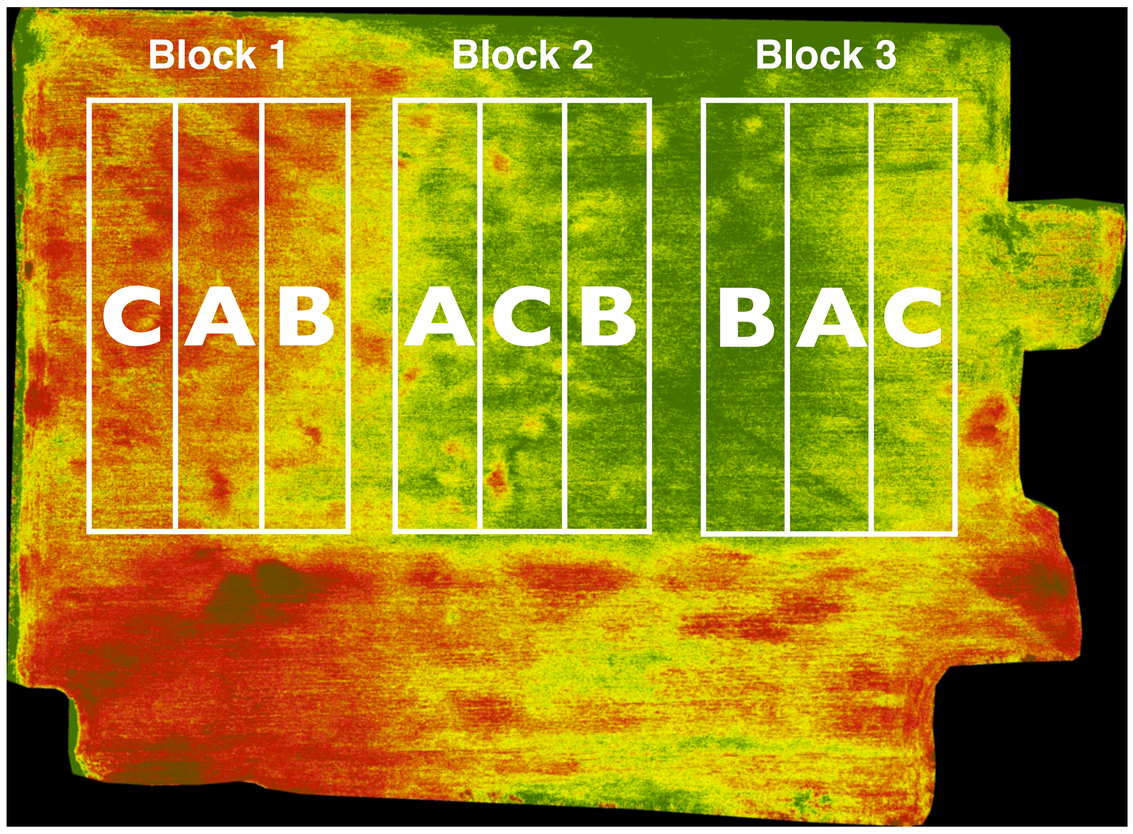
Completely **R**andomized **D**esign

Structure	Variable	Type	#levels	Block	EU
Treatment	Insecticide	Categ	3	None	Plot
Design	Plot	Categ	9		
Response	Counts	Num	9		

lm(Counts ~ Insecticide)

Randomized **C**omplete **B**lock **D**esign



Structure	Variable	Type	#levels	Block	EU
Treatment	Insecticide	Categ	3	Block	Plot
Design	Block	Categ	3		
	Ins:Block	Categ	9		
	Plot	Categ	9		
Response	Counts	Num	9		

lm(Counts ~ Insecticide + Block)

RCBD Design Table

EU follow the normal rules

Declare “random” if in the model

“Block” is a replicate/block for the Treatment

Must be a row in the Design structure

Also must include “Treatment:Block” in the Design structure

Declare random: (1|Treatment:Block) if in the model

RCBD analysis

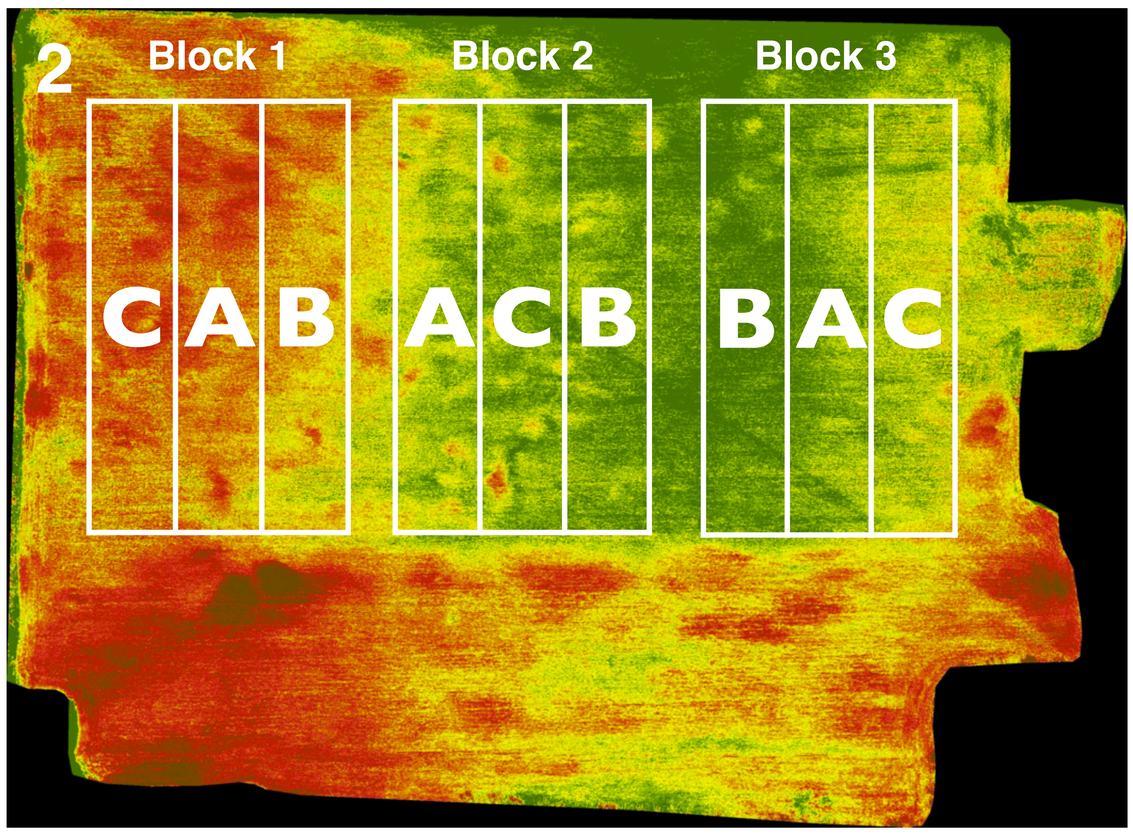
emmeans(model,specs = ‘Insecticide’)

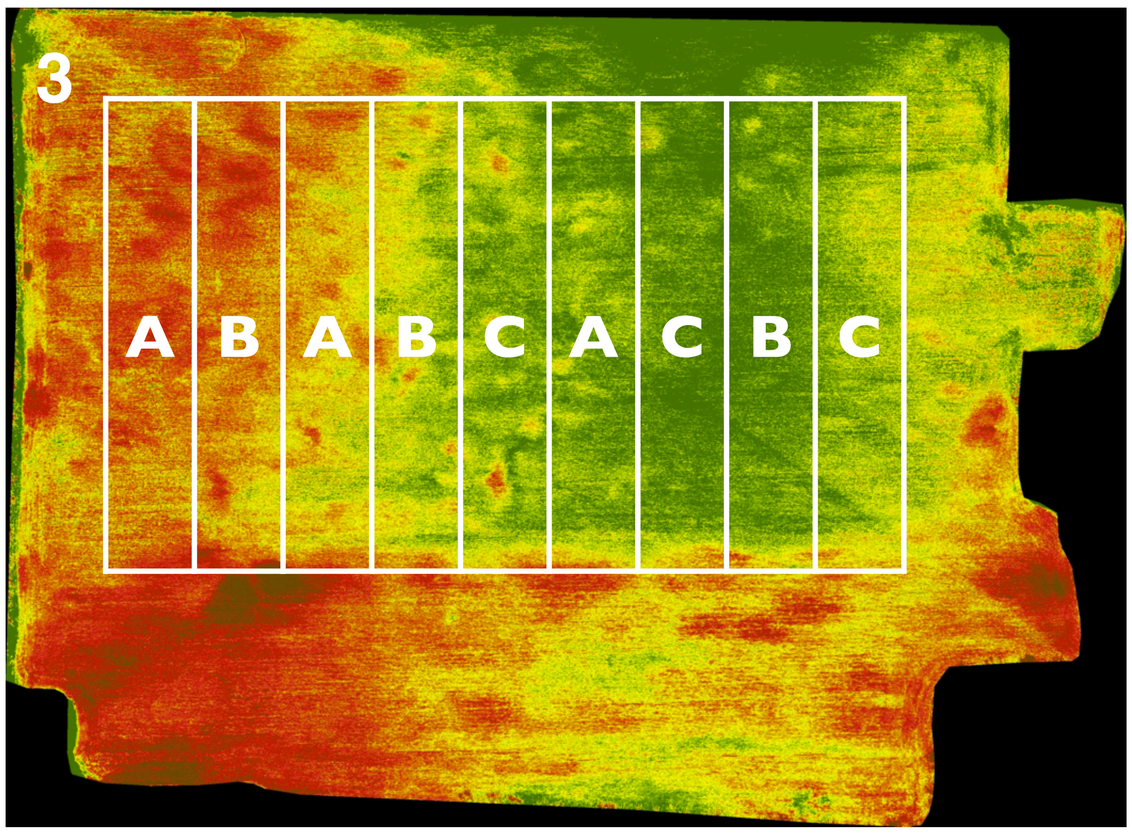
contrast(means,’pairwise’)

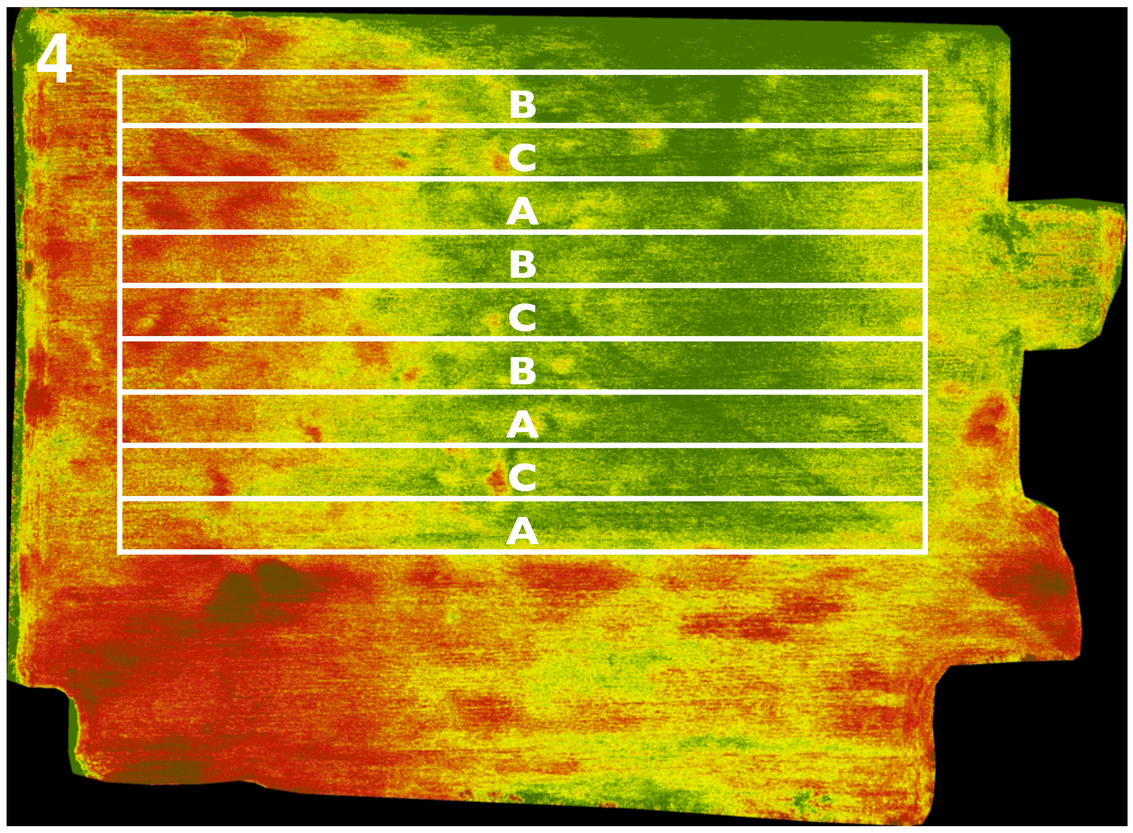
```
contrast estimate    SE df t.ratio p.value
a - b      -0.901 0.515  4  -1.752  0.2949
a - c       0.474 0.515  4   0.922  0.6570
b - c       1.376 0.515  4   2.673  0.1144

Results are averaged over the levels of: B
P value adjustment: tukey method for comparing a family of 3 estimates
```

Is the RCBD the best design for this experiment?







2 is a RCBD

DF = (3-1)*(3-1) = 4 $s^2_{effects}$

1, 3, 4 are all Completely Randomized Designs (CRD)

DF = 3*(3-1) = 6 s^2_{plots}

Which Design has plots that are the **least variable**?

Design 4 - all of them span good -> bad areas of the field. s^2_{plots} would be smallest

Always good to run EU **along gradients** to average over this variation

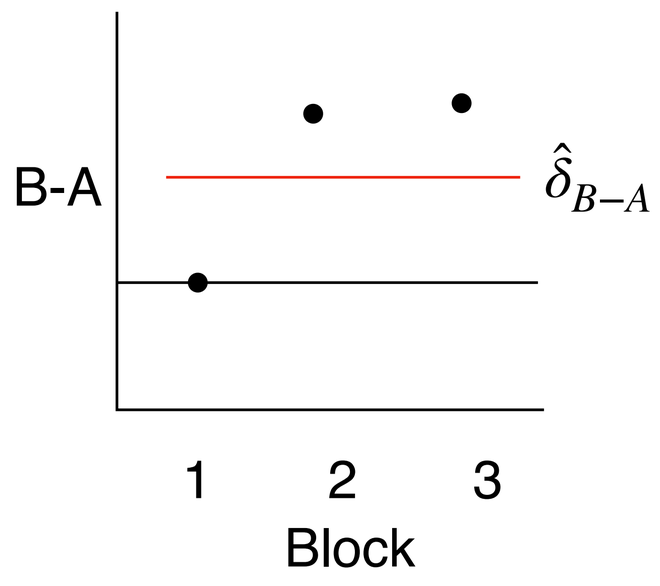
Only use RCBD if you can't do this

What about variation in **treatment effects** between good (green) and bad (red) areas?

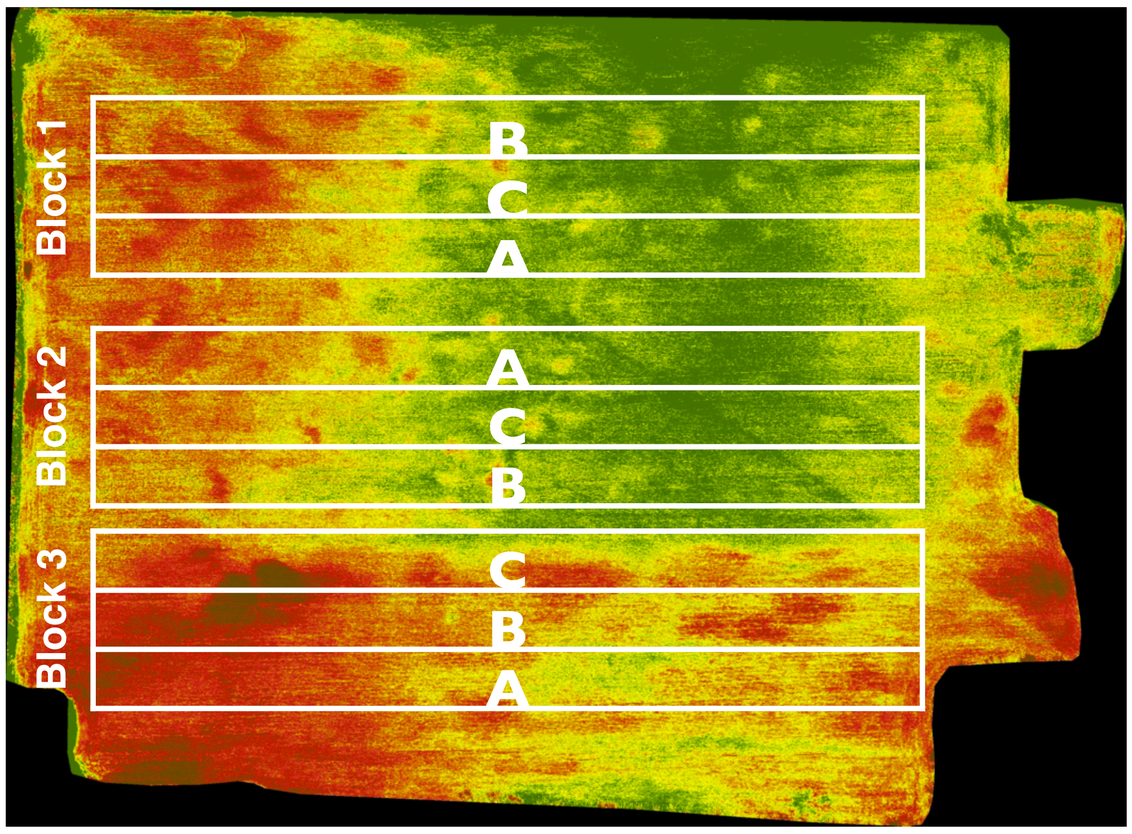
Can observe this using RCBD (but no error bars)

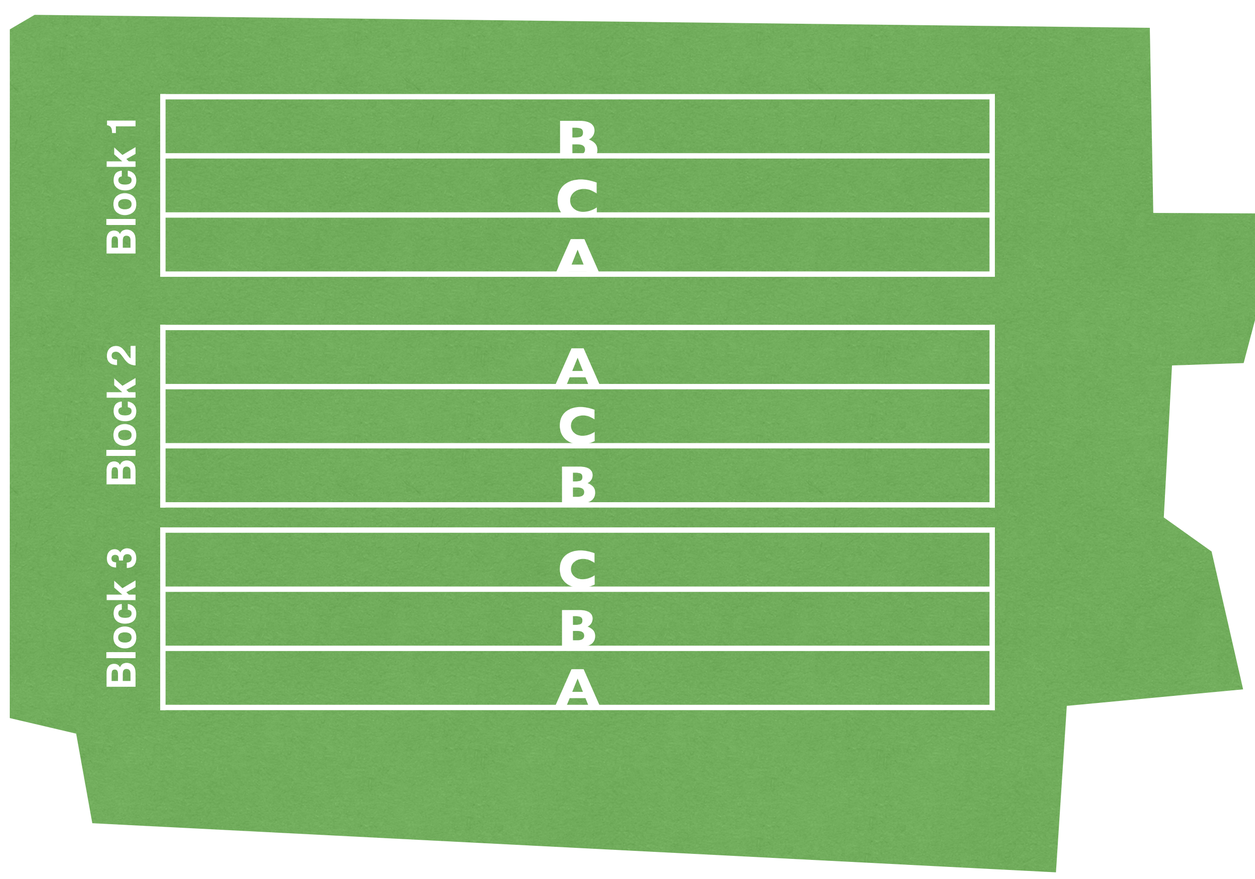
Increases uncertainty (s^2) in Designs 1-3

Less so in 4, because this is averaged over **within EU**



What makes good blocks?





You can block by any factor that you can observe **before the experiment**

Area of a field that you know has different water

Growth chamber

Person doing the measurements

Time of day / year

Think of Blocks as Experimental Replicates

You measure each treatment in each block, make treatment effect estimates, then compare among blocks

So, experimental replicates **are blocks**

Blocks are most useful when the EU within blocks are similar (correlated) relative to EU in other blocks

If so, $s^2_{effect} < s^2_{value}$

But, Blocks don't have to be good/useful to be **valid**

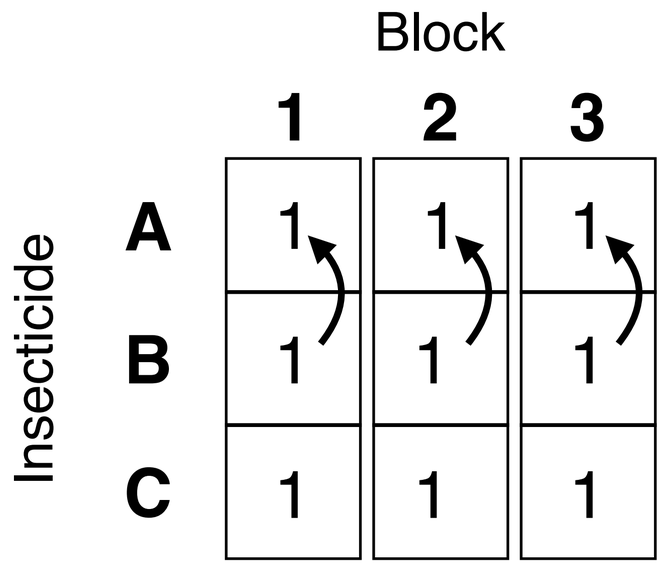
If you block by regions of the field based on a previous year's data

But this year the whole file grows well, the blocks weren't very useful

But you'll still include them in your analysis

And your analysis will still be valid

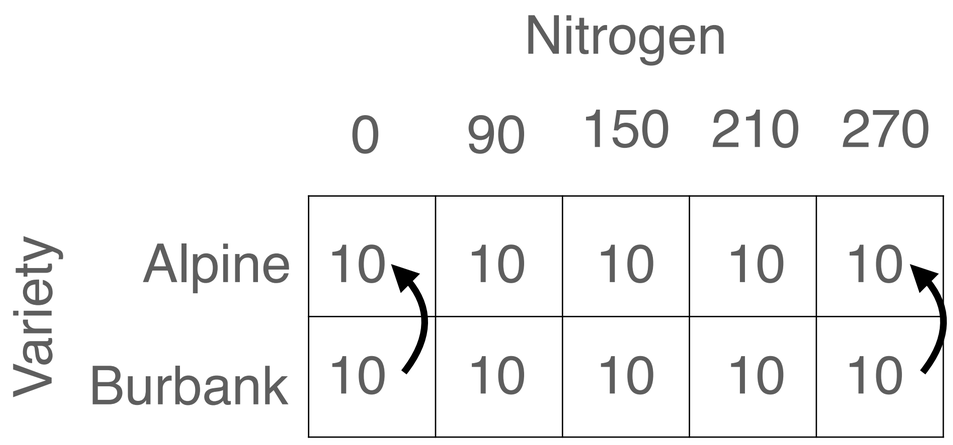
Randomized **C**omplete **B**lock **D**esign



Focal: Insecticide Moderator: Block

Structure	Variable	Type	#levels	Block	EU
Treatment	Insecticide	Categ	3	Block	Plot
Design	Block	Categ	3		
	Ins:Block	Categ	9		
	Plot	Categ	9		
Response	Counts	Num	9		

Factorial



Focal: Variety Moderator: Nitrogen

Structure	Variable	Type	#levels	Block	EU
Focal	Variety	Categ	2	Nitrogen	Plot
Moderator	Nitrogen	Categ	5	None	Plot
Combo	Var:Nitro	Categ	10	None	Plot
Design	Plot	Categ	100		
Response	Yield	Num	100		

Differences

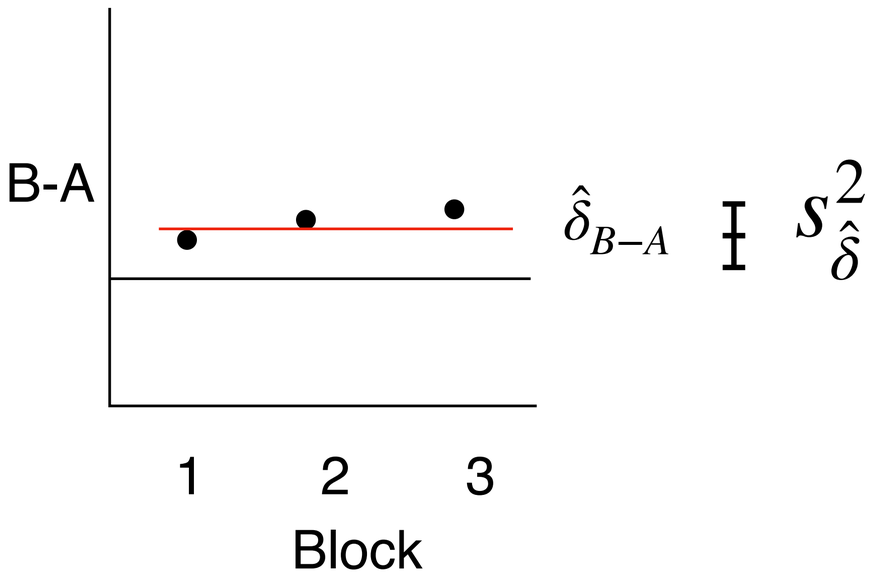
lm(Counts ~ Insecticide + Block)

Can’t put Block:Insectide in model

Consequence: Can’t estimate **specific effects** of Insecticide using emmeans()

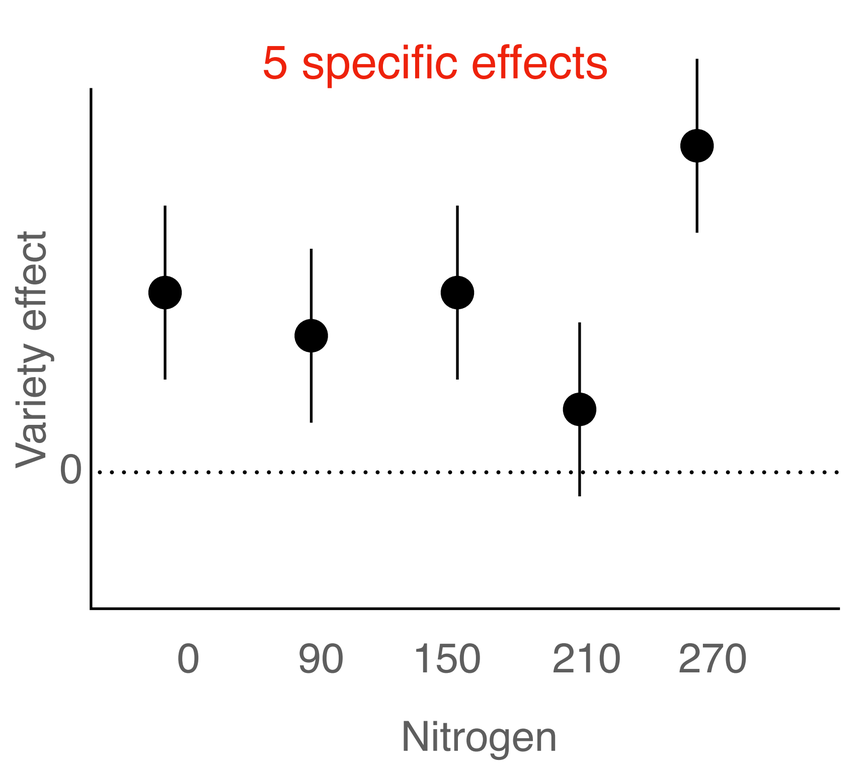
We can only estimate the **main effect: the average effect across blocks**

No replicates of Block:Treatment combinations



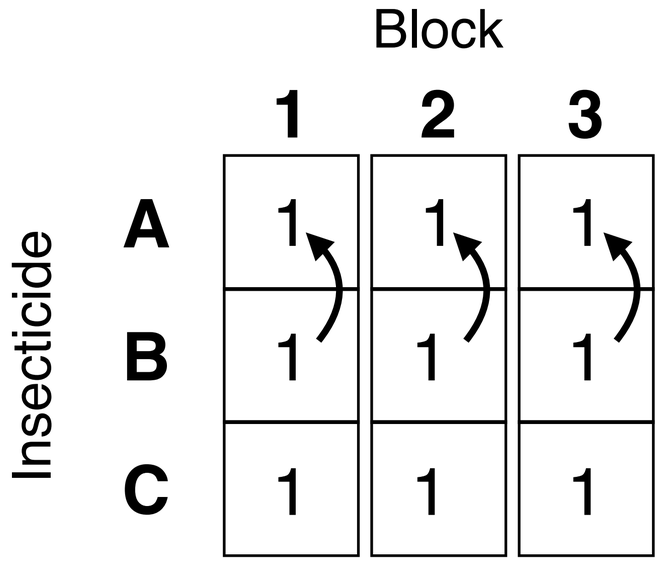
No CIs for treatment effect in each block

Variety:Nitrogen combos repeated 10 times each



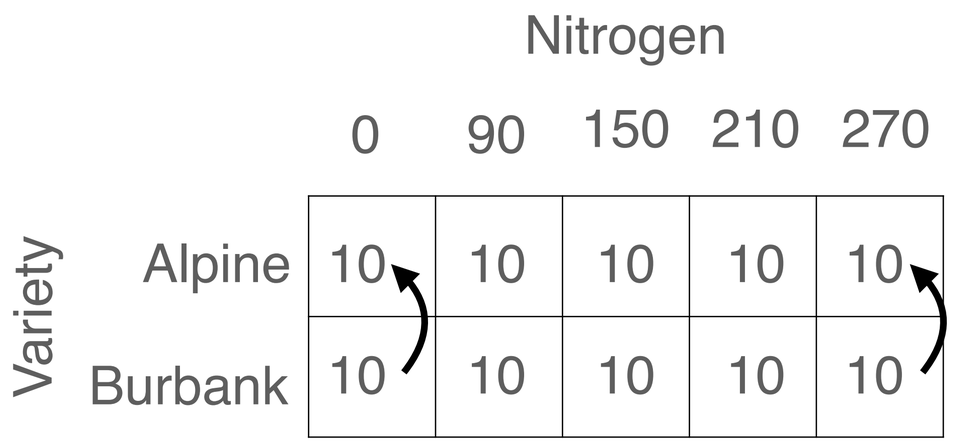
These aren’t needed for estimating the **main effect** because for this we just use $s^2_{\hat{\delta}}$

Randomized **C**omplete **B**lock **D**esign



Goal: Main Effect

Factorial



Goal: Specific Effects / Interaction Effects

Key Difference

"Block" is **NOT** a treatment!

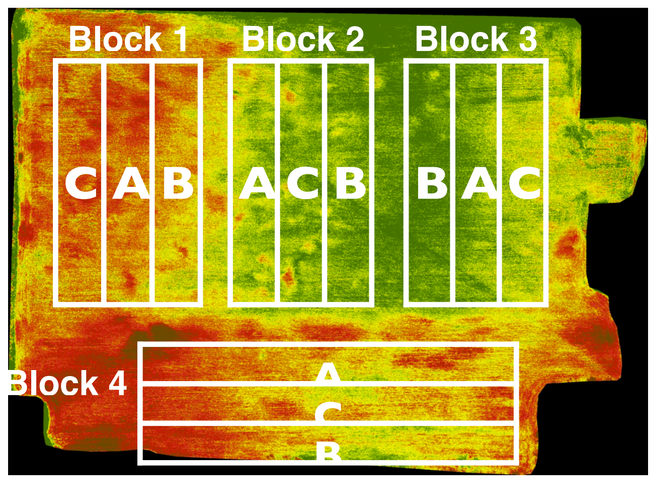
We haven't done a manipulation

We aren't trying to **explain** differences among blocks

We **don't care** about these blocks *per se*

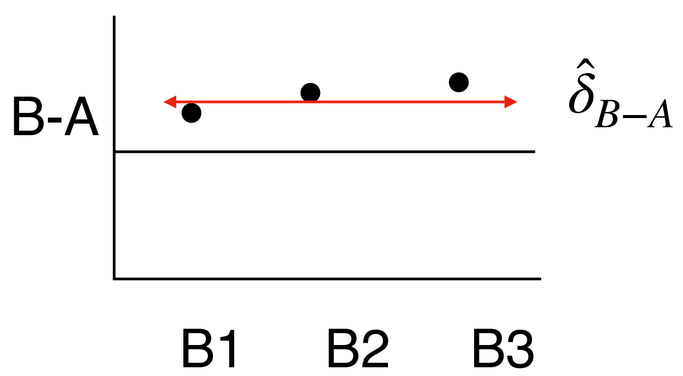
We don't really know **which factors** that differs among the blocks are relevant

So we can't predict what will happen in a specific new block



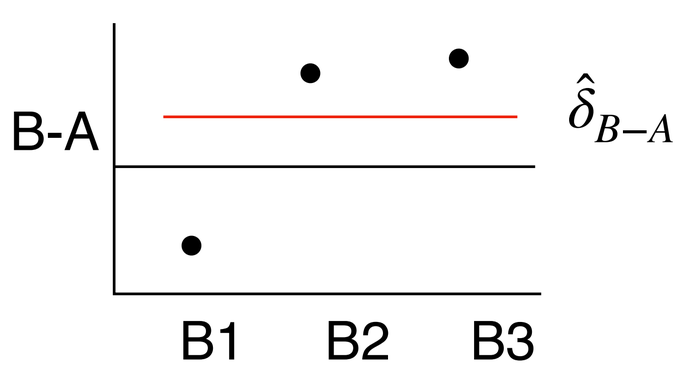
If the treatment effect estimates are similar among blocks (low $s^2_{\hat{\delta}}$)

We will be confident predicting the response into new settings



If the treatment effect estimates are NOT similar among blocks $s^2_{\hat{\delta}}$

We will NOT be confident predicting the response into new settings



Also:

EUs of each block **are not interspersed**

So we wouldn't be confident about interpreting block differences anyway!

This is why "Block" is put in the **Design Structure,** not the **Treatment Structure**

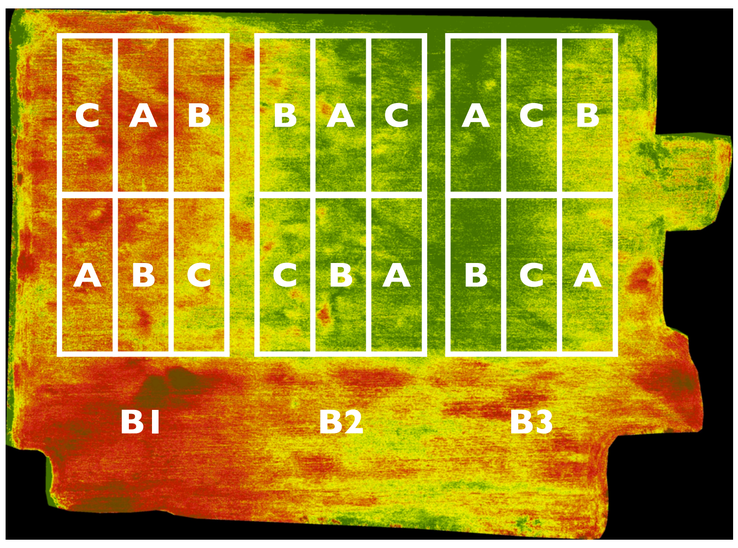
Key Questions to determine if a factor is a block or a treatment:

Is the factor **manipulated**?

Are the EUs **interspersed**?

Are the Treatment:Factor combinations **replicated**?

Replication of treatment levels within blocks



Structure	Variable	Type	#levels	Block	EU
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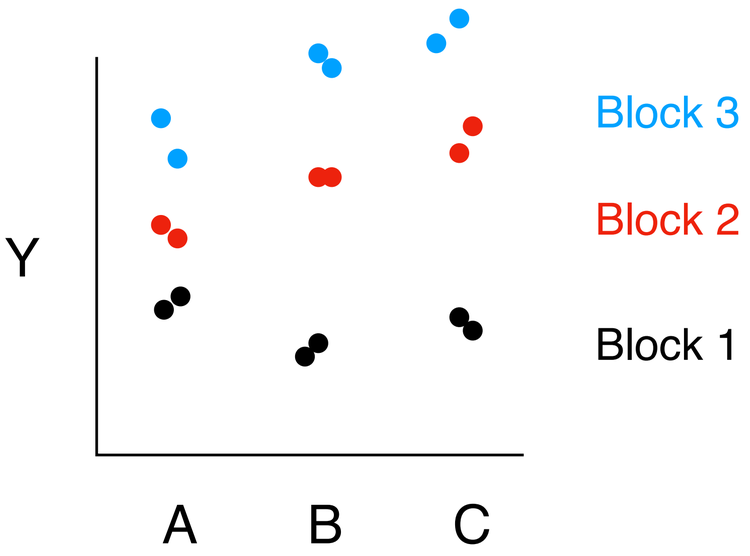
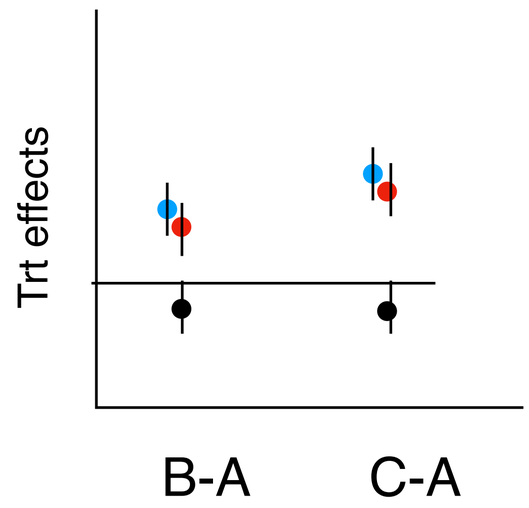




Now we can make confidence intervals on the **specific effects** in each block

Can analyze like a factorial:

focal: Insecticide

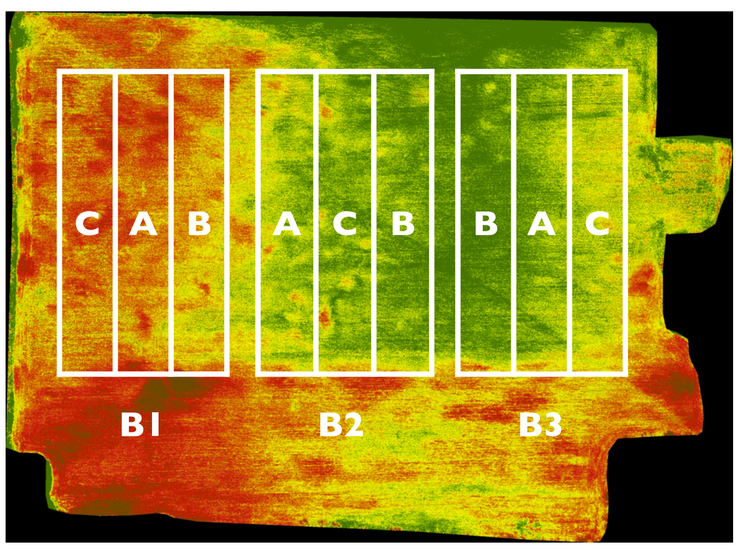
moderator: Block

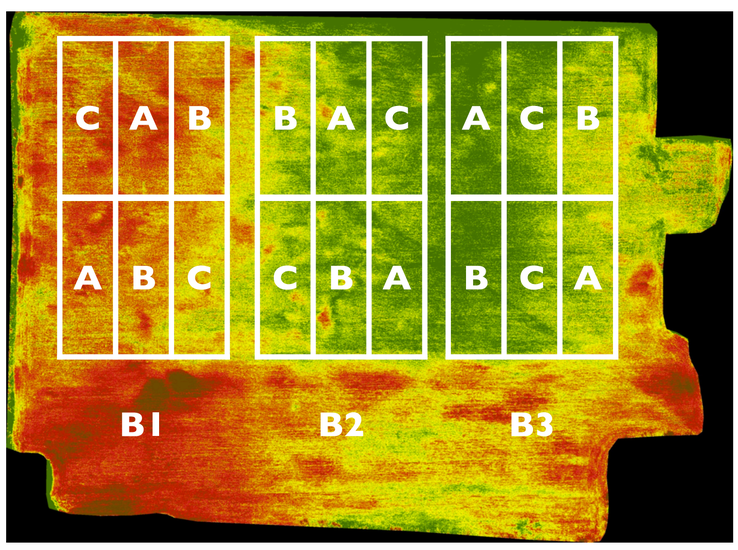
Test for Block:Insecticide interactions

Describe specific effects / block

But: We can't **explain** them

~~plant health?~~





RCBD

Describe **main effects**

Average over blocks

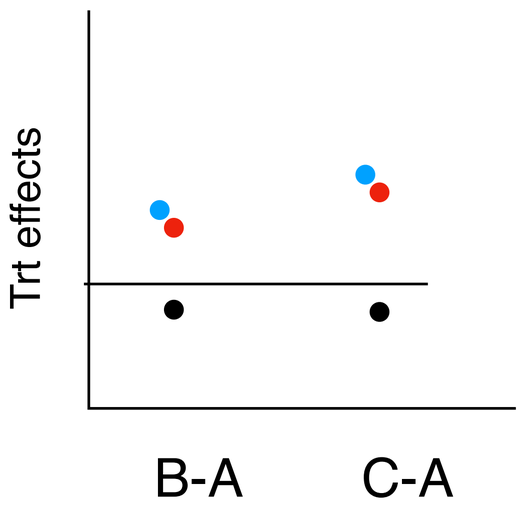
RCBD with Reps

Test for Block:Insecticide interactions

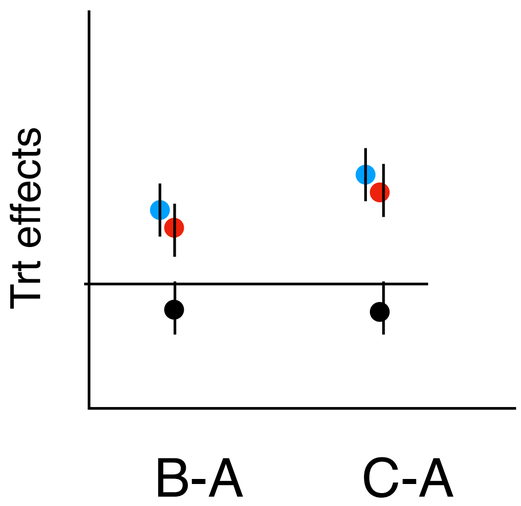
Describe specific effects / block

Describe **main effects**

RCBD



RCBD with Reps



In either case, we when reporting **main effects**

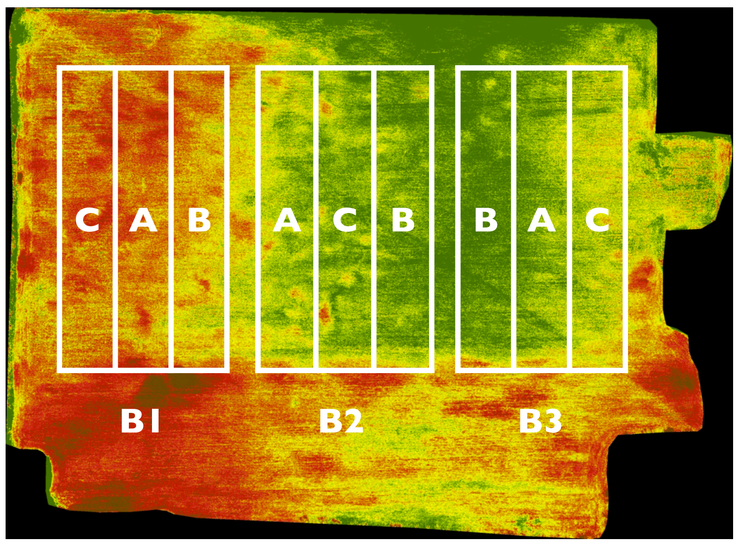
Analysis is the same

We have 3 replicates of B-A

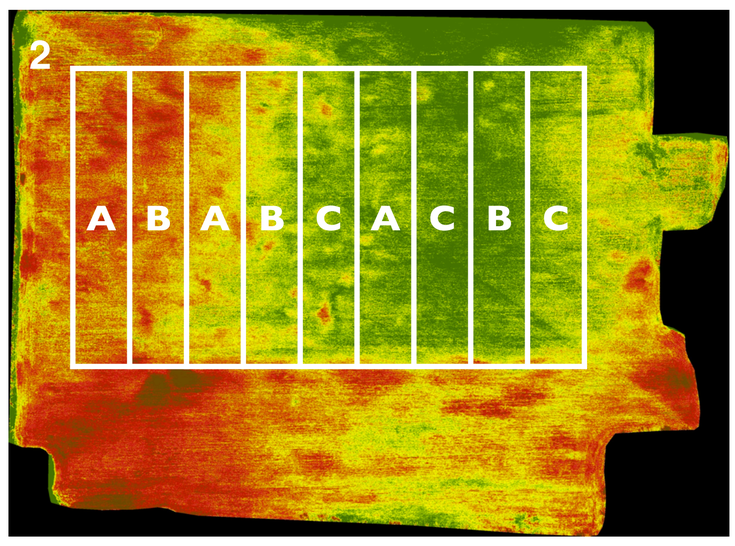
Not 6 reps of B and 6 reps of A

Treatment:Block interactions

What happens if the Insecticide effects change across the field?



RCBD

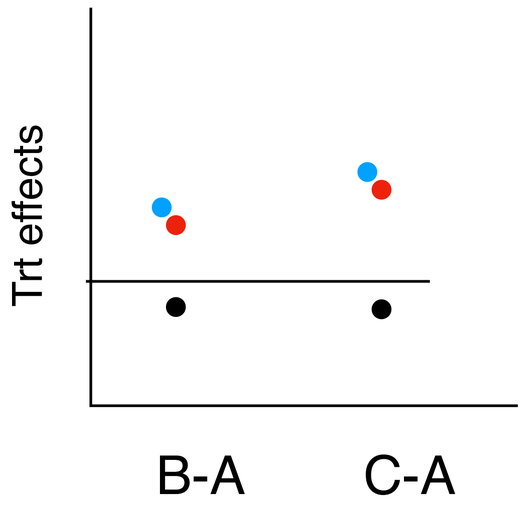


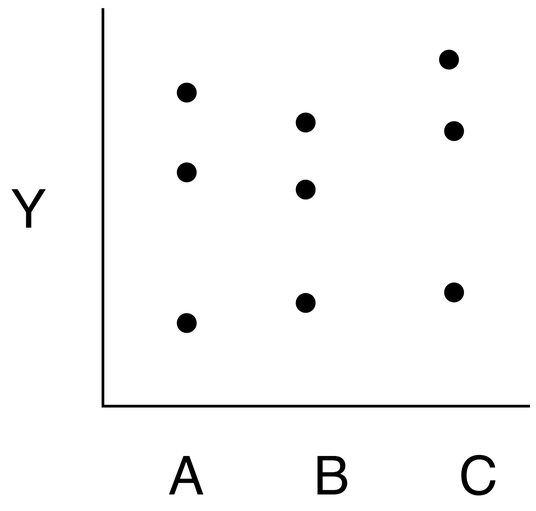
CRD

CRD

We can't even observe it at all

Just part of σ^2_{EU}

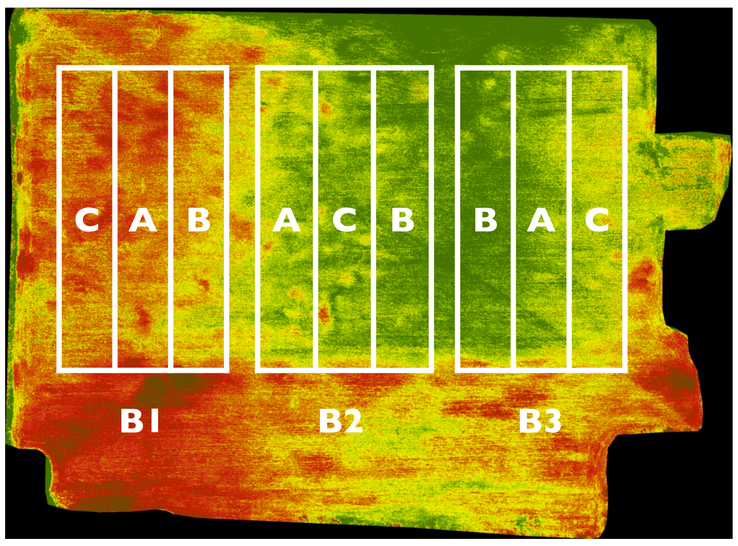




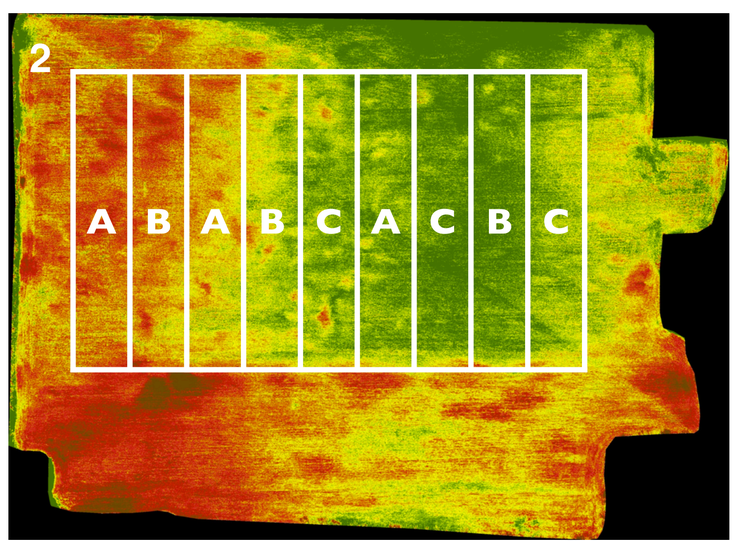
Treatment:Block interactions mean we are less sure about **the treatment effect**

Inflate s^2 in both designs

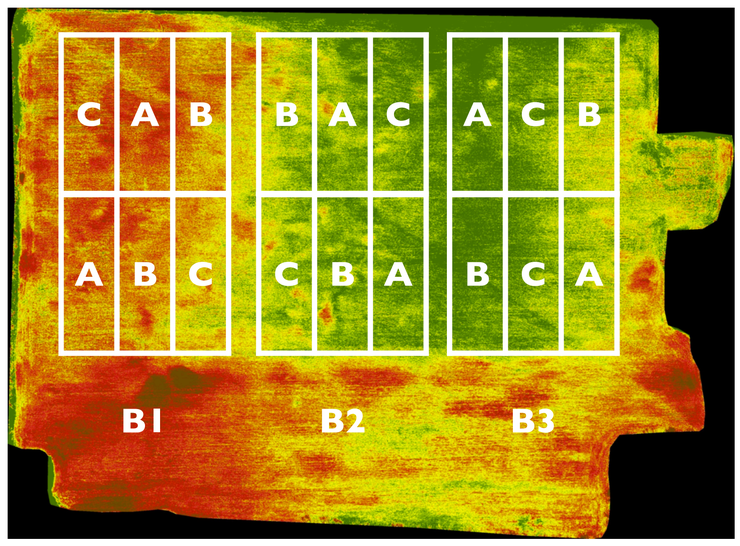
With RCBD we can look for evidence of these, but can't state confidence unless we replicate within blocks



RCBD



CRD



RCBD with Reps

Which design would you use to make an Insecticide recommendation to **this farmer** (in this field)?

Reps are overkill, replicate plots within blocks are sub-samples; not-interspersed

Say the farmer could target regions within a field? Which would you use?

RCBD with reps is necessary (more like a factorial)

What design would you use to make a recommendation in a new field?

RCBD with Fields as blocks to estimate **main effect** of insecticide across all fields

Factorial with Fields as moderator to estimate **specific effects** in **certain types of fields**

Rules for making Design Table

1) Response: One Variable, always numeric

2) Treatments: Variables we want to study

Focal, Moderator, in a factorial

List Blocks and EUs for every treatment variable

Don’t list Focal as a Block

3) Create Treatment:Block variables

If both “Treatment” and “Block” are treatments, include these as Combo treatment

Otherwise, Treatment:Block is a Design variable

4) Design: All other variables necessary to describe the experiment

Must be random → Every EU variable

Every Block variable that **is not a Treatment**

Can be random → Every Treatment:Block variable that **is not a Combo Treatment**

A variable to describe each unique observation
(same # levels as the response)

5) Check **variable relationships** and simplify if possible

EU Variable must be **nested** in the Treatment variable

If two variables are **aliased**, keep only 1 of them

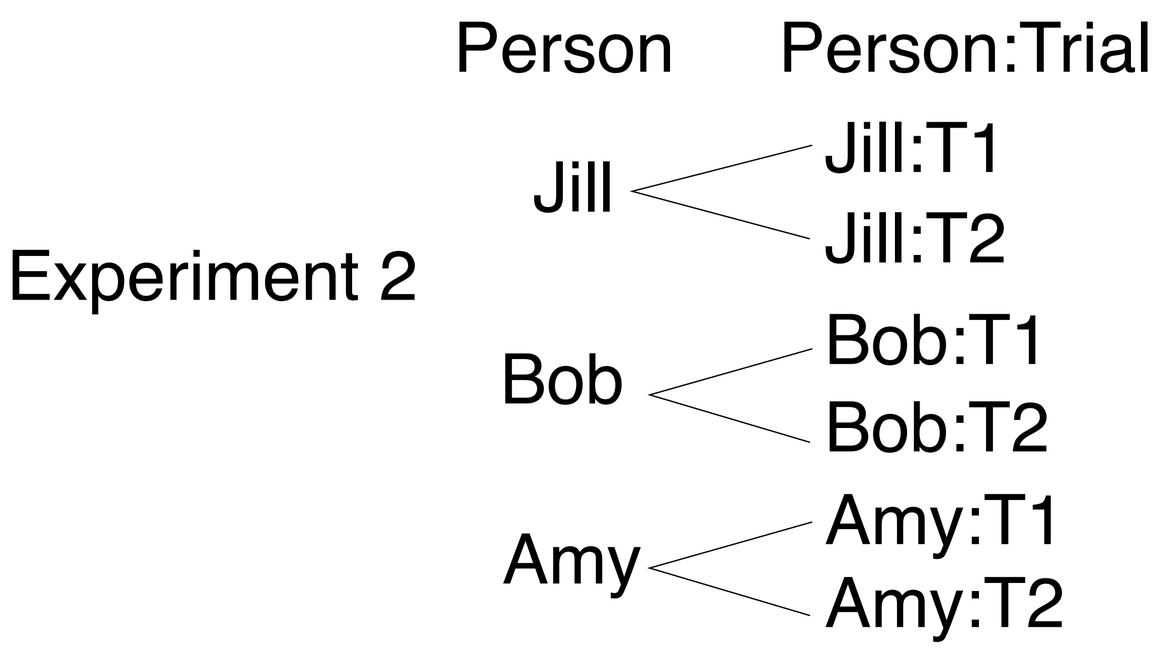
If two variables are **crossed**, keep both

order of variables does not matter

Relationships among variables

nested one:many Keep both, if first is random, so is second

2nd has more levels

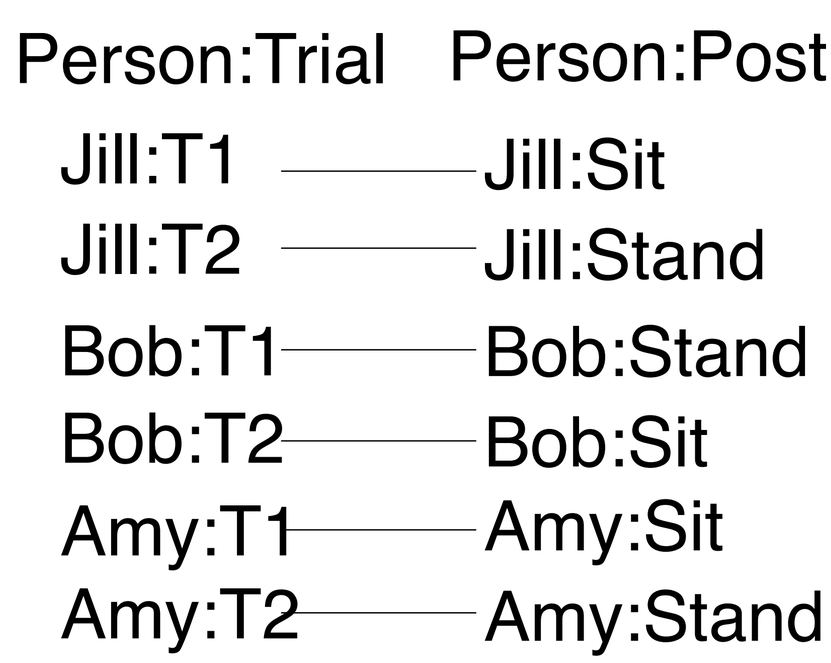


Experiment 2

is_nested(Person~Person:Trial)

aliased one:one Keep one, particularly Treatment:Block

always same # levels

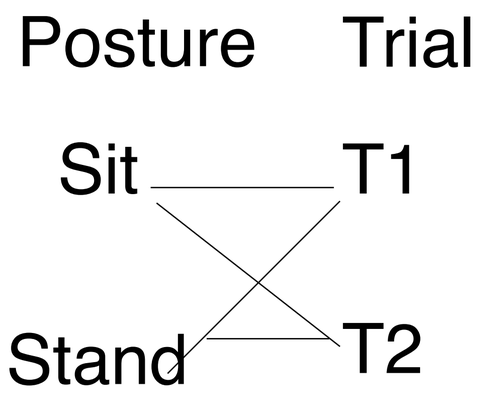


Experiment 2

is_aliased(A~B)

crossed many:many Keep both

at least 1 level of A matched with 2+ levels of B and vice versa

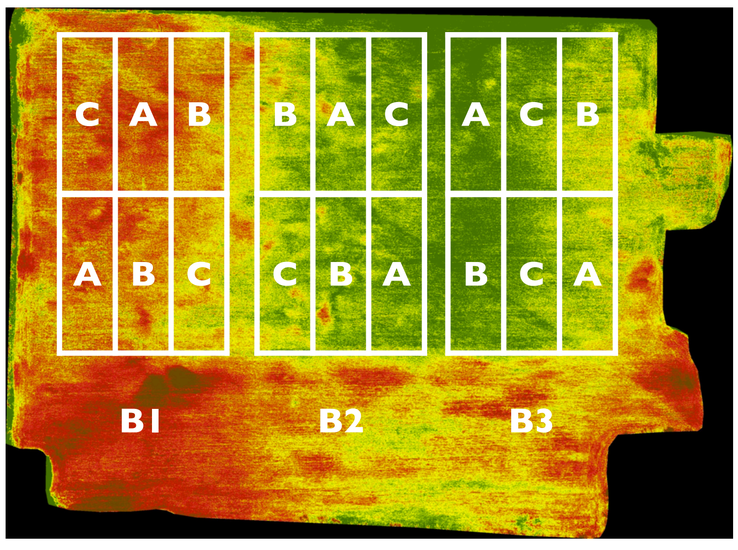


Experiment 2

Experiment 3

is_crossed(A~B)

Practice



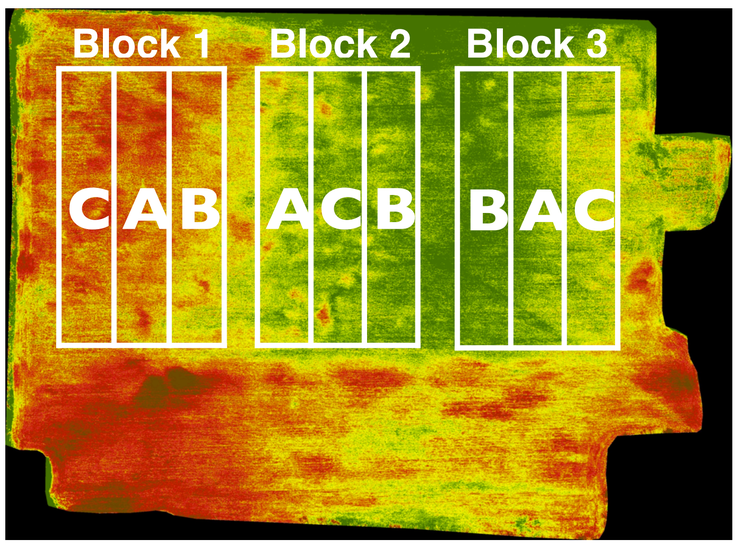
Structure	Variable	Type	#levels	Block	EU
Treatment	Insecticide	Categ	3	Block	Plot
Design	Block	Categ	3		
	Ins:Block	Categ	9		
	Plot	Categ	18		
Response	Yield	Num	18		

Describe these relationships: nested / aliased / crossed

Insecticide ~ Block — crossed

Insecticide ~ Plot — nested

Insecticide:Block ~ Plot — nested



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Response	Counts	Num	9		

Describe these relationships: nested / aliased / crossed

Insecticide ~ Block — crossed

Insecticide ~ Plot — nested

Insecticide:Block ~ Plot — aliased