Structure balance and ANOVA tables for experiments which are randomized in stages

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joint work with C. J. Brien, University of South Australia

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An experiment on an industrial process (Gelman, 2005)

4 treatments

4 Variations → 20 Machines

6 Times in M

120 runs

An experiment on an industrial process (Gelman, 2005)

4 treatments

$$\boxed{4 \;\text{Variations}} \longrightarrow \boxed{\begin{array}{l}20 \;\text{Machines}\\ 6 \;\text{Times in M}\end{array}}$$

120 runs

runs tier	
source	df
Mean	1
Machines	19
Times[Machines]	100

An experiment on an industrial process (Gelman, 2005)

4 treatments — 4 Variations $\rightarrow$ 20 Machines, 6 Times in M — 120 runs

runs tier	
source	df
Mean	1
Machines	19
Times[Machines]	100

treatments tier	
source	df
Mean	1
Variations	3

An experiment on an industrial process (Gelman, 2005)

4 treatments | 4 Variations → 20 Machines, 6 Times in M | 120 runs

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runs tier		
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source	df
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Variations	3

runs tier		treatments tier	
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source	df	source	df
Mean	1	Mean	1
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runs tier		treatments tier	
source	df	source	df
Mean	1	Mean	1
Machines	19	Variations	3
		Residual	16
Times[Machines]	100		

An experiment on an industrial process: skeleton anova

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Mean	1	Mean	1
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The skeleton analysis of variance shows

- which "block" term the Variations term is confounded with, hence the likely magnitude of the variance of the estimator of the contrast between any two variations

An experiment on an industrial process: skeleton anova

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source	df	source	df
Mean	1	Mean	1
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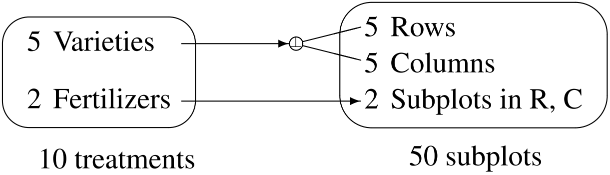
Times[Machines]	100		

The skeleton analysis of variance shows

- which “block” term the Variations term is confounded with,
  hence the likely magnitude of the variance of the estimator of the contrast between any two variations
- the relevant residual term, and its degrees of freedom,
  hence the likely precision of the estimator of that variance,
  and information about the power of a hypothesis test.

An agricultural experiment (Gelman, 2005)



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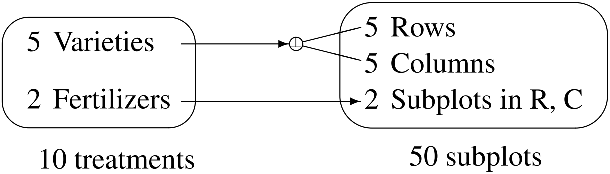

subplots tier		
source	df	
Mean	1	
Rows	4	
Columns	4	
Rows#Columns	16	
Subplots[R,C]	25	

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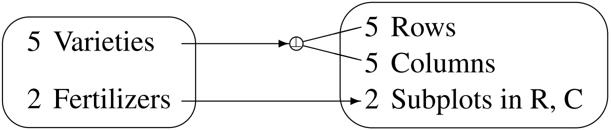

10 treatments

50 subplots

subplots tier		treatments tier	
source	df	source	df
Mean	1		
Rows	4		
Columns	4		
Rows#Columns	16		
Subplots[R,C]	25		

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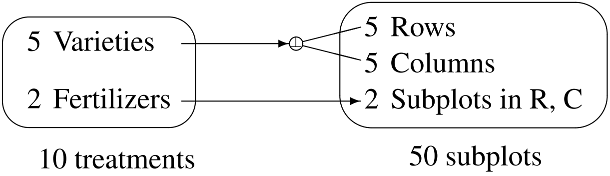

subplots tier		treatments tier	
source	df	source	df
Mean	1	Mean	1
Rows	4		
Columns	4		
Rows#Columns	16		
Subplots[R,C]	25		

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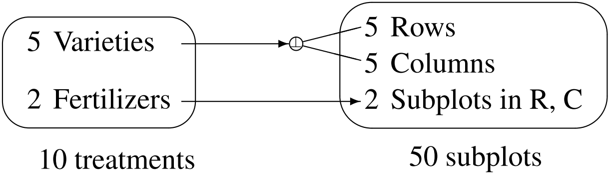

subplots tier		treatments tier	
source	df	source	df
Mean	1	Mean	1
Rows	4		
Columns	4		
Rows#Columns	16	Varieties	4
Subplots[R,C]	25		

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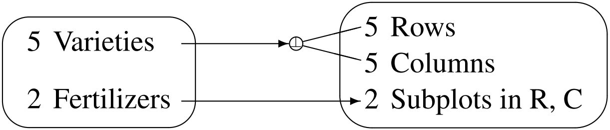

10 treatments

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subplots tier		treatments tier	
source	df	source	df
Mean	1	Mean	1
Rows	4		
Columns	4		
Rows#Columns	16	Varieties	4
Subplots[R,C]	25	Fertilizers	1
		Varieties#Fertilizers	4

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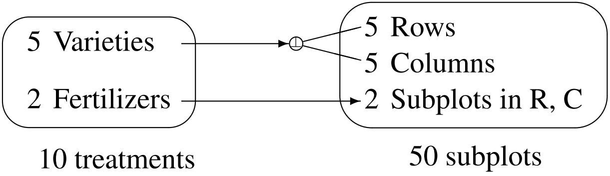

<table>
<tr><th colspan="2">subplots tier</th><th colspan="2">treatments tier</th></tr>
<tr><td>source</td><td>df</td><td>source</td><td>df</td></tr>
<tr><td>Mean</td><td>1</td><td>Mean</td><td>1</td></tr>
<tr><td>Rows</td><td>4</td><td></td><td></td></tr>
<tr><td>Columns</td><td>4</td><td></td><td></td></tr>
<tr><td rowspan="2">Rows#Columns</td><td rowspan="2">16</td><td>Varieties</td><td>4</td></tr>
<tr><td>Residual</td><td>12</td></tr>
<tr><td rowspan="3">Subplots[R,C]</td><td rowspan="3">25</td><td>Fertilizers</td><td>1</td></tr>
<tr><td>Varieties#Fertilizers</td><td>4</td></tr>
<tr><td></td><td></td></tr>
</table>

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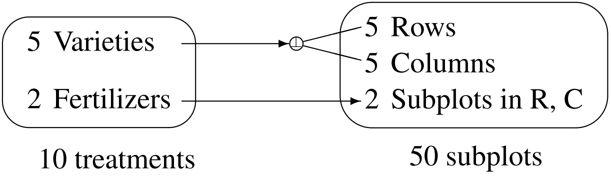


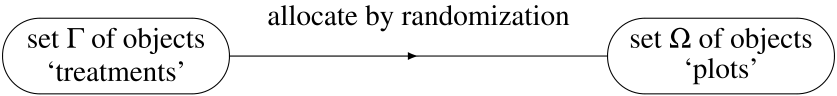
subplots tier		treatments tier	
source	df	source	df
Mean	1	Mean	1
Rows	4		
Columns	4		
Rows#Columns	16	Varieties	4
		Residual	12
Subplots[R,C]	25	Fertilizers	1
		Varieties#Fertilizers	4
		Residual	20

Basic idea for a single randomization

set Γ of objects
'treatments'

set Ω of objects
'plots'

Basic idea for a single randomization



Basic idea for a single randomization

set Γ of objects ‘treatments’ $\xrightarrow{\text{allocate by randomization}}$ set Ω of objects ‘plots’

vector space $V_\Gamma = \mathbb{R}^\Gamma$

vector space $V_\Omega = \mathbb{R}^\Omega$

Basic idea for a single randomization

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allocate by randomization $\longrightarrow$

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Decomposition $\mathscr{Q}$ of V_Γ into orthogonal subspaces

Decomposition $\mathscr{P}$ of V_Ω into orthogonal subspaces

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Decomposition $\mathscr{Q}$ of V_Γ into orthogonal subspaces

Decomposition $\mathscr{P}$ of V_Ω into orthogonal subspaces

$\mathscr{Q}$ further decomposes $\mathscr{P}$

Basic idea for a single randomization

$$\begin{array}{c}\text{set } \Gamma \text{ of objects}\\ \text{`treatments'}\end{array} \xrightarrow{\text{allocate by randomization}} \begin{array}{c}\text{set } \Omega \text{ of objects}\\ \text{`plots'}\end{array}$$

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Decomposition $\mathscr{Q}$ of V_Γ
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$\mathscr{Q}$ further decomposes $\mathscr{P}$

- What happens if the design (allocation) is not orthogonal?

Basic idea for a single randomization

set Γ of objects
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allocate by randomization →

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vector space $V_\Gamma = \mathbb{R}^\Gamma$ $\qquad$ $V_\Gamma \rightarrow\leq V_\Omega$ $\qquad$ vector space $V_\Omega = \mathbb{R}^\Omega$

Decomposition $\mathscr{Q}$ of V_Γ
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Decomposition $\mathscr{P}$ of V_Ω
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$\mathscr{Q}$ further decomposes $\mathscr{P}$

- What happens if the design (allocation) is not orthogonal?
- What happens if there are 2 or more stages of (random) allocation?

A pair of orthogonal decompositions

A decomposition $\mathscr{P}$ of V_Ω into n pairwise orthogonal subspaces
$\equiv$ a set of real $\Omega \times \Omega$ matrices $\mathbf{P}_1, \ldots, \mathbf{P}_n$ which

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- sum to $\mathbf{I}$.

A decomposition $\mathscr{Q}$ of V_Γ into m pairwise orthogonal subspaces
$\equiv$ a set of real $\Gamma \times \Gamma$ matrices $\mathbf{Q}_1, \ldots, \mathbf{Q}_m$ which ...

Given an allocation of Γ to Ω, we can regard subspaces of V_Γ as subspaces of V_Ω and hence regard $\mathbf{Q}_1, \ldots, \mathbf{Q}_m$ as $\Omega \times \Omega$ matrices.

A pair of orthogonal decompositions: continued

$$\begin{aligned}
\mathbf{P}_1 + \mathbf{P}_2 + \cdots + \mathbf{P}_n &= \mathbf{I} \quad \text{(identity for } V_\Omega\text{)} \\
\mathbf{Q}_1 + \mathbf{Q}_2 + \cdots + \mathbf{Q}_m &= \mathbf{I}_{\mathscr{Q}} \quad \text{(identity for } V_\Gamma \text{ in } V_\Omega\text{)}
\end{aligned}$$

A pair of orthogonal decompositions: continued

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The design is orthogonal if
each subspace in $\mathscr{Q}$ is contained in a subspace in $\mathscr{P}$;

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each subspace in $\mathscr{Q}$ is contained in a subspace in $\mathscr{P}$;
that is, for each $\mathbf{Q}_i$ there is some j such that

- $\mathbf{Q}_i\mathbf{P}_j = \mathbf{P}_j\mathbf{Q}_i = \mathbf{Q}_i$
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The designs in the preceding examples are both orthogonal.

Structure balance (following Nelder's 'general balance')

$$\begin{array}{llcll} \mathscr{P} & \mathbf{P}_1+\mathbf{P}_2+\cdots+\mathbf{P}_n & = & \mathbf{I} & \text{(identity for } V_\Omega) \\ \mathscr{Q} & \mathbf{Q}_1+\mathbf{Q}_2+\cdots+\mathbf{Q}_m & = & \mathbf{I}_{\mathscr{Q}} & \text{(identity for } V_\Gamma \text{ in } V_\Omega) \end{array}$$

Definition

A structure $\mathscr{Q}$ is structure-balanced in relation to a structure $\mathscr{P}$ if there are scalars $\lambda_{\mathbf{PQ}}$ for $\mathbf{P}$ in $\mathscr{P}$ and $\mathbf{Q}$ in $\mathscr{Q}$ such that

(i) $\mathbf{QPQ} = \lambda_{\mathbf{PQ}}\mathbf{Q}$ for all $\mathbf{P}$ in $\mathscr{P}$ and all $\mathbf{Q}$ in $\mathscr{Q}$, and

(ii) $\mathbf{Q}_1\mathbf{P}\mathbf{Q}_2 = \mathbf{0}$ for all $\mathbf{P}$ in $\mathscr{P}$ and all $\mathbf{Q}_1 \neq \mathbf{Q}_2$ in $\mathscr{Q}$.

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The structure $\mathscr{Q}$ is orthogonal in relation to $\mathscr{P}$ if (i) and (ii) hold with each $\lambda_{\mathbf{PQ}}$ equal to either 1 or 0.

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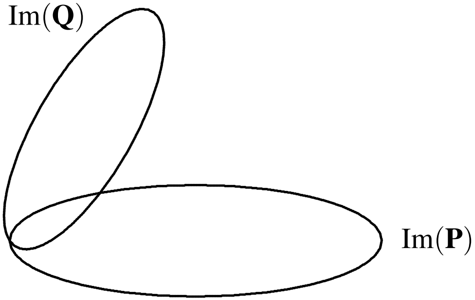
The $\lambda_{\mathbf{PQ}}$ are called efficiency factors and are summarized in the $\mathscr{P} \times \mathscr{Q}$ efficiency matrix $\Lambda_{\mathscr{P}\mathscr{Q}}$.

Structure balance (using James and Wilkinson)

Fix $\mathbf{P}$ and $\mathbf{Q}$.



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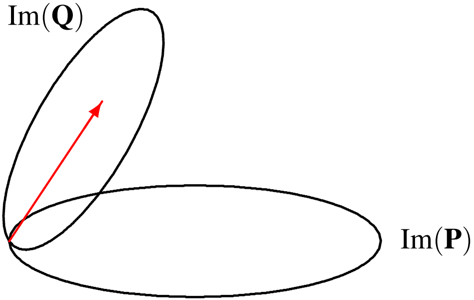

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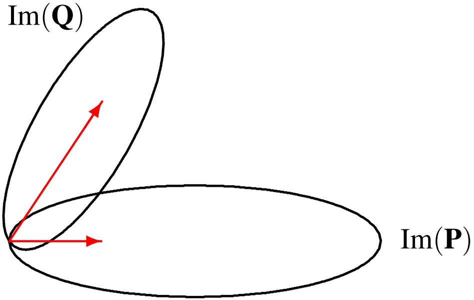

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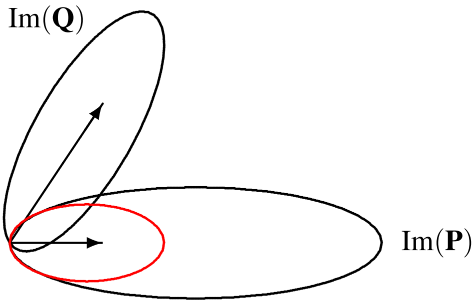

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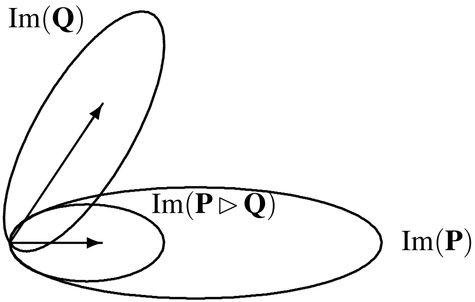
- write $\mathbf{P} \triangleright \mathbf{Q}$ for $\lambda_{\mathbf{PQ}}^{-1}\mathbf{PQP}$ (the part of $\mathbf{P}$ explained by $\mathbf{Q}$).



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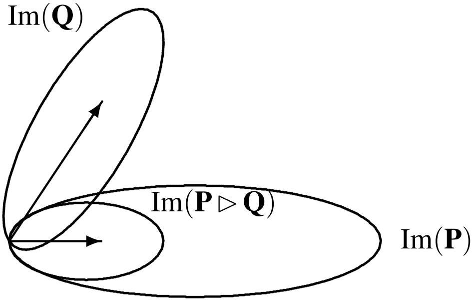
- $\lambda_{\mathbf{PQ}}^{-1}\mathbf{PQP}$ is the matrix of orthogonal projection onto $\mathbf{P}(\mathrm{Im}\,\mathbf{Q})$;
- write $\mathbf{P} \triangleright \mathbf{Q}$ for $\lambda_{\mathbf{PQ}}^{-1}\mathbf{PQP}$ (the part of $\mathbf{P}$ explained by $\mathbf{Q}$).



Fix $\mathbf{Q}$, let $\mathbf{P}$ vary.

- $\sum \mathbf{P} = \mathbf{I}$ implies that $\sum_{\mathbf{P}} \lambda_{\mathbf{PQ}} = 1$.

Structure balance

Fix $\mathbf{P}$, let $\mathbf{Q}$ vary.

- $\mathbf{Q}_1\mathbf{P}\mathbf{Q}_2 = \mathbf{0}$ implies that

$$\mathbf{P}(\mathrm{Im}(\mathbf{Q}_1)) \quad \perp \quad \mathbf{P}(\mathrm{Im}(\mathbf{Q}_2)), \qquad \text{so}$$

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$$\mathscr{P} \triangleright \mathscr{Q} = \{\mathbf{P} \triangleright \mathbf{Q} : \mathbf{P} \in \mathscr{P},\ \mathbf{Q} \in \mathscr{Q},\ \lambda_{\mathbf{PQ}} \neq 0\} \cup \{\mathbf{P} \vdash \mathscr{Q} : \mathbf{P} \in \mathscr{P}\}.$$

Toy example from micorarrays

	slides							
	1	2	3	4	5	6	7	8
red	0	1	0	2	0	3	0	4
green	1	0	2	0	3	0	4	0

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observations		
source	df	
Mean	1	
Colours	1	
Slides	7	
Colours # Slides	7	

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observations		treatments		
source	df	eff	source	df
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Colours # Slides	7	1	Control-v-rest	1

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observations		treatments		
source	df	eff	source	df
Mean	1	1	Mean	1
Colours	1			
Slides	7	$\frac{1}{2}$	Within-rest	3
Colours # Slides	7	1	Control-v-rest	1
		$\frac{1}{2}$	Within-rest	3

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observations		treatments		
source	df	eff	source	df
Mean	1	1	Mean	1
Colours	1			
Slides	7	$\frac{1}{2}$	Within-rest	3
			Residual	4
Colours # Slides	7	1	Control-v-rest	1
		$\frac{1}{2}$	Within-rest	3
			Residual	3

Experiments with two randomizations

Laboratory animals (White, 1975)

$$\boxed{\text{2 Drugs}} \longrightarrow \boxed{\text{10 Days}} \longrightarrow \boxed{\text{60 Animals}}$$

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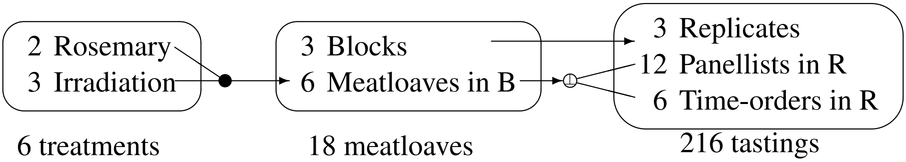
Laboratory animals (White, 1975)

Meat-loaves (T. B. Bailey)



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Laboratory animals: skeleton anova

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2 Drugs → 10 Days → 60 Animals

animals tier			
source	df		
Mean	1		
Animals	59		

Laboratory animals: skeleton anova

$\boxed{\text{2 Drugs}} \longrightarrow \boxed{\text{10 Days}} \longrightarrow \boxed{\text{60 Animals}}$

animals tier		days tier		
source	df	source	df	
Mean	1	Mean	1	
Animals	59	Days	9	

Laboratory animals: skeleton anova

2 Drugs → 10 Days → 60 Animals

animals tier		days tier		
source	df	source	df	
Mean	1	Mean	1	
Animals	59	Days	9	
		Residual	50	

Laboratory animals: skeleton anova

animals tier		days tier		treatments tier	
source	df	source	df	source	df
Mean	1	Mean	1	Mean	1
Animals	59	Days	9	Drugs	1
		Residual	50		

Laboratory animals: skeleton anova

2 Drugs → 10 Days → 60 Animals

<table>
<tr><th colspan="2">animals tier</th><th colspan="2">days tier</th><th colspan="2">treatments tier</th></tr>
<tr><td>source</td><td>df</td><td>source</td><td>df</td><td>source</td><td>df</td></tr>
<tr><td>Mean</td><td>1</td><td>Mean</td><td>1</td><td>Mean</td><td>1</td></tr>
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</table>

Laboratory animals: skeleton anova

2 Drugs → 10 Days → 60 Animals

animals tier		days tier		treatments tier	
source	df	source	df	source	df
Mean	1	Mean	1	Mean	1
Animals	59	Days	9	Drugs	1
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- Differences between Drugs are confounded with differences between Days and differences between Animals.

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$$\boxed{2\ \text{Drugs}} \longrightarrow \boxed{10\ \text{Days}} \longrightarrow \boxed{60\ \text{Animals}}$$

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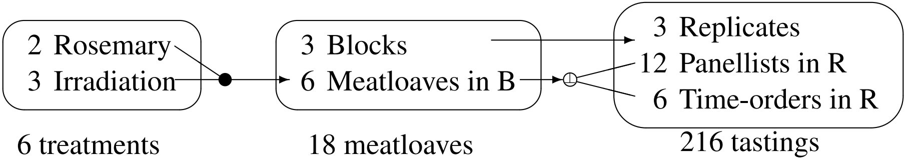
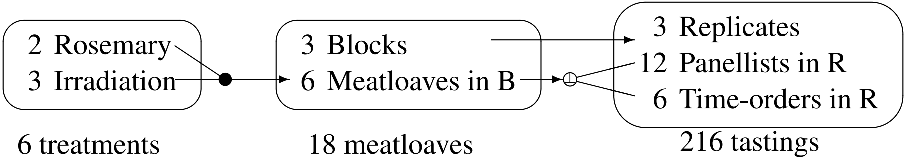
source	df	source	df	source	df
Mean	1	Mean	1	Mean	1
Animals	59	Days	9	Drugs	1
				Residual	8
		Residual	50		

- Differences between Drugs are confounded with differences between Days and differences between Animals.
- The 8-df Residual gives the variability between Days plus the variability between Animals.

Meatloaves: skeleton anova



Meatloaves: skeleton anova



tastings tier		meatloaves tier		treatments tier	
source	df	source	df	source	df
Mean	1	Mean	1	Mean	1
Replicates	2	Blocks	2		
Panellists[Reps]	33				
Time-orders[Reps]	15				
P#T[Reps]	165	Meatloaves[B]	15	Rosemary	1
				Irradiation	2
				R# I	2
				Residual	10
		Residual	150		

Structure balance when two arrows have the same end (1)

$$\mathscr{Q} \longrightarrow \mathscr{P} \longleftarrow \mathscr{R}$$

There are three possibilities.

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Unrandomized-inclusive randomizations

The outcome of the randomization $\mathscr{Q} \longrightarrow \mathscr{P}$ is known;
the design for $\mathscr{R} \longrightarrow \mathscr{P}$ and method of randomizing $\mathscr{R} \longrightarrow \mathscr{P}$ both use knowledge of $\mathscr{P} \rhd \mathscr{Q}$.

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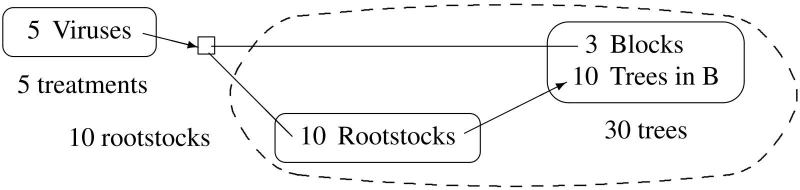
Assume that $\mathscr{Q}$ is structure-balanced in relation to $\mathscr{P}$,
and that $\mathscr{R}$ is structure-balanced in relation to $\mathscr{P} \rhd \mathscr{Q}$.
Use the decompostion $(\mathscr{P} \rhd \mathscr{Q}) \rhd \mathscr{R}$.

Superimposed Experiment in a Row-Column Design



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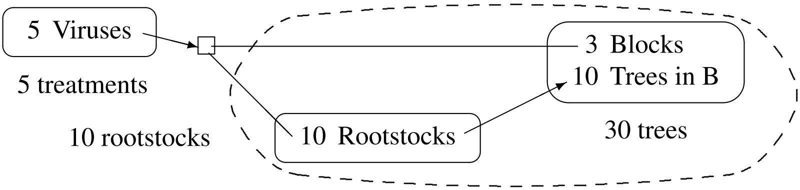

trees tier		rootstocks tier		treatments tier		
source	df	source	df	eff	source	df
Mean	1	Mean	1		Mean	1
Blocks	2					
Trees[Blocks]	27	Rootstocks	9	$\frac{1}{6}$	Viruses	4
					Residual	5
		Residual	18	$\frac{5}{6}$	Viruses	4
					Residual	14

Structure balance when two arrows have the same end (2)

$$\mathscr{Q} \longrightarrow \mathscr{P} \longleftarrow \mathscr{R}$$

Independent randomizations

The two structurally balanced designs are chosen so that,
for all **P** except the Mean,
either every **PQ** is zero or every **PR** is zero.
Thus $\mathscr{Q}$ and $\mathscr{R}$ do not interfere with each other in $\mathscr{P}$.

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Coincident randomizations

The two structurally balanced designs are chosen so that, for all $\mathbf{P}$, $\mathbf{Q}$, $\mathbf{R}$

- either $\mathbf{PQ}$ is zero (after $\mathbf{P}$, ignore $\mathbf{Q}$)
- or $\mathbf{PR}$ is zero (after $\mathbf{P}$, ignore $\mathbf{R}$)
- or $\mathbf{P} \rhd \mathbf{Q} = \mathbf{P}$ (after $\mathbf{P}$, do $\mathbf{Q}$ before $\mathbf{R}$)
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$$\{\mathbf{AB} : \mathbf{A} \in \mathscr{P} \rhd \mathscr{Q},\ \mathbf{B} \in \mathscr{P} \rhd \mathscr{R}\}$$

gives an orthogonal decomposition of V_Ω.

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  - the same treatment contrasts with block terms at both stages (thus obtaining very poor precision on those contrasts)
  - or some treatment contrasts with Stage 1 blocks and different treatment contrasts with Stage 2 blocks (thus decreasing the number of residual degrees of freedom)?
- In many cases, the models can be justified by the randomization employed.

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