK}^2
τ_{Ak}	b	0	f_B	σ_A^2
$\tau_{BLK\ X\ Ajk}$	1	0	f_B	$\sigma_{BLK\times A}^2$
τ_{Bk}	b	f_A	0	σ_B^2
τ_{ABkl}	b	0	0	σ_{AB}^2
$\tau_{BLK\ X\ Bjl}$	1	f_A	0	$\sigma_{BLK\times B}^2$
$\tau_{BLK\ X\ ABjkl}$	1	0	0	$\sigma_{BLK\times AB}^2$

For Block by Factor B, the E[MS$_{\text{BLK X B}}$] is:

$$f_A \sigma_{BLK\times B}^2$$

For the error term, the subscript is *jkl*:

Type:	R	F	F	
	b	f_A	f_B	
Effect	j	k	l	Symbol
τ_{BLKj}	1	f_A	f_B	σ_{BLK}^2
τ_{Ak}	b	0	f_B	σ_A^2
$\tau_{BLK\ X\ Ajk}$	1	0	f_B	$\sigma_{BLK\times A}^2$
τ_{Bk}	b	f_A	0	σ_B^2
τ_{ABkl}	b	0	0	σ_{AB}^2
$\tau_{BLK\ X\ Bjl}$	1	f_A	0	$\sigma_{BLK\times B}^2$
$\tau_{BLK\ X\ ABjkl}$	1	0	0	$\sigma_{BLK\times AB}^2$

The E[MS$_{\text{BLK X AB]}}$ is simply: $\sigma_{BLK\times AB}^2$.

“Error 2” is a combination of BLK X B with BLK X AB, which is:

$$\sigma_{\varepsilon 2}^2 = f_A \sigma_{BLK\times B}^2 + \sigma_{BLK\times AB}^2$$

Assuming no interaction between Blocks and Factor B, this

$$\sigma_{\varepsilon 2}^2 \cong \sigma_{BLK\times AB}^2$$

For the ANOVA table then: Using j=1 to J blocks; k=1 to K Factor A levels; l=1 to L Factor B levels; and using error 1 and error 2 (as per the notes RCB Split-Plot):

Source	*df*	*MS*	Both A and B are Fixed; Blocks are Random
Block	J-1	MS_{BLK}	$KL\sigma_{BLK}^2$
Factor A	K-1	MS_A	$L\sigma_{\varepsilon 1}^2 + \phi_A$
Exp. Err. #1	(J-1)(K-1)	MS_{E1}	$L\sigma_{\varepsilon 1}^2$
Factor B	L-1	MS_B	$\sigma_{\varepsilon 2}^2 + \phi_B$
A x B	(K-1) (L-1)	MS_{AXB}	$\sigma_{\varepsilon 2}^2 + \phi_{A\times B}$
Exp. Err. #2	K(J-1) (L-1)	MS_{E2}	$\sigma_{\varepsilon 2}^2$
Total	JKL-1		

Generalized RCB, one-fixed factor with subsampling. Blocks assumed fixed.

1. Write up linear model.

$$y_{ijkl} = \mu_{\bullet\bullet\bullet} + \tau_{BLK\ j} + \tau_{TR\ k} + \tau_{BLK\times TR\ jk} + \varepsilon_{i(jk)} + \varepsilon_{l(ijk)}$$

for j=1 to J, k=1 to K,
(blocks) (Treatment=Factor A)
i=1 to n, (Exp. units in jk)
and l=1 to m (sampling in each exp. unit)

NOTE: will use instead:
for j=1 to b, k=1 to f_A
(blocks) (Factor A)
Then b is taken from B possible blocks;
f_A is taken from F_A possible levels of Factor A;
n is taken from N possible experimental units;
m is taken from M possible samples in each experimental unit.

The first error term, is the EU error; the second error term is the SU error.

Steps 2 and 3: Generate table of indices and number of factor levels etc. Indicate which factors are fixed versus random and add a symbol for each component. Note that we will use the symbol for variance (random-effects) for all components, and change this to ϕ for the fixed-effects treatment at the end.

Type: Effect	F b j	F f_A k	R n i	R m l	Symbol
τ_{BLKj}					σ^2_{BLK}
τ_{TRk}					σ^2_{TR}
$\tau_{BLK\ X\ TRjk}$					$\sigma^2_{BLK\times TR}$
$\varepsilon_{i(jk)}$					σ^2_{EE}
$\varepsilon_{l(ijk)}$					σ^2_{SE}

4. Fill in the table by:
   a. Put down a "1", where subscript is bracketed (nested)
   b. For each effect, put down the end value (e.g., f_A for number of levels of Factor A) for each subscript that does *not* appear for the effect

Type: Effect	F b j	F f_A k	R n i	R m l	Symbol
τ_{BLKj}		f_A	n	m	σ^2_{BLK}
τ_{TRk}	b		n	m	σ^2_{TR}
$\tau_{BLK\ X\ TRjk}$			n	m	$\sigma^2_{BLK\times TR}$
$\varepsilon_{i(jk)}$	1	1			σ^2_{EE}
$\varepsilon_{l(ijk)}$	1	1	1		σ^2_{SE}

c. Add the "finite population correction factor" for each of the other factors: e.g., for Blocks, this is $\left(\frac{B-b}{B}\right)=\left(1-\frac{b}{B}\right)$

Type:	F	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	$\left(1-\frac{b}{B}\right)$	f_A	n	m	σ^2_{BLK}
τ_{TRk}	b	$\left(1-\frac{f_A}{F_A}\right)$	n	m	σ^2_{TR}
$\tau_{BLK\ X\ TRjk}$	$\left(1-\frac{b}{B}\right)$	$\left(1-\frac{f_A}{F_A}\right)$	n	m	$\sigma^2_{BLK\times TR}$
$\varepsilon_{i(jk)}$	1	1	$\left(1-\frac{n}{N}\right)$	m	σ^2_{EE}
$\varepsilon_{l(ijk)}$	1	1	1	$\left(1-\frac{m}{M}\right)$	σ^2_{SE}

5. Change FPC values to either 1 or zero.

a. If factors are random and there is a very large number of available levels, e.g., $N\approx\infty$. Thus FPC→1

b. If factors are fixed, then the number of available factors is the number of factors sampled, e.g., $f_A = F_A$. Thus, FPC→0

c. If factors are random and there is a finite number of available factors, then no change is made (we will assume we have none of these).

Type:	F	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	0	f_A	n	m	σ^2_{BLK}
τ_{TRk}	b	0	n	m	σ^2_{TR}
$\tau_{BLK\ X\ TRjk}$	0	0	n	m	$\sigma^2_{BLK\times TR}$
$\varepsilon_{i(jk)}$	1	1	1	m	σ^2_{EE}
$\varepsilon_{l(ijk)}$	1	1	1	1	σ^2_{SE}

6. Write up components
   a. For each effect, select all the row(s) with effects that contain the same subscript(s)
   b. Ignore any columns with the heading for that (those) subscript(s). (i.e., select all columns that <u>do not</u> have the subscript.
   c. Add up the product of the remaining columns for the selected row(s)

For Blocks, the subscript is *j*.

Type:	F	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	0	f_A	n	m	σ_{BLK}^2
τ_{TRk}	b	0	n	m	σ_{TR}^2
$\tau_{BLK\ X\ TRjk}$	0	0	n	m	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^2
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^2

For Block, the E[MS$_{\text{BLK}}$] is:

$$f_A nm\sigma_{BLK}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$$

Since Blocks are fixed:

$$\phi_{BLK} + m\sigma_{EE}^2 + \sigma_{SE}^2$$

For Factor A (treatment), the subscript is *k*:

Type:	F	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	0	f_A	n	m	σ_{BLK}^2
τ_{Ak}	b	0	n	m	σ_{TR}^2
$\tau_{BLK\ X\ Ajk}$	0	0	n	m	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^2
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^2

For treatments (Factor A), the E[MS$_{\text{TR}}$] is:

$$bnm\sigma_{TR}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$$

Since treatments are fixed:

$$\phi_{TR} + m\sigma_{EE}^2 + \sigma_{SE}^2$$

For Block X Factor A, the subscript is *jk*:

Type: Effect	F b j	F f_A k	R n i	R m l	Symbol
τ_{BLKj}	0	f_A	n	m	σ_{BLK}^2
τ_{Ak}	b	0	n	m	σ_{TR}^2
$\tau_{BLK\ X\ Ajk}$	0	0	n	m	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^2
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^2

For Block by Factor A, the $E[MS_{BLK\ X\ TR}]$ is:

$$nm\sigma_{BLK\times TR}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$$

Since Blocks and treatments (Factor A) are fixed:

$$\phi_{BLK\times TR} + m\sigma_{EE}^2 + \sigma_{SE}^2$$

For the experimental units nested in blocks by treatments, the subscript is *ijk*:

Type: Effect	F b j	F f_A k	R n i	R m l	Symbol
τ_{BLKj}	0	f_A	n	m	σ_{BLK}^2
τ_{Ak}	b	0	n	m	σ_{TR}^2
$\tau_{BLK\ X\ Ajk}$	0	0	n	m	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^2
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^2

For the experimental units, the $E[MS_{EE}]$ is:

$$m\sigma_{EE}^2 + \sigma_{SE}^2$$

And for the samples in each experimental unit, the $E[MS_{SE}]$ is:

$$\sigma_{SE}^2$$

If Blocks are random and treatments are fixed, steps 1 to 4 are the same:

Type:	R	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	$\left(1-\frac{b}{B}\right)$	f_A	n	m	σ_{BLK}^2
τ_{TRk}	b	$\left(1-\frac{f_A}{F_A}\right)$	n	m	σ_{TR}^2
$\tau_{BLK\ X\ TRjk}$	$\left(1-\frac{b}{B}\right)$	$\left(1-\frac{f_A}{F_A}\right)$	n	m	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	$\left(1-\frac{n}{N}\right)$	m	σ_{EE}^2
$\varepsilon_{l(ijk)}$	1	1	1	$\left(1-\frac{m}{M}\right)$	σ_{SE}^2

5. Change FPC values to either 1 or zero.
   - d. If factors are random and there is a very large number of available levels, e.g., $N \approx \infty$. Thus FPC→1
   - e. If factors are fixed, then the number of available factors is the number of factors sampled, e.g., $f_A = F_A$. Thus, FPC→0
   - f. If factors are random and there is a finite number of available factors, then no change is made (we will assume we have none of these).

Type:	R	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	1	f_A	n	m	σ_{BLK}^2
τ_{TRk}	b	0	n	m	σ_{TR}^2
$\tau_{BLK\ X\ TRjk}$	1	0	n	m	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^2
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^2

6. Write up components
   d. For each effect, select all the row(s) with effects that contain the same subscript(s)
   e. Ignore any columns with the heading for that (those) subscript(s). (i.e., select all columns that <u>do not</u> have the subscript.
   f. Add up the product of the remaining columns for the selected row(s)

For Blocks, the subscript is *j*.

Type:	R	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	1	f_A	n	m	σ_{BLK}^2
τ_{TRk}	b	0	n	m	σ_{TR}^2
$\tau_{BLK\ X\ TRjk}$	1	0	n	m	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^2
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^2

For Block, the E[MS$_{\text{BLK}}$] is:

$$f_A nm\sigma_{BLK}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$$

For Factor A (treatment), the subscript is *k*:

Type:	R	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	0	f_A	n	m	σ_{BLK}^2
τ_{Ak}	b	0	n	m	σ_{TR}^2
$\tau_{BLK\ X\ Ajk}$	1	0	n	m	$\sigma_{BLK\times TR}^2$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^2
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^2

For Factor A, the E[MS$_{\text{TR}}$] is:

$$bnm\sigma_{TR}^2 + nm\sigma_{BLK\times TR}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$$

Since treatments are fixed, but blocks are random:

$$\phi_{TR} + nm\sigma_{BLK\times TR}^2 + m\sigma_{EE}^2 + \sigma_{SE}^2$$

For Block X Factor A, the subscript is *jk*:

Type:	R	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	0	f_A	n	m	σ_{BLK}^{2}
τ_{Ak}	b	0	n	m	σ_{TR}^{2}
$\tau_{BLK\ X\ Ajk}$	1	0	n	m	$\sigma_{BLK\times TR}^{2}$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^{2}
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^{2}

For Block by Factor A, the E[$\mathrm{MS}_{\mathrm{BLK\ X\ TR}}$] is:

$$nm\sigma_{BLK\times TR}^{2}+m\sigma_{EE}^{2}+\sigma_{SE}^{2}$$

For the experimental units nested in blocks by treatments, the subscript is *ijk*:

Type:	R	F	R	R	
	b	f_A	n	m	
Effect	j	k	i	l	Symbol
τ_{BLKj}	0	f_A	n	m	σ_{BLK}^{2}
τ_{Ak}	b	0	n	m	σ_{TR}^{2}
$\tau_{BLK\ X\ Ajk}$	1	0	n	m	$\sigma_{BLK\times TR}^{2}$
$\varepsilon_{i(jk)}$	1	1	1	m	σ_{EE}^{2}
$\varepsilon_{l(ijk)}$	1	1	1	1	σ_{SE}^{2}

For the experimental units, the E[$\mathrm{MS}_{\mathrm{EE}}$] is:

$$m\sigma_{EE}^{2}+\sigma_{SE}^{2}$$

And for the samples in each experimental unit, the E[$\mathrm{MS}_{\mathrm{SE}}$] is:

$$\sigma_{SE}^{2}$$

Power of the Test

Four possible results from Hypothesis testing:

	Reject H0	Accept H0
H0 True	α	1-α
H0 False	1-β	β

1. H0 is true, and we accept H0 (we fail to reject it). Correct outcome. Probability of this is 1-α

2. H0 is false (H1 is true instead) and we reject H0. Correct outcome. Probability of this is 1-β. This is called the **Power of the Test**.

3. H0 is true, but we reject H0. Not correct! Called the Type I error rate, the chance of rejecting a null hypothesis when it is true. For example, you reject when the means are actually the same, for a fixed-effects factor The probability of this happening is α, the significance level that you select.

4. H0 is false, but we accept H0 (we fail to reject it). Not correct! Called the Type II error rate, with a probability of β, the chance of accepting a null hypothesis when it is false. For example, you fail to reject H0: when the underlying population means are actually different.

Let's say we are looking at a simple hypothesis, that the true mean is equal to a value, $\mu=\mu_0$:

H0: $\mu=\mu_0$

We then test this by:

- Collecting a number of observations (n) from the population with mean of μ
- Calculating the sample mean, $\bar{y}$ is an unbiased estimate of μ
- If we repeat this a number of times, the sample means will vary around the real mean, with some sample means being far away from μ
- The variance of the sample means among different sample sets will depend upon:
  - The number of observations in each sample set: As $n\uparrow$, the variance of these means will decrease.
  - If the variance in the observations is low, the variance of these means will also be low, for a given n.

Let's say the alternative is that the true mean is greater than μ_0:

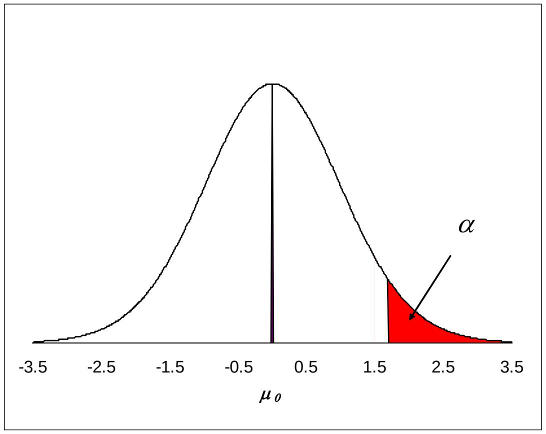
H1:$\mu>\mu_0$

and state this as:

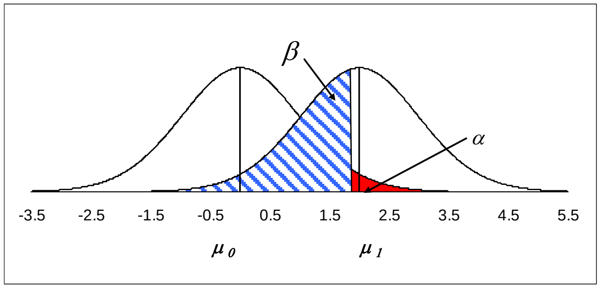
H1 $\mu=\mu_1$ where this is larger than μ_0.

Using a t-test (the y values follow a normal distribution, or *n* is large), sometimes we will reject H0: $\mu=\mu_0$, even when the sample was from that population.

α is the significance level that we set.
α is the probability that we reject H0 when it is true, a Type I error, and conclude that it came from the population with $\mu=\mu_1$. An error!



We choose α but how do we get β?



β = Type II error; β is the probability that we Accept H0 (*do not reject)* when it is false, e.g., if μ is really equal to μ_1 . The **Power of the Test** is 1-β.

β is directly related to the α level that we chose.
If we set α smaller (Type I error), β will get larger (Type II error)!

Examples:
1. sample mean = -2.5. Conclusion?

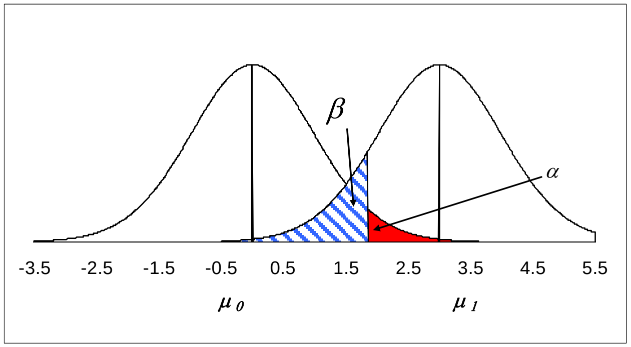
2. sample mean =0.5. Conclusion? Correct? Depends!

3. sample mean=2.5. Conclusion? Correct? Depends!

4. sample mean =4.5. Conclusion? Correct?

How do we increase Power of the Test?

1. If we set α *larger*, β will get smaller. But then the Type I error is larger!
   "lumpers" – large α; "splitters" – small α
2. If $\mu=\mu_1$ is very far from $\mu=\mu_0$, β will get smaller.



As our alternative hypothesis (e.g., μ_1) moves farther away from the null value (e.g., μ_0), β decreases and the power of the test increases.

3. Reduce the variance of the sample mean between different sample sets by:
   - ○ ⇧ number of observations in each sample: As n ⇧, the variance of these means will decrease.
   - ○ If the variance in the observations is low, the variance of these means will also be low, for a given n. Can do this via stratifying, or in experiments, by blocking.

For <u>experiments</u>, for a given α level, power changes with:

- the sizes of the real differences between true (population) treatment means, and
- variation between experimental unit means (the means from the experiment) for a given treatment.
- the type of test we use to test our hypothesis. For experimental design, we use an F-test (or more than one F-test)
- CAUTION: If there are repeated measures, spatial correlations, unequal variances, and/or non-normality for the error term(s), this becomes very complex. Can use transformations to meet the assumptions in some cases.

In Power Analysis for experiments, we want to either:

1. Calculate the Type II error and the power after the experiment is done, given the size of differences that we had in our experimental data, OR

2. Calculate the Type II error before conducting the experiment
   - putting in the size of the differences that we wish to detect (e.g., how much more does height growth have to be before we would add fertilizer?)
   - the α level, and
   - change the experiment (more experimental units) to achieve a certain power (e.g., 0.80)

If Power analysis is used to alter the experiment, <u>prior</u> to it being conducted, then any differences that are detected, *WILL BE DIFFERENCES OF PRACTICAL IMPORTANCE***.**

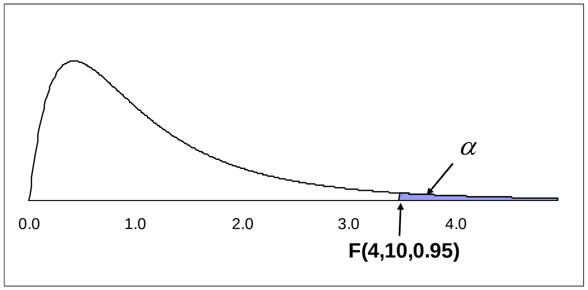
How do we calculate Power after conducting the experiment (*post-hoc power analysis)?* Steps:

1. The experimental design is already set, along with the number of experimental units in each treatment, and the sizes of differences that were detected in the experiment.

2. Choose α. e.g., α=0.05

3. Find the critical region using α.

e.g., suppose we have a CRD: one fixed-effect factor, with:
J=5 treatments, and df treatment is 5-1=4
n=3 observations in each treatment, and df error is 5(3-1)=10
Therefore, Fcritical is F(0.95,4,10)=3.48



4. Power is the probability that we would get the Fcritical or a larger value, if H1 was true (the means differed by the amounts given in the experiment). Need to estimate the size of the treatment effects (differences between means and the grand mean) based on the experiment to get this probability.

E.g., for the example, the experimenter calculated:
SS_{TR}=753 so MS_{TR}=753/(5-1)=188.25
MSE=5.23

We know that $E[MS_{TR}]=\phi_{TR}+\sigma_{\varepsilon}^{2}$ and $E[MSE]=\sigma_{\varepsilon}^{2}$, and that:

$$\phi_{TR}=\frac{n\sum_{j=1}^{J}\tau_j^{2}}{J-1} \quad where \quad \tau_j=\mu_{\bullet j}-\mu$$

$$so \quad E[MS_{TR}]=\frac{n\sum_{j=1}^{J}\tau_j^{2}}{J-1}+\sigma_{\varepsilon}^{2}$$

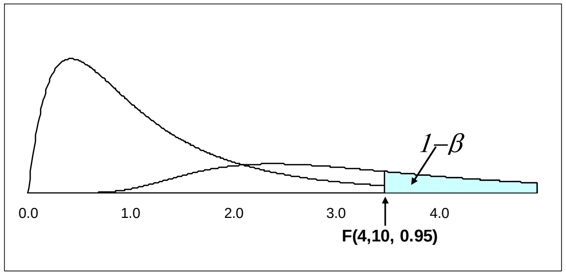
$$then \quad E[MS_{TR}]-E[MSE]=\frac{n\sum_{j=1}^{J}\tau_j^{2}}{J-1}+\sigma_{\varepsilon}^{2}-\sigma_{\varepsilon}^{2}$$

$$\sum_{j=1}^{J}\hat{\tau}_j^{2}=\frac{J-1}{n}(MS_{TR}-MSE)$$

$$\sum_{j=1}^{J}\hat{\tau}_j^{2}=\frac{5-1}{3}(188.75-5.23)=244.69$$

Power is then Prob(F>Fcritical | Noncentral) where Noncentral is the noncentrality parameter, when H1 is true. This is called a "Noncentral F-distribution".

Using the treatment effects we did get in the experiment, we can then calculate the noncentrality parameter, and find this probability.



$$\delta=noncentral=\frac{n\sum_{j=1}^{J}\tau_j^{2}}{\sigma_{\varepsilon}^{2}}$$

$$\hat{\delta}=noncentral=\frac{3\times 244.69}{5.23}=140.36$$

for n=3.

Then use SAS:

```
Data power;
*  Power=1-probf(Fcritical,df Treatment, df
Error, Noncentral);
Power=1-probf(3.48,4,10,140.36);
Run;
```

The temporary file will have the result in it, which is 0.9999. Very high power. Often try to get power between 0.80 and 0.95.

How do we calculate Power before conducting the experiment? Steps:

1. Select the experimental design
   E.g., simplest is CRD with one fixed-effect factor. Power analysis changes with the design, since the numerator and the denominator of the F-tests change.

2. State each H0 and H1. BUT H1 must be explicit, as to the size of the differences that you wish to detect.
   E.g. CRD with one fixed-effect factor:
   H_1: $\mu_1=10$, $\mu_2=11$, $\mu_3 = 12$, $\mu_4 = 13$, $\mu_5 = 14$
   With a grand mean of 12, so the treatment effects are
   $\tau_1=-2$, $\tau_2=-1$, $\tau_3=0$, $\tau_4=+1$, $\tau_5=+2$, and:
   $$\sum_{j=1}^{J} \tau_j^{\,2} = 10$$
   We would like to detect quite small differences. If we reject H0, and conclude H1, the differences are at least this large (called minimum distances). And if these differences are detected, this is a difference of practical importance.

3. Choose α. e.g., α=0.05. Find the critical F value using α. e.g, for 3 experimental units per treatment, df(error) is 5(3-1)=10. $F_{(4,\,10,\,0.95)} = 3.48$. Therefore, the critical region is $F>3.48$

4. Power is the probability that we will get Fcalculated that is greater than 3.48, given that the means are as given in H1 (i.e. H1 is true). We again need use the noncentral F distribution:
   Power=Prob(F>Fcritical | Noncentral)
   where Noncentral is the noncentrality parameter, when H1 is true. Using the treatment effects we wish to be able to detect (or larger differences), we can then calculate the noncentrality parameter, and find this probability. BUT we need an estimate of the variance of the error terms from a previous similar experiment!

Using the last experiment as being similar: *MSE*=5.23 is our estimate of the variance of the errors.

$$\delta = noncentral = \frac{n\sum_{j=1}^{J}\tau_j^{\,2}}{\sigma_\varepsilon^{\,2}} \qquad \hat{\delta} = \frac{3\times 10}{5.23} = 5.74$$

for n=3.

Then use SAS:

```
Data power;
*  Power=1-probf(Fcritical,df Treatment, df
Error, Noncentral);
Power=1-probf(3.48,4,10,140.36);
Run;
```

The temporary file “power” will have the result in it, which is 0.30. Very low power. Often try to get power between 0.80 and 0.95. These are small differences which will be harder to detect.

Options:

1. What about increasing this to n=4 experimental units per treatment (20 experimental units for the experiment)? The df treatment is still 4, but the df(error) is J(n-1) which is 5(4-1)=15. This has a critical $F_{(4,15,0.95)}$= 3.06

$$\delta = noncentral = \frac{n\sum_{j=1}^{J}\tau_j^2}{\sigma_\varepsilon^2} \qquad \hat{\delta} = \frac{4\times 10}{5.23} = 7.65$$

for n=4.

```
Data power;
*  Power=1-probf(Fcritical,df Treatment, df
Error, Noncentral);
Power=1-probf(3.06,4,15,7.65);
Run;
```

This results in a power of 0.44. The chance of rejecting H0 when there is at least these differences is only 44%. There is a large chance of accepting H0, when it is false (Type II error).

2. Another option is to use a different experimental design. What if we think we can reduce the MSE to 1.5 by using 2 Blocks in the design, but only n=2 experimental units per treatment (5 X 2 X 2=20 experimental units in total). We then have J=2 blocks, K=5 treatments, and n=2 experimental unit in each Block/Treatment combination. The df(error) is then JK(n-1) which is 2 X 5 (2-1)=10. The F critical is $F_{(4,10,0.95)}$=3.48.

$$\delta = noncentral = \frac{n\sum_{j=1}^{J}\tau_j^2}{\sigma_\varepsilon^2} \qquad \hat{\delta} = \frac{2\times 10}{1.5} = 13.3$$

```
Data power;
*  Power=1-probf(Fcritical,df Treatment, df
Error, Noncentral);
Power=1-probf(3.48,4,10,13.3);
Run;
```

The power is now 0.63.

3. Power is still not high enough, but cannot afford more experimental units or blocks? Change your expectations, also:

H_1: $\mu_1=9$, $\mu_2=11$, $\mu_3 = 12$, $\mu_4 = 13$, $\mu_5 = 15$

With a grand mean of 12, so the treatment effects are

$\tau_1=-3$, $\tau_2=-1$, $\tau_3=0$, $\tau_4=+1$, $\tau_5=+3$, and: $\sum_{j=1}^{J}\tau_j^2 = 20$

The F critical is $F_{(4,10,0.95)}=3.48$, as in option 2.

$$\delta = noncentral = \frac{n\sum_{j=1}^{J}\tau_j^2}{\sigma_\varepsilon^2} \qquad \hat{\delta} = \frac{2\times 20}{1.5} = 26.7$$

For n=2 and using the estimated variance of the error terms when 2 blocks are used.

```
Data power;
*  Power=1-probf(Fcritical,df Treatment, df
Error, Noncentral);
Power=1-probf(3.48,4,10,26.7);
Run;
```

The power is now 0.92! Only an 8% chance of a Type II error.

See SAS code called
One_way_anova_power_using_min_differences.sas
Gives power for different alpha levels, and *n*.

References:

Textbook: [newest edition in White]
Ch. 16.10; 19.11; 21.9;

Biometrics Information Handbook and Pamphlets (see **www.forestry.ubc.ca/biometrics** and click on “link” to find the website for these handbooks), particularly:

Nemec, A.F. 1991. Power analysis handbook for the design and analysis of forestry trials, Handbook No. 2. BC Ministry of Forests, Research Branch, Victoria, BC.

Bergerud, W. 1995. Post-hoc power analyses for ANOVA F-tests. Pamphlet #52. BC Ministry of Forests, Research Branch, Victoria, BC.

Bergerud, W. 1992. A general description of hypothesis testing and power analysis. Pamphlet #37. BC Ministry of Forests, Research Branch, Victoria, BC.

Bergerud, W.1995. Power analysis and sample sizes for completely randomized designs with subsampling. Pamphlet #49. BC Ministry of Forests, Research Branch, Victoria, BC.

Bergerud, W.1995. Power analysis and sample sizes for randomized block designs with subsampling. Pamphlet #50. BC Ministry of Forests, Research Branch, Victoria, BC.

Bergerud, W.1995. Programs for power analysis/sample size calculations for CR and RB designs with subsampling. Pamphlet #51. BC Ministry of Forests, Research Branch, Victoria, BC.

Example from
Nemec, A.F. 1991. Power analysis handbook for the design and analysis of forestry trials, Handbook No. 2. BC Ministry of Forests, Research Branch, Victoria, BC.
Pp 15-16.

1. Experiment:
   J=5 treatments, and df treatment is 5-1=4
   n=3 observations in each treatment, and df error is 5(3-1)=10

Therefore, Fcritical is F(0.90,4,10)=2.605

2. Set means for H1:
   H_1: μ_1=600, μ_2=500, μ_3 = 500, μ_4 = 400, μ_5 =400
   With a grand mean of 480, so the treatment effects are
   τ_1=120, τ_2=20, τ_3=20, τ_4=-80, τ_5=-80, and: $\sum_{j=1}^{J} \tau_j^{\,2} = 28{,}000$

3. Estimate standard deviation of the errors as 200 cm, so variance of the errors is 2002.
4. Calculate noncentrality parameter:

$$\delta = noncentral = \frac{n\sum_{j=1}^{J} \tau_j^{\,2}}{\sigma_\varepsilon^{\,2}} \qquad \hat{\delta} = \frac{3 \times 28{,}000}{40{,}000} = 2.1$$

For n=3.

4. Calculate power using SAS:

```
Data power;
*  Power=1-probf(Fcritical,df Treatment, df
Error, Noncentral);
Power=1-probf(2.605,4,10,2.1);
Run;
```

The power is 0.224.

Use of Linear Mixed Models for Experimental Design

<u>What are linear mixed models?</u>

They are a group of linear models that include:

- **<u>One dependent variable</u>, that is continuous (usually labeled as *Y or y* in textbooks)**
- **<u>fixed components</u>**
  - **continuous variables, and/or class variables represented by dummy (indicator) variables;**
  - **fixed-effects in experimental design, predictor variables in regression, usually labeled as *X or x*;**
  - **associated coefficients are labeled as β in most texts.**
- **<u>error term</u>**
  - **usually labeled as *ε* (use *e* if this is estimated errors, not population errors)**
  - **covariance matrix: variances and covariances of the errors; labeled the *R* matrix in many mixed models text books**
  - **error terms follow a normal distribution**
  - **error terms may have unequal variance, and /or correlations (time and/or space) between error terms**
  - **error terms are a random component.**

and may include, also:

- **<u>random components</u>**
  - **covariance matrix (variances and covariances of these random components) is labeled the *G* matrix in many texts**
  - **the “variables” (really a design matrix) are labeled as *Z*, with associated coefficients “u”.**
  - **these also follow a normal distribution**
  - **some models have only random components, and no fixed components**

Aside: In math symbols, this becomes:

$$\mathbf{y} = \boldsymbol{\beta}\mathbf{x} + \mathbf{u}\mathbf{Z} + \boldsymbol{\varepsilon} \qquad \mathbf{V(y)} = \mathbf{G'ZG} + \mathbf{R}$$

- **Estimates of all parameters:**
  - **the fixed component coefficients (including the intercept),**
  - **the variances for:**
    - **the random components variances and covariances; and random-effects coefficients**
    - **variances (and covariances) of the error term**
- **are estimated using <u>maximum likelihood</u>**

<u>Likelihood</u>

Given a set of the estimated parameters (coefficients and variances/covariances), what is the chance that we would get the data that we did get?

For a discrete distribution of y (not the case in linear mixed models), this would be a probability for the first observation X the prob of the second observation, etc. to the last observation – between 0 and 1.

For a continuous distribution, e.g., normal, this is the value of the probability density function for the first observation X the probability density function for the second observation, etc to the last observation – not necessarily less than 1.

<u>Maximum Likelihood</u>

Change the set of estimated parameters until we get the largest possible likelihood.

Often easier to take the logarithm of the likelihood to do this – <u>most packages report the log likelihood, or -2 X log likelihood.</u>

<u>Searching for the Maximum Likelihood</u>

Most packages get the maximum likelihood by:

- **Searching for a set of all of these estimated parameters that will result in the maximum likelihood of obtaining the data that we did get (ML method)**

OR

- **Finding estimates of the fixed component coefficients first (sometimes using least squares methods), and then using the residuals from that to get the random components (REML).**

Because this is a <u>search</u> to find a solution (the estimates that give the maximum likelihood), the search proceeds by :

- **getting estimates, calculating the (log) maximum likelihood (<u>one iteration</u>),**
- **altering the estimates, and recalculating the maximum likelihood (another iteration), and**
- **so on, <u>until the estimates don't change</u> (or this may stop based on <u>the likelihood does not change</u>.**

However, the search <u>may not converge</u> –

- **means that the estimates are not becoming the same over the iterations of the search.**
- **You may need to:**
  - **increase the number of iterations,**
  - **change the way the search is done (e.g., Marquardt is one method for searching that is commonly used)**
  - **It may mean that your model is not correctly specified, or it is just very hard to find a solution if your models if very complex.**

The search may converge, but with the statement that the "Hessian is not positive definite"

- **This will mean that the variance estimates are not reliable.**
- **This can occur with a complex model, or when the model is not correctly specified.**

<u>Mixed models for experimental design</u>

Linear mixed models enable us to get estimates for mixed-effects models, including:

- **testing the fixed-effects factors for interactions, and main effects (Type III SS, F-tests). SAS will use the <u>correct F-tests</u> based on Expected Means Squares.**
- **Get t-tests for pairs of means using the correct denominator Mean Squares (same as the one used in the F-test)**
- **Get estimates of the variances for the random effects, including the variance of the residual error.**
- **Testing assumptions: bit harder to do!**
  - **Use residuals from GLM and do the tests?**
  - **Check the log likelihood – should be better (higher log likelihood OR lower -2 log L) as you better meet the assumptions.**

Example 1: CRD with one-fixed and one-random factor (handed out in class) -- discussion.

Others used in class: Time permitting only.
Example 2: Randomized Block Design with replicates in each block (Generalized Block Design; handed out in class as one of the designs under *Randomized Block Design with other Experiments*)

Example 3: CRD: one fixed-effect factor with subsampling

References:
Littell, R.C., G. A. Milliken, W.W. Stroup, and R.D. Wolfinger. 1996. SAS system for Mixed Models. SAS Institute Inc., Cary, NC.

Pineiro, J.C. and D.M. Bates. 2000. Mixed-effects models in S and S-plus. Springer, New York.

Schabenberger, O. and F. J. Pierce. 2002. Contemporary Statistical Models. CRC Press, New York (available electronically to UBC students as by accessing:

1. **www.library.ubc.ca**
2. **Indexes and Databases**
3. **Stats Net Base**
4. **Then search for "Schabenberger"**
5. **Then select Chapter 7. "Linear mixed models for clustered data."**

NOTES:

1. **Generalized Linear Mixed Models allow for class variables and count variables also (PROC GLMMIX).**
2. **Nonlinear Mixed Models allow for nonlinear models (PROC NLMIX).**

CRD: Random and Mixed Effects

Example Using SAS: Two Factors, CRD.

- Factor A, (three levels of fertilization: A1, A2, and A3) (J=3) – fixed-effects
- Factor B (four species: B1, B2, B3 and B4) (K=4) Random-effects
- Crossed: 12 treatments
- Four replications per treatment (n=4) for a total of 48 experimental units
- Measured Responses: height growth in mm

species is random -- these are a few of the species that we are interested in and we wish to look at the variance in height growth that is due to species.

- Expected Mean Square Values Comparison:

Mean Square	Model I Both A and B are Fixed	Model II Both A and B are Random	Model III A is Fixed B is Random
A (MSA)	$\sigma_{\varepsilon}^{2} + \phi_{A}^{*}$	$\sigma_{\varepsilon}^{2} + nK\sigma_{A}^{2} + n\sigma_{AB}^{2}$	$\sigma_{\varepsilon}^{2} + \phi_{A} + n\sigma_{AB}^{2}$
B (MSB)	$\sigma_{\varepsilon}^{2} + \phi_{B}$	$\sigma_{\varepsilon}^{2} + nJ\sigma_{B}^{2} + n\sigma_{AB}^{2}$	$\sigma_{\varepsilon}^{2} + nJ\sigma_{B}^{2}$
A X B (MSAB)	$\sigma_{\varepsilon}^{2} + \phi_{AB}$	$\sigma_{\varepsilon}^{2} + n\sigma_{AB}^{2}$	$\sigma_{\varepsilon}^{2} + n\sigma_{AB}^{2}$
Error (MSE)	σ_{ε}^{2}	σ_{ε}^{2}	σ_{ε}^{2}

SAS CODE:

```
PROC IMPORT OUT= WORK.twofactor
     DATAFILE=
"E:\frst430\lemay\examples\encyl_examples.xls"
     DBMS=EXCEL REPLACE;
     SHEET="crd$";       GETNAMES=YES;
     MIXED=NO;           SCANTEXT=YES;
     USEDATE=YES;        SCANTIME=YES;
RUN;

options ls=70 ps=50 pageno=1;

*  Using the same data as for fixed two-factor
experiment, but assuming that factor b is random;
PROC GLM  data=twofactor;
class a b;
model result=a b a*b;
random b a*b/test;
test h=a e=a*b;
lsmeans a /e=a*b pdiff tdiff;
output out=glmout r=resid p=predict;
run;

proc plot data=glmout;
plot resid*predict='*';
run;

proc univariate data=glmout normal plot;
var resid;
run;

PROC MIXED data=twofactor;
class a b;
model result=a;
lsmeans a/pdiff;
random b a*b;
run;
```

```
                 The SAS System                   1

                The GLM Procedure

             Class Level Information

          Class         Levels    Values

          A                  3    1 2 3
          B                  4    1 2 3 4

       Number of Observations Read          48
       Number of Observations Used          48

                The SAS System                    2

              The GLM Procedure

Dependent Variable: result   result

                     Sum of
Source      DF      Squares     Mean Square F Value

Model       11    2209.916667   200.901515  164.37
Error       36      44.000000     1.222222
Corrected
   Total    47    2253.916667

           Source                 Pr > F

           Model                  <.0001
           Error
           Corrected Total

R-Square  Coeff Var   Root MSE    result Mean

0.980478  4.850640     1.105542     22.79167
```

Removed Type I SAS output.

```
Source    DF    Type III SS    Mean Square   F Value

A          2    1258.166667     629.083333    514.70
B          3     934.750000     311.583333    254.93
A*B        6      17.000000       2.833333      2.32

              Source                 Pr > F

              A                      <.0001
              B                      <.0001
              A*B                    0.0539

                 The SAS System                  4

                The GLM Procedure

Source         Type III Expected Mean Square

A          Var(Error) + 4 Var(A*B) + Q(A)
B          Var(Error) + 4 Var(A*B) + 12 Var(B)  ????
A*B        Var(Error) + 4 Var(A*B)
```

These are not reliable – do not match textbooks nor determination of EMS using the rules. Tests on the following page also not useful.

```
              The SAS System                   5

              The GLM Procedure

Tests of Hypotheses for Mixed Model Analysis of
Variance

Dependent Variable: result   result

Source     DF   Type III SS   Mean Square  F Value

 *  A      2   1258.166667    629.083333   514.70
    B      3    934.750000    311.583333   254.93
    A*B    6     17.000000      2.833333     2.32

Error:
MS(Error) 36     44.000000      1.222222

* This test assumes one or more other fixed effects are
zero.

          Source                Pr > F

          *  A                     <.0001
             B                     <.0001
             A*B                   0.0539

Error: MS(Error)
* This test assumes one or more other fixed effects are
zero.
```

```
                    The SAS System                6

                 Least Squares Means
Standard Errors and Probabilities Calculated Using the
Type III MS for A*B as an Error Term

                         result      LSMEAN
            A            LSMEAN      Number
            1      16.2500000           1
            2      23.3750000           2
            3      28.7500000           3


         Least Squares Means for Effect A
       t for H0: LSMean(i)=LSMean(j) / Pr > |t|

            Dependent Variable: result

i/j         1            2           3

1                  -11.9724      -21.0042
                     <.0001        <.0001
2      11.97239                  -9.03181
         <.0001                    0.0001
3       21.0042   9.031807
         <.0001     0.0001


NOTE: To ensure overall protection level, only
probabilities associated with pre-planned comparisons
should be used.
```

MUST use the Bonferroni correction. For every test, compare the p-value to alpha/# pairs.

```
                    The SAS System                    7
```

```
Dependent Variable: result   result

Tests of Hypotheses Using the Type III MS for A*B as an
Error Term

Source    DF    Type III SS    Mean Square   F Value
A         2    1258.166667     629.083333    222.03

              Source                  Pr > F

                A                     <.0001
```

From class, we estimated the variance for Factor B as (n=

$$E[MSB] = \sigma_{\varepsilon}^{2} + nJ\sigma_{B}^{2}$$

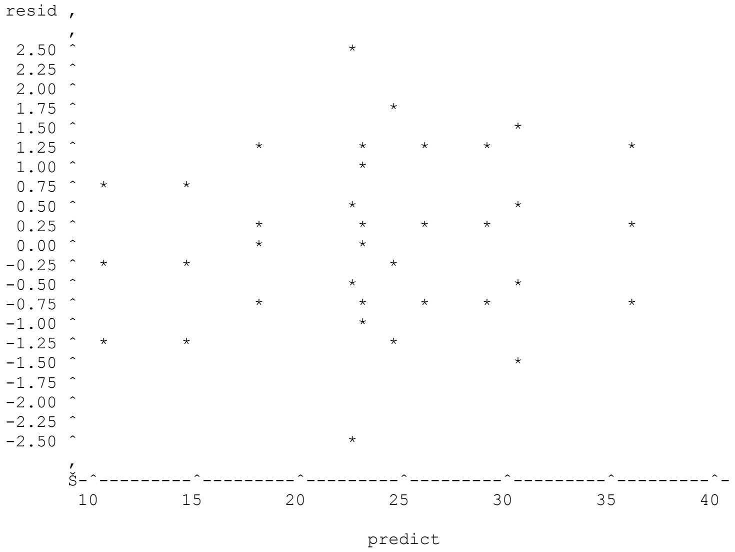
$$E[MSE] = \sigma_{\varepsilon}^{2}$$

$$E[MSB] - E[MSE] = \sigma_{\varepsilon}^{2} + nJ\sigma_{B}^{2} - \sigma_{\varepsilon}^{2}$$

$$\sigma_{B}^{2} = \frac{E[MSB] - E[MSE]}{nJ}$$

$$\hat{\sigma}_{B}^{2} = \frac{MSB - MSE}{nJ} = \frac{311.58 - 1.22}{4 \times 3} = 25.86$$

```
                    The SAS System                    8

      Plot of resid*predict.  Symbol used is '*'.
```



```
NOTE: 12 obs hidden.
```

Some SAS outputs removed.

```
                The SAS System                9

           The UNIVARIATE Procedure
              Variable:  resid
```

```
                  Tests for Normality

Test                 --Statistic--   --p Value----

Shapiro-Wilk       W     0.977162 Pr < W   0.4666
Kolmogorov-Smirnov D     0.114207 Pr > D   0.1169
Cramer-von Mises   W-Sq  0.082279 Pr >W-Sq 0.1963
Anderson-Darling   A-Sq  0.513709 Pr >A-Sq 0.1926
```

```
          The UNIVARIATE Procedure
              Variable:  resid

Stem Leaf                     #             Boxplot
   2 5                        1                |
   2                                           |
   1 58                       2                |
   1 022222                   6                |
   0 558888                   6             +-----+
   0 00000022222             11             *--+--*
  -0 2222                     4             |     |
  -0 888888888855            12             +-----+
  -1 2220                     4                |
  -1 5                        1                |
  -2                                           |
  -2 5                        1                |
   ----+----+----+----+


              Normal Probability Plot
   2.75+                                               *
       |                                              +++++
       |                                         *+*++
       |                                  ***+**+
       |                              **+*++
       |                        *****+*
       |                    +****+
       |             **+**+**
       |       * *++*++
       |     +++++
       |++++*+
  -2.75+
        +----+----+----+----+----+----+----+----+----+----+
            -2        -1         0        +1        +2
```

The Mixed Procedure

```
              Model Information

Data Set                      WORK.TWOFACTOR
Dependent Variable            result
Covariance Structure          Variance Components
Estimation Method             REML
Residual Variance Method      Profile
Fixed Effects SE Method       Model-Based
Degrees of Freedom Method     Containment

          Class Level Information

        Class    Levels    Values
        A             3    1 2 3
        B             4    1 2 3 4
```

Levels for A and B correct.

```
              Dimensions
      Covariance Parameters            3
      Columns in X                     4
      Columns in Z                    16
      Subjects                         1
      Max Obs Per Subject             48
```

Have 3 covariance parameters, as there are 3 random components: B, A X B, and the error term.

Columns in X: 4. Why? Factor A uses 3 dummy variables for 3 levels, plus the intercept.

(NOTE: can use “noint” – to remove the intercept)

Columns in Z: 16. Why?

Factor B has 4 levels. Uses 4 dummy variables

Factor A X B is 3 dummy variables for Factor A X 4 dummy variables for Factor B= 12

Subjects: only one dataset – not subdivided by anything. So 48 obs in one subject (n=4 exp. units per treatment)

```
                    Number of Observations

        Number of Observations Read               48
        Number of Observations Used               48
        Number of Observations Not Used            0

                        Iteration History

 Iteration  Evaluations  -2 Res Log Like   Criterion

   0             1       275.37975211
   1             1       166.72010292     0.00000000

                           The SAS System              13

                         The Mixed Procedure
                      Convergence criteria met.


                      Covariance Parameter
                           Estimates

                     Cov Parm     Estimate

                      B             25.7292
                      A*B            0.4028
                      Residual       1.2222

                          Fit Statistics

        -2 Res Log Likelihood           166.7
        AIC (smaller is better)         172.7
        AICC (smaller is better)        173.3
        BIC (smaller is better)         170.9
```

Instead of R Squared used in least squares, we have -2 Res (residual) log likelihood.
Instead of R squared adjusted, we have AIC, AICC, BIC

```
         Type 3 Tests of Fixed Effects

                          Num      Den
 Effect            DF      DF    F Value     Pr > F

 A                  2       6     222.03     <.0001
```

Correct F-test.

```
                  Least Squares Means

                          Standard
Effect    A   Estimate    Error    DF  t Value   Pr>|t|
A         1   16.2500     2.5709    6     6.32   0.0007
A         2   23.3750     2.5709    6     9.09   <.0001
A         3   28.7500     2.5709    6    11.18   <.0001
```

df(MSAB)=(3-1)X(4-1)=6

From the GLM output, we expected:

$$S.E(Factor\ A\ level\ mean) = \sqrt{\left(\frac{MSAB}{Kn}\right)}$$

For mixed models, MSAB is replaced with:

$$MSAB = \hat{\sigma}_{\varepsilon}^{\ 2} + n\hat{\sigma}_{AB} = 1.22 + (4)(0.4028)$$ **=2.8312**

[was 2.833 using least squares)

$$S.E(Factor\ A\ means) = \sqrt{\left(\frac{2.833}{4 \times 4}\right)} = 0.4207$$

WHY is this given as 2.5709?? VERY different using PROC MIXED vs PROC GLM. Why?

Littell and others (1996) indicate that the ones in GLM are not correct. That we should add in all of the random variances.

Using the population model for two factors:

Population: $y_{ijk} = \mu + \tau_{Aj} + \tau_{Bk} + \tau_{AB\,jk} + \varepsilon_{ijk}$

They suggest that for the Factor A level means are calculated as:

$$\bar{y}_{\bullet j \bullet} = \mu + \tau_{Aj} + \bar{\tau}_{B\bullet} + \bar{\tau}_{AB\,j\bullet} + \bar{\varepsilon}_{\bullet j \bullet}$$

When Factor B is fixed, the effects due to B and AB do not contribute to the variance (the average effect for B is 0, as well as the other terms). Then the variance of the Factor A level means is simply the variance of the error term (estimated by MSE), divided by the number of observations for that Factor A level (and the F-test is MSA/MSE).

When Factor B is random, the F-test is MSA/MSAB, to isolate the effects for Factor A.

For confidence intervals on Factor A level means, there is the variance of the error term + variance of B + variance of AB divided by the number of observations in this Factor A level. This means the standard error would be changed to:

$$\text{Estimated Variance (Factor A level means)}$$
$$= V\hat{a}r(\bar{\tau}_{B\bullet}) + V\hat{a}r(\bar{\tau}_{AB\,j\bullet}) + V\hat{a}r(\bar{\varepsilon}_{\bullet j \bullet})$$
$$= \left(\frac{\hat{\sigma}_B{}^2}{K} + \frac{\hat{\sigma}_{AB}{}^2}{K} + \frac{\hat{\sigma}_\varepsilon{}^2}{Kn} \right) = \left(\frac{n\hat{\sigma}_B{}^2 + n\hat{\sigma}_{AB}{}^2 + \hat{\sigma}_\varepsilon{}^2}{Kn} \right)$$

Divisors:

- **K values used to calculate the average Factor B effect;**
- **K values used to calculate the average interaction effect for each Factor A level;**
- **Kn values used to calculate the average error for each Factor A level.**

Standard Error (Factor A level means) is the square root of this. For the example:

$$\sqrt{\left(\frac{1.22+(4)0.4028+(4)25.76}{4\times 4}\right)}$$

$$=2.5723$$

As per the MIXED output [shows 2.5709]

```
          Differences of Least Squares Means

                             Standard
Effect   A   A Estimate  Error     DF  t Value Pr>|t|

A        1  2   -7.1250  0.5951     6  -11.97  <.0001
A        1  3 -12.5000  0.5951     6  -21.00  <.0001
A        2  3   -5.3750  0.5951     6   -9.03  0.0001
```

Pairs of means t-tests same as for GLM using A X B as the error term for Factor A.

$$S.E(mean1-mean2)=\sqrt{MSAB\left(\frac{1}{nobs1}+\frac{1}{nobs2}\right)}$$

$$=\sqrt{2.8312\left(\frac{1}{4X4}+\frac{1}{4X4}\right)}=0.5949$$

Corresponds with least squares means, as other variance terms cancel out when we get the variance in the difference of the means.

<u>Randomized Block Design with replicates in each block</u>

Example: Randomized Block Design (RCB), with Factor A (three types of food: A1 to A3), and two labs (blocks). Randomization of Factor A is restricted to within labs.

Lab 1		Lab 2	
A1 = 6	A1=5	A3=11	A3=12
A3=10	A2=8	A1=4	A2=9
A2=7	A3=12	A2=8	A1=5

Response variable: weight gain of fish (kg)
Experimental unit: one tank of fish; 6 tanks in each lab

Use the SAME analysis as for CRD with one fixed and one random factor – no difference in analysis. However, the conclusions WILL vary, as we are only interested in sites as a way to remove variation for the F-test, and for pairs of means t-tests.

CRD: One Factor Experiment, Fixed Effects with subsampling [26.7 of textbook (White)]

Example from Textbook:

- Have three temperatures: low, medium, and high
- For each, we have two experimental units (batches)
- For each batch, we have three loaves of bread
- The response variable is crustiness of bread.

Data:

temp	batch	observation	yijl
low	1	1	4
low	1	2	7
low	1	3	5
low	2	1	12
low	2	2	8
low	2	3	10
medium	1	1	14
medium	1	2	13
medium	1	3	11
medium	2	1	9
medium	2	2	10
medium	2	3	12
high	1	1	14
high	1	2	17
high	1	3	15
high	2	1	16
high	2	2	19
high	2	3	18

SAS code: Three options presented

4. Using PROC GLM and the sample observations. **Model yijk= treat batch(treat);**
5. Using PROC MIXED, and the sample observations. **Model yijk=treat; Random batch(treat);**

The F-test for the treatment is F=MS_{TR}/MS_{EE}

For the mean of the treatment:

$$\bar{y}_{\bullet j \bullet} = \mu + \tau_{TRj} + \bar{\varepsilon}_{EU \bullet j} + \bar{\varepsilon}_{SU \bullet j \bullet}$$

Where experimental errors are random, and the sampling errors are random, with a fixed treatment.

$$\text{Estimated Variance (Factor A level means)}$$
$$= Var(\bar{\tau}_{EU \bullet j}) + Var(\bar{\varepsilon}_{SU \bullet j \bullet})$$
$$= \left(\frac{\sigma_{EE}{}^{2}}{n} + \frac{\sigma_{SE}{}^{2}}{nm} \right) = \left(\frac{m\sigma_{EE}{}^{2} + \sigma_{SE}{}^{2}}{nm} \right)$$

Since the numerator is the Expected value for MS_{EE}, the standard error of the mean is estimated by:

$$S.E(Factor\ A\ level\ mean) = \sqrt{\left(\frac{MS_{EE}}{nm} \right)}$$

Get the same results using GLM as using MIXED. [also get the same results using the mean values for each experimental unit as the y-variable]

```
PROC IMPORT OUT= WORK.onesub
    DATAFILE= "E:\frst430\lemay\examples\
         subsampling_neter_newest_p1109.xls"
    DBMS=EXCEL REPLACE;       SHEET="data$";
    GETNAMES=YES;  MIXED=NO;   SCANTEXT=YES;
    USEDATE=YES;   SCANTIME=YES;
RUN;

options ls=70 ps=50 pageno=1;

* Analysis 1. first, use GLM and bring in the
Experimental error and the Sampling error into the
design;
PROC GLM data=onesub;
class temp batch;
model yijl=temp batch(temp);
random batch(temp)/test;
test h=temp e=batch(temp);
lsmeans temp /e=batch(temp) pdiff tdiff;
output out=glmout r=resid p=predict;
run;
proc plot data=glmout;
plot resid*predict='*';
run;
proc univariate data=glmout normal plot;
var resid;
run;

* Analysis 2: this is using maximum likelihood for
a mixed model to estimate variances and get correct
F-tests;

PROC MIXED data=onesub;
class temp batch;
model yijl=temp;
lsmeans temp/pdiff;
random batch(temp);
run;
```

Analysis 1: GLM using samples with experimental error given as batch(treat), and sampling error as the Error term.

```
                 The SAS System             1

                 The GLM Procedure

              Class Level Information

        Class         Levels    Values
        temp               3    high low medium
        batch              2    1 2

    Number of Observations Read          18
    Number of Observations Used          18

               The SAS System

              The GLM Procedure

Dependent Variable: yijl   yijl

                      Sum of
Source      DF       Squares  Mean Square   F Value

Model        5    284.4444444  56.8888889     21.79
Error       12     31.3333333   2.6111111
Corrected
   Total    17    315.7777778

                 Source                 Pr > F
                 Model                  <.0001
                 Error
                 Corrected Total


R-Square     Coeff Var      Root MSE     yijl Mean

0.900774      13.59163      1.615893      11.88889
```

(**NOTE: Type I SS removed)**

```
Source        DF    Type III SS  Mean Square   F Value
temp           2    235.4444444  117.7222222     45.09
batch(temp)  3      49.0000000   16.3333333       6.26

                    Source                  Pr > F
                    temp                    <.0001
                    batch(temp)             0.0084
```

NOTE: Variance components and GLM Mixed model analysis given by SAS removed – often not correct.

```
                 Least Squares Means
Standard Errors and Probabilities Calculated Using the
Type III MS for batch(temp) as an Error Term



                                LSMEAN
temp         yijl LSMEAN        Number
high          16.5000000             1
low            7.6666667             2
medium        11.5000000             3

     Least Squares Means for Effect temp
    t for H0: LSMean(i)=LSMean(j) / Pr > |t|

    Dependent Variable: yijl

i/j            1             2             3
1                     3.785714      2.142857
                        0.0323        0.1215
2      -3.78571                     -1.64286
         0.0323                       0.1990
3      -2.14286       1.642857
         0.1215         0.1990

NOTE: To ensure overall protection level, only
probabilities associated with pre-planned comparisons
should be used.
```

```
Dependent Variable: yijl   yijl

  Tests of Hypotheses Using the Type III
    MS for batch(temp) as an Error Term

Source        DF   Type III SS  Mean Square   F Value
temp           2   235.4444444  117.7222222      7.21

              Source                   Pr > F
              temp                     0.0715

       Plot of resid*predict.  Symbol used is '*'.

 resid ,
 2.000 ^                    *
       ,
       ,
 1.667 ^ *                   *                   *
       ,
       ,
 1.333 ^                               *                   *
       ,
       ,
 1.000 ^
       ,
       ,
 0.667 ^
       ,
       ,
 0.333 ^                               *                   *
       ,
       ,
 0.000 ^                    *
       ,
       ,
-0.333 ^ *                   *                   *
       ,
       ,
-0.667 ^
       ,
       ,
-1.000 ^
       ,
       ,
-1.333 ^ *                   *                   *
       ,
       ,
-1.667 ^                               *                   *
       ,
       ,
-2.000 ^                    *
       ,
       Š^---------^---------^---------^---------^---------^---------^-
       5.0       7.5      10.0      12.5      15.0      17.5      20.0

                                   predict
```

```
               The UNIVARIATE Procedure
                  Variable:  resid
```

NOTE: All outputs removed except for Normality tests and box plot and normality plot

```
              Tests for Normality

Test                  --Statistic---    -p Value------

Shapiro-Wilk          W     0.908031    Pr<W      0.0794
Kolmogorov-Smirnov    D      0.17031    Pr>D     >0.1500
Cramer-von Mises      W-Sq  0.084708    Pr>W-Sq   0.1732
Anderson-Darling      A-Sq  0.605378    Pr>A-Sq   0.0984
```

```
    Stem Leaf                     #            Boxplot
       2 0                        1               |
       1 777                      3               |
       1 33                       2            +------+
       0                                       |      |
       0 033                      3            |   +  |
      -0 333                      3            *------*
      -0                                       |      |
      -1 333                      3            +------+
      -1 77                       2               |
      -2 0                        1               |
         ----+----+----+----+
```

```
               The UNIVARIATE Procedure
                  Variable:  resid

                    Normal Probability Plot
  2.25+                                        +++*
      |                                 *  *+*+
      |                              * *++++
  0.75+                             ++++
      |                         +**+*
      |                     *+**
 -0.75+                  ++++
      |              +++** *
      |       *   +*+*
 -2.25+       ++++
       +----+----+----+----+----+----+----+----+----+----+
           -2        -1         0        +1        +2
```

Analysis 2: MIXED using each sample unit value.

```
                The SAS System
             The Mixed Procedure

            Model Information
Data Set                         WORK.ONESUB
Dependent Variable               yijl
Covariance Structure             Variance
                                 Components
Estimation Method                REML
Residual Variance Method         Profile
Fixed Effects SE Method          Model-Based
Degrees of Freedom Method        Containment

              Class Level Information
          Class    Levels    Values
          temp          3    high low medium
          batch         2    1 2

                  Dimensions
     Covariance Parameters                2
     Columns in X                         4
     Columns in Z                         6
     Subjects                             1
     Max Obs Per Subject                 18

          Number of Observations
 Number of Observations Read               18
 Number of Observations Used               18
 Number of Observations Not Used            0

                Iteration History
Iteration Evaluations -2 Res Log Like Criterion
0              1        73.11545106
1              1        67.84036856    0.00000000
            Convergence criteria met.
```

```
              Covariance Parameter
              Estimates
        Cov Parm        Estimate
        batch(temp)       4.5741
        Residual          2.6111
```

```
           Fit Statistics
       -2 Res Log Likelihood            67.8
       AIC (smaller is better)          71.8
       AICC (smaller is better)         72.8
       BIC (smaller is better)          71.4
```

```
            Type 3 Tests of Fixed Effects
          Num    Den
Effect     DF     DF    F Value    Pr > F
temp        2      3       7.21    0.0715
```

```
                     Least Squares Means

                            Standard
Effect temp   Estimate   Error    DF   t Value  Pr>|t|
temp   high    16.5000   1.6499    3     10.00  0.0021
temp   low      7.6667   1.6499    3      4.65  0.0188
temp   medium  11.5000   1.6499    3      6.97  0.0061
```

```
Differences of Least Squares Means

                                  Std.
Effect temp temp    Estimate  Error  DF t Value  Pr>|t|
temp   high  low      8.8333  2.3333 3  3.79     0.0323
temp   high medium    5.0000  2.3333 3  2.14     0.1215
temp   low  medium   -3.8333  2.3333 3 -1.64     0.1990
```

Brief Summary of the Course

- All linear models
- Regression analysis and analysis of variance (ANOVA) or analysis of covariance (ANCOVA) for experiments.
- y – is a continuous variable; “dependent” variable in regression; “response” variable in experiments

Regression (Fitting Equations):

Reason: Prediction of the dependent variable (y; hard to measure) from related variables (x’s; easy to measure). Started with only continuous x variables, and then added class variables as predictors.

Model:

$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_m x_{mi} + \varepsilon_i$

- Used least squares regression to find estimated coefficients and standard errors of the coefficients

- Used “hand calculations” for SLR only.

SAS:

```
PROC REG data=yourdata;
 model y=X1 X2 X3;
 output out=out1 p=yhat1 r=resid1;
run;
*-----------------------------------------;
PROC PLOT DATA=out1;
 plot resid1*yhat1;
run;
*----------------------------------------;
PROC univariate data=out1 plot normal;
Var resid1;
Run;
```

Process:

1. Collect data on y and x's.
2. Run a model.
3. Check assumptions. If met, go to step 5.
4. If not met, transform the x and go back to step 2. If this does not work, try transforming the y and repeat step 2.
5. Goodness of fit measures: R^2 (or r^2) and root MSE (SE_E).
6. Use an F-test to see if the model is significant. Null hypothesis: H0: $\beta_1 = \beta_2 = \beta_3 = . . . = \beta_m = 0$ [all slopes are zero meaning no relationship with x's]
7. If the regression is significant, test each predictor variable (in the presence of the other x-variables), using a t-test.
8. Can calculate confidence intervals for each coefficient, and for the predicted values (mean predicted value, new observation, OR mean of *g* new observations).

Adding class variables:

- Convert these to dummy variables.
- The set of dummy variables represents that class variable
- Dummy variables alter the intercept
- Interactions between dummy variables and the continuous variables alter the slopes.
- Use a partial F-test as this can be used to test a group of variables (the group of dummy variables, or the group of interactions between dummy variables and continuous variables), whereas a t-test is for a single variable (testing a single dummy variable has no meaning – the group of dummy variables represents that class; unless there is only two levels in the class, since this would be only 1 dummy variable)

$$partial\ F = \frac{\left(SSreg(full) - SSreg(reduced)\right)/r}{SSE/(n-m-1)(full)}$$

Where *r* is the df(model) for the full model – df(model) for the reduced model.

Stepwise methods (as guides to selecting variables):

1. All possible regressions
2. R^2 (or Adjusted R^2).
3. Stepwise.
4. Backwards Stepwise
5. Forward Stepwise 2^m-1

CAUTION: Careful with dummy variables! Must come in or out of the model as a group, as the group represents one class variable.

Experimental Design:

- Manipulate by using treatments
- We are interested in CAUSE and EFFECT
- NOTE: We did “hand” calculations for CRD, one-factor only

Designs:

- Select homogeneous experimental units
- Randomly assign treatments to experimental units
- Treatments can be divided into Factors
- A crossed experiment (factorial) includes all combinations of the factor levels from all Factor
- Factors can be nested in another factor – more difficult to interpret and cannot look at interactions among factors
- Factors can be fixed-effect or random-effect

NOTE: differences in the use of the word random:

  - Random sampling
  - Random assignment of treatments to experimental units
  - Random-effects

- Can “block” before assigning treatments to experimental units to reduce variability among experimental units
- Can “split” experimental units for a second factor, or even split again “split-split plot for a third level – will affect the analysis and conclusions made
- Can add “covariates” as measurements on continuous variables from each experimental unit, to reduce variability

- Can have one measurement from each experimental unit (or an average for that unit), or can retain sampling unit measures but must divide the error in that case.
- Error terms (experimental error and sampling error) are random-effects
- Blocks are often random-effects
- F-tests are used to test for interactions (1^{st}), and main effects.
- Expected means squares are used to determine which F-tests to use to test each factor.
- If there is an interaction among factors, you cannot interpret the main effects (each Factor) separately
- If there is a significant difference in means (for a main effect, or there is an interaction), post comparison tests can be used to determine which means differ, IF the factor(s) are fixed-effects.
- For random-effects factors (and interactions), we can use the MS’s to estimate the variance for that factor (or interaction)

Process for Analysis:

1. Set up data in excel, by giving a label to each observation as to which block, and factor levels it was measured for, experimental unit, sampling unit, etc.
2. Set up SAS (or other package) with
   - **a.** the correct class statements,
   - **b.** model statements,
   - **c.** any necessary test statements (use the expected mean squares to decide if the default is ok or not), and
   - **d.** multiple comparisons (use LSMEANS for this in SAS).
   - **e.** Also, get a residual plot, normal probability plot, and normality tests (for the residuals)
3. Check the assumptions first. May have to transform the y-variable until assumptions are met.
4. When assumptions are met, use F-tests for interactions (if any) first. Make sure you have the right F-test.
5. If no interactions, check F-tests for main effects (e.g., Factor A, Factor B, etc).
6. For fixed-effects (main or interactions) that show significant differences among mean values, do pairs of means t-tests (or other multiple comparisons) to decide which means differ. Remember to divide alpha by the number of pairs of means when interpreting pairs of means t-tests.
7. For random-effects, estimate the variance for that factor. (can do this for error terms also as they are random-effects)

Models:

CRD with one factor:

Model: $y_{ij} = \mu + \tau_j + \varepsilon_{ij}$

SAS:

```
PROC GLM data=yourdata;
CLASS Treatment;
MODEL y=treatment;
MEANS treatment/scheffe hovtest=bartlett;
estimate '1 VS others' treatment 4 -1 -1 -1 -
1/divisor=4;
OUTPUT OUT=GLMOUT PREDICTED=PREDICT
RESIDUAL=RESID;
RUN;
PROC PLOT DATA=GLMOUT;
PLOT RESID*PREDICT='*';
RUN;
PROC UNIVARIATE DATA=GLMOUT PLOT NORMAL;
VAR RESID;
RUN;
```

OR:

Can use:

```
MEANS treatment/pdiff tdiff hovest=bartlett;
```

Instead.

2-factor, CRD:

Model: $y_{ijk} = \mu + \tau_{A\,j} + \tau_{Bk} + \tau_{AB\,jk} + \varepsilon_{ijk}$

SAS: both factors are fixed-effects

```
PROC GLM  data=yourdata;
class factorA factorB;
model result=factorA factorB factorA*factorB;
output out=glmout r=resid p=predict;
lsmeans factorA factorB
factorA*factorB/pdiff tdiff;
run;
proc plot data=glmout;
plot resid*predict='*';
run;
PROC univariate data=glmout plot normal;
Var resid;
Run;
```

SAS: mixed-effects, A fixed-effect; B random-effect

```
PROC GLM  data=yourdata;
class factorA factorB;
model result= factorA factorB factorA*factorB;
random factorB/test;
test h= factorA e= factorA*factorB;
lsmeans factorA/e= factorA* factorB pdiff tdiff;
output out=glmout r=resid p=predict;
run;
proc plot data=glmout;
plot resid*predict='*';
run;
proc univariate data=glmout normal plot;
var resid;
run;
```

RCB, one fixed-effect

Model: $y_{jk} = \mu + +\tau_{Bj} + \tau_{Ak} + \varepsilon_{jk}$

SAS:

```
PROC GLM  data=yourdata;
class block treatment;
model y=block treatment;
random block;
lsmeans treatment/pdiff tdiff;
output out=glmout r=resid p=predict;
run;
[plus statements to obtain the residual plot and
normality plot/tests]
```

RCB, two Factors:

Model: $y_{jkl} = \mu + \tau_{BLK\,j} + \tau_{A\,k} + \tau_{Bl} + \tau_{A\,Bkl} + \varepsilon_{jkl}$

SAS both Factors are fixed-effects, and blocks are random-effects:

```
PROC GLM  data=yourdata;
class block factorA factorB;
model y=block factorA factorB factorA* factorB;
random block;
lsmeans factorA/pdiff tdiff;
lsmeans factorB/pdiff tdiff;
lsmeans factorA* factorB/pdiff tdiff;
output out=glmout r=resid p=predict;
run;
[plus statements to obtain the residual plot and
normality plot/tests]
```

Generalized RCB, one Factor (RCB with replicates in each block)

Model: $y_{ijk} = \mu + \tau_{BLK\,j} + \tau_{TR\,k} + \tau_{BLK\times TR\,jk} + \varepsilon_{ijk}$

SAS (treatment is a fixed effect; blocks are random-effects)

```
PROC GLM  data=yourdata;
class block treatment;
model y=site treatment block*treatment;
random block block*treatment;
test h=treatment e=site*treatment;
lsmeans treatment/e=site*treatment pdiff tdiff;
output out=glmout r=resid p=predict;
run;
[plus statements to obtain the residual plot and
normality plot/tests]
```

Latin Square, with blocking in two directions
One fixed-effect factor:

Model: $y_{jkl} = \mu + \tau_{A\,k} + \tau_{Rj} + \tau_{Cl} + \varepsilon_{jkl}$

SAS:

```
PROC GLM  data=yourdata;
class row column treatment;
model y=row column treatment;
random row column;
lsmeans treatment/pdiff tdiff;
output out=glmout r=resid p=predict;
run;
[plus statements to obtain the residual plot and
normality plot/tests]
```

Split plots (and split-split plots):
Model for a 2-factor RCB, split-plot:

$$y_{jkl} = \mu_{\bullet\bullet\bullet} + \tau_{BLK\,j} + \tau_{A\,k} + \tau_{BLK\times A\,jk} + \tau_{Bl} + \tau_{A\,Bkl} + \varepsilon_{jkl}$$

SAS: blocks random-effects, Factor A fixed-effects, FactorB is applied to the split-plot

```
PROC GLM data=yourdata;
TITLE 'split plot, blocks random, treatments fixed';
CLASS block factorA factorB;
MODEL y=block factorA block*factorA factorB
factorA*factorB;
Test h=factorA e=factorA*block;
LSMEANS factorA/e=block*factorA tdiff pdiff;
LSMEANS factorB factorA*factorB/tdiff pdiff;
OUTPUT OUT=GLMOUT PREDICTED=PREDICT RESIDUAL=RESID;
RUN;
[plus statements to obtain the residual plot and
normality plot/tests]
```

Nested factors:
For a *crossed* experiment (Factorial):

$$y_{ijk} = \mu + \tau_{A\,j} + \tau_{Bk} + \tau_{AB\,jk} + \varepsilon_{ijk}$$

However, for a *nested* experiment, B nested in A, we have:

Model: $y_{ijk} = \mu + \tau_{A\,j} + \tau_{Bk(j)} + \varepsilon_{ijk}$

SAS:

```
PROC GLM  data=yourdata;
class factorA  factorA;
model y= factorA factorB(factorA);
output out=glmout r=resid p=predict;
lsmeans factorA factorB(factorA)/pdiff tdiff;
run;
[plus statements to obtain the residual plot and
normality plot/tests]
```

CRD: One Factor Experiment, Fixed Effects with subsampling

Model: $y_{ijl} = \mu + \tau_{TRj} + \varepsilon_{EUij} + \varepsilon_{SUijl}$

SAS: (note: expunitlabel is the label for the exp. units, eg., batch, board, etc)

```
PROC GLM data=yourdata;
class treatment expunitlabel;
model y=treatment expunitlabel(treatment);
random expunitlabel(treatment)/test;
test h=treatment e= expunitlabel(treatment);
lsmeans treatment /e= expunitlabel(treatment)pdiff
tdiff;
output out=glmout r=resid p=predict;
run;
[plus statements to obtain the residual plot and
normality plot/tests]
```

NOTE: could instead average the sample values for each experimental unit, to obtain one value for that experimental unit, and analyze this as if there were no samples (error term is experimental unit).

Generalized RCB [randomized block design, also called randomized complete block] with subsampling:

Model: $y_{ijl} = \mu + \tau_{BLKj} + \tau_{TRk} + \tau_{BLK \times TRjk} + \varepsilon_{EUijk} + \varepsilon_{SUijkl}$

[not given in class, but can modify the SAS code for generalized RCB]

Analysis of Covariance

Model: shown for CRD with two fixed-effect factors and one covariate; covariates are continuous variables; assuming no interactions between covariate and factors

$$y_{jkl} = \mu + \beta(x_{jkl} - \bar{x}) + \tau_{BLK\,j} + \tau_{Ak} + \tau_{Bl} + \tau_{ABkl} + \varepsilon_{jkl}$$

SAS code [full model with interactions which are not shown in the model above, and reduce to only one factor]

```
PROC GLM data=yourdata;
CLASS factorA;
Full: MODEL y=factorA x factorA*x/solution;
OUTPUT OUT=GLMOUT2 PREDICTED=PREDICT2 RESIDUAL=RESID2;
RUN;
PROC PLOT DATA=GLMOUT2;
PLOT RESID2*PREDICT2='*';
RUN;
PROC UNIVARIATE DATA=GLMOUT2 PLOT NORMAL;
VAR RESID2;
RUN;
```

Compare to the classical analysis of covariance model with no interaction between the covariates and the factors:

```
PROC GLM data=yourdata;
CLASS factorA;
Full: MODEL y=factorA x/solution;
OUTPUT OUT=GLMOUT3 PREDICTED=PREDICT3 RESIDUAL=RESID3;
RUN;
PROC PLOT DATA=GLMOUT3;
PLOT RESID3*PREDICT3='*';
RUN;
PROC UNIVARIATE DATA=GLMOUT3 PLOT NORMAL;
VAR RESID3;
RUN;
```

Using a partial F-test:

$$partial\ F = \frac{\left(SSreg(full) - SSreg(reduced)\right)/r}{SSE/(dferror)(full)}$$

OR

$$partial\ F = \frac{\left(SSE(reduced) - SSE(full)\right)/r}{SSE/(dferror)(full)}$$

$$= \frac{(SS \text{ due to dropped interaction variable(s)})/r}{MSE(full)}$$

SSreg=SSmodel
r=df(model for full model)-df(model for reduced model)

df for numerator of F is r
df for denominator of F is df(error full model)

Expected Mean Squares:

- Given for all models covered
- Can calculate this using the “rules” for any model (not be required to do this on an exam)

Power analysis:
Four possible results from Hypothesis testing:

	Reject H0	Accept H0
H0 True	α	1-α
H0 False	1-β	β

- Set Type I error (α)
- Solve for Type II error (β)
- Power is 1- β