

SE for g1&f1

are based on CS-approx.
using "lmerTest"

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)	
(Intercept)	126.025	7.581	6.740	16.624	1.01e-06	***
<u>g2</u>	<u>22.500</u>	<u>7.314</u>	11.154	3.076	0.010384	*
g3	-12.275	7.314	11.154	-1.678	0.121064	
f2	13.750	4.456	27.000	3.086	0.004649	**
f3	22.425	4.456	27.000	5.033	2.79e-05	***
f4	19.025	4.456	27.000	4.270	0.000216	***
g2:f2	-2.825	6.301	27.000	-0.448	0.657499	
g3:f2	17.875	6.301	27.000	2.837	0.008540	**
g2:f3	3.750	6.301	27.000	0.595	0.556721	
g3:f3	24.525	6.301	27.000	3.892	0.000588	***
g2:f4	8.600	6.301	27.000	1.365	0.183583	
g3:f4	35.800	6.301	27.000	5.681	4.92e-06	***

--- there are 12 distinct treatments and all treatment means have an estimated SE

= 7.581

end
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SE = 7.314 is associated with g2, which is the estimated change in the mean response when switching from g1 & f1 to g2 & f1

Correlation of Fixed Effects:

	(Intr)	g2	g3	f2	f3	f4	g2:f2	g3:f2	g2:f3	g3:f3	g2:f4
g2	-0.482										
g3	-0.482	0.500									
f2	-0.294	0.305	0.305								
f3	-0.294	0.305	0.305	0.500							
f4	-0.294	0.305	0.305	0.500	0.500						
g2:f2	0.208	-0.431	-0.215	-0.707	-0.354	-0.354					
g3:f2	0.208	-0.215	-0.431	-0.707	-0.354	-0.354	0.500				
g2:f3	0.208	-0.431	-0.215	-0.354	-0.707	-0.354	0.500	0.250			
g3:f3	0.208	-0.215	-0.431	-0.354	-0.707	-0.354	0.250	0.500	0.500		
g2:f4	0.208	-0.431	-0.215	-0.354	-0.354	-0.707	0.500	0.250	0.500	0.250	
g3:f4	0.208	-0.215	-0.431	-0.354	-0.354	-0.707	0.250	0.500	0.250	0.500	0.500

```
> anova(o)
```

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)	
g	673.3	336.65	2	<u>6.0013</u>	8.4784	0.0178463	*
f	8737.7	2912.57	3	<u>26.9999</u>	73.3529	4.234e-13	***
g:f	1557.3	259.56	6	<u>26.9999</u>	6.5369	0.0002381	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '1'

table of all marginal means
and cell means (next slide)

```
> ls_means(o)
```

Least Squares Means table:

	Estimate	Std. Error	df	t value	lower	upper	Pr(> t)	
g1	139.825	7.073	5.1	19.769	121.779	157.870	4.870e-06	***
g2	164.706	7.073	5.1	23.287	146.661	182.752	2.120e-06	***
g3	147.100	7.073	5.1	20.797	129.054	165.145	3.765e-06	***
f1	129.433	6.296	3.4	20.558	110.696	148.171	0.000107	***
f2	148.200	6.296	3.4	23.539	129.463	166.937	6.758e-05	***
f3	161.283	6.296	3.4	25.617	142.546	180.020	5.071e-05	***
f4	163.258	6.296	3.4	25.930	144.521	181.995	4.865e-05	***

└ reflect marginal means
g1 is the marginal mean of genotype 1
averaging over all fertilizers

treatment means



	<u>Estimate</u>	Std. Error	df	t value	lower	upper	Pr(> t)	
g1:f1	<u>126.025</u>	7.581	6.7	16.624	107.958	144.092	1.012e-06	***
g2:f1	148.525	7.581	6.7	19.592	130.458	166.592	3.411e-07	***
g3:f1	113.750	7.581	6.7	15.005	95.683	131.817	1.986e-06	***
g1:f2	139.775	7.581	6.7	18.437	121.708	157.842	5.102e-07	***
g2:f2	159.450	7.581	6.7	21.033	141.383	177.517	2.129e-07	***
g3:f2	145.375	7.581	6.7	19.176	127.308	163.442	3.932e-07	***
g1:f3	148.450	7.581	6.7	19.582	130.383	166.517	3.423e-07	***
g2:f3	174.700	7.581	6.7	23.044	156.633	192.767	1.159e-07	***
g3:f3	160.700	7.581	6.7	21.198	142.633	178.767	2.021e-07	***
g1:f4	145.050	7.581	6.7	19.133	126.983	163.117	3.991e-07	***
g2:f4	176.150	7.581	6.7	23.236	158.083	194.217	1.097e-07	***
g3:f4	168.575	7.581	6.7	22.236	150.508	186.642	1.470e-07	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Confidence level: 95%

Degrees of freedom method: Satterthwaite

```
> betahat=fixef(o)
```

```
> betahat
```

(Intercept)		g2		g3	
126.025		22.500		-12.275	
	f2		f3		f4
13.750		22.425		19.025	
	g2:f2		g3:f2		g2:f3
-2.825		17.875		3.750	
				24.525	
				g2:f4	
				8.600	
					g3:f4
					35.800

we get estimates of $\mu, g^2, g^3, f^2, \dots, f^4,$
 g^2f^2, \dots, g^3f^4

> #The following table shows the cell means
 > #in terms of the R parameterization.

> #####

> #

on slide 9

> # f1=0units f2=50units f3=100units f4=150units

> #

	mu	mu + <u>f2</u>	mu + <u>f3</u>	mu + <u>f4</u>
#g1				
#				
#g2	mu+g2	mu+g2+f2+ <u>g2f2</u>	mu+g2+f3+ <u>g2f3</u>	mu+g2+f4+ <u>g2f4</u>
#				
#g3	mu+ <u>g3</u>	mu+g3+f2+ <u>g3f2</u>	mu+g3+f3+ <u>g3f3</u>	mu+g3+f4+ <u>g3f4</u>
#				

> # $\hat{\mu} = 126.025$

> #g2 mu+g2 mu+g2+f2+g2f2 mu+g2+f3+g2f3 mu+g2+f4+g2f4

> # $126.025 + 22.5 = 148.525$

> #g3 mu+g3 mu+g3+f2+g3f2 mu+g3+f3+g3f3 mu+g3+f4+g3f4

> #

> #####

is the estimated cell mean for g2 & f1

first row in cell means table on
slide 15

```
> #Coefficients for geno 1 marginal mean
```

```
>
```

```
> C1 = matrix(c(1,
```

```
+ 0, 0,
```

```
+ 1/4, 1/4, 1/4,
```

```
+ 0, 0, 0, 0, 0, 0), nrow=1)
```

```
>
```

$\beta =$ $\begin{pmatrix} \mu \\ g_2 \\ g_3 \\ p_1 \\ p_2 \\ p_3 \\ p_4 \\ g_2:p_2 \\ \vdots \\ g_3:p_4 \end{pmatrix}$

$$= \frac{\mu + (\mu + p_2) + (\mu + p_3) + (\mu + p_4)}{4}$$


```

> #Coefficients for geno 1 - geno 2 marginal mean
>
> C2 = matrix(c(0,
+               g2 - (-1, 0,
+                   0, 0, 0,
+                   -1/4, 0, -1/4, 0, -1/4, 0), nrow=1)
>
>

```

```
> #Coefficients for geno 1 - geno 2 with no fertilizer
>
> C3 = matrix(c(0,
+               -1, 0,
+               0, 0, 0,
+               0, 0, 0, 0, 0, 0), nrow=1)
>
```

Handwritten orange annotations:
A circle around the value -1, with an arrow pointing to it from the text $-g_2$ written to the left.

```
> C = rbind(C1, C2, C3)
```

```
> contest(o, L = C, joint = F, confint = T)
```

	Estimate	Std. Error	df	t value	lower	upper	Pr(> t)
-1	139.82500	7.072992	5.129	<u>19.768862</u>	121.77948	157.870523	4.870369e-06
-2	-24.88125	6.213453	6.001	<u>-4.004416</u>	-40.08425	-9.678254	7.080208e-03
-3	-22.50000	7.314154	11.154	<u>-3.076227</u>	-38.57124	-6.428757	1.038405e-02

False: if set to True
we will get $C\beta = \underline{0}$ and
a single F-statistic

this makes sense here bc we wanted to
test 3 distinct hypotheses.

```
> #The degrees of freedom, sums of squares,  
> #and mean squares from a sequential ANOVA  
> #table could be used to estimate variance  
> #components and compute test statistics.  
>  
> a = anova(lm(y ~ b + g + b:g + f + g:f))
```

this model does not account for the
random effects \Rightarrow some of the lines in the
ANOVA table will be incorrect
on next slide

Reference slide 42 of Chapter 15

> a

Analysis of Variance Table

Response: y

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
b	3	5349.5	1783.16	44.9089	1.252e-10 ***
g	2	5237.2	2618.62	65.9500	4.057e-11 ***
f	3	8737.7	2912.57	73.3531	4.233e-13 ***
b:g	6	1853.4	<u>308.90</u>	7.7796	6.355e-05 ***
g:f	6	1557.3	259.56	6.5370	0.0002381 ***
Residuals	27	1072.1	39.71		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1

inference for genotype: $F = \frac{2618.62}{308.90} = 8.47728$
see slide 24

all F-statistics
are based on
the MSE (39.71)
in the denominator!

F-statistics
are correct

> #For example, based on expected mean squares
 > #presented in slide set 15, an unbiased
 > #estimator of variance for the whole-plot
 > #random effects is (MSbg - MSe) / 4.

Chapter 15

>
 > MSbg = a[4,3]

> MSbg

[1] 308.8985

> MSe = a[6,3]

> MSe

[1] 39.70613

> (MSbg - MSe) / 4

[1] 67.2981

$$E(MS_{bg}) = S \cdot \sigma_w^2 + \sigma_e^2$$

$$S=4 = 4 \sigma_w^2 + \sigma_e^2$$

$$\frac{(4 \sigma_w^2 + \sigma_e^2) - \sigma_e^2}{4} = \sigma_w^2$$

end lecture 33

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```
> #The F tests and p-values in the  
> #ANOVA table "a" all use MSe as the  
> #denominator because the lm function  
> #implies a Gauss-Markov model rather  
> #than a linear mixed-effects model.  
> #This is fine for f and g:f, but not  
> #for the other lines of the ANOVA  
> #table.
```

```
> #The correct F statistic for testing
> #for genotype main effects is
> #MSg/MSbg
>
> MSg = a[2,3]
> MSg
[1] 2618.619
>
> MSbg = a[4,3]
> MSbg
[1] 308.8985
>
> MSg / MSbg
[1] 8.47728
```