

# Randomized Complete Block Design

Bret Larget

Departments of Botany and of Statistics  
University of Wisconsin—Madison

March 22, 2007

## The Big Picture

- A *blocking variable* is a categorical variable that is not the primary variable of interest where observations within each level ought to be homogeneous except for treatment.
- In a *randomized complete block design*, each treatment is applied to individuals selected at random within each block.
- In a *randomized incomplete block design*, treatments are assigned at random within blocks, but every treatment may not be represented in every block.

## Seed Germination Experiment

- In an experiment, four sites were selected where the soil and climate conditions were expected to be very similar within the site.
- Here we will treat each site as a block.
- Within each block, five plots were identified.
- The treatment was applying a seed disinfectant to seeds. There were four different treatments (brands) plus a control.
- The researchers planted 100 seeds from a single treatment in each plot.
- The response is the number of seeds that germinated.
- We will also analyze this data using a *generalized linear model* later in the semester. The response variable is better modeled as *binomial* than as *normal*.

## Data

Treatment	Block			
	1	2	3	4
Control	86	90	88	87
Arasan	98	94	93	89
Spergon	96	90	91	92
Semesan	97	95	91	92
Fermate	91	93	95	95

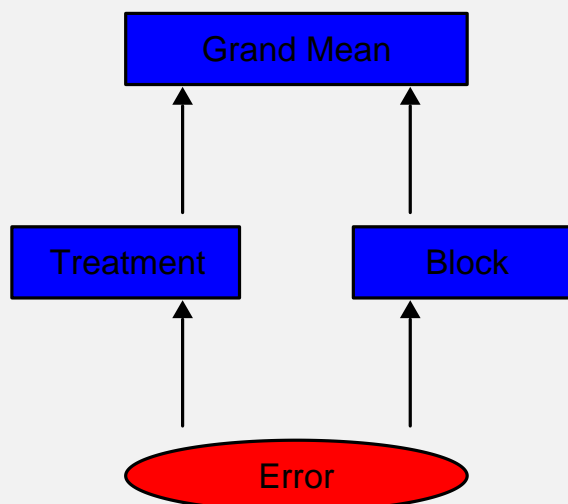
**Lines show treatment**

Treatment	Block			
	1	2	3	4
Control	86	90	88	87
Arasan	98	94	93	89
Spergon	96	90	91	92
Semesan	97	95	91	92
Fermate	91	93	95	95

**Lines show blocking**

## Crossed Variables

- A categorical variable  $A$  is *crossed* with a categorical variable  $B$  if there is one or more observations for each combination of levels of  $A$  and  $B$ .
- Here, treatment and blocking are *crossed*.
- Both treatment and blocking are *nested* within the grand mean.
- Individual error is *nested* within each other variable.
- Block could be random or fixed.



## Model

- A model is

$$y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}$$

where:

- $\mu$  is an overall mean,
- $\alpha_i$  is the effect of treatment  $i$  where  $\sum_i \alpha_i = 0$ , for  $i = 1, \dots, 5$ ,
- $\beta_j$  is the effect in block  $j$  where  $\sum_j \beta_j = 0$ , for  $j = 1, \dots, 4$ ,
- and  $e_{ij} \sim \text{iid } N(0, \sigma_e^2)$  is individual random error.
- Note that  $\mu_{ij} = \mu + \alpha_i + \beta_j$ .
- Instead of the sum constraints, we could instead assume  $\alpha_1 = \beta_1 = 0$  (the default in R).

## Data

```

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

'data.frame': 20 obs. of 3 variables:
 $ count   : int  86 90 88 87 98 94 93 89 96 90 ...
 $ treatment: Factor w/ 5 levels "AControl","Arasan",...: 1 1 1 1 2 2 2 2 5 5 ...
 $ block   : Factor w/ 4 levels "b1","b2","b3",...: 1 2 3 4 1 2 3 4 1 2 ...

> seed

  count treatment block
1     86 AControl  b1
2     90 AControl  b2
3     88 AControl  b3
4     87 AControl  b4
5     98  Arasan  b1
6     94  Arasan  b2
7     93  Arasan  b3
8     89  Arasan  b4
9     96 Spergon  b1
10    90 Spergon  b2
11    91 Spergon  b3
12    92 Spergon  b4
13    97 Semesan  b1
14    95 Semesan  b2
15    91 Semesan  b3
16    92 Semesan  b4
17    91 Fermate  b1
18    93 Fermate  b2
19    95 Fermate  b3
20    95 Fermate  b4

```

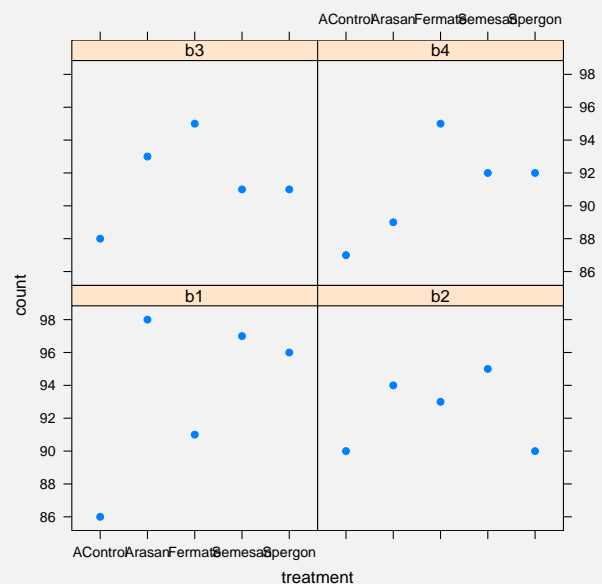
## Plot of Data

```

> library(lattice)
> fig1 = xyplot(count ~ treatment | block, pch = 16)
> print(fig1)

```

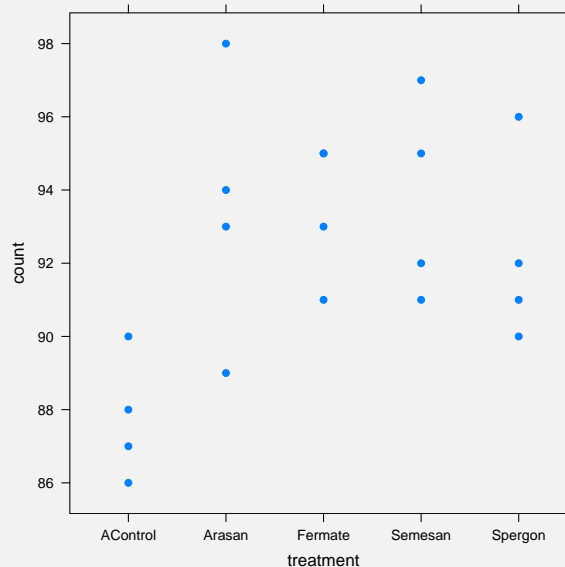
- The block effect seems pretty weak.



## Alternative Plot of Data

```
> library(lattice)
> fig1 = xyplot(count ~ treatment, pch = 16)
> print(fig1)
```

- It looks like each treatment improves germination rate over the control.
- The spread is similar within treatments.



## Linear Model Analysis

```
> seed.lm = lm(count ~ treatment + block)
> anova(seed.lm)
```

## Analysis of Variance Table

```
Response: count
      Df Sum Sq Mean Sq F value Pr(>F)
treatment 4 102.300  25.575  3.5979 0.03775 *
block      3  18.950   6.317  0.8886 0.47480
Residuals 12  85.300   7.108
---
```

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

```
> summary(seed.lm)
```

```
Call:
lm(formula = count ~ treatment + block)
```

## Residuals:

```
      Min       1Q   Median       3Q      Max
-3.950 -1.113  0.325  1.850  3.050
```

## Coefficients:

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    89.200     1.686   52.899 1.37e-15 ***
treatmentArasan  5.750     1.885    3.050 0.01008 *
treatmentFermate  5.750     1.885    3.050 0.01008 *
treatmentSemesan  6.000     1.885    3.183 0.00788 **
treatmentSpergon  4.500     1.885    2.387 0.03433 *
blockb2         -1.200     1.686   -0.712 0.49028
blockb3         -2.000     1.686   -1.186 0.25854
blockb4         -2.600     1.686   -1.542 0.14904
---
```

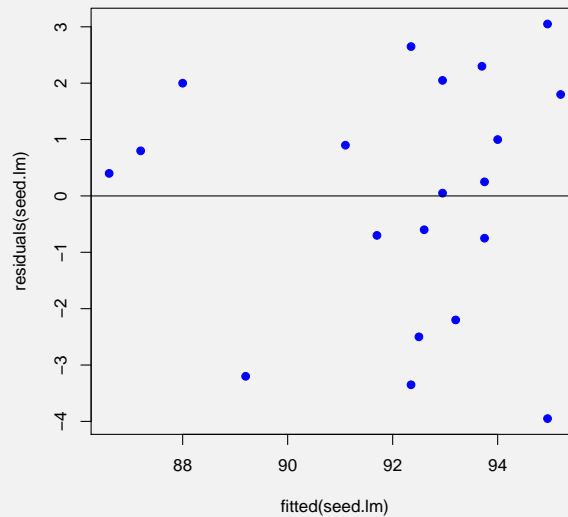
```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 2.666 on 12 degrees of freedom
Multiple R-Squared:  0.587, Adjusted R-squared:  0.3461
F-statistic: 2.437 on 7 and 12 DF, p-value: 0.08395
```

## Residual Plot

```
> plot(fitted(seed.lm), residuals(seed.lm))
> abline(h = 0)
```

- Residual plot looks okay.
- Normal approximation to binomial is still not too bad as there are sufficient numbers of successes and failures in each treatment group.



## Random Effects Model

- There are very few differences in a random effects model (treating block as random).
- The variance of the block variable is essentially 0.
- It is more difficult to carry out hypothesis tests.

# Comparison

```

> library(lme4)
> seed.lmer = lmer(count ~ treatment + (1 | block))
> summary(seed.lmer)

Linear mixed-effects model fit by REML
Formula: count ~ treatment + (1 | block)
   AIC   BIC logLik MLdeviance REMLdeviance
 90.58 96.56 -39.29    89.78      78.58
Random effects:
 Groups   Name      Variance Std.Dev.
block    (Intercept) 3.475e-09 5.8949e-05
Residual                    6.950e+00 2.6363e+00
number of obs: 20, groups: block, 4

Fixed effects:
              Estimate Std. Error t value
(Intercept)    87.750     1.318    66.57
treatmentArasan  5.750     1.864     3.08
treatmentFermate 5.750     1.864     3.08
treatmentSemesan 6.000     1.864     3.22
treatmentSpergon 4.500     1.864     2.41

Correlation of Fixed Effects:
      (Intr) trtmnA trtmnF trtmntSm
tretmntArasn -0.707
tretmntFrmnt -0.707  0.500
tretmntSmsn  -0.707  0.500  0.500
trtmntSprgn  -0.707  0.500  0.500  0.500

> summary(seed.lm)

Call:
lm(formula = count ~ treatment + block)

Residuals:
    Min       1Q   Median       3Q      Max
-3.950 -1.113  0.325  1.850  3.050

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    89.200     1.686  52.899 1.37e-15 ***
treatmentArasan  5.750     1.885   3.050 0.01008 *
treatmentFermate 5.750     1.885   3.050 0.01008 *
treatmentSemesan 6.000     1.885   3.183 0.00788 **
treatmentSpergon 4.500     1.885   2.387 0.03433 *
blockb2         -1.200     1.686  -0.712 0.49028
blockb3         -2.000     1.686  -1.186 0.25854
blockb4         -2.600     1.686  -1.542 0.14904
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.666 on 12 degrees of freedom
Multiple R-Squared: 0.587, Adjusted R-squared: 0.3461
F-statistic: 2.437 on 7 and 12 DF, p-value: 0.08395

```