Blocking

When I run this in Rstudio, we get the following output:

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
block	4	6.9465	1.7366	3.6692	0.0555884	.
recipe	2	29.1472	14.5736	30.7918	0.0001747	***
Residuals	8	3.7864	0.4733			

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

A. Reject the null hypothesis and include block in further analysis

B. Reject the null hypothesis and DON'T include block in further analysis

C. Fail to reject the null hypothesis and include block

D. Fail to reject the null hypothesis and DON'T include block

Blocking

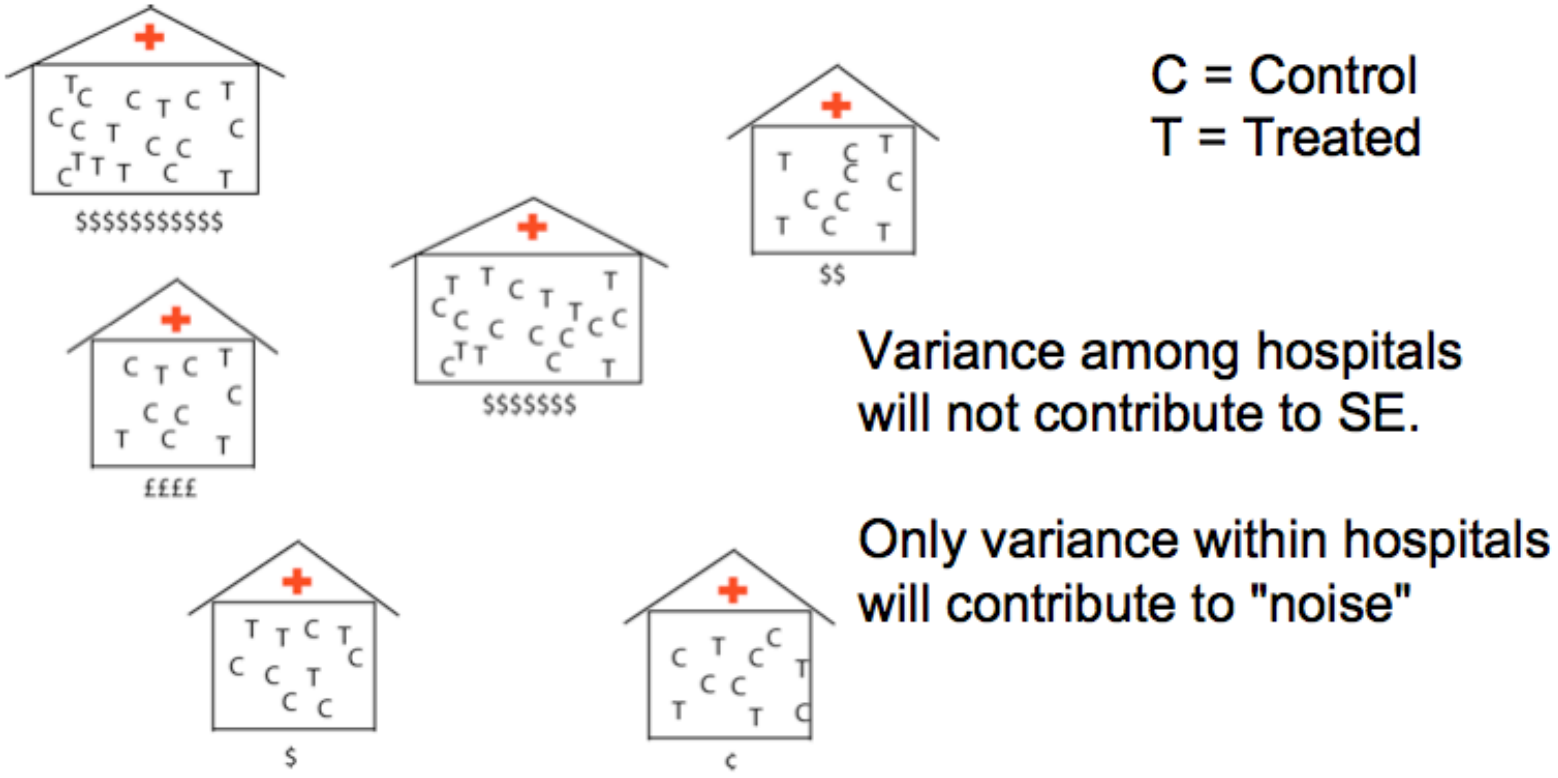
- Results in an additional variable, a block, that must be included in analysis
  - Can no longer use simple one-factor ANOVA
- Randomized block design
  - **Paired design** for > 2 treatments
  - Example:
    - Every treatment is replicated **once** within each block
    - Minimize "noise"
- Accounting for any variation caused by blocking **can improve our treatment effect detection** (i.e. increase the power of our test)
- Treatment effects are assessed by different treatments **within** each block so there is no interaction term

Goals of experiments:

determine how explanatory variable (treatment) affects response variable

- Eliminate Bias

- Reduce Sampling Error
  - Blocking:



C = Control
T = Treated

Variance among hospitals will not contribute to SE.

Only variance within hospitals will contribute to "noise"

Blocking

Response = Constant + Treatment + Block

H_0: Response = Constant + Block

H_A: Response = Constant + Block + Treatment

– Determine significance via ANOVA table which includes a row for the **block**

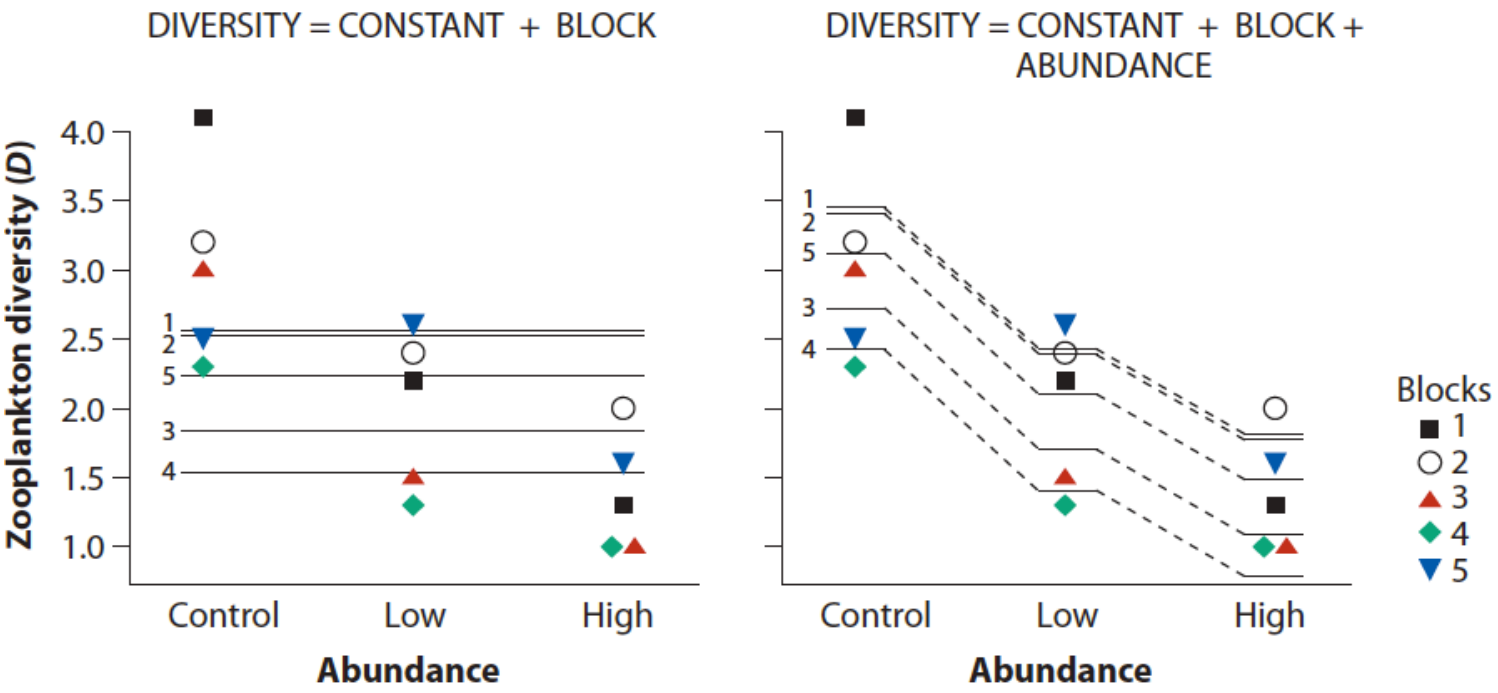
- Calculates a F value for block - examines how much better fit is with the block versus without

Blocking

Response = Constant + Treatment + Block

H_0: Response = Constant + Block

H_A: Response = Constant + Block + Treatment



Blocking

Response = Constant + Treatment + Block

H_0: Response = Constant + Block

H_A: Response = Constant + Block + Treatment

Source of variation	Sum of Squares	df	Mean Square	F	P
BLOCK	2.340	4	0.5850		
Treatment	6.8573	2	3.4287	16.37	0.001
Residual	1.6760	8	0.2095		
Total	10.8733	14			

$$F = \frac{H_A = \text{Constant+Block+Treatment}}{H_0 \quad \text{Constant + Block}}$$

$$= \frac{\text{residual+location+fish Abundance}}{\text{residual+location}}$$

Response = Constant + Treatment + Block

H_0: Response = Constant + Block

H_A: Response = Constant + Block + Treatment

Source of variation	Sum of Squares	df	Mean Square	F	P
BLOCK	2.340	4	0.5850		
Treatment	6.8573	2	3.4287	16.37	0.001
Residual	1.6760	8	0.2095		
Total	10.8733	14			

$$F_{treatment} = \frac{H_A}{H_0} = \frac{\text{Residual+Block+ Treatment}}{\text{Residual + Block}} = \frac{MS_{treatment}}{Ms_{block}} = \frac{3.4287}{0.5850} = 16.37$$

$\mathbf{F_{0.05(1),2,14} = 3.74}$ so we reject the H_O

Response = Constant + Block

H_0: Response = Constant +treatment

H_A: Response = Constant + treatment+Block

Source of variation	Sum of Squares	df	Mean Square	F	P
BLOCK	2.340	4	0.5850		
Treatment	6.8573	2	3.4287	16.37	0.001
Residual	1.6760	8	0.2095		
Total	10.8733	14			

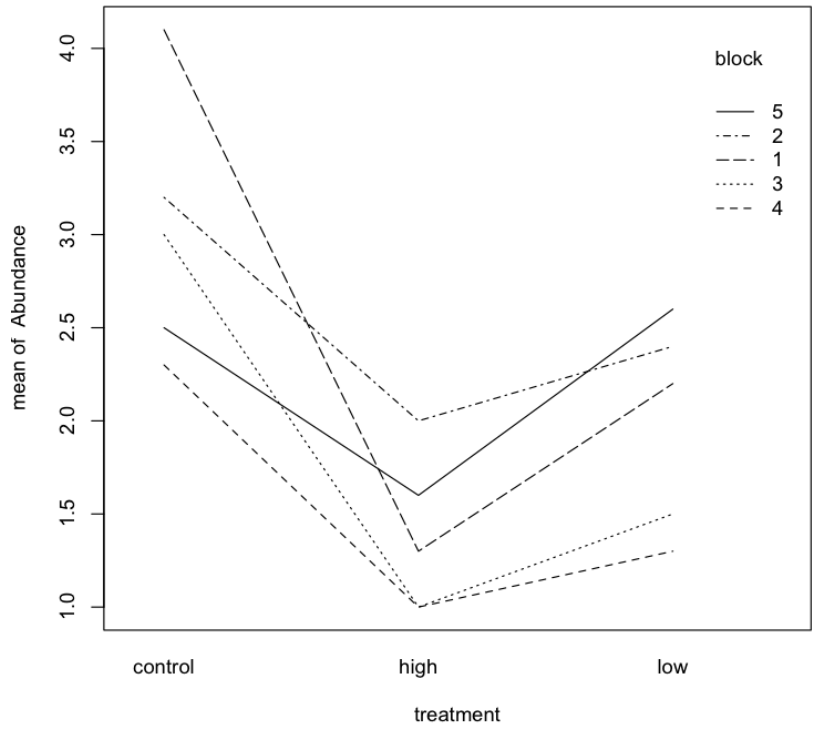
$$F_{Block} = \frac{H_A}{H_0} = \frac{\text{Residual+treatment+Block}}{\text{Residual +treatment}} = \frac{MS_{block}}{MS_{residual}} = \frac{0.5850}{0.2095} = 2.79$$

$F_{0.05(1),4,8} = 3.84$ so we fail to reject the H_O

* note: this is for illustration, though – you always want to include the block when it has been designed that way!

Blocking

Source of variation	Sum of Squares	df	Mean Square	F	P
BLOCK	2.340	4	0.5850		
VARIABLE	6.8573	2	3.4287	16.37	0.001
Residual	1.6760	8	0.2095		
Total	10.8733	14			

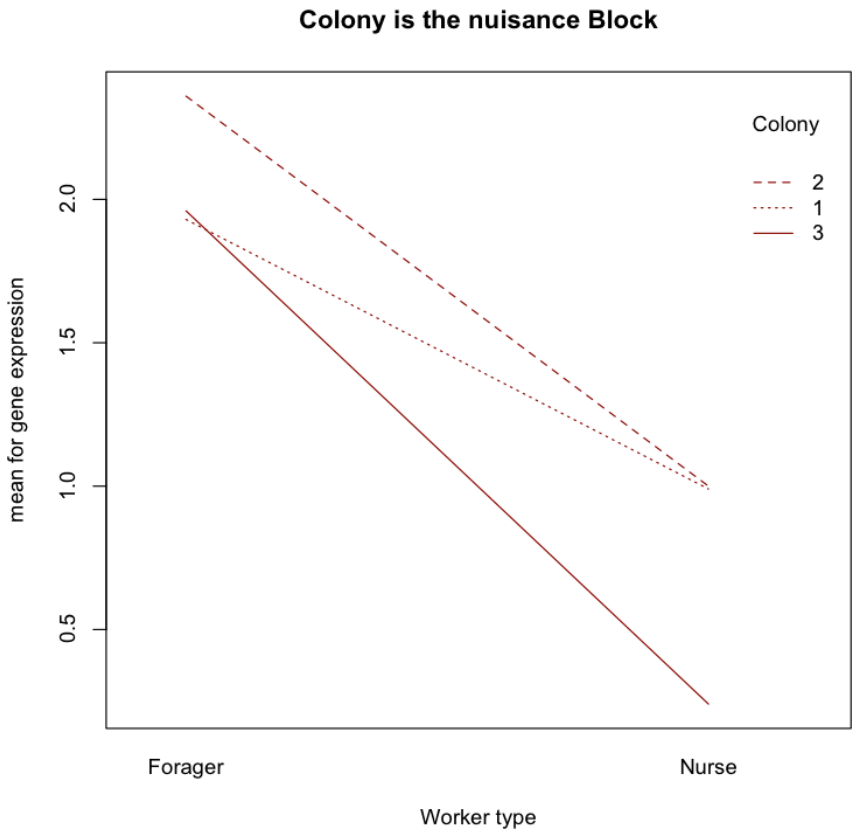


Blocking:

The foraging gene, *for*, has been found to underlie variation in foraging behavior in several insect species. Researchers examined if the gene might influence behavioral differences in the honey bee. Worker bees perform tasks in the hive such as brood care when they are young and switch to foraging for nectar and pollen as they age. The authors compared *for* gene expression in nurse and foraging workers bees in three bee colonies.

Blocking:

Worker type	Colony	*for* gene expression
Nurse	1	0.99
Forager	1	1.93
Nurse	2	1.00
Forager	2	2.36
Nurse	3	0.24
Forager	3	1.96



Blocking

Worker type	Colony	*for* gene expression
Nurse	1	0.99
Forager	1	1.93
Nurse	2	1.00
Forager	2	2.36
Nurse	3	0.24
Forager	3	1.96

For Expression = Constant + Worker Type + Colony

Constant = ‘grand mean’ for gene expression

Worker type = treatment

Colony = block

Blocking:

Worker type	Colony	*for* gene expression
Nurse	**1**	**0.99**
Forager	**1**	**1.93**
Nurse	**2**	**1.00**
Forager	**2**	**2.36**
Nurse	**3**	**0.24**
Forager	**3**	**1.96**

H_0: *For Expression* = Constant + COLONY

H_A: *For Expression* = Constant + Worker TYPE+COLONY

Blocking:

Worker type	Colony	*for* gene expression
Nurse	1	0.99
Forager	1	1.93
Nurse	2	1.00
Forager	2	2.36
Nurse	3	0.24
Forager	3	1.96

For Expression = Constant + Worker Type + Colony

H_0: *For Expression* = Constant + COLONY

H_A: *For Expression* = Constant + Worker TYPE+COLONY

Source of variation	Sum of Squares	df	Mean Square	F	P
Colony	0.342	2	0.171		
Worker Type	2.69340	1	2.6930	35.53	0.0271
Residual	0.152	2	0.076		
Total		5			

$$F_{treatment} = \frac{H_A}{H_0} = \frac{\text{Residual+Block+ Treatment}}{\text{Residual + Block}} = \frac{MS_{treatment}}{Ms_{block}} = \frac{2.693}{0.076} = 35.53$$

$F_{0.05(1),1,2}$ = 18.51 so we reject the H_O

Blocking:

Worker type	Colony	*for* gene expression
Nurse	1	0.99
Forager	1	1.93
Nurse	2	1.00
Forager	2	2.36
Nurse	3	0.24
Forager	3	1.96

Is worker type a random effect or a fixed effect?

What is the purpose of a blocking variable in experimental design?