Split-Plot Designs

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March 27, 2007

The Big Picture

- In a *split-plot design*, plots are assigned at random to a first treatment.
- Within each plot individuals are assigned at random to a second treatment.
- The key feature of a *split-plot design* is that there are two different levels for comparing treatments of interest.
- Differences in treatment effects of the first variable must be examined relative to plot level variation.
- Differences in treatment effects of the second variable must be examined relative to plot level variation.

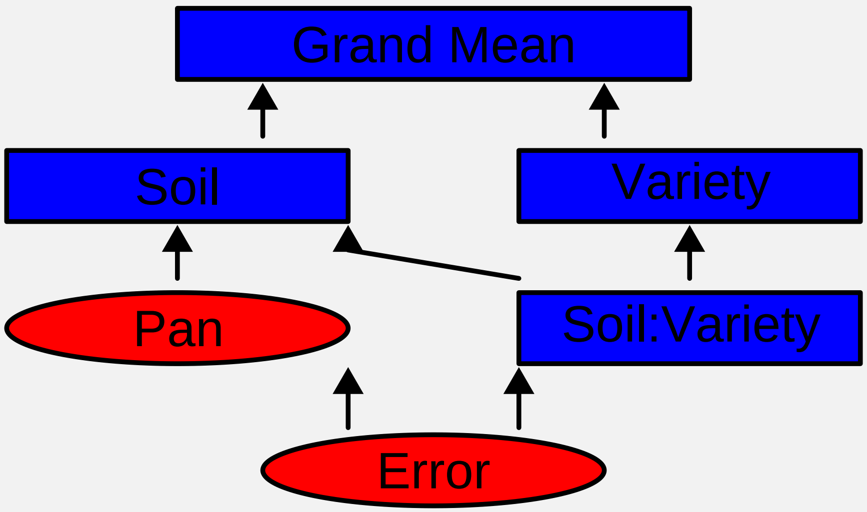
Barley Yield Experiment

- In an experiment, there are two treatments of interest, soil type (3 types) and barley variety (4 types).
- Each soil type is placed into two pans (plots).
- Within each pan, each variety is planted in a single subplot.
- The response variable is the yield of the barley.

Data

	Soil 1		Soil 2		Soil 3	
	Pan 1	Pan 2	Pan 1	Pan 2	Pan 1	Pan 2
Var 1	9.2	11.8	12.9	19.1	16.8	21.7
Var 2	11.3	14.6	15.5	22.6	19.5	23.7
Var 3	6.9	9.3	12.9	16.6	16.8	21.0
Var 4	6.5	9.9	11.2	16.6	15.8	17.8

Split-Plot Design with Interaction



Model

- $$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + c_{ik} + e_{ijk}$$

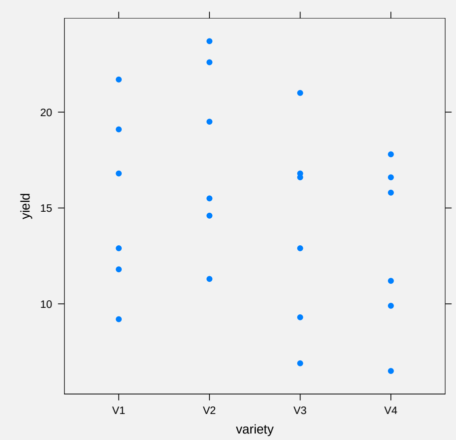
  where
  - μ is a population mean.
  - α_i is the main effect of soil type (A) i, $i = 1, \ldots, 3$, $\sum_{i=1}^{3} \alpha_i = 0$.
  - β_j is a main effect of barley variety (B) j, $j = 1, \ldots, 4$, $\sum_{j=1}^{4} \beta_j = 0$.
  - $(\alpha\beta)_{ij}$ is the interaction effect of A and B, $\sum_i (\alpha\beta)_{ij} = 0$ for each j and $\sum_j (\alpha\beta)_{ij} = 0$ for each i
  - $c_{ik} \sim \text{iid } \mathrm{N}(0, \sigma_a^2)$ is the plot (pan) error distribution, $k = 1, 2$.
  - $e_{ijk} \sim \text{iid } \mathrm{N}(0, \sigma_e^2)$ is the subplot (individual) error distribution, $k = 1, 2$.

Data

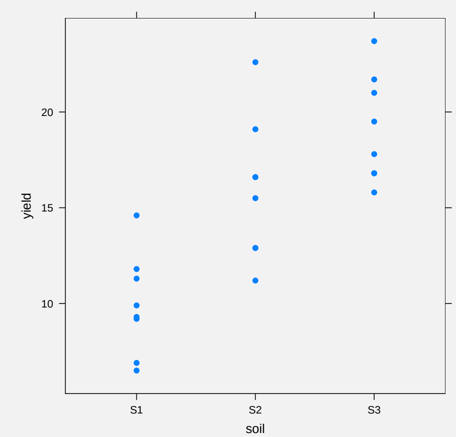
```
> barley = read.table("barley.txt", header = T)
> attach(barley)
> str(barley)

'data.frame': 24 obs. of  4 variables:
 $ variety: Factor w/ 4 levels "V1","V2","V3",..: 1 1 2 2 3 3 4 4 1 1 ...
 $ soil   : Factor w/ 3 levels "S1","S2","S3": 1 1 1 1 1 1 1 1 2 2 ...
 $ pan    : Factor w/ 2 levels "P1","P2": 1 2 1 2 1 2 1 2 1 2 ...
 $ yield  : num  9.2 11.8 11.3 14.6 6.9 9.3 6.5 9.9 12.9 19.1 ...
```


Plot of Data

```
> library(lattice)
> fig1 = xyplot(yield ~ variety, pch = 16)
> print(fig1)
```




```
> library(lattice)
> fig2 = xyplot(yield ~ soil, pch = 16)
> print(fig2)
```



Numerical Summaries

```
> sapply(split(yield, soil), mean)

     S1      S2      S3
 9.9375 15.9250 19.1375

> sapply(split(yield, soil), sd)

      S1       S2       S3
2.647337 3.710121 2.798948

> sapply(split(yield, variety), mean)

      V1       V2       V3       V4
15.25000 17.86667 13.91667 12.96667

> sapply(split(yield, variety), sd)

      V1       V2       V3       V4
4.750895 4.868128 5.239625 4.448221

> sapply(split(yield, soil:variety), mean)

S1:V1 S1:V2 S1:V3 S1:V4 S2:V1 S2:V2 S2:V3 S2:V4 S3:V1 S3:V2 S3:V3 S3:V4
10.50 12.95  8.10  8.20 16.00 19.05 14.75 13.90 19.25 21.60 18.90 16.80

> sapply(split(yield, soil:variety), sd)

   S1:V1    S1:V2    S1:V3    S1:V4    S2:V1    S2:V2    S2:V3    S2:V4
1.838478 2.333452 1.697056 2.404163 4.384062 5.020458 2.616295 3.818377
   S3:V1    S3:V2    S3:V3    S3:V4
3.464823 2.969848 2.969848 1.414214
```


Mixed Effects Analysis

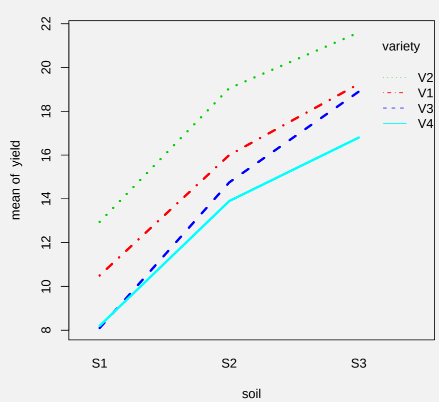
```
> library(lme4)
> options(contrasts = c("contr.sum", "contr.poly"))
> bf = formula(yield ~ soil * variety + (1 | soil:pan))
> barley.lmer = lmer(bf)
> summary(barley.lmer)
```

```
Linear mixed-effects model fit by REML
Formula: bf
   AIC   BIC logLik MLdeviance REMLdeviance
 92.44 107.8 -33.22       65.4        66.44
Random effects:
 Groups   Name        Variance Std.Dev.
 soil:pan (Intercept) 8.88775  2.9812
 Residual             0.65512  0.8094
number of obs: 24, groups: soil:pan, 6

Fixed effects:
               Estimate Std. Error t value
(Intercept)    15.00000    1.22825  12.213
soil1          -5.06250    1.73700  -2.915
soil2           0.92500    1.73700   0.533
variety1        0.25000    0.28616   0.874
variety2        2.86667    0.28616  10.018
variety3       -1.08333    0.28616  -3.786
soil1:variety1  0.31250    0.40470   0.772
soil2:variety1 -0.17500    0.40470  -0.432
soil1:variety2  0.14583    0.40470   0.360
soil2:variety2  0.25833    0.40470   0.638
soil1:variety3 -0.75417    0.40470  -1.864
soil2:variety3 -0.09167    0.40470  -0.227

Correlation of Fixed Effects:
            (Intr) soil1  soil2  varty1 varty2 varty3 sl1:v1
soil1        0.000
soil2        0.000 -0.500
variety1     0.000  0.000  0.000
variety2     0.000  0.000  0.000 -0.333
soil2:vrty1  0.000  0.000  0.000  0.000  0.000  0.000 -0.500
soil1:vrty2  0.000  0.000  0.000  0.000  0.000  0.000 -0.333
soil2:vrty2  0.000  0.000  0.000  0.000  0.000  0.000  0.167
soil1:vrty3  0.000  0.000  0.000  0.000  0.000  0.000 -0.333
.167
```


Interaction Plots

```
> interaction.plot(soil, variety, yield, col = 2:5)
```

- Points are of group means.
- Lines indicate change, but are meaningless between x values.
- Lines that are nearly parallel indicate little potential *interaction*.
- Lines that are far from parallel indicate possible interaction.



Likelihood Ratio Tests

- Two *nested models* can be fit with a *likelihood ratio test*.
- When L_1 is the likelihood of the smaller model and L_2 is the likelihood of the larger model,
- the statistic $-2 \times (\log(L_1) - \log(L_2))$ has approximately a chi-square distribution with degrees of frredom equal to the difference in the number of parameters in the model.
- The `anova` function is useful to carry out likelihood ratio tests for models fit with `lmer`.

Nested Models

```
> barley1 = lmer(yield ~ 1 + (1 | soil:pan))
> barleyA = lmer(yield ~ soil + (1 | soil:pan))
> barleyB = lmer(yield ~ variety + (1 | soil:pan))
> barleyAB = lmer(yield ~ soil + variety + (1 | soil:pan))
> barleyABi = lmer(yield ~ soil * variety + (1 | soil:pan))
```


Testing for a Soil Effect 1

```
> anova(barley1, barleyA)

Data:
Models:
barley1: yield ~ 1 + (1 | soil:pan)
barleyA: yield ~ soil + (1 | soil:pan)
        Df     AIC     BIC  logLik  Chisq Chi Df Pr(>Chisq)
barley1  2 127.392 129.748 -61.696
barleyA  4 123.665 128.377 -57.832 7.7267      2    0.02100 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Testing for a Soil Effect 2

```
> anova(barleyB, barleyAB, barleyABi)

Data:
Models:
barleyB: yield ~ variety + (1 | soil:pan)
barleyAB: yield ~ soil + variety + (1 | soil:pan)
barleyABi: yield ~ soil * variety + (1 | soil:pan)
          Df     AIC     BIC  logLik  Chisq Chi Df Pr(>Chisq)
barleyB    5  92.860  98.750 -41.430
barleyAB   7  88.786  97.032 -37.393 8.0739      2    0.01765 *
barleyABi 13  91.396 106.711 -32.698 9.3899      6    0.15281
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Comparison to F test

```
> barley.lm = lm(yield ~ variety + soil/pan)
> anova(barley.lm)

Analysis of Variance Table

Response: yield
          Df Sum Sq Mean Sq F value    Pr(>F)
variety    3  81.53   27.18  42.331 1.473e-07 ***
soil       2 348.83  174.41 271.673 1.655e-12 ***
soil:pan   3 109.09   36.36  56.642 2.055e-08 ***
Residuals 15   9.63    0.64
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> 1 - pf(174.41/36.36, 2, 3)

[1] 0.1162684
```

Observations

- Using the likelihood ratio test, there is strong evidence that `soil` has an effect on `yield` both in the absence ($p = 0.02$) and the presence ($p = 0.18$) of `variety`.
- There is little evidence that the interaction between `soil` and `yield` is important ($p = 0.15$).
- Using an F test, there is much less evidence for the effect of `soil` in the presence of `variety` ($p = 0.12$).
- Notice that the larger apparent effect due to `soil` based on the magnitude of the difference in sample means is offset by the much larger standard errors in estimating the size of the effect.