# ANOVA Models

*Advanced Biostatistics*
Dean Adams
Lecture 3
EEOB 590C

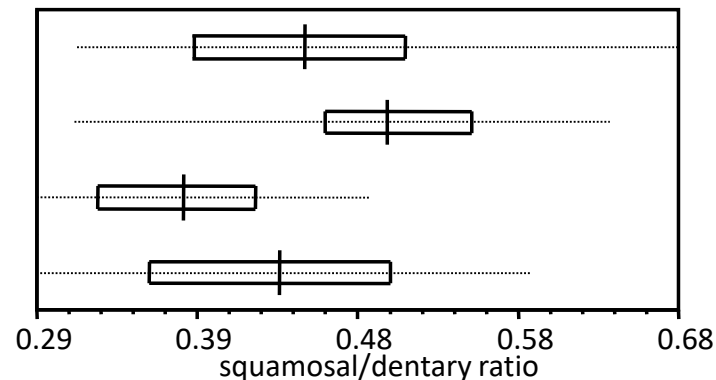**ANOVA (Analysis of Variance)**:  Y~X

     -X is categorical (groups), Y is continuous

$H_0$: no relationship between X & Y (i.e., no difference among groups)

     -Compare variation between groups to variation within groups (e.g., are males & female different in height?)

Model: $Y_{ij} = \mu + \alpha_i + \varepsilon_{ij}$ ($\mu$ is grand mean, $\alpha_i$ is $i^{th}$ group mean, and $\varepsilon_{ij}$ is error)

    -Standard test statistic: F-ratio (ratio of variances)

$$F \approx \frac{\sigma^2_{btwngroups}}{\sigma^2_{withingroups}}$$

If no difference amongst groups for null hypothesis, the "value of central tendency" will be on 1.



squamosal/dentary ratio

Errors

## 1: **Independence**: $\varepsilon_{ij}$ of variates must be independent

-SOME reasons for violation: spatial or temporal autocorrelation (variates close in space or time are similar).
-Autocorrelation test: Serial Independence (if data not independent, model non-independence in error variance)

## 2: **Normality**: requires normally distributed $\varepsilon_{ij}$

-Test distribution of deviates from mean for skewness, kurtosis (also other methods).
-If not normal, transform, use nonparametric methods, or randomization

## 3: **Homoscedasticity**: equal variance

-Test: F-tests, Bartlett's test, F-max test.
-If heteroscedastic, transform or use nonparametric (NOTE: ANOVA models fairly robust to homoscedasticity violations)

ANOVA based on partitioning Total Sums-of-Squares SST

Sample size per group.

Double bars means grand mean.

$$SST = \sum_{i=1}^{a} \sum_{j=1}^{n} \left( Y_{ij} - \bar{\bar{Y}} \right)^2$$

Total variation in the data set.

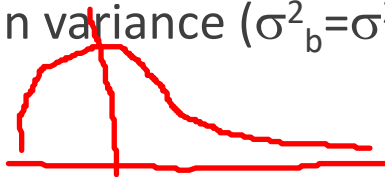SST=SSM+SSE        (M = model; E = error)

Variance components and F-ratio obtained

$$\sigma^2 = \frac{1}{n-1} \sum_{i=1}^{n} \left( Y_i - \bar{Y} \right)^2 = \frac{1}{df} SS$$

$$F \approx \frac{\sigma^2_{btwngroups}}{\sigma^2_{withingroups}}$$

If F-ratio = 1.0, no difference in variance ($\sigma^2_b = \sigma^2_w$)

Expected value under the null hypothesis.

SST can be partitioned into various components (for more complex designs)

Model contains single grouping variable (e.g., species or sex)

Procedure

$$Y \sim A$$

-Obtain overall and group means

-Estimate SSM (and $\sigma^2$=MSM) of group means vs. overall mean

-Estimate SSE (and $\sigma^2$=MSE) of individuals vs. their group mean

-Calculate F and assess significance (df1,df2)

| Source | df | SS | MS=$\sigma$ | F | P |
|--------|-----|----|-----|---|---|
| Group | a-1 | $SSM = \sum_{i=1}^{a} n_i \left( \bar{Y_i} - \bar{\bar{Y}} \right)^2$ | SSM/df | MSM/MSE | |
| Error | $\sum n_i - a$ | $SSE = \sum_{i=1}^{a} \sum_{j=1}^{n} \left( Y_{ij} - \bar{Y_i} \right)^2$ | SSE/df | | |
| Total | n-1 | $SST = \sum_{i=1}^{a} \sum_{j=1}^{n} \left( Y_{ij} - \bar{\bar{Y}} \right)^2$ | | | |

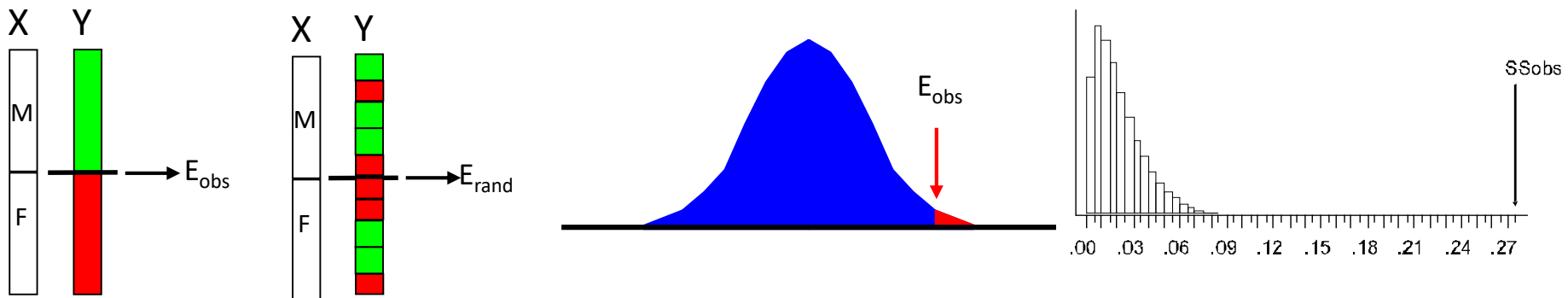*Note: SSE for can be obtained as SSE = SST − SSB

Standard approach:

-Compare F-ratio to F-distribution with appropriate df
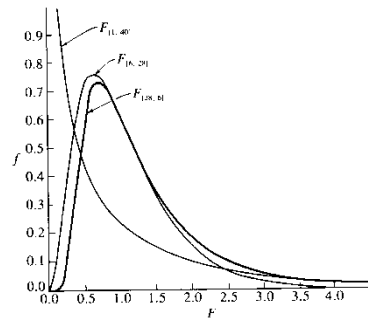


Resampling Alternative:

-Shuffle individuals among groups and generate distribution of possible

F-values (note: for single-factor ANOVA, shuffling individuals IS a residual randomization)

## For 2 groups ($n_1=n_2$), ANOVA will yield identical results to t-test

$$\mathbf{X} = \begin{bmatrix} m & m & m & m & m & f & f & f & f & f \end{bmatrix}$$
$$\mathbf{Y} = \begin{bmatrix} 5 & 4 & 4 & 4 & 3 & 7 & 5 & 6 & 6 & 6 \end{bmatrix}$$

```
> t.test(y~x)

t = 4.4721, df = 8, p-value = 0.002077

> anova(lm(y~x))

          Df  Sum Sq  Mean Sq  F value   Pr(>F)
x          1      10     10.0       20 0.002077 **
```

NOTE: For this case, one can derive F-ratio from the t-statistic

$$t^2 = \frac{\left(\overline{Y}_1 - \overline{Y}_2\right)^2}{s_p^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)} = \frac{n\left(\overline{Y}_1 - \overline{Y}_2\right)^2}{2s_p^2}$$

Numerator:

$$n\left(\overline{Y}_1 - \overline{Y}_2\right)^2 = \left(n\left(\overline{Y}_1 - \overline{\overline{Y}}\right)^2 + n\left(\overline{Y}_2 - \overline{\overline{Y}}\right)^2\right) = \sum n\left(\overline{Y}_i - \overline{\overline{Y}}\right)^2$$

b/c $n_1=n_2=n$ rewrite as:

ANOVA identifies group differences, but not WHICH ONES

Pairwise multiple comparisons required (1 vs 2, 1 vs 3, etc)

MANY approaches (most derived from t-statistic)

-Example: Fishers' LSD (Least Significant Difference)

-Calculate    $t_{obs} = \left| \bar{Y}_i - \bar{Y}_j \right|$

-Compare to smallest significant standardized difference:

$$LSD = t_{\alpha/2} \sqrt{MSE \left( \frac{1}{n_i} + \frac{1}{n_j} \right)}$$

Other approaches: T', Tukey-Kramer, GT2, Duncan's multiple range, Scheffe's F-test

(choice depends on = or ≠ sample sizes, etc.)

Resampling method for pairwise comparisons

Euclidian distance =
absolute value of the
differences in mean for
univariate data.

-Estimate group means

-Calculate matrix of $D_{euclid}$

$$\mathbf{D}_{obs} = \sqrt{\left(\overline{\mathbf{X}}_i - \overline{\mathbf{X}}_j\right)^t \left(\overline{\mathbf{X}}_i - \overline{\mathbf{X}}_j\right)}$$

-Shuffle specimens into groups

-Estimate means and $D_{rand}$
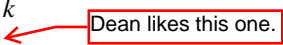
-Assess $D_{obs}$ vs. $D_{rand}$

-Repeat

$D_{Euclid}$

e.g., Adams 2004. *Ecology*
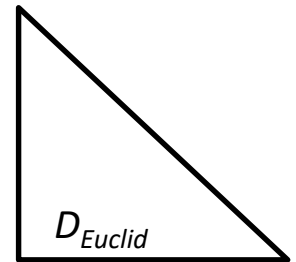
Multiple testing of data increases chance of 'finding' significance, so adjust critical-$\alpha$ for # comparisons (k)

Various approaches

Dunn-Sidak:  $\alpha' = 1 - \left(1 - \alpha\right)^{1/k}$ ← Dean likes this one.

Bonferroni:  $\alpha' = \dfrac{\alpha}{k}$

Sequential Bonferroni: , $\alpha_k^1 = \dfrac{\alpha}{k}$  but recalculated each time (k=1,2,3. . . ) for ORDERED comparisons

Bonferroni considered quite conservative: sequential Bonferroni much less so

After a bad winter storm (Feb. 1, 1898), Bumpus retrieved 136 sparrows in Rhode Island (about ½ died)

Collected the following measurements on each:

1) Alive/dead

2) Weight

3) Total length

4) Wing extent

5) Beak-head length

6) Humerus

7) Femur

8) Tibiotarsal

9) Skull

10) Keel-sternum

11) male/female

To investigate natural selection, examined whether there was a difference in alive vs. dead birds

Bumpus, H. C. 1898. *Woods Hole Mar. Biol. Sta.*

## Single-factor ANOVA

```
> anova(lm(TotalLength~sex))
             Df    Sum Sq   Mean Sq F value     Pr(>F)
sex           1 0.007460 0.0074597  16.667 7.617e-05 ***
Residuals   134 0.059975 0.0004476
```



Histogram of sexdata$m
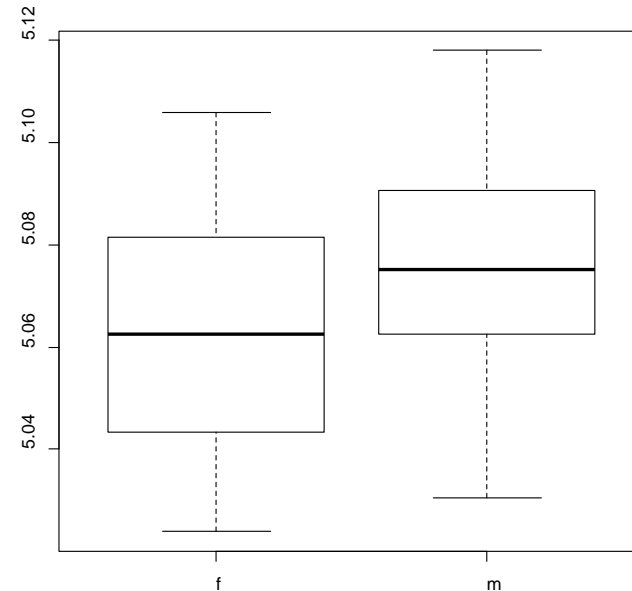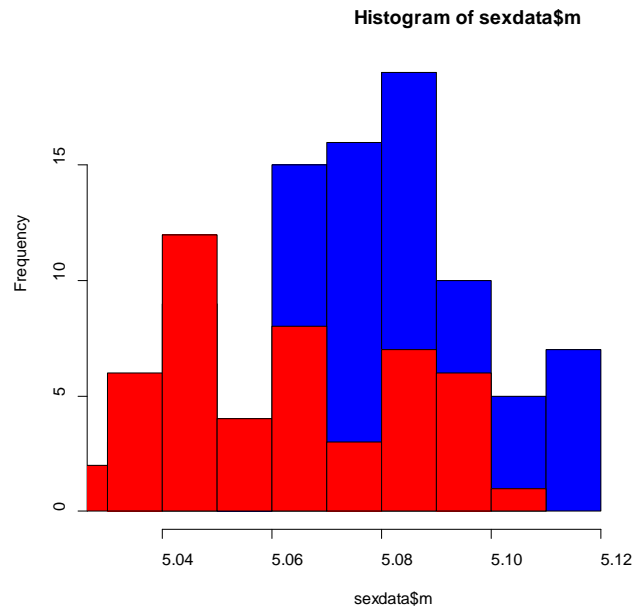


Males larger than females

ANOVA with 4 groups (male-alive, male-dead, female-alive,female-dead)

```
> gp<-as.factor(paste(sex,surv))
> anova(lm(TotalLength~gp))
             Df    Sum Sq   Mean Sq F value     Pr(>F)
gp            3 0.014515 0.0048382  12.068 4.957e-07 ***
```

Pairwise comparisons*

DON'T EVER CHANGE THIS NUMBER.

```
> pairwise.t.test(TotalLength, gp, p.adj = "none")

        f FALSE f TRUE  m FALSE
f TRUE  0.259    -       -
m FALSE 1.2e-05 3.5e-07 -
m TRUE  0.260   0.024   9.1e-05
```

*Shows P-values only

Via Randomization (D$_{euclid}$ below, P above diagonal)

|          | Fem Dead | Fem Surv | Male Dead | Male Surv |
|----------|----------|----------|-----------|-----------|
| Fem Dead | 0        | 0.330 NS | **0.002** | 0.328 NS  |
| Fem Surv | 0.0066   | 0        | **0.001** | **0.042** |
| Male Dead| 0.0229   | 0.0295   | 0         | **0.002** |
| Male Surv| 0.0053   | 0.0118   | 0.0176    | 0         |

ANOVA multiple X variables (e.g, species AND sex)

Model: $Y_{ijk} = \mu + \alpha_i + \beta_j + \varepsilon_{ijk}$

$$Y \sim A + B$$

In simple case, SSA & SSB are independent of one another, and are thus calculated as before: e.g.  $SSA = \sum_{i=1}^{a} n_i \left( \bar{Y}_i - \bar{\bar{Y}} \right)^2$

| Source | df | SS | MS | F | P |
|---|---|---|---|---|---|
| Factor A | a-1 | SSA | SSA/df | MSA/MSE | |
| Factor B | b-1 | SSB | SSB/df | MSB/MSE | |
| Error | $df_{tot}$-($df_A$+$df_B$) | SSE | SSE/df | | |
| Total | n-1 | SSA+SSB+SSE | | | |

*Note: SSE IS affected by factors (SSE = SST −(SSA+SSB)

Think of data for Factorial ANOVA as table of reactions

|  | Factor B (gp 1) | Factor B (gp 2) |
|---|---|---|
| Factor A (gp1) | Responses $AB_{11}$ | Responses $AB_{12}$ |
| Factor A (gp 2) | Responses $AB_{21}$ | Responses $AB_{22}$ |

Assumes changes in Factor A are constant across Factor B and vice versa. (Ignores the interaction between A and B)

Find means of rows, columns, and individual cells, and comparison of these yields tests for Factors A & B

NOTE: This ignores the interaction (A:B)

Interactions measure the joint effect of main effects A & B

Identifies whether response to A dependent on level of B

$$Y_{ijk} = \mu + \alpha_i + \beta_j + \boxed{(\alpha\beta)_{ij}} + \varepsilon_{ijk}$$

Y ~ A + B+A:B

Y ~ A*B

Estimated as:

Row mean

Column mean

$$SSAB = \sum_{i=1}^{a}\sum_{j=1}^{b} n_{ij}\left(\bar{Y}_{AB} - \bar{Y}_i - \bar{Y}_j + \bar{\bar{Y}}\right)^2 = n_{AB}\sum_{AB=1}^{rc}\left(\bar{Y}_{AB} - \bar{\bar{Y}}\right)^2 - SSA - SSB$$

Significant interaction: main effects not interpretable without clarification (e.g., species 1 larger than species 2 ONLY in wet environments…)

IF HAVE SIGNIFICANT INTERACTION TERM, MUST INTERPRET THAT BEFORE MOVING ONTO MAIN EFFECTS

**VERY** common in biology



Growth rate — Species 1 — Species 2 — Wet — Dry
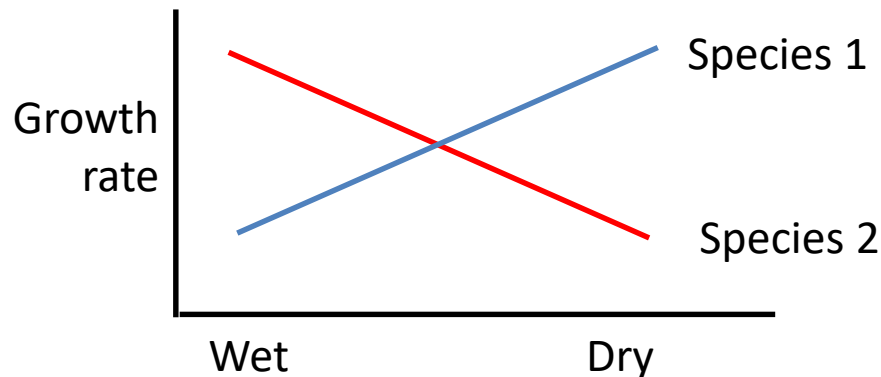
Note: The study of trade-offs (reaction norms) in evolutionary ecology is based on the study of interactions

Other factors can be added for general factorial designs (e.g., 3-way factorial with interaction)

$$Y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + \varepsilon_{ijkl}$$

Y ~ A + B+C+A:B+A:C+B:C+A:B:C

Adding factors also means adding many interactions

In general, assess significance of interactions, pool non-significant interaction Mean Square with MSE**, then interpret main effects whenever possible

Inclusion of more factors is 'neater', and allows assessment of **interactions**, but requires larger N

**Rules for pooling MSA*B with MSE depend upon significance, the type of effect (fixed or random), and several other factors (See Box 10.3 in *Biometry* for details)
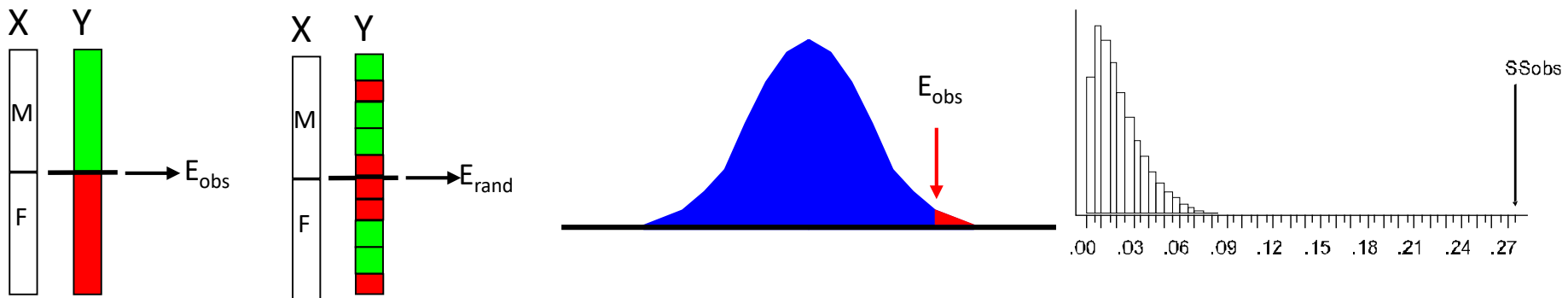
Standard approach:

-Compare F-ratio to F-distribution with appropriate df
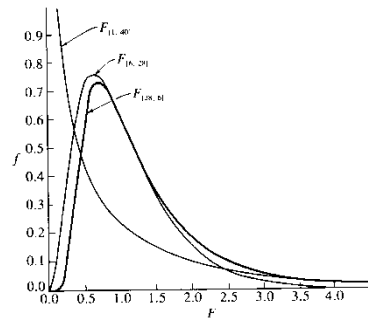


Resampling Alternative:

-Residual randomization: shuffle residuals from reduced model to assess that factor (e.g., remove A×B and use randomization to test A×B factor)

Bumpus data with two factors (sex, surv):

```
> anova(lm(TotalLength~sex*surv))
             Df    Sum Sq    Mean Sq  F value     Pr(>F)
sex           1  0.007460  0.0074597  18.6069  3.122e-05  ***
surv          1  0.006121  0.0061212  15.2683  0.0001483  ***
sex:surv      1  0.000934  0.0009337   2.3289  0.1293803
```

*NOTE: no significant interaction

Pairwise comparisons

Previous:

| | Fem Dead | Fem Surv | Male Dead | Male Surv |
| --- | --- | --- | --- | --- |
| Fem Dead | 0 | 0.330 NS | **0.002** | 0.328 NS |
| Fem Surv | 0.0066 | 0 | **0.001** | **0.042** |
| Male Dead | 0.0229 | 0.0295 | 0 | **0.002** |
| Male Surv | 0.0053 | 0.0118 | 0.0176 | 0 |

***NOTE: significance of pairwise

tests depends *heavily on null model*

*used for permutation!!*

Via Randomization ($D_{euclid}$ below, P above diagonal)

Values above diagonal are p-values
NS = Non significant

| | Fem Dead | Fem Surv | Male Dead | Male Surv |
| --- | --- | --- | --- | --- |
| Fem Dead | 0 | 0.883 NS | 0.154 NS | 0.427 NS |
| Fem Surv | 0.0066 | 0 | 0.625 NS | 0.875 NS |
| Male Dead | 0.0229 | 0.0295 | 0 | 0.179 NS |
| Male Surv | 0.0053 | 0.0118 | 0.0176 | 0 |

Values below diagonal are Euclidian distances

## *TRADITIONAL STATISTICAL VIEW*

For standard approaches, evaluating factors (via F-tests) requires knowledge of *expected mean squares (EMS)*

   -EMS describe the sources of variation for the effects in the model, and the sources against which effects are evaluated

**FIXED EFFECTS** (model I ANOVA): assumes differences among groups are due to treatment effects determined (FIXED) by the investigator (e.g., compare 3 drugs)

**RANDOM EFFECTS** (model II ANOVA): differences among groups are due to treatment effects and a random component NOT fixed by the investigator.  Groups are chosen as a *random* sample from a larger population (e.g., compare variation among families: the variation is of interest, not the chosen families)

## *TRADITIONAL STATISTICAL VIEW*

$$Y_{ij} = \mu + \alpha_i + \varepsilon_{ij}$$

**FIXED EFFECTS**: Var of $Y_{ij}$ = variance of $\mu$ + variance of $\alpha_i$ + variance of $\varepsilon_{ij}$

But since $\alpha$ are fixed, expected $k\sigma^2_\alpha = 0$

- Thus, $EMS_{trt}$ = variance of $\varepsilon_{ij}$

= $\sigma^2_\varepsilon$

**RANDOM EFFECTS**: Var of $Y_{ij}$ = variance of $\mu$ + variance of $\alpha_i$ + variance of $\varepsilon_{ij}$

$EMS_{trt}$ = variance of $\alpha_i$ + variance of $\varepsilon_{ij}$

= $k\sigma^2_\alpha + \sigma^2_\varepsilon$ (EMS contains variation among treatments)

## *TRADITIONAL STATISTICAL VIEW*

Determining whether a factor is fixed or random is tricky but *can be* important

This must be determined prior to final assembly and analysis of ANOVA table, because EMS is not the same (thus MS comparisons in F-tests will be different)

-Consider whether you have 'set' the levels of a factor in experiment, or have chosen 'representatives'

-Then consider what other levels may or may not exist

-Determine EMS for various factors

-When all else fails…

**CONSULT STATISTICIAN AND STATISTIC BOOKS!!**

Some factors are not independent, but are hierarchical
Levels of B 'nested' within levels of A:

Example: Compare $CO_2$ production among habitats (A) measured from multiple trees (B)

A1

B1  B2  B3

A2

B1  B2  B3
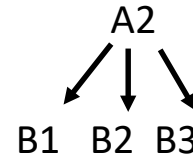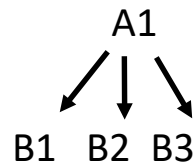
Trees logically nested within habitats

Note: B1 in each group is NOT the same! It is a place-holder (e.g., 1st tree sampled)

**Nested factors ALWAYS RANDOM effects!**

*NOTE: no interaction of A:B obtained when nested terms are used!!!
        -because SS(A/B) = SSB + SSA:B

Model:

SSA: $Y_{ijk} = \mu + \alpha_i + \beta_j(\alpha_i) + \varepsilon_{ijk}$     (reflects summation across levels of B)

SS(A/B): $SSA = nb\sum_{i=1}^{a}\left(\bar{Y}_i - \bar{\bar{Y}}\right)^2$     ('subgroups' of A)

NOTE: SS for Nested term [SS(A/B)] is sum of SSB + SSA:B

$$SS(A/B) = n\sum_{i=1}^{a}\sum_{j=1}^{b}\left(\bar{Y}_j - \bar{Y}_i\right)^2$$

| Source | df | SS | MS | | F | P |
|:---:|:---:|:---:|:---:|:---:|:---:|:---:|
| Factor A | a-1 | SSA | SSA/df | | **MSA/MS(A/B)** | |
| Factor A/B | a(b-1) | SS(A/B) | SS(A/B)/df | | **MS(A/B) /MSE** | |
| Error | ab(n-1) | SSE | SSE/df | | | |
| Total | n-1 | SSA+SS(A/B)+SSE | | | | |

NOTE: because of nested relationship and because B is a random effect, MSA tested vs. MS(A/B)

Determining independent vs. nested can be tricky. Consider:

1: Is there correspondence of levels across factors, or do they represent sub-divisions?

2: Is second factor fixed/random?

3: Is interaction term meaningful?

Example 1: Is sex nested within species, or is it an independent factor?

**SEX IS AN INDEPENDENT FACTOR**:

Levels of sex correspond across species

Sex is fixed effect

Sex:species interaction term meaningful

Example 2: Is tree nested within habitat (for $CO_2$ experiment), or is it an independent factor?

**TREE COULD BE NESTED FACTOR:**

Levels of tree not common across habitats

Trees are random effects (trees selected as representatives of the sample)

Tree:habitat interaction not biologically meaningful

Because SS can be partitioned, much more complicated ANOVA models are possible (e.g., 5 way factorial with 2 nested effects, some fixed some random...)

Often, researchers are prohibited by $$$ and cannot measure replicates for all levels of various treatments

Various experimental designs exist to extract SS for factors in incomplete data (e.g., latin-squares, randomized complete block, randomized incomplete block, etc.)

Maximize the power of analysis vs. sampling effort, **PROVIDED THEY ARE SET UP CORRECTLY** (i.e. are considered a priori)

SEE STATISTICS Dept. for HOW to generate such designs

For balanced data sets, everything above holds

For unbalanced data, things are more complicated

Different factor SS can be obtained with different ORDER of factors in the model

```
> anova(lm(TotalLength~sex+surv))
             Df    Sum Sq    Mean Sq F value      Pr(>F)
sex           1 0.007460 0.0074597  18.423 3.383e-05 ***
surv          1 0.006121 0.0061212  15.117 0.0001588 ***

> anova(lm(TotalLength~surv+sex))
             Df    Sum Sq    Mean Sq F value      Pr(>F)
surv          1 0.004127 0.0041266  10.191  0.001761 **
sex           1 0.009454 0.0094544  23.349 3.666e-06 ***
```

Why is this the case?

Difference due to calculations of type I vs. type III SS

Type 1 is default in R

**Type I (sequential) SS**: calculated in order found in model

Estimate SS for effect given model up to that point

e.g., $\quad SSA = A\left(\beta_A \mid \overline{\overline{Y}}\right) \quad$ then find $\quad SSB = B\left(\beta_B \mid \beta_A, \overline{\overline{Y}}\right)$

**Type III (marginal) SS**: calculated relative to all other model effects

All terms in model and estimate effect SS by removing it

e.g., $\quad SSA = A\left(\beta_A \mid \beta_B, \overline{\overline{Y}}\right) \quad SSB = B\left(\beta_B \mid \beta_A, \overline{\overline{Y}}\right)$

Type I SS can change depending on order, while Type III do not

Type I SS remain additive (they sum to SSModel) while Type III do not

For balanced designs, Type I = Type III

This matters when you have unbalanced data, which most data is.

**Type III: Issues**

1: $H_0$ and $H_a$ illogical for type III:

        -Obtain $SS_A$ by doing $SS_{Full} - SS_{Full\ w.out\ A}$

        -Obtain $SS_B$ by doing $SS_{Full} - SS_{Full\ w.out\ B}$

        -Obtain $SS_{A:B}$ by doing $SS_{Full} - SS_{Full\ w.out\ A:B}$

BUT what sense is this model: Y~A + A:B (ie, how can one have an interaction without the main effect???)


2: SS from Type III VIOLATE original property described by Fisher

        SS partitioning: SST= SSA+SSB, etc. ___**NOT**___ the case with type III


```
> anova(lm(TotalLength~paste(sex,surv))) # total SSModel: A, B, A:B
Analysis of Variance Table

Response: TotalLength
             Df   Sum Sq   Mean Sq F value    Pr(>F)
paste(sex, surv)  3 0.014515 0.0048382  12.068 4.957e-07 ***
Residuals       132 0.052920 0.0004009
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> sum(anova(lm(TotalLength~sex*surv))[[2]][1:3])  #TYPE I
[1] 0.01451466
> sum(drop1(aov(TotalLength~sex*surv),.~.)[[2]][2:4]) #TYPE III
[1] 0.00973504
```

DCA perspective: Type I preferred (though it forces user to think about $H_0$ $H_a$!).

Some software (SAS, JMP, Minitab) use Type III

Other packages (R, S-plus, Mathematica) use Type I

       Philosophical debate amongst statisticians

Venables argues logic behind type III SS nonsensical:

> "The objection to Type III sums of squares is that they encourage naive users to do silly things such as test main effects in the presence of interactions, without really asking whether the test makes sense or not, that is, whether it really addresses a question of any interest."

> "There is, by any sensible reckoning, only ONE type of sum of squares, and it always represents an improvement **sum of squares of the outer (or alternative) model over the inner (or null hypothesis) model. What the SAS highly dubious classification of sums of squares does is to encourage users to concentrate on the null hypothesis model and to forget about the alternative.**"

Translation: $H_a$ matters, so think CAREFULLY about your model before pushing buttons!

Y ~ A + B + A:B    This *IS* a set of sequential hypotheses tests (Type I SS)

| Model | Test | $H_0$ |
|---|---|---|
| Y ~ A | Does A explain more variation than the grand mean? | Y ~ 1 |
| Y ~ A + B | Does B\|A explain more variation than A alone? | Y ~ A |
| Y ~ A + B + A:B | Does the interaction help in explaining more variation than A and B separately? | Y ~ A + B |

Requires appropriate resampling procedure with exchangeable units for each $H_0$

*Residual randomization* is the most appropriate for factorial models

Anderson and ter Braak 2003. *J. Stat. Comput. Simul.*
Collyer and Adams 2007. *Ecology.*
Collyer et al. 2015. *Heredity.*

Sequentially permute $Y_{resid}$ from reduced model ($H_{0.r}$) with fewer terms
Tests SS for $H_1$, while holding constant SS in corresponding $H_0$

**Procedure**

> 1: Estimate parameters and observed test statistic ($E_{obs}$) from full model
> 2: Remove one term from the model; calculate predicted values ($\widehat{\mathbf{Y}}$) and residuals ($\varepsilon$) for the reduced model
> 3: Permute residuals ($\varepsilon$) and add them to the predicted values to obtain randomized values
> 4: Calculate test statistic for random data ($E_{rand}$)
> 5: Repeat *i* times to obtain empirical distribution of statistic

Higher statistical power for factorial designs (Anderson and terBraak, 2003)
Tests appropriate $H_0$ for each term in model (Collyer, Sekora, and Adams 2015)
Uses correct exchangeable units for hypothesis testing (Collyer, Sekora, and Adams 2015)

Expected mean squares

NOTE: Using permutation, the concepts of EMS are more clear. One is explicitly describing what hypothesis is tested against which.

(DCA: using permutation, traditional concepts such as EMS, type of SS, etc. come clearly into focus. Type I SS requires clear thinking of $H_0$ & $H_a$, so hypothesis testing is rigorously defined).

ANOVA an incredibly flexible tool for testing hypotheses

Can add factors, based on theory of partitioning SS

Type I retains that theory, type III does not

Permutations are incredibly useful

Think critically about $H_0$ & $H_a$: BOTH matter!