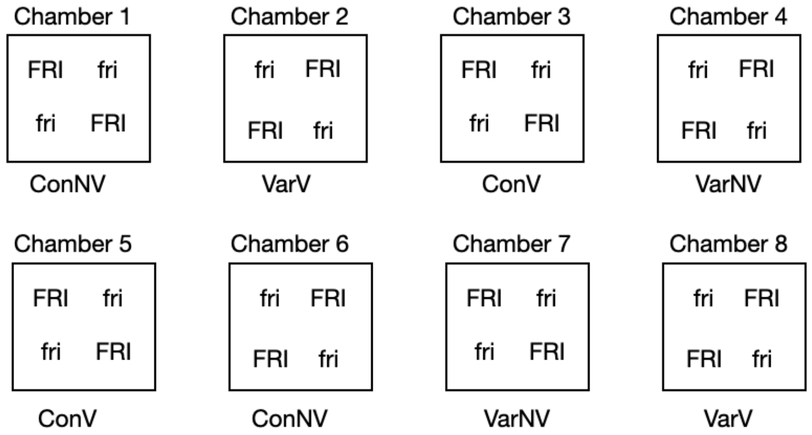
Design Table -> Model statement



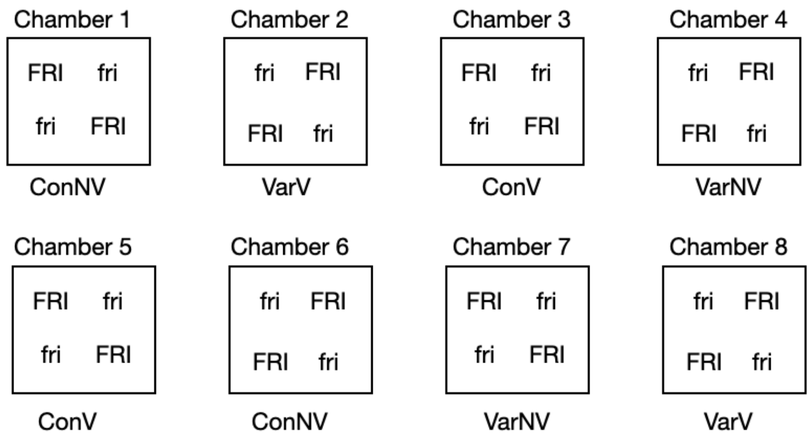
	Pot	Genotype	FRI	mutant	Treatment.V	Chamber	Days.to.Bolt
	<dbl>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	3	Col FRI	FRI	WT	22ConLDNV	1	70
2	7	Col	fri	WT	22ConLDNV	1	20
3	8	Col	fri	WT	22ConLDNV	1	21
4	9	Col FRI	FRI	WT	22ConLDNV	1	53

Structure	Variable	# levels	Block	EU
Response	Days.to.Bolt	64		
focal treatment	FRI	2	Chamber	Pot
moderator treatment	Treatment.V	4	None	Chamber
combo treatment	FRI:Treatment.V	8	Chamber	Pot
Design	Chamber	8		
	Pot	64		
	FRI:Chamber	16		
	FRI:Treatment.V:Chamber	64		

Response Treatments Design

model = lmer(Days.to.Bolt ~ FRI + Treatment.V + FRI:Treatment.V + (1|Chamber) + (1|FRI:Chamber))

Design Table - 1. Response



Structure	Variable	# levels	Block	EU
Response	Days.to.Bolt	64		

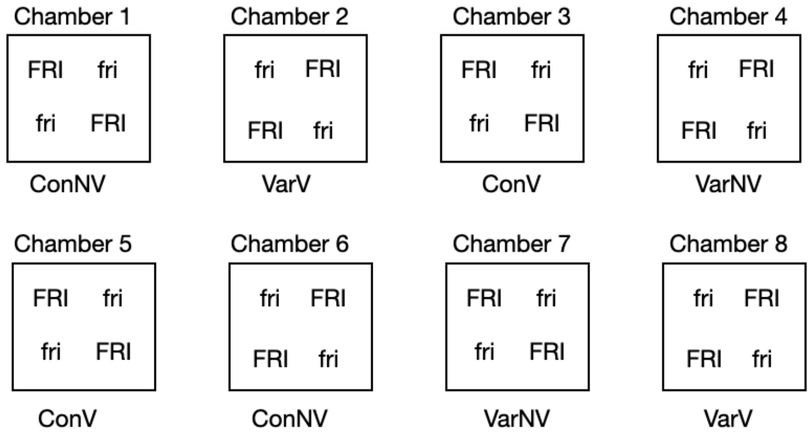
Variable: name of column in data.frame

or inverse(Days.to.Bolt/100)

 # levels: # rows in data.frame

	Pot	Genotype	FRI	mutant	Treatment.V	Chamber	Days.to.Bolt
	<dbl>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	3	Col FRI	FRI	WT	22ConLDNV	1	70
2	7	Col	fri	WT	22ConLDNV	1	20
3	8	Col	fri	WT	22ConLDNV	1	21
4	9	Col FRI	FRI	WT	22ConLDNV	1	53

Design Table - 2. Treatment



Structure	Variable	# levels	Block	EU
Response	Days.to.Bolt	64		
focal treatment	FRI	2	Chamber	Pot
moderator treatment	Treatment.V	4	None	Chamber

	Pot	Genotype	FRI	mutant	Treatment.V	Chamber	Days.to.Bolt
	<dbl>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	3	Col FRI	FRI	WT	22ConLDNV	1	70
2	7	Col	fri	WT	22ConLDNV	1	20
3	8	Col	fri	WT	22ConLDNV	1	21
4	9	Col FRI	FRI	WT	22ConLDNV	1	53

Variable: name of column in data.frame

 # levels: # levels of each treatment

Block and **EU:**

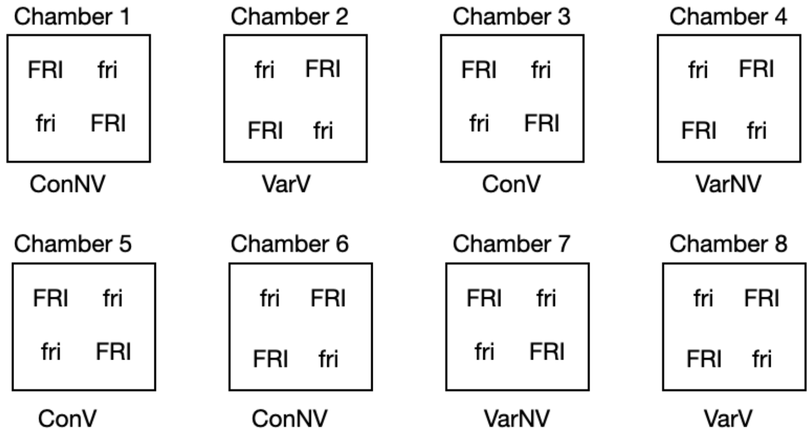
Based on the design

Use the column names in data.frame

focal and moderator treatment

When 2+ treatments, declare 1 “focal”

Design Table - 2. Treatment combos



Structure	Variable	# levels	Block	EU
Response	Days.to.Bolt	64		
focal treatment	FRI	2	Chamber	Pot
moderator treatment	Treatment.V	4	None	Chamber
combo treatment	FRI:Treatment.V	8	Chamber	Pot

	Pot	Genotype	FRI	mutant	Treatment.V	Chamber	Days.to.Bolt
	<dbl>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	3	Col FRI	FRI	WT	22ConLDNV	1	70
2	7	Col	fri	WT	22ConLDNV	1	20
3	8	Col	fri	WT	22ConLDNV	1	21
4	9	Col FRI	FRI	WT	22ConLDNV	1	53

Terminology:

"FRI" and "Treatment.V" are **crossed**

rows and columns have 2+ entries

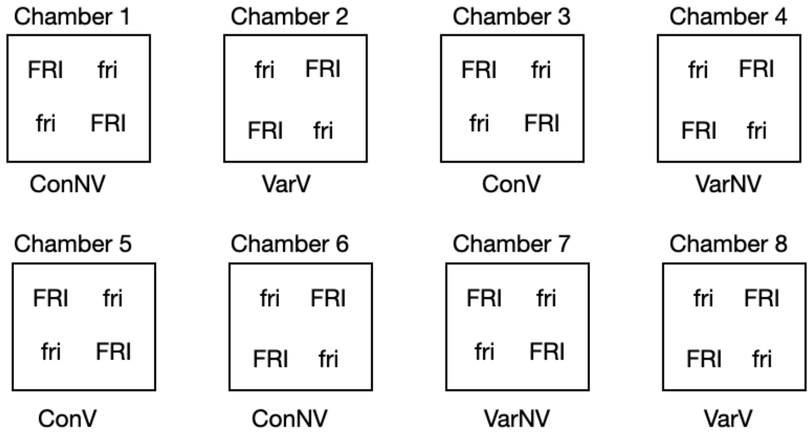
Combos are combined variables

combine names with "**:**" *e.g.* FRI:Treatment.V

	ConNV	VarNV	ConV	VarV
fri	fri:ConNV	fri:VarNV	fri:ConV	fri:VarV
FRI	FRI:ConNV	FRI:VarNV	FRI:ConV	FRI:VarV

 # levels: # unique combinations *in the experiment*

Design Table - 3. Design



	Pot	Genotype	FRI	mutant	Treatment.V	Chamber	Days.to.Bolt
	<dbl>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	3	Col FRI	FRI	WT	22ConLDNV	1	70
2	7	Col	fri	WT	22ConLDNV	1	20
3	8	Col	fri	WT	22ConLDNV	1	21
4	9	Col FRI	FRI	WT	22ConLDNV	1	53

Structure	Variable	# levels	Block	EU
Response	Days.to.Bolt	64		
focal treatment	FRI	2	Chamber	Pot
moderator treatment	Treatment.V	4	None	Chamber
combo treatment	FRI:Treatment.V	8	Chamber	Pot
Design	Chamber	8		
	Pot	64		
	FRI:Chamber	16		
	FRI:Treatment.V:Chamber	64		

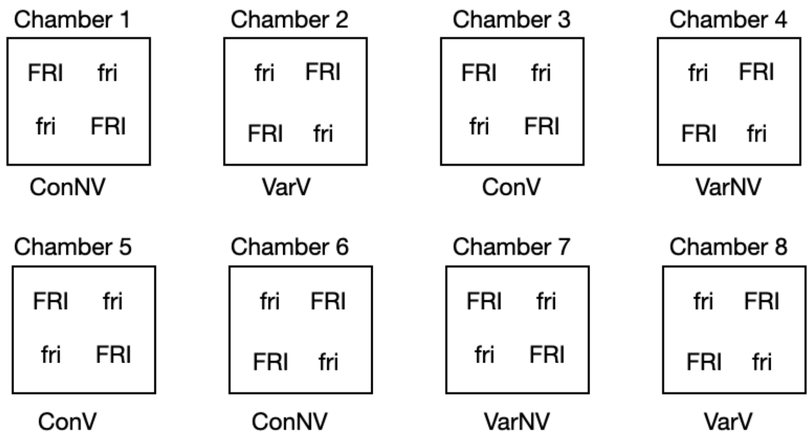
Variable:

List all Block and EUs Check that they are named **uniquely**!

Form all possible **combination terms** among **crossed variables** count # levels

all Treatment:Block some Block:Block

Design Table - 3. Design



	Pot	Genotype	FRI	mutant	Treatment.V	Chamber	Days.to.Bolt
	<dbl>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	3	Col FRI	FRI	WT	22ConLDNV	1	70
2	7	Col	fri	WT	22ConLDNV	1	20
3	8	Col	fri	WT	22ConLDNV	1	21
4	9	Col FRI	FRI	WT	22ConLDNV	1	53

Structure	Variable	# levels	Block	EU
Response	Days.to.Bolt	64		
focal treatment	FRI	2	Chamber	Pot
moderator treatment	Treatment.V	4	None	Chamber
combo treatment	FRI:Treatment.V	8	Chamber	Pot
Design	Chamber	8		
	Pot	64		
	FRI:Chamber	16		
	FRI:Treatment.V:Chamber	64		

Crossed Rows and Columns have 2+ entries

Nested Rows **or** Columns have 2+ entries. The other has only 1

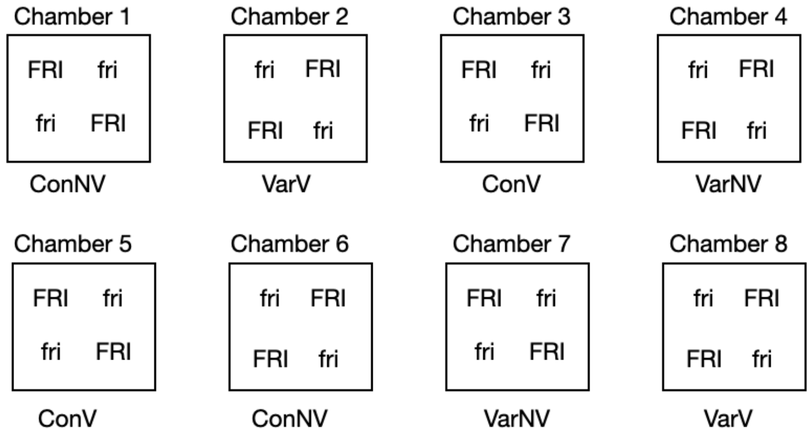
Aliased one-to-one labels

Keep adding rows for any **crossed** combos

If B is **nested in** A, or **aliased with** A, don't form a combo

If C and A are **aliased**, don't need C (unless it is an EU)

Design Table - 4. Model



	Pot	Genotype	FRI	mutant	Treatment.V	Chamber	Days.to.Bolt
	<dbl>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	3	Col FRI	FRI	WT	22ConLDNV	1	70
2	7	Col	fri	WT	22ConLDNV	1	20
3	8	Col	fri	WT	22ConLDNV	1	21
4	9	Col FRI	FRI	WT	22ConLDNV	1	53

Structure	Variable	# levels	Block	EU
Response	Days.to.Bolt	64		
focal treatment	FRI	2	Chamber	Pot
moderator treatment	Treatment.V	4	None	Chamber
combo treatment	FRI:Treatment.V	8	Chamber	Pot
Design	Chamber	8		
	~~Pot~~	~~64~~		
	FRI:Chamber	16		
	~~FRI:Treatment.V:Chamber~~	~~64~~		

1. Drop rows with same # levels as the Response

2. List all other terms, separated by “+”

Response ~ FRI + Treatment.V + FRI:Treatment.V + (1| Chamber) + (1|FRI:Chamber)

3. Convert **EUs**, terms **nested in EUs**, and (usually) **Treatment:Block combos** to random

model function:

Any random terms: lmer()

NO random terms: lm()

(1|Variable)