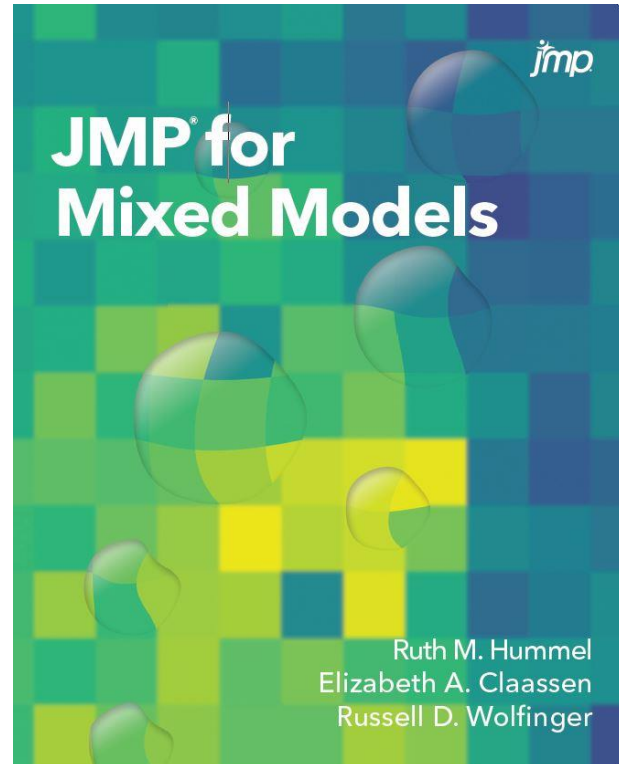


# Mixed Models Part 1 - A Critical Tool When You Have More Than One Source of Variation

*Elizabeth A Claassen, PhD  
Research Statistician Developer, JMP*

# JMP for Mixed Models

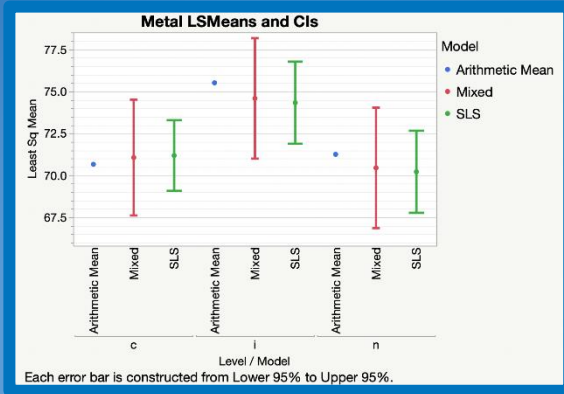
- Example driven
  - Focus on concepts rather than formulas
  - Get modelers modeling!
- Data available
  - JMP Journal organized by chapter
  - [support.sas.com/hummel](https://support.sas.com/hummel)
  - [support.sas.com/claassen](https://support.sas.com/claassen)
  - [support.sas.com/wolfinger](https://support.sas.com/wolfinger)



# Overview

- Introduction to the various concepts in mixed modeling
  - Fixed vs Random Effects
  - Correlation between experimental units
  - Different size experimental units for different effects
- Teach through example
  - Formulas only when necessary
  - Focus on conceptual understanding
- JMP and JMP Pro
  - A lot of mixed models can be fit in JMP
  - But some more complicated models require JMP Pro

## Why use Mixed Models?



## What we will cover:

- What is a **Random Effect**?
- **Mixed Models** → possibly different results for estimates, CIs, and pairwise comparisons
- **REML** – Use it! Especially when you have missing data or unequal group sizes
- **LSMeans** – better than arithmetic means. ;)



Prepare the experimental unit  
and assign the Treatment  
Level (i.e., which metal?)

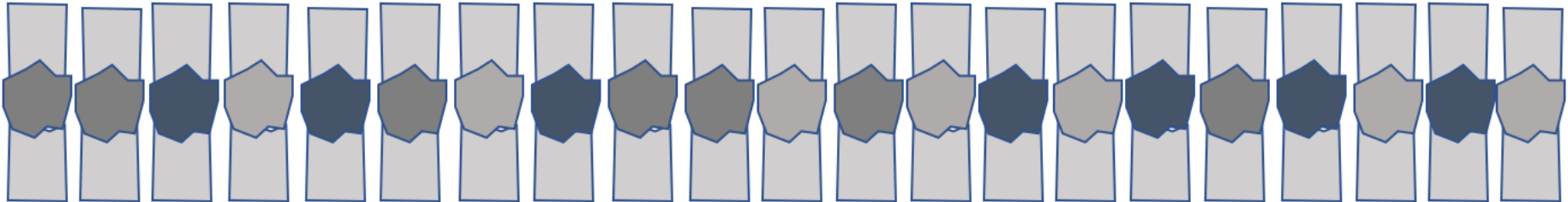


*Metal = Copper*

Explore “Bond” data:  
No Blocks



Conduct the experiment:  
test the breaking  
strength of the metal  
bond.





Divide each ingot into three experimental units



Prepare the experimental unit and assign the Treatment Level (i.e., which metal?)

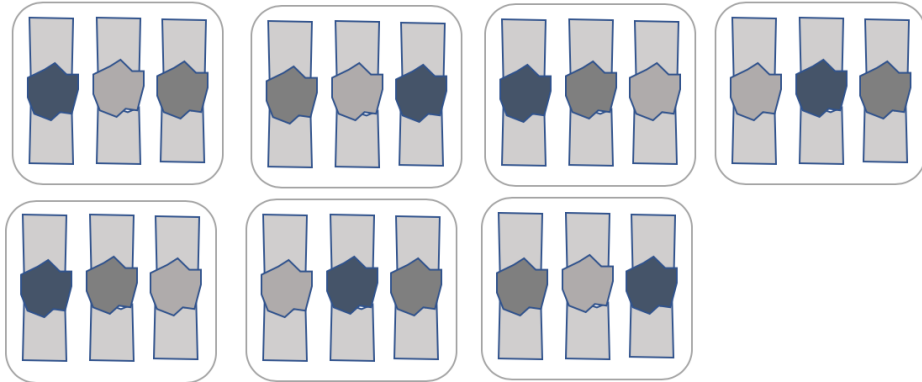


*Metal = Copper*



Conduct the experiment: test the breaking strength of the metal bond.

# Explore “Bond” data: With Blocks (Fixed? Or Random?)



# Definitions

- Fixed Effect
  - When you care about exactly those levels, and you want to make inference for a future observation from exactly those levels
- Random Effect
  - when the levels are a sample from a larger population, and you want to make inference to the larger population and not just to those specific levels, and/or
  - when you are primarily interested in explaining the variability coming from that effect rather than, say, pairwise comparisons

Do I care about only those seven ingots? Or do I want to understand which bonding metal will work best on a future ingot?

# Determining a 'Sensible' Model

## Repurposing the ANOVA table

- ANOVA tables originally designed to aid construction of F-tests
  - Degrees of freedom
  - Expected Mean Squares
  - F-ratios
- Modern software computes these statistics automatically
- Repurpose the ANOVA table to describe a 'sensible' model
  - Sources of Variation
    - Experiment Design
    - Treatment Design
  - One-to-one match of ANOVA effects and model parameters



# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Total				Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Ingot	7-1=6				
Total				Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Ingot	$7-1=6$				
Ingot-third	$(3-1)*7=14$				
Total				Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Ingot	$7-1=6$				
Ingot-third	$(3-1)*7=14$				
Total	$21-1=20$			Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Ingot	$7-1=6$				
		Metal	$3-1=2$		
Ingot-third	$(3-1)*7=14$				
Total	$21-1=20$			Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Ingot	$7-1=6$			Ingot	6
		Metal	$3-1=2$		
Ingot-third	$(3-1)*7=14$				
Total	$21-1=20$			Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Ingot	$7-1=6$			Ingot	6
		Metal	$3-1=2$	Metal	2
Ingot-third	$(3-1)*7=14$			Ingot-third   Metal -> Residual	12
Total	$21-1=20$			Total	20

# From ANOVA to Model

## One-to-one ANOVA source & Model Parameter

Skeleton ANOVA	
Source	df
Ingot	6
Metal	2
Ingot-third   Metal -> Residual	12
Total	20

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

$y_{ij}$  is the observation of the  $i^{\text{th}}$  Metal in the  $j^{\text{th}}$  Ingot

$\mu$  is the intercept

$r_j$  is the  $j^{\text{th}}$  Ingot effect and  $\sim N(0, \sigma_r^2)$

$\alpha_i$  is the  $i^{\text{th}}$  Metal effect

$e_{ij}$  is the residual error and  $\sim N(0, \sigma^2)$



# Bond with random Ingots

## Fit Mixed

### Fit Statistics

-2 Residual Log Likelihood	109.98743
-2 Log Likelihood	115.94455
AICc	129.94455
BIC	131.16716

### Random Effects Covariance Parameter Estimates

Variance Component	Estimate	Std Error	95% Lower	95% Upper	Wald p-Value
ingot	11.447778	8.7203658	-5.643825	28.539381	0.1893
Residual	10.371587	4.2341828	5.3331979	28.261813	
Total	21.819365	9.056538	11.11697	60.718883	

### Fixed Effects Parameter Estimates

### Random Coefficients

### Fixed Effects Tests

Source	Nparm	DFNum	DFDen	F Ratio	Prob > F
metal	2	2	12.0	6.358764	0.0131*

# Bond with random Ingots

## Fit Mixed

### Fixed Effects Tests

### Multiple Comparisons for metal

#### Least Squares Means Estimates

metal	Estimate	Std Error	DF	Lower 95%	Upper 95%
c	70.185714	1.7655175	11.609	66.324558	74.046870
i	75.900000	1.7655175	11.609	72.038844	79.761156
n	71.100000	1.7655175	11.609	67.238844	74.961156

#### Tukey HSD All Pairwise Comparisons

Quantile = 2.66776, Adjusted DF = 12.0, Adjustment = Tukey-Kramer

#### All Pairwise Differences

metal	-metal	Difference	Std Error	t Ratio	Prob> t	Lower 95%	Upper 95%
c	i	-5.71429	1.721427	-3.32	0.0156*	-10.3066	-1.12194
c	n	-0.91429	1.721427	-0.53	0.8578	-5.5066	3.67806
i	n	4.80000	1.721427	2.79	0.0404*	0.2077	9.39235

Why bother using a mixed model? Why not just include the random effect like a fixed effect?

Metal and Ingot both fixed effects

Response pressure

Summary of Fit

AICc	BIC
138.964	127.4092

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	8	400.19048	50.0238	4.8232
Error	12	124.45905	10.3716	<b>Prob &gt; F</b>
C. Total	20	524.64952		<b>0.0076*</b>

Parameter Estimates

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
metal	2	2	131.90095	6.3588	<b>0.0131*</b>
ingot	6	6	268.28952	4.3113	<b>0.0151*</b>

## Bond with random Ingots

Fit Mixed

Fit Statistics

-2 Residual Log Likelihood	109.98743
-2 Log Likelihood	115.94455
AICc	129.94455
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Fixed Effects Parameter Estimates

Random Coefficients

Fixed Effects Tests

Source	Nparm	DFNum	DFDen	F Ratio	Prob > F
metal	2	2	12.0	6.358764	<b>0.0131*</b>

Answer #1: Ingot is used in the model to explain variance.

# Bond with random Ingots: adjustments to one-group CIs

Metal and Ingot both fixed effects

Response pressure

Multiple Comparisons for metal

Least Squares Means Estimates

metal	Estimate	Std Error	DF	Lower 95%	Upper 95%	Arithmetic Mean Estimate	N
c	70.185714	1.2172327	12	67.533592	72.837836	70.185714	7
i	75.900000	1.2172327	12	73.247878	78.552122	75.900000	7
n	71.100000	1.2172327	12	68.447878	73.752122	71.100000	7

Tukey HSD All Pairwise Comparisons

Quantile = 2.66776, Adjusted DF = 12.0, Adjustment = Tukey

All Pairwise Differences

metal	-metal	Difference	Std Error	t Ratio	Prob> t	Lower 95%	Upper 95%
c	i	-5.71429	1.721427	-3.32	0.0156*	-10.3066	-1.12194
c	n	-0.91429	1.721427	-0.53	0.8578	-5.5066	3.67806
i	n	4.80000	1.721427	2.79	0.0404*	0.2077	9.39235

Fit Mixed

Fixed Effects Tests

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Quantile = 2.66776, Adjusted DF = 12.0, Adjustment = Tukey-Kramer

All Pairwise Differences

metal	-metal	Difference	Std Error	t Ratio	Prob> t	Lower 95%	Upper 95%
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c	n	-0.91429	1.721427	-0.53	0.8578	-5.5066	3.67806
i	n	4.80000	1.721427	2.79	0.0404*	0.2077	9.39235

Answer #2: And that effects CIs for the fixed effects.

# Bond with random Ingots: adjustments to one-group CIs

Metal and Ingot both fixed effects

Response pressure

Multiple Comparisons for metal

Least Squares Means Estimates

metal	Estimate	Std Error	DF	Lower 95%	Upper 95%	Arithmetic Mean Estimate	N
c	70.185714	1.2172327	12	67.533592	72.837836	70.185714	7
i	75.900000	1.2172327	12	73.247878	78.552122	75.900000	7
n	71.100000	1.2172327	12	68.447878	73.752122	71.100000	7

Tukey HSD All Pairwise Comparisons

Quantile = 2.66776, Adjusted DF = 12.0, Adjustment = Tukey

All Pairwise Differences

metal	-metal	Difference	Std Error	t Ratio	Prob> t	Lower 95%	Upper 95%
c	i	-5.71429	1.721427	-3.32	0.0156*	-10.3066	-1.12194
c	n	-0.91429	1.721427	-0.53	0.8578	-5.5066	3.67806
i	n	4.80000	1.721427	2.79	0.0404*	0.2077	9.39235

Fit Mixed

Fixed Effects Tests

Multiple Comparisons for metal

Least Squares Means Estimates

metal	Estimate	Std Error	DF	Lower 95%	Upper 95%
c	70.185714	1.7655175	11.609	66.324558	74.046870
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Tukey HSD All Pairwise Comparisons

Quantile = 2.66776, Adjusted DF = 12.0, Adjustment = Tukey-Kramer

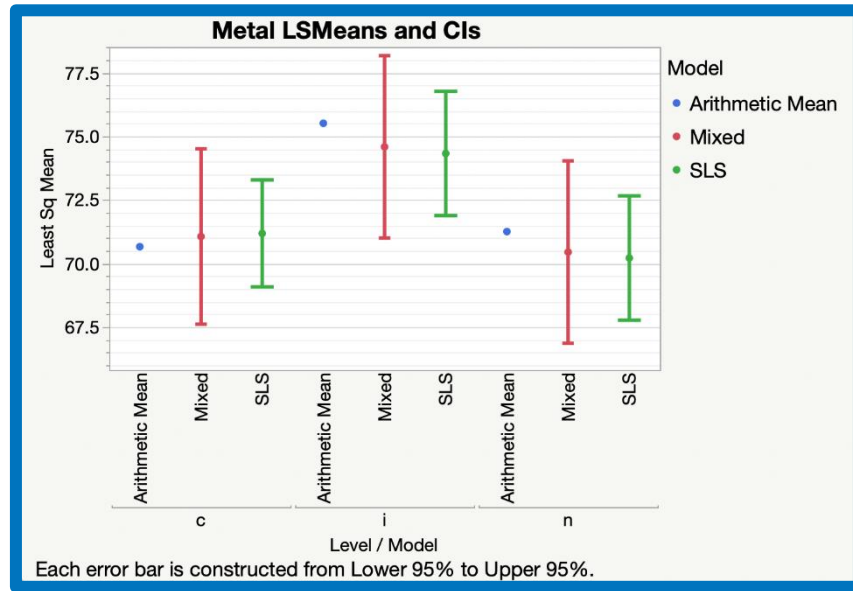
All Pairwise Differences

metal	-metal	Difference	Std Error	t Ratio	Prob> t	Lower 95%	Upper 95%
c	i	-5.71429	1.721427	-3.32	0.0156*	-10.3066	-1.12194
c	n	-0.91429	1.721427	-0.53	0.8578	-5.5066	3.67806
i	n	4.80000	1.721427	2.79	0.0404*	0.2077	9.39235

Answer #2: (But not the CIs for differences if the design is balanced).

# Summary/Tips

- You are dealing with Random Effects:
  - when the levels are a sample from a larger population, and/or
  - when you are primarily interested in explaining the variability rather than, say, pairwise comparisons.



- If you treat a random effect as fixed, your standard errors (and therefore your CIs on the other fixed effects) will be less appropriate. “All models are wrong, but some are useful.”  
“When you know better, do better.”

- LSMMeans are not necessarily the arithmetic means. Missing data / imbalance needs REML to better estimate the LSMMeans.
- With missing data / imbalance, the pairwise comparisons for the other fixed effects are also affected by the choice to model an effect as random.
- Don't rely only on the p-value – remember that  $p=0.049$  and  $p=0.050$  are basically the same thing.

## Models with Factorial Designs

Dark Blue	Medium Blue	Light Blue
Dark Blue	Medium Blue	Light Blue
Dark Blue	Medium Blue	Light Blue
Dark Blue	Medium Blue	Light Blue

## What we will cover:

- What is a Factorial Design and why would we use one?
- How is discussion of Factorials a Mixed Model topic?
- Beyond the split plot



# Factorial Treatment Designs

- A factorial treatment design occurs when the experiment has two or more treatment factors of interest
- These designs are more efficient than one factor at a time experiments
  - Reduce the number of experiments and therefore experimental units required
  - Enables the measurement of *interactions* between the factors
  - Improved statistical properties for *main effects* and *simple effects*
- Factorial treatment designs are often used with split-plot experiment designs
  - Often one factor is harder to change treatment levels than the other
  - The hard-to-change factor is the *whole plot* factor
  - The easier-to-change factor is the *split plot* factor

# Main Effects

## When there's negligible interaction

- A main effect is the effect of a single factor averaging over any other factors in the model
- Because we have determined there is no interaction, it does not matter what level the other factor(s) are at. Thus, we can use the “average” level/effect.
- Use LSMeans comparisons of the factor to make decisions about optimal factor settings.

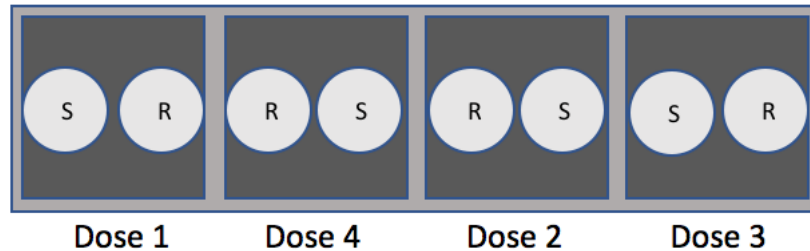
# Simple effects

## When an interaction is non-negligible

- A simple effect is the effect of one factor given a particular level of the other factor(s).
- An interaction by definition is when the simple effect *changes* depending on the level of the other factor.
- Look at *slices* of the interaction LSMeans to determine optimal factor settings.

# Greenhouse Example

- A plant researcher has two plant varieties and a pesticide meant to protect the plants against disease
- The amount of pesticide can be applied to sections of greenhouse benches.
- Bench sections can hold multiple plants.
- From past experiments the researcher knows there is variability between benches within the greenhouse, so benches should be a blocking factor.



# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	5-1=4				
Total				Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	$5-1=4$				
WP(Block)	$(4-1)*5=15$				
Total				Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	$5-1=4$				
WP(Block)	$(4-1)*5=15$				
SP(WP)	$(2-1)*20=20$				
Total				Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	$5-1=4$				
WP(Block)	$(4-1)*5=15$				
SP(WP)	$(2-1)*20=20$				
Total	$40-1=39$			Total	



# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	$5-1=4$				
		Dose	$4-1=3$		
WP(Block)	$(4-1)*5=15$				
SP(WP)	$(2-1)*20=20$				
Total	$40-1=39$			Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	$5-1=4$				
		Dose	$4-1=3$		
WP(Block)	$(4-1)*5=15$				
		Type	$2-1=1$		
		Type*Dose	3		
SP(WP)	$(2-1)*20=20$				
Total	$40-1=39$			Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	$5-1=4$			Block	4
		Dose	$4-1=3$		
WP(Block)	$(4-1)*5=15$				
		Type	$2-1=1$		
		Type*Dose	3		
SP(WP)	$(2-1)*20=20$				
Total	$40-1=39$			Total	

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	$5-1=4$			Block	4
		Dose	$4-1=3$	Dose	3
WP(Block)	$(4-1)*5=15$			WP(Block)   Dose -> Block*Dose	12
		Type	$2-1=1$		
		Type*Dose	3		
SP(WP)	$(2-1)*20=20$				
Total	$40-1=39$			Total	39

# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Block	$5-1=4$			Block	4
		Dose	$4-1=3$	Dose	3
WP(Block)	$(4-1)*5=15$			WP(Block)   Dose -> Block*Dose	12
		Type	$2-1=1$	Type	1
		Type*Dose	3	Type*Dose	3
SP(WP)	$(2-1)*20=20$			SP(WP)   Dose, Type -> Residual	16
Total	$40-1=39$			Total	39

# ANOVA to Model

Skeleton ANOVA	
Source	df
Block	4
Dose	3
WP(Block)   Dose -> Block*Dose	12
Type	1
Type*Dose	3
SP(WP)   Dose, Type -> Residual	16
Total	39

- $y_{ijk} = \mu + r_k + \delta_i + w_{ik} + \tau_j + \delta\tau_{ij} + e_{ijk}$
- $y_{ijk}$  is the observation of the  $i^{th}$  Dose,  $j^{th}$  Type, and  $k^{th}$  block.
- $\mu$  is the intercept
- $r_k$  is the  $k^{th}$  block effect and  $\sim N(0, \sigma_r^2)$
- $\delta_i$  is the  $i^{th}$  Dose effect
- $w_{ik}$  is the  $ik^{th}$  whole-plot (Block\*Dose) effect and  $\sim N(0, \sigma_w^2)$
- $\tau_j$  is the  $j^{th}$  Type effect
- $\delta\tau_{ij}$  is the  $ij^{th}$  Dose\*Type interaction effect
- $e_{ijk}$  is the split-plot, residual error and  $\sim N(0, \sigma^2)$

# Dialog boxes

$$y_{ijk} = \mu + r_k + \delta_i + w_{ik} + \tau_j + \delta\tau_{ij} + e_{ijk}$$

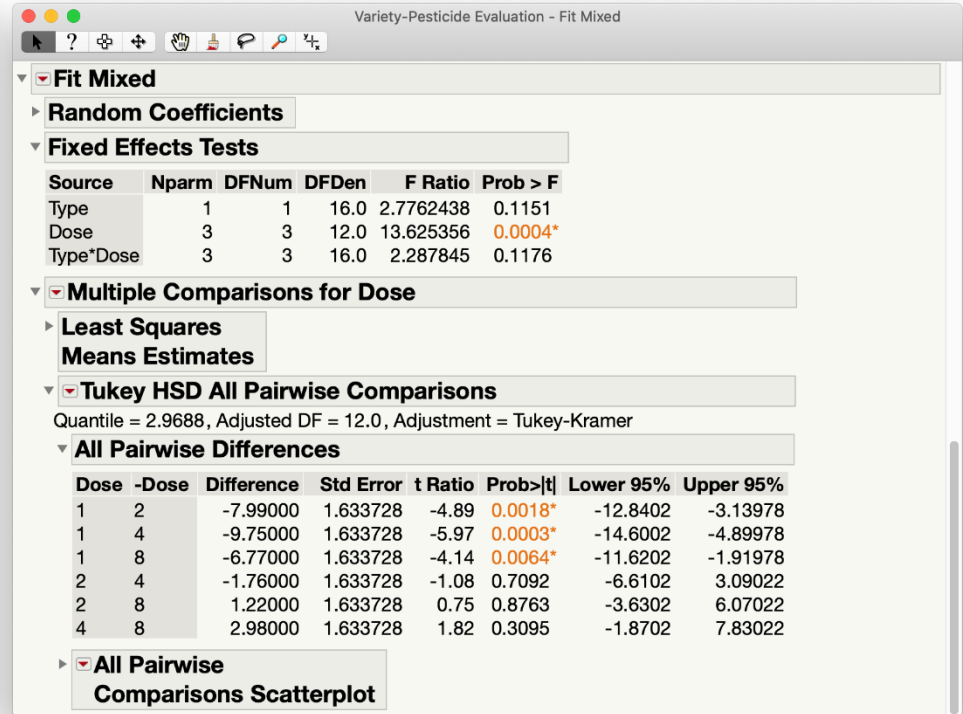
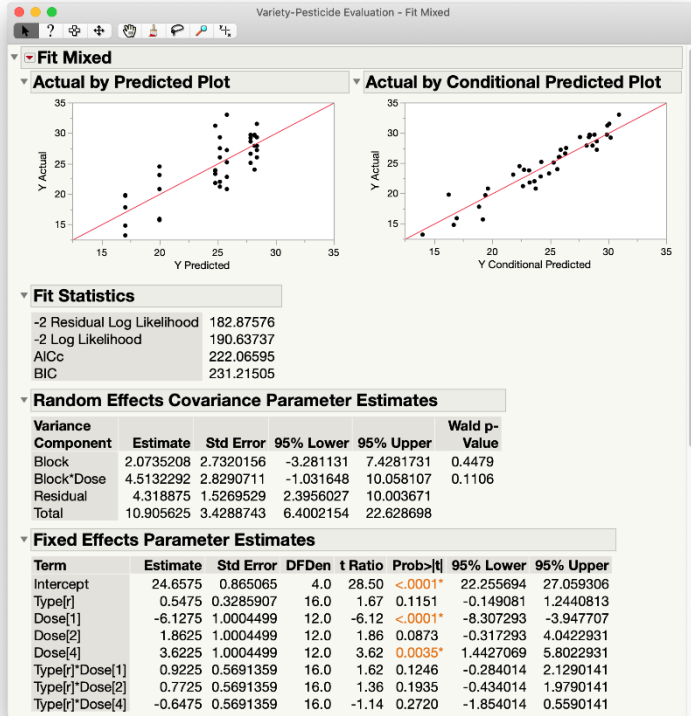
The image displays the JMP software interface for model specification. The main window is titled "Report: Fit Model" and shows the "Model Specification" dialog box. The dialog is divided into several sections:

- Select Columns:** A list of 4 columns: Block, Type, Dose, and Y.
- Pick Role Variables:** Fields for "Y" (containing "Y") and "By" (containing "optional").
- Personality:** Set to "Mixed Model".
- Options:** "Unbounded Variance Components" is checked. Buttons for "Help", "Run", "Recall", "Remove", and "Keep dialog open" are present.
- Construct Model Effects:** Three tabs: "Fixed Effects", "Random Effects", and "Repeated Structure".

The "Random Effects" tab is active, showing a list of effects: "Type", "Dose", and "Type\*Dose". A blue arrow points from this tab to a zoomed-in view of the "Random Effects" sub-dialog. This sub-dialog shows:

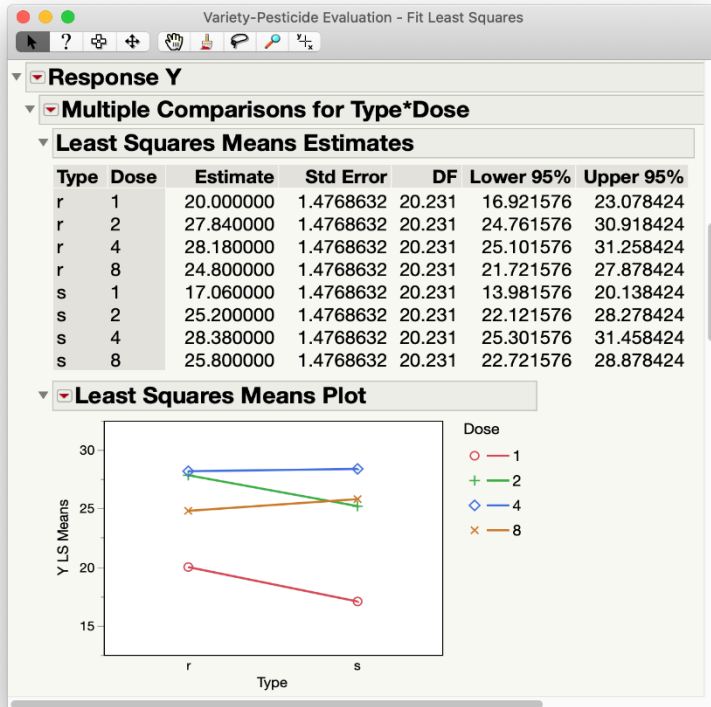
- Buttons for "Add", "Cross", "Nest", and "Nest Random Coefficients".
- A "Macros" dropdown menu.
- A "Degree" field set to "2".
- A list of effects: "Block" and "Block\*Dose".

# Results





# Results



Variety-Pesticide Evaluation - Fit Least Squares

Response Y

Multiple Comparisons for Type\*Dose

Tukey HSD All Pairwise Comparisons

Quantile = 3.46215, Adjusted DF = 16.0, Adjustment = Tukey-Kramer

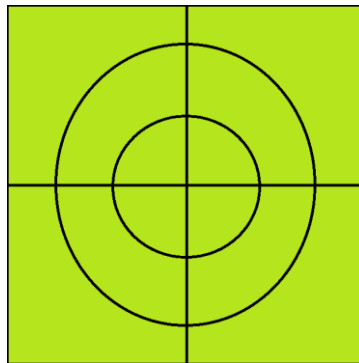
All Pairwise Differences

Type	Dose	-Type	-Dose	Difference	Std Error	t-Ratio	Prob> t	Lower 95%	Upper 95%
r	1	r	2	-7.8400	1.879586	-4.17	0.0128*	-14.3474	-1.3326
r	1	r	4	-8.1800	1.879586	-4.35	0.0090*	-14.6874	-1.6726
r	1	r	8	-4.8000	1.879586	-2.55	0.2417	-11.3074	1.7074
r	1	s	1	2.9400	1.314363	2.24	0.3814	-1.6105	7.4905
r	1	s	2	-5.2000	1.879586	-2.77	0.1721	-11.7074	1.3074
r	1	s	4	-8.3800	1.879586	-4.46	0.0073*	-14.8874	-1.8726
r	1	s	8	5.8000	1.879586	3.09	0.0095	-12.3074	0.7074
r	2	r	4	-0.3400	1.879586	-0.18	1.0000	-6.8474	6.1674
r	2	r	8	3.0400	1.879586	1.62	0.7345	-3.4674	9.5474
r	2	s	1	10.7800	1.879586	5.74	0.0006*	4.2726	17.2874
r	2	s	2	2.6400	1.314363	2.01	0.5057	-1.9105	7.1905
r	2	s	4	-0.5400	1.879586	-0.29	1.0000	-7.0474	5.9674
r	2	s	8	2.0400	1.879586	1.09	0.9510	-4.4674	8.5474
r	4	r	8	3.3800	1.879586	1.80	0.6298	-3.1274	9.8874
r	4	s	1	11.1200	1.879586	5.92	0.0005*	4.6126	17.6274
r	4	s	2	2.9800	1.879586	1.59	0.7521	-3.5274	9.4874
r	4	s	4	-0.2000	1.314363	-0.15	1.0000	-4.7505	4.3505
r	4	s	8	2.3800	1.879586	1.27	0.8986	-4.1274	8.8874
r	8	s	1	7.7400	1.879586	4.12	0.0142*	1.2326	14.2474
r	8	s	2	-0.4000	1.879586	-0.21	1.0000	-6.9074	6.1074
r	8	s	4	-3.5800	1.879586	-1.90	0.5666	-10.0874	2.9274
r	8	s	8	-1.0000	1.314363	-0.76	0.9930	-5.5505	3.5505
s	1	s	2	-8.1400	1.879586	-4.33	0.0094*	-14.6474	-1.6326
s	1	s	4	-11.3200	1.879586	-6.02	0.0004*	-17.8274	-4.8126
s	1	s	8	-8.7400	1.879586	-4.65	0.0050*	-15.2474	-2.2326
s	2	s	4	-3.1800	1.879586	-1.69	0.6922	-9.6874	3.3274
s	2	s	8	-0.6000	1.879586	-0.32	1.0000	-7.1074	5.9074
s	4	s	8	2.5800	1.879586	1.37	0.8567	-3.9274	9.0874

# Beyond the Split-Plot

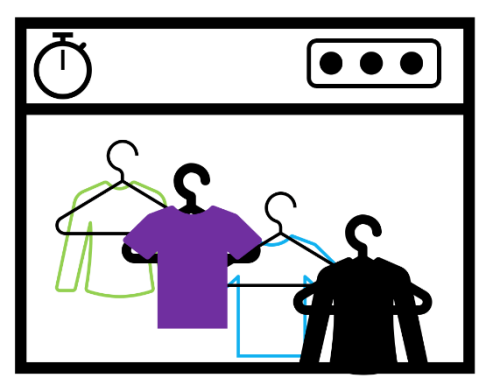
## Factorial Treatments with other Experiment Designs

- Many variations and extensions of the basic split-plot exist
  - Split-split-plot
  - Strip-split-plot
  - Combinations of any of these!
- Nested designs (often look like split-plots)
- With the skeleton ANOVA process, can translate virtually any design to model



# Multiple Random Effects (and negative variance components)

## Fabric Shrinkage



3	9	1	2	8	6	5	7	4
4	8	7	3	5	9	1	2	6
6	5	2	7	1	4	8	3	9
8	7	5	4	3	1	6	9	2
2	1	3	9	6	7	4	8	5
9	6	4	5	2	8	7	1	3
1	4	9	6	7	3	2	5	8
5	3	8	1	4	2	9	6	7
7	2	6	8	9	5	3	4	1

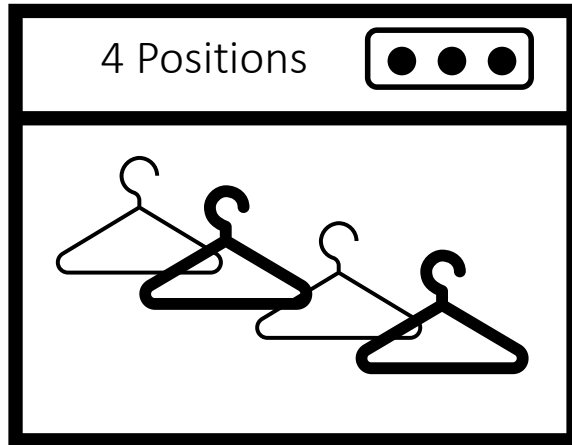
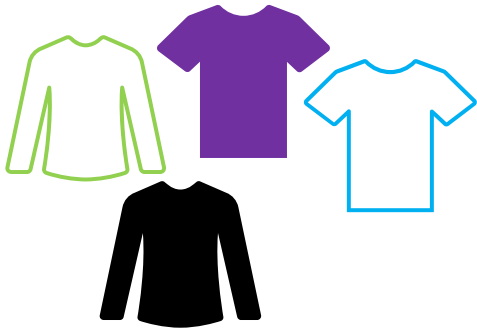
## What we will cover:

- Just like we can have several treatment effects, and cross them (or nest them) – we can also do this with random effects
- **Latin Square** is a special kind of crossed random effects
- A note about **Negative Variance Components**

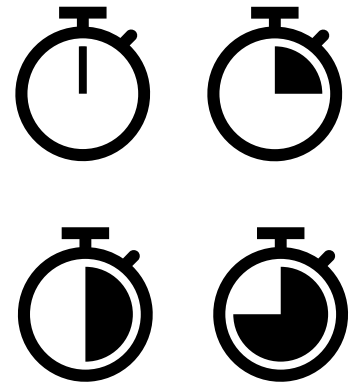
# Describe the data

- **Fabric Shrinkage** — A fabric manufacturer needs to test four new materials to be used in permanent press garments. The heat chamber used to test fabrics has four positions. Each fabric should be tested under each position, and due to time constraints, the manufacturer is limited to four runs. Fabric shrinkage is the response of interest.

4 Materials



4 Runs



# Skeleton ANOVA

Experiment Design		Treatment Design		Skeleton ANOVA	
Source	df	Source	df	Source	df
Run	$4-1=3$			Run	3
Position	$4-1=3$			Position	3
		Material	$4-1=3$	Material	3
Run*Position (the e.u.)	$(4-1)*(4-1)=9$			(Run*Position)   Material → Residual	$9-3=6$
Total	$16-1=15$			Total	15

# Negative Variance Components?

The screenshot shows the 'Fit Model' dialog box in JMP. The 'Model Specification' section is expanded, showing 'Select Columns' with 4 columns: Cage, Condition, Diet, and Gain. The 'Pick Role Variables' section has 'Y' set to 'Gain' (optional) and 'By' set to 'optional'. The 'Personality' is set to 'Mixed Model', and 'Unbounded Variance Components' is checked. The 'Construct Model Effects' section has three tabs: 'Fixed Effects', 'Random Effects', and 'Repeated Structure'. The 'Random Effects' tab is active, showing 'Condition', 'Diet', and 'Condition\*Diet'. A blue arrow points from this tab to a zoomed-in view of the 'Random Effects' section. The zoomed-in view shows the 'Random Effects' tab with 'Cage' and 'Cage\*Condition' listed. The 'Degree' is set to 2.

**Fit Model**

**Model Specification**

Select Columns: 4 Columns  
Cage  
Condition  
Diet  
Gain

Pick Role Variables  
Y: Gain (optional)  
By: optional

Personality: Mixed Model  
 Unbounded Variance Components  
Buttons: Help, Run, Recall, Keep dialog open (unchecked), Remove

Construct Model Effects

Fixed Effects | **Random Effects** | Repeated Structure

Condition  
Diet  
Condition\*Diet

Fixed Effects | **Random Effects** | Repeated Structure

Add  
Cross  
Nest  
Macros

Degree: 2  
Attributes:  No Intercept

Cage  
Cage\*Condition

Macros

Degree: 2

Mouse Condition - Fit Least Squares

Window Tools Graph Tools Show Data Table Local Data Filter

**Response Gain**

**Summary of Fit**

RSquare	0.351969
RSquare Adj	0.054955
Root Mean Square Error	5.617433
Mean of Response	57.19444
Observations (or Sum Wgts)	36

**Parameter Estimates**

**Random Effect Predictions**

**REML Variance Component Estimates**

Random Effect	Var Ratio	Var Component	Std Error	95% Lower	95% Upper	Wald p-Value	Pct of Total
Cage	0.1593643	5.0288294	4.7149355	-4.212274	14.269933	0.2862	13.746
Condition*Cage	-0.197757	-6.240346	4.8693074	-15.78401	3.3033207	0.2000	0.000
Residual		31.555556	11.156574	17.503302	73.091115		86.254
Total		36.584385	12.111967	20.956243	79.50077		100.000

-2 LogLikelihood = 179.29117789

Note: Total is the sum of the positive variance components.  
Total including negative estimates = 30.344039


**Covariance Matrix of Variance Component Estimates**

**Iterations**

**Fixed Effect Tests**

Source	Nparm	DF	DFDen	F Ratio	Prob > F
Condition	3	3	4.718	4.3123	0.0798
Diet	2	2	16	0.8248	0.4561
Condition*Diet	6	6	16	1.5232	0.2333

**Effect Details**



# BUT WHY????

- Negative variance component estimates might happen when, for example, a variance is very small or when there is negative correlation among experimental units. This latter situation often happens when there is competition for resources among plots or units, as here with mice in a cage. In such cases, the REML optimal value for the variance estimate can cross into the negative region.
- Although it might seem strange to report negative variance component estimates, this unbounded fit is the best model for estimating the fixed effects comparisons.
- Allowing the negative variance component(s), you get better control over Type 1 error for your fixed effects comparisons, and in some cases better power.



# Summary

- You can have multiple random effects to account for multiple sources of variance (multiple restrictions on randomization for the treatment).
- A Latin Square is a special restriction when you have the (number of treatments) = (number of runs from restriction 1) = (number of runs from restriction 2).
- Allow negative variance estimates. It's better for your model fit and better inference.