Not all n_{ij} the same

STAT 516 Lec 07

Unbalanced two-way factorial design

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2024-03-26

Mice example

Change in mRNA expression of esr1 in wild-type vs gen-modified mice on low- and high-fat diets.

Data from Trey Hope in Dr. Enos' lab in the USC School of Medicine.

2 Factors

A: Diet (LFD, HFD)

B: Gene (WT, ADIPO)

WT LFD	ADIPO-ERα LFD	WT HFD	ADIPO-ERα HFD
493	555	595.5	1153
172	302	418.5	890.5
617	434	642	539
534	90	743.5	651.5
500.5	72	1351	585
127	489	1180	783.5
1224	453	938.5	533.5
143	552.5	670	895
852	635.5	1319	579
134	330.9	1007	551
547.5	169.5	589	800
	737.5	481.5	1026
		785	308
		1060	1415
		435	342.5
		535.5	197.5

Does the diet affect the response? The genetic modification? Is the effect of the diet the same in the wild-type and the gen-modified mice?

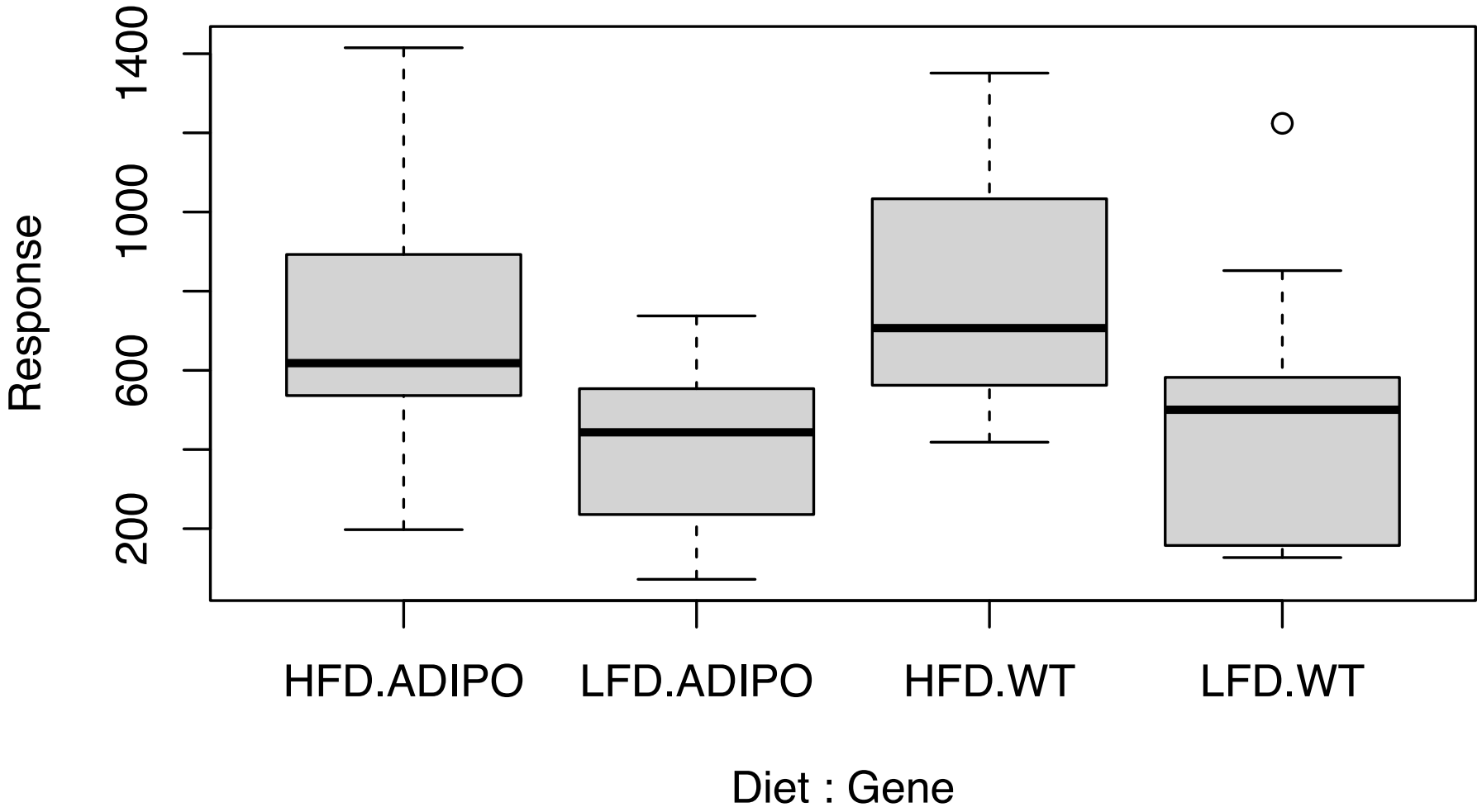
Now in a `.csv` file with one column for each factor.

```
Response,Gene,Diet
493,WT,LFD
172,WT,LFD
617,WT,LFD
534,WT,LFD
500.5,WT,LFD
127,WT,LFD
1224,WT,LFD
143,WT,LFD
852,WT,LFD
134,WT,LFD
547.5,WT,LFD
555,ADIPO,LFD
302,ADIPO,LFD
434,ADIPO,LFD
90,ADIPO,LFD
72,ADIPO,LFD
489,ADIPO,LFD
453,ADIPO,LFD
552.5,ADIPO,LFD
635.5,ADIPO,LFD
330.9,ADIPO,LFD
169.5,ADIPO,LFD
737.5,ADIPO,LFD
595.5,WT,HFD
418.5,WT,HFD
```

```r
link <- url("https://people.stat.sc.edu/gregorkb/data/ADIPOER.csv")
adipoer <- read.csv(link)
head(adipoer,n = 14)
```

```
   Response  Gene Diet
1     493.0    WT  LFD
2     172.0    WT  LFD
3     617.0    WT  LFD
4     534.0    WT  LFD
5     500.5    WT  LFD
6     127.0    WT  LFD
7    1224.0    WT  LFD
8     143.0    WT  LFD
9     852.0    WT  LFD
10    134.0    WT  LFD
11    547.5    WT  LFD
12    555.0 ADIPO  LFD
13    302.0 ADIPO  LFD
14    434.0 ADIPO  LFD
```

```r
boxplot(Response ~ Diet + Gene, data = adipoer)
```



```r
grp_means <- aggregate(Response ~ Diet + Gene, data = adipoer, mean)
grp_means
```

```
  Diet  Gene Response
1  HFD ADIPO 703.1250
2  LFD ADIPO 401.7417
3  HFD    WT 796.9375
4  LFD    WT 485.8182
```

$\hat{\mu}$ in R

$\bar{Y}_{11\cdot}$ $\bar{Y}_{21\cdot}$ $\bar{Y}_{12\cdot}$ $\bar{Y}_{22\cdot}$

```r
grp_counts <- aggregate(Response ~ Diet + Gene, data = adipoer, length)
grp_counts
```

```
  Diet  Gene Response
1  HFD ADIPO       16
2  LFD ADIPO       12
3  HFD    WT       16
4  LFD    WT       11
```

n_{11} n_{21} n_{12} n_{22}

Two-way treatment effects model

The two-way treatment effects model gives

$$Y_{ijk} = \mu + \tau_i + \gamma_j + (\tau\gamma)_{ij} + \varepsilon_{ijk}$$

for $i = 1, \ldots, a$, $j = 1, \ldots, b$, and $k = 1, \ldots, n_{ij}$, where

- Y_{ijk} is the response for EU k under level i of A and level j of B.
- μ represents a baseline or overall mean.
- The τ_i are the main effects for Factor A.
- The γ_j are the main effects for Factor B.
- The $(\tau\gamma)_{ij}$ are the interaction effects between A and B.
- The ε_{ijk} are Normal$(0, \sigma^2)$ error terms.

Now suppose n_{ij} are not all the same, so the design is unbalanced.

Parameter constraints in the unbalanced case

We have $1 + a + b + ab$ parameters for ab treatment means...

1. To give μ a baseline interpretation, set

$$\tau_a = 0, \quad \gamma_b = 0, \quad \text{and} \quad (\tau\gamma)_{aj} = (\tau\gamma)_{ib} = 0 \text{ for all } i, j.$$

2. To give μ an overall mean interpretation, set

$$\sum_{i=1}^{a} n_{i\cdot}\tau_i = 0, \quad \sum_{j=1}^{b} n_{\cdot j}\gamma_j = 0,$$

where $n_{i\cdot} = \sum_{j=1}^{b} n_{ij}$ and $n_{\cdot j} = \sum_{i=1}^{a} n_{ij}$, as well as

$$\sum_{j=1}^{b} n_{ij}(\tau\gamma)_{ij} = 0 \text{ for all } i \text{ and } \sum_{i=1}^{a} n_{ij}(\tau\gamma)_{ij} = 0 \text{ for all } j.$$

Estimating the error term variance

An unbiased estimator of the error term variance σ^2 is given by

$$\hat{\sigma}^2 = \frac{1}{N-ab} \sum_{i=1}^{a} \sum_{j=1}^{b} \sum_{k=1}^{n_{ij}} (Y_{ijk} - \bar{Y}_{ij.})^2,$$

where $N = \sum_{i=1}^{a} \sum_{j=1}^{b} n_{ij}$.

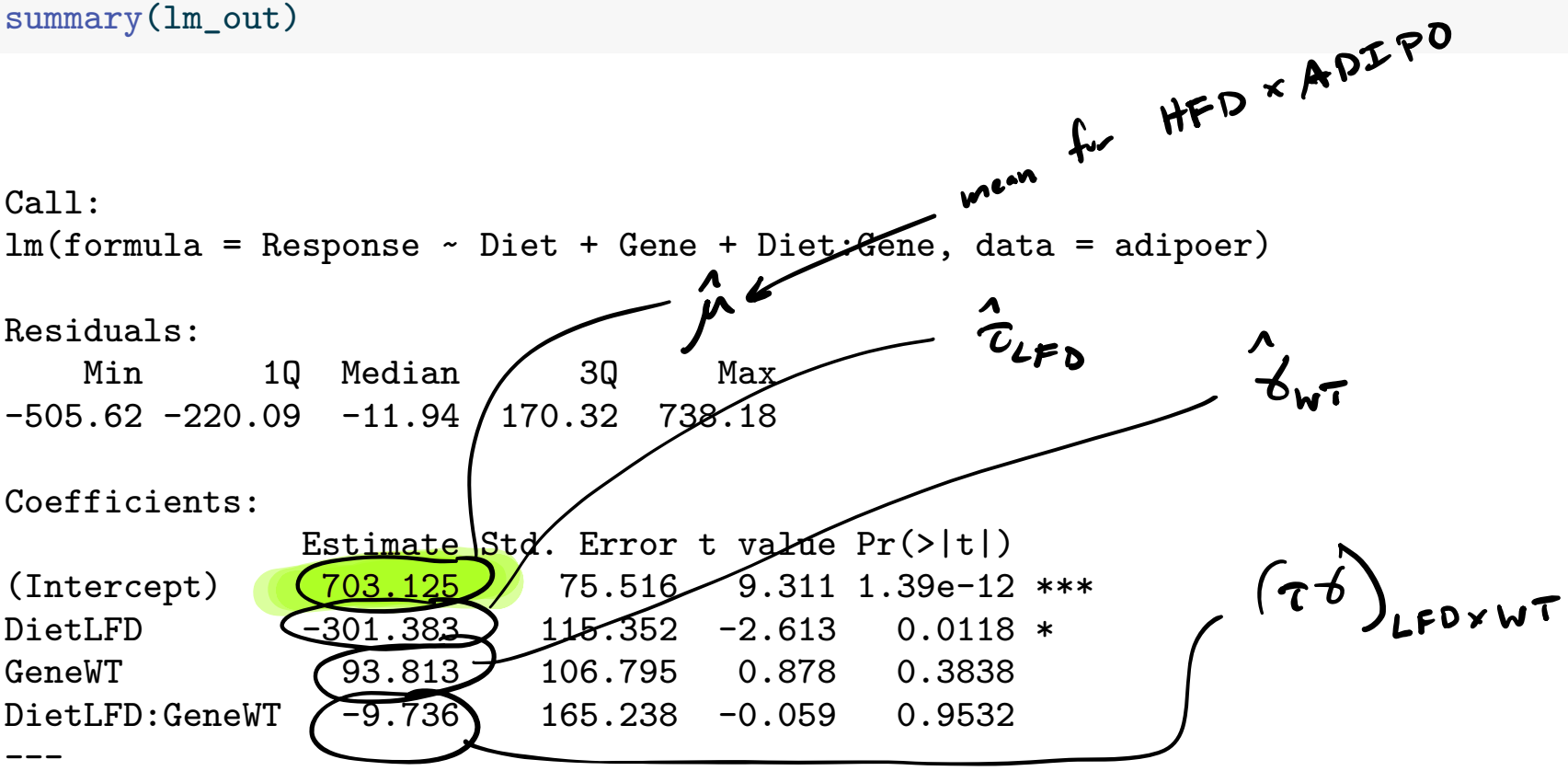
In balanced case $n_{ij} = n \ \forall \ i,j$, so $N = abn$.

$N - ab = abn - ab = ab(n-1)$.

Mice data (cont)

R uses the μ-as-baseline constraint.

```
lm_out <- lm(Response ~ Diet + Gene + Diet:Gene, data = adipoer)
summary(lm_out)
```




```
Call:
lm(formula = Response ~ Diet + Gene + Diet:Gene, data = adipoer)

Residuals:
    Min      1Q  Median      3Q     Max
-505.62 -220.09  -11.94  170.32  738.18

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   703.125     75.516   9.311 1.39e-12 ***
DietLFD      -301.383    115.352  -2.613   0.0118 *
GeneWT         93.813    106.795   0.878   0.3838
DietLFD:GeneWT -9.736    165.238  -0.059   0.9532
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 302.1 on 51 degrees of freedom
Multiple R-squared:  0.2289,    Adjusted R-squared:  0.1835
F-statistic: 5.045 on 3 and 51 DF,  p-value: 0.003882
```

Sums of squares in the unbalanced design

Decompose variability in Y_{ijk}

Sum of squares	Symbol	Formula
Total	$\mathrm{SS}_{\mathrm{Tot}}$	$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n_{ij}}(Y_{ijk}-\bar{Y}_{\dots})^2$
Treatments	$\mathrm{SS}_{\mathrm{Trt}}$	$\sum_{i=1}^{a}\sum_{j=1}^{b} n_{ij}(\bar{Y}_{ij\cdot}-\bar{Y}_{\dots})^2$
Error	$\mathrm{SS}_{\mathrm{Error}}$	$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n_{ij}}(Y_{ijk}-\bar{Y}_{ij\cdot})^2$

We have the decomposition $\mathrm{SS}_{\mathrm{Tot}} = \mathrm{SS}_{\mathrm{Trt}} + \mathrm{SS}_{\mathrm{Error}}$.

Effects of A, B, and A×B all together

The Analysis of Variance (ANOVA) table

Obtain the MS values by dividing the SS values by the Df values.

Source	Df	SS	MS	F value
Treatments	$ab-1$	$\mathrm{SS}_{\mathrm{Trt}}$	$\mathrm{MS}_{\mathrm{Trt}}$	$F_{\mathrm{stat}} = \mathrm{MS}_{\mathrm{Trt}} / \mathrm{MS}_{\mathrm{Error}}$
Error	$N-ab$	$\mathrm{SS}_{\mathrm{Error}}$	$\mathrm{MS}_{\mathrm{Error}}$	
Total	$N-1$	$\mathrm{SS}_{\mathrm{Tot}}$		

Reject H_0: μ_{ij} all the same if $F_{\mathrm{stat}} > F_{ab-1,N-ab,\alpha}$.

In the unbalanced case we have $N = \sum_{i=1}^{a} \sum_{j=1}^{b} n_{ij}$ in place of abn.

Main effect sums of squares under unbalancedness

Balanced Case: $SS_{Trt} = SS_A + SS_B + SS_{AB}$

Unbalanced Case: No nice decomposition like this.

- In the balanced case, we decomposed $\mathrm{SS}_{\mathrm{Trt}}$ as $\mathrm{SS}_{\mathrm{A}} + \mathrm{SS}_{\mathrm{B}} + \mathrm{SS}_{\mathrm{AB}}$.
- No such "clean" decomposition of $\mathrm{SS}_{\mathrm{Trt}}$ under unbalancedness.
- Specifically, it is not obvious how to define SS_{A} and SS_{B}.
- Three versions of SS_{A} and SS_{B} measure main effect importance:
  1. Sequentially ← anova( ) in R gives these.
  2. After other main effect in the *absence* of interaction
  3. After other main effect in the *presence* of interaction

  These are called Type I, Type II, and Type III sums of squares.

Type I SS (meaningless for unbalanced designs)

Sequential SS

```
anova(lm(Response ~ Gene + Diet + Gene:Diet, data = adipoer))
```

```
Analysis of Variance Table

Response: Response
          Df  Sum Sq Mean Sq F value    Pr(>F)
Gene       1  127271  127271  1.3949 0.2430621
Diet       1 1253492 1253492 13.7381 0.0005184 ***
Gene:Diet  1     317     317  0.0035 0.9532452
Residuals 51 4653342   91242
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

SS_{Gene} SS_{Diet} $SS_{Gene*Diet}$

If design is balanced, you will get the same output.

If unbalanced, do not use this!

```
anova(lm(Response ~ Diet + Gene + Diet:Gene, data = adipoer))
```

```
Analysis of Variance Table

Response: Response
          Df  Sum Sq Mean Sq F value    Pr(>F)
Diet       1 1270105 1270105 13.9202 0.0004804 ***
Gene       1  110659  110659  1.2128 0.2759481
Diet:Gene  1     317     317  0.0035 0.9532452
Residuals 51 4653342   91242
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

SS_{Diet} SS_{Gene} $SS_{Diet*Gene}$

Type II SS (assumes no interaction)

```
# fit model with both main effects
lm_Diet_Gene <- lm(Response ~ Diet + Gene, data = adipoer)
SSE_Diet_Gene <- sum(lm_Diet_Gene$residuals^2)

# fit model with just Gene
lm_Gene <- lm(Response ~ Gene, data = adipoer)
SSE_Gene <- sum(lm_Gene$residuals^2)
SS_Diet <- SSE_Gene - SSE_Diet_Gene # take difference in SSE
SS_Diet
```

```
[1] 1253492
```

```
# fit model with just Diet
lm_Diet <- lm(Response ~ Diet, data = adipoer)
SSE_Diet <- sum(lm_Diet$residuals^2)
SS_Gene <- SSE_Diet - SSE_Diet_Gene # take difference in SSE
SS_Gene
```

```
[1] 110658.6
```

Obtain Type II SS with `Anova()` function from R package `car`.

```r
library(car)
Anova(lm(Response ~ Diet + Gene + Diet:Gene, data = adipoer),type = "II")
```

```
Anova Table (Type II tests)

Response: Response
           Sum Sq Df F value    Pr(>F)
Diet      1253492  1 13.7381 0.0005184 ***
Gene       110659  1  1.2128 0.2759481
Diet:Gene     317  1  0.0035 0.9532452
Residuals 4653342 51
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Type III SS (Use this one for unbalanced designs)

- In the unbalanced case we should use the so-called Type III SS.
- We will denote them by $\mathrm{SS}_{\mathrm{A}}^{\mathrm{III}}$ and $\mathrm{SS}_{\mathrm{B}}^{\mathrm{III}}$.
- Type III SS are tedious to obtain in the unbalanced case; they are like full-reduced model differences in the error sum of squares, where the reduced model is the model without the main effect in question.
- The `anova()` or `aov()` functions in R give sequential SS, which are not meaningful in the unbalanced case; however, the Type III SS are equal to the sequential (i.e. Type I) SS when $n_{ij} = n \ \forall ij$.
- Under unbalancedness $\mathrm{SS}_{\mathrm{Trt}} \neq \mathrm{SS}_{\mathrm{A}}^{\mathrm{III}} + \mathrm{SS}_{\mathrm{B}}^{\mathrm{III}} + \mathrm{SS}_{\mathrm{AB}}$.

Type III sums of squares for unbalanced designs

ANOVA table with Type III SS and MS for A and B:

Source	Df	SS	MS	F value
A	$a-1$	$\mathrm{SS}_{\mathrm{A}}^{\mathrm{III}}$	$\mathrm{MS}_{\mathrm{A}}^{\mathrm{III}}$	$F_{\mathrm{A}} = \mathrm{MS}_{\mathrm{A}}^{\mathrm{III}} / \mathrm{MS}_{\mathrm{Error}}$
B	$b-1$	$\mathrm{SS}_{\mathrm{B}}^{\mathrm{III}}$	$\mathrm{MS}_{\mathrm{B}}^{\mathrm{III}}$	$F_{\mathrm{B}} = \mathrm{MS}_{\mathrm{B}}^{\mathrm{III}} / \mathrm{MS}_{\mathrm{Error}}$
AB	$(a-1)(b-1)$	$\mathrm{SS}_{\mathrm{AB}}$	$\mathrm{MS}_{\mathrm{AB}}$	$F_{\mathrm{AB}} = \mathrm{MS}_{\mathrm{AB}} / \mathrm{MS}_{\mathrm{Error}}$
Error	$N-ab$	$\mathrm{SS}_{\mathrm{Error}}$	$\mathrm{MS}_{\mathrm{Error}}$	
Total	$N-1$	$\mathrm{SS}_{\mathrm{Tot}}$		

1. Reject H_0: $\bar{\mu}_{1.} = \cdots = \bar{\mu}_{a.}$ if $F_{\mathrm{A}} > F_{a-1,N-ab,\alpha}$.
2. Reject H_0: $\bar{\mu}_{.1} = \cdots = \bar{\mu}_{.b}$ if $F_{\mathrm{B}} > F_{b-1,N-ab,\alpha}$.
3. Reject H_0: $\mu_{ij} = \bar{\mu}_{i.} + \bar{\mu}_{.j} - \bar{\mu}_{..} \quad \forall ij$ if $F_{\mathrm{AB}} > F_{(a-1)(b-1),N-ab,\alpha}$.

Tensile strength data (cont)

Obtain Type III SS with `Anova()` from the R package `car`.

Important to specify all the options exactly!

```
library(car)
Anova(lm(Response ~ Gene + Diet + Gene:Diet,
         contrasts = list(Gene = contr.sum, Diet = contr.sum),# specify constraint
         data = adipoer),
      type = "III")
```

```
Anova Table (Type III tests)

Response: Response
             Sum Sq Df  F value    Pr(>F)
(Intercept) 19050576  1 208.7917 < 2.2e-16 ***
Gene          105749  1   1.1590 0.2867411
Diet         1253698  1  13.7404 0.0005179 ***
Gene:Diet        317  1   0.0035 0.9532452
Residuals    4653342 51
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Correct output.

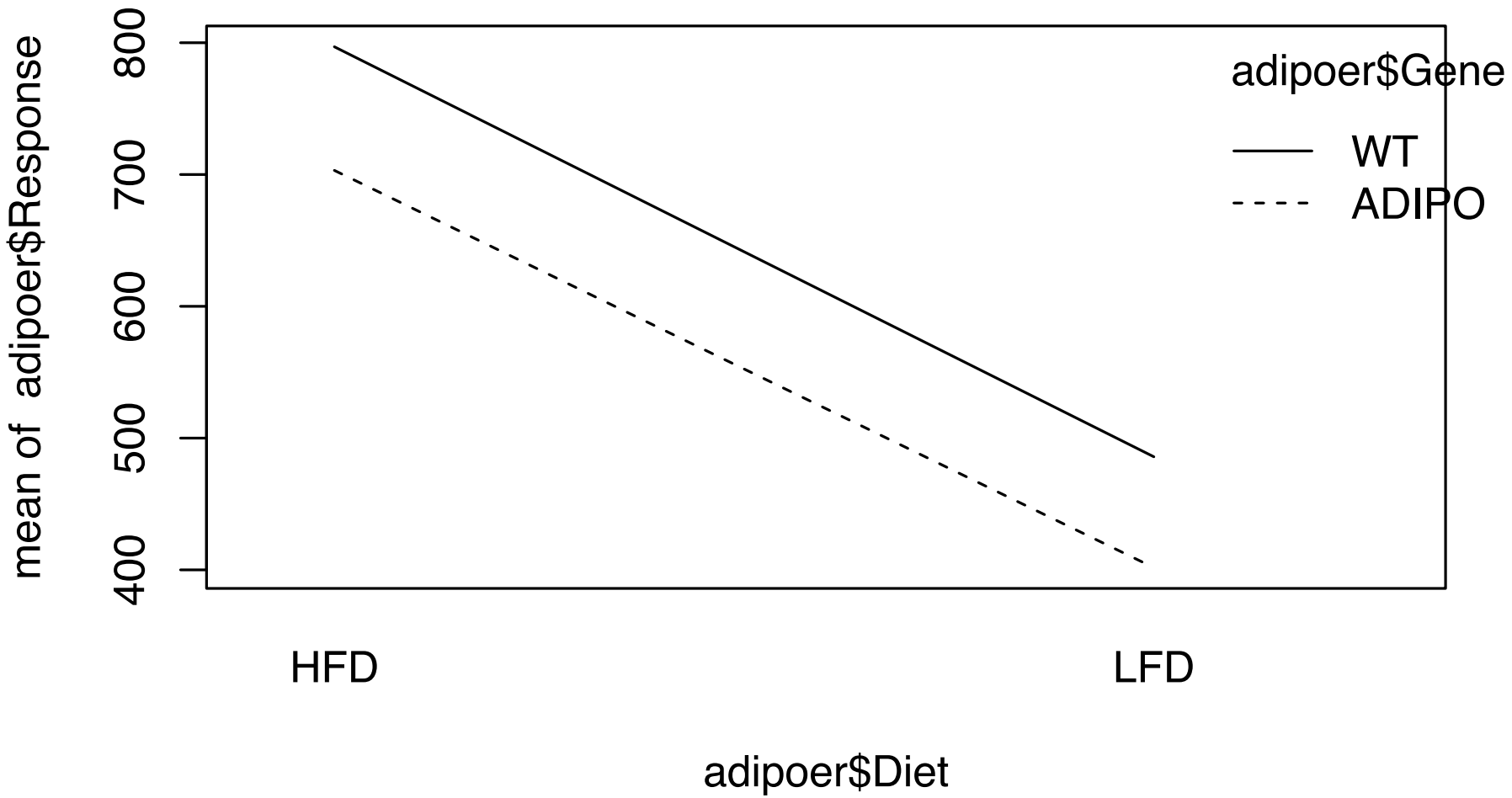
Same as from anova() output

No sign. interaction

Since interaction is not significant, we can focus on main effects...

Mice data (cont)

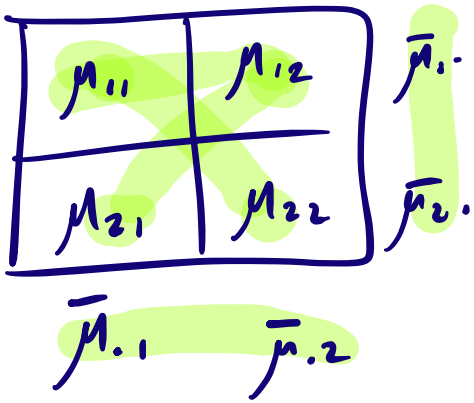
```
interaction.plot(adipoer$Diet, adipoer$Gene, adipoer$Response)
```



Estimates of cell and marginal means in unbalanced case

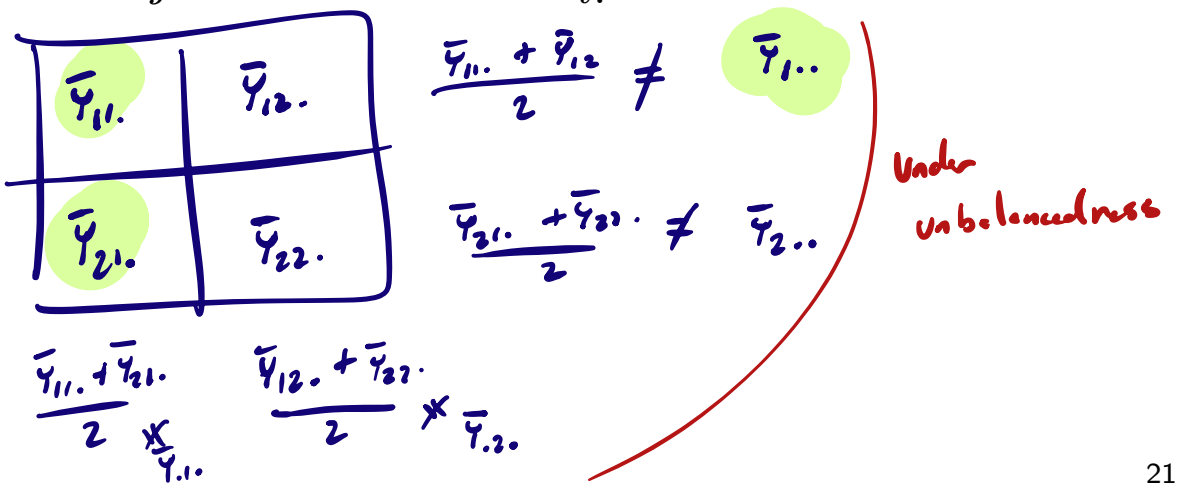
The estimators of the cell and marginal means are given by

- $\hat{\mu}_{ij} = \bar{Y}_{ij.}$, $i = 1, \ldots, a$, $j = 1, \ldots, b$.
- $\hat{\bar{\mu}}_{i.} = \frac{1}{b} \sum_{j=1}^{b} \hat{\mu}_{ij}$, $i = 1, \ldots, a$.
- $\hat{\bar{\mu}}_{.j} = \frac{1}{a} \sum_{i=1}^{a} \hat{\mu}_{ij}$, $j = 1, \ldots, b$.



We estimate $\hat{\bar{\mu}}_{i.}$ with $\bar{Y}_{i..}$ (and $\hat{\bar{\mu}}_{.j}$ with $\bar{Y}_{.j.}$) only when $n_{ij} = n \; \forall ij$.

Exercise: Write $\hat{\bar{\mu}}_{i.}$ in terms of Y_{ijk} and find $\operatorname{Var} \hat{\bar{\mu}}_{i.}$.



Some CI formulas (without familywise adjustment)

Under unbalancedness our CI formulas become more complicated.

Target	$(1-\alpha)100\%$ confidence interval
μ_{ij}	$\hat{\mu}_{ij} \pm t_{N-ab,\alpha/2}\hat{\sigma}\sqrt{\frac{1}{n_{ij}}}$
$\mu_{ij} - \mu_{i'j'}$	$\hat{\mu}_{ij} - \hat{\mu}_{i'j'} \pm t_{N-ab,\alpha/2}\hat{\sigma}\sqrt{\frac{1}{n_{ij}} + \frac{1}{n_{i'j'}}}$
$\bar{\mu}_{i.}$	$\hat{\bar{\mu}}_{i.} \pm t_{N-ab,\alpha/2}\hat{\sigma}\sqrt{\frac{1}{b^2}\sum_{j=1}^{b}\frac{1}{n_{ij}}}$
$\bar{\mu}_{.j}$	$\hat{\bar{\mu}}_{.j} \pm t_{N-ab,\alpha/2}\hat{\sigma}\sqrt{\frac{1}{a^2}\sum_{i=1}^{a}\frac{1}{n_{ij}}}$
$\bar{\mu}_{i.} - \bar{\mu}_{i'.}$	$\hat{\bar{\mu}}_{i.} - \hat{\bar{\mu}}_{i'.} \pm t_{N-ab,\alpha/2}\hat{\sigma}\sqrt{\frac{1}{b^2}\sum_{j=1}^{b}(\frac{1}{n_{ij}} + \frac{1}{n_{i'j}})}$
$\bar{\mu}_{.j} - \bar{\mu}_{.j'}$	$\hat{\bar{\mu}}_{.j} - \hat{\bar{\mu}}_{.j'} \pm t_{N-ab,\alpha/2}\hat{\sigma}\sqrt{\frac{1}{a^2}\sum_{i=1}^{a}(\frac{1}{n_{ij}} + \frac{1}{n_{i'j}})}$

In the above $\hat{\sigma} = \sqrt{\mathrm{MS}_{\mathrm{Error}}}$.

Mice data (cont)

Diet (A): $\bar{\mu}_{1\cdot} - \bar{\mu}_{2\cdot}$.

Gene (B): $\bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 2}$

The interaction appears to be negligible, so we can focus on main effects.

Build 95% CIs for the differences in marginal means for

- Diet: $\hat{\bar{\mu}}_{1\cdot} - \hat{\bar{\mu}}_{2\cdot} \pm t_{55-4,0.05/2}\hat{\sigma}\sqrt{\frac{1}{2^2}\sum_{j=1}^{2}(\frac{1}{n_{1j}} + \frac{1}{n_{2j}})}$
- Gene: $\hat{\bar{\mu}}_{\cdot 1} - \hat{\bar{\mu}}_{\cdot 2} \pm t_{55-4,0.05/2}\hat{\sigma}\sqrt{\frac{1}{2^2}\sum_{i=1}^{2}(\frac{1}{n_{i1}} + \frac{1}{n_{i2}})}$,

where $\hat{\sigma} = \sqrt{\mathrm{MS}_{\mathrm{Error}}}$.

```r
mu_hat <- grp_means$Response
nn <- grp_counts$Response
mu11_hat <- mu_hat[1] ; n11 <- nn[1] # HFD x ADIPO
mu21_hat <- mu_hat[2] ; n21 <- nn[2] # LFD x ADIPO
mu12_hat <- mu_hat[3] ; n12 <- nn[3] # HFD x WT
mu22_hat <- mu_hat[4] ; n22 <- nn[4] # LFD x WT

mu1.hat <- (mu11_hat + mu12_hat)/2 # HFD mean
mu2.hat <- (mu21_hat + mu22_hat)/2 # LFD mean
mu.1hat <- (mu11_hat + mu21_hat)/2 # ADIPO mean
mu.2hat <- (mu12_hat + mu22_hat)/2 # WT mean

N <- sum(nn)
a <- 2
b <- 2
MSE <- sum(lm_out$residuals^2)/(N - a*b)
alpha <- 0.05

me <- qt(1-alpha/2,N-a*b)*sqrt(MSE)*sqrt(1/2^2*(1/n11 + 1/n12 + 1/n11 + 1/n22))

ci_diet <- c(mu1.hat - mu2.hat - me, mu1.hat - mu2.hat + me)
ci_gene <- c(mu.1hat - mu.2hat - me, mu.1hat - mu.2hat + me)
```

We obtain the intervals:

- Diet: $(146.27, 466.24)$
- Gene: $(-248.93, 71.04)$

Significant diff between $\bar{\mu}_{1\cdot}$ and $\bar{\mu}_{2\cdot}$.

Unbalanced tensile strength data from Kuehl (2000)

Table 6.19 Tensile strength (psi) of asphaltic concrete specimens for two aggregate types with each of three kneading compaction methods

	Compaction Method			
	Kneading			
Aggregate Type	*Regular*	*Low*	*Very Low*	*Aggregate Means* ($\bar{y}_{i\cdot\cdot}$)
Basalt	106	93	56	
	108	101		
		98		
Means ($\bar{y}_{1j\cdot}$)	107.0	97.3	56	93.7
Silicious	107	63	40	
	110	60	41	
	116		44	
Means ($\bar{y}_{2j\cdot}$)	111.0	61.5	41.7	72.6
Compaction means ($\bar{y}_{\cdot j\cdot}$)	109.4	83.0	45.3	

```
y <- c(106,108,93,101,98,56,107,110,116,63,60,40,41,44)
agg <- as.factor(c("b","b","b","b","b","b","s","s","s","s","s","s","s","s"))
comp <- as.factor(c("r","r","l","l","l","vl","r","r","r","l","l","vl","vl","vl"))
tensile <- data.frame(y = y, agg = agg, comp = comp)
```

Compute group means:

```
aggregate(y ~ agg + comp,data = tensile, mean)
```

```
  agg comp         y
1   b    l  97.33333
2   s    l  61.50000
3   b    r 107.00000
4   s    r 111.00000
5   b   vl  56.00000
6   s   vl  41.66667
```

Unbalanced tensile strength data (cont)

Again the meaninglessness of sequential SS under unbalancedness:

```
anova(lm(y ~ agg + comp + agg:comp, data = tensile))
```

```
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq F value    Pr(>F)
agg        1 1518.0  1518.0 135.184 2.726e-06 ***
comp       2 8401.9  4201.0 374.112 1.252e-08 ***
agg:comp   2  953.4   476.7  42.454 5.497e-05 ***
Residuals  8   89.8    11.2
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Incorrect

okay

```
anova(lm(y ~ comp + agg + agg:comp, data = tensile))
```

```
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq F value    Pr(>F)
comp       2 9159.3  4579.6 407.834 8.899e-09 ***
agg        1  760.7   760.7  67.740 3.557e-05 ***
comp:agg   2  953.4   476.7  42.454 5.497e-05 ***
Residuals  8   89.8    11.2
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Incorrect

okay

Tensile strength data (cont)

Obtain Type III SS with `Anova()` from the R package `car`.

```
library(car)
Anova(lm(y ~ agg + comp + agg:comp, data = tensile,
         contrasts = list(agg = contr.sum, comp = contr.sum)),
      type = "III")
```

```
Anova Table (Type III tests)

Response: y
             Sum Sq Df  F value    Pr(>F)
(Intercept)  75050  1 6683.495 5.589e-13 ***
agg            710  1   63.269 4.551e-05 ***
comp          6806  2  303.070 2.879e-08 ***
agg:comp       953  2   42.454 5.497e-05 ***
Residuals       90  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Correct

← same as from ordinary anova output.

Now we could make comparisons of means, noting the interaction.

References

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