17. R Analysis of Split-Plot Experiments

Field Split-Plot Experiment $\mathcal{RCBD}$

Field

	Genotype C				Genotype A				Genotype B			
Block 1	0	100	150	50	50	100	150	0	150	100	50	0
Block 2	Genotype B				Genotype A				Genotype C			
	150	100	50	0	0	50	150	100	100	50	150	0
Block 3	Genotype A				Genotype B				Genotype C			
	100	50	0	150	0	100	150	50	50	100	150	0
Block 4	Genotype B				Genotype C				Genotype A			
	0	50	100	150	150	100	50	0	50	150	100	0

Install and Load Packages for Linear Mixed-Model Analysis in R

> install.packages("lme4")

for fitting the linear mixed effects models

> install.packages("lmerTest")

for obtaining correct df and p-values associated with inference of mixed effects

> library(lme4)

> library(lmerTest)

Read Data

```
> fd = read.delim(
  "https://dnett.github.io/S510/FieldSplitPlotData.txt")

> head(fd)
  block geno fert     y
1     1    1     0 148.7
2     1    1    50 150.4
3     1    1   100 166.7
4     1    1   150 156.5
5     1    2     0 162.5
6     1    2    50 168.6
```

```
> #Define factors and shorten names.

> y = fd$y

> b = factor(fd$block)

> g = factor(fd$geno)
                                    ⎧ 4 levels: 1, 2, 3, 4
> f = factor(fd$fert/50+1)
```

Fit the Model

we are allowing for a random intercept for each level of b

```
> o = lmer(y ~ g + f + g:f + (1 | b) + (1 | b:g))
```

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + b_k + w_{ik} + e_{ijk}$$

$$b_k \stackrel{iid}{\sim} N(0, \sigma_b^2)$$

$$w_{ik} \stackrel{iid}{\sim} N(0, \sigma_w^2)$$

$$e_{ijk} \stackrel{iid}{\sim} N(0, \sigma_e^2)$$

```
> summary(o)
Linear mixed model fit by REML.

t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: y ~ g + f + g:f + (1 | b) + (1 | b:g)

REML criterion at convergence: 275.1

Scaled residuals:
     Min       1Q   Median       3Q      Max
-1.43560 -0.60942 -0.07892  0.53263  2.09822
```

$$\hat{\sigma}_w^2$$

```
Random effects:
 Groups    Name         Variance Std.Dev.
 b:g       (Intercept)   67.29    8.203
 b         (Intercept)  122.89   11.086
 Residual                39.71    6.301
Number of obs: 48, groups:  b:g, 12; b, 4
```

$$MSE: \hat{\sigma}_e^2 \qquad \hat{\sigma}_b^2$$

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	***
g2	22.500	7.314	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	***

$\hat{\mu}$ $\hat{g_2}$ $\hat{g_3}$

$\hat{\beta} =$

$\widehat{g_3 f_4}$

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here are 12 distinct treatments and all
treatment means have an estimated SE
_= 7.581_

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