

SE for  $g_1 g_2 f_1$

are based on CS-approx.

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )	
(Intercept)	126.025	7.581	6.740	16.624	1.01e-06	***
<u>g<sub>2</sub></u>	<u>22.500</u>	<u>7.314</u>	<u>11.154</u>	<u>3.076</u>	<u>0.010384</u>	<u>*</u>
<u>g<sub>3</sub></u>	<u>-12.275</u>	<u>7.314</u>	<u>11.154</u>	<u>-1.678</u>	<u>0.121064</u>	
f <sub>2</sub>	13.750	4.456	27.000	3.086	0.004649	**
f <sub>3</sub>	22.425	4.456	27.000	5.033	2.79e-05	***
f <sub>4</sub>	19.025	4.456	27.000	4.270	0.000216	***
g <sub>2</sub> :f <sub>2</sub>	-2.825	6.301	27.000	-0.448	0.657499	
g <sub>3</sub> :f <sub>2</sub>	17.875	6.301	27.000	2.837	0.008540	**
g <sub>2</sub> :f <sub>3</sub>	3.750	6.301	27.000	0.595	0.556721	
g <sub>3</sub> :f <sub>3</sub>	24.525	6.301	27.000	3.892	0.000588	***
g <sub>2</sub> :f <sub>4</sub>	8.600	6.301	27.000	1.365	0.183583	
g <sub>3</sub> :f <sub>4</sub>	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

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$SE = 7.314$  is associated with  $g_2$ , which is the estimated change in the mean response when switching from  $g_1 \& f_1$  to  $g_2 \& f_1$

Correlation of Fixed Effects:

	(Intr)	$g_2$	$g_3$	$f_2$	$f_3$	$f_4$	$g_2:f_2$	$g_3:f_2$	$g_2:f_3$	$g_3:f_3$	$g_2:f_4$
$g_2$	-0.482										
$g_3$	-0.482	0.500									
$f_2$	-0.294	0.305	0.305								
$f_3$	-0.294	0.305	0.305	0.500							
$f_4$	-0.294	0.305	0.305	0.500	0.500						
$g_2:f_2$	0.208	-0.431	-0.215	-0.707	-0.354	-0.354					
$g_3:f_2$	0.208	-0.215	-0.431	-0.707	-0.354	-0.354	0.500				
$g_2:f_3$	0.208	-0.431	-0.215	-0.354	-0.707	-0.354	0.500	0.250			
$g_3:f_3$	0.208	-0.215	-0.431	-0.354	-0.707	-0.354	0.250	0.500	0.500		
$g_2:f_4$	0.208	-0.431	-0.215	-0.354	-0.354	-0.707	0.500	0.250	0.500	0.250	
$g_3:f_4$	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							

```
> 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

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

## treatment means



Estimate Std. Error df t value lower upper Pr(>|t|)

g1:f1	126.025	7.581	6.7	16.624	107.958	144.092	1.012e-06	***	
g2:f1	148.525	$f_1 + g_2$	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
```

	g2	g3
--	----	----

126.025	22.500	-12.275
---------	--------	---------

	f2	f3	f4
--	----	----	----

13.750	22.425	19.025
--------	--------	--------

	g2:f2	g3:f2	g2:f3	g3:f3	g2:f4	g3:f4
--	-------	-------	-------	-------	-------	-------

-2.825	17.875	3.750	24.525	8.600	35.800
--------	--------	-------	--------	-------	--------

we get estimates of  $\mu, g^2, g^3, f_2, \dots, f_4,$

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

> #####

> #

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

> #

#	g1	mu	mu +f2	mu +f3	mu +f4
> #	g1	mu	mu +f2	mu +f3	mu +f4
> #	g2	mu+g2	mu+g2+f2+g2f2	mu+g2+f3+g2f3	mu+g2+f4+g2f4
> #	g3	mu+g3	mu+g3+f2+g3f2	mu+g3+f3+g3f3	mu+g3+f4+g3f4
> #		$\hat{\mu} = 126.025$	$126.025 + 22.5 = 148.525$		

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)

>

$$\beta = \begin{pmatrix} \mu \\ g_2 \\ g_3 \\ f_1 \\ f_3 \\ f_4 \\ g_2:f_2 \\ \vdots \\ g_3:f_4 \end{pmatrix}$$

$$= \frac{\mu + (\mu + f_2) + (\mu + f_3) + (\mu + f_4)}{4}$$

```
> #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,  
+               -g2, 0, 0, 0, 0, 0, 0), nrow=1)  
>
```

```

> 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 19.768862 121.77948 157.870523 4.870369e-06
-2 -24.88125 6.213453 6.001 -4.004416 -40.08425 -9.678254 7.080208e-03
-3 -22.50000 7.314154 11.154 -3.076227 -38.57124 -6.428757 1.038405e-02

```

False ; if set to True  
 we will get  $C\beta = 0$  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	308.90	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 1

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

all F-statistics  
are based on  
the MS $E$  (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.
>
> MSbg = a[4,3]
> MSbg
[1] 308.8985
> MSe = a[6,3]
> MSe
[1] 39.70613
> (MSbg - MSe) / 4
[1] 67.2981

```

$$E(MSbg) = S \cdot \sigma_w^2 + \sigma_e^2$$

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

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

end lecture 33

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Chapter 15

```
> #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
                  
```