

# Design of two-phase experiments

R. A. Bailey



`r.a.bailey@qmul.ac.uk`

DEMA, Isaac Newton Institute, Cambridge  
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# Abstract

In a two-phase experiment, treatments are (typically) allocated to experimental units in the first phase, and the products from those experimental units are allocated to a second sort of experimental unit in the second phase.

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Usually we want to estimate the most important contrasts with low variance and with a large number of degrees of freedom for the appropriate residual. In a two-phase experiment, these criteria may conflict.

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In a two-phase experiment, treatments are (typically) allocated to experimental units in the first phase, and the products from those experimental units are allocated to a second sort of experimental unit in the second phase. The appropriate data analysis (and therefore the quality of the overall design) depends on the designs used for the two phases and on how they fit together.

Usually we want to estimate the most important contrasts with low variance and with a large number of degrees of freedom for the appropriate residual. In a two-phase experiment, these criteria may conflict.

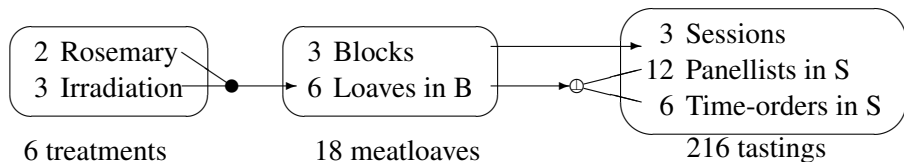
I will discuss some of the issues to think about when designing such experiments, and show how sometimes Patterson's design key can help.

# Thanks

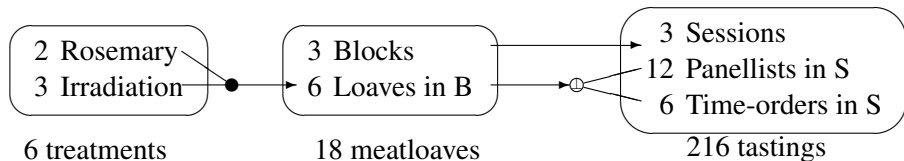
Based on

- ▶ joint work with Chris Brien
- ▶ discussions about particular examples with
  - ▶ Ruth Butler
  - ▶ Andrew Mead
  - ▶ Kathy Ruggiero
  - ▶ Andy Lynch
  - ▶ Tristan Mary-Huard
  - ▶ Terry Speed
  - ▶ Carla Vivacqua
- ▶ discussions with Ching-Shui Cheng

# Meatloaves (T. B. Bailey): a tasting experiment



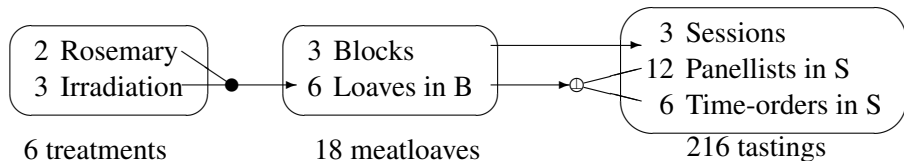
# Meatloaves (T. B. Bailey): a tasting experiment



The systematic design for Phase I is randomized by randomly permuting blocks and randomly permuting loaves within each block.

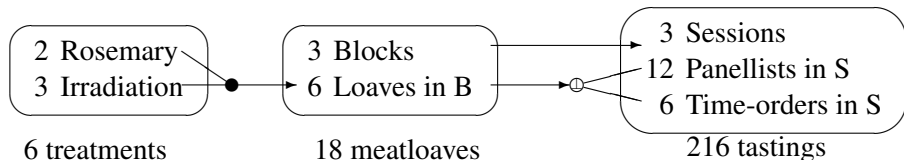


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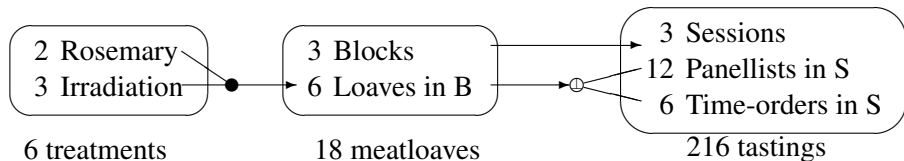
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$$= \eta_{BL} \left( \mathbf{I}_L - \frac{\mathbf{J}_B}{6} \right) + \eta_B \left( \frac{\mathbf{J}_B}{6} - \frac{\mathbf{J}}{18} \right) + \eta_0 \frac{\mathbf{J}}{18}$$

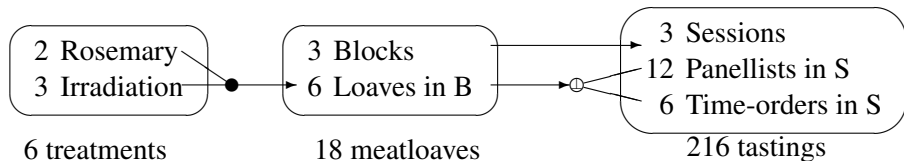
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$$\begin{aligned} &= \eta_{BL} \left( \mathbf{I}_L - \frac{\mathbf{J}_B}{6} \right) + \eta_B \left( \frac{\mathbf{J}_B}{6} - \frac{\mathbf{J}}{18} \right) + \eta_0 \frac{\mathbf{J}}{18} \\ &= \eta_{BL} \mathbf{Q}_{BL} + \eta_B \mathbf{Q}_B + \eta_0 \mathbf{Q}_0 \end{aligned}$$

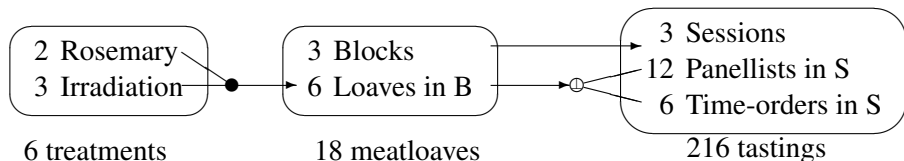
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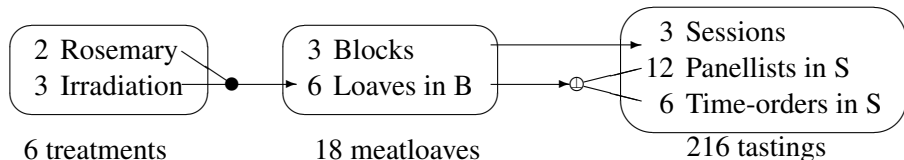
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$$\begin{aligned} &= \eta_{BL} \left( \mathbf{I}_L - \frac{\mathbf{J}_B}{6} \right) + \eta_B \left( \frac{\mathbf{J}_B}{6} - \frac{\mathbf{J}}{18} \right) + \eta_0 \frac{\mathbf{J}}{18} \\ &= \underbrace{\eta_{BL} \mathbf{Q}_{BL} + \eta_B \mathbf{Q}_B + \eta_0 \mathbf{Q}_0}_{\text{positive}} \quad \leftarrow \text{orthogonal idempotents} \end{aligned}$$

# Meatloaves (T. B. Bailey): a tasting experiment

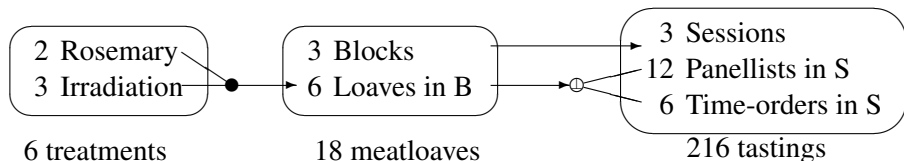


# Meatloaves (T. B. Bailey): a tasting experiment



The systematic design for Phase II (a pair of  $6 \times 6$  Latin squares) is randomized by randomly permuting sessions, randomly permuting panellists within each session, and randomly permuting time-orders within each session.

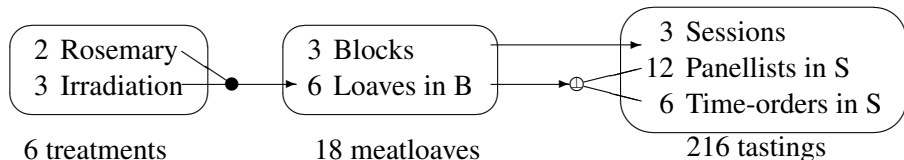
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$$\xi_0 \mathbf{P}_0 + \xi_S \mathbf{P}_S + \xi_{SP} \mathbf{P}_{SP} + \xi_{ST} \mathbf{P}_{ST} + \xi_{SPT} \mathbf{P}_{SPT}.$$

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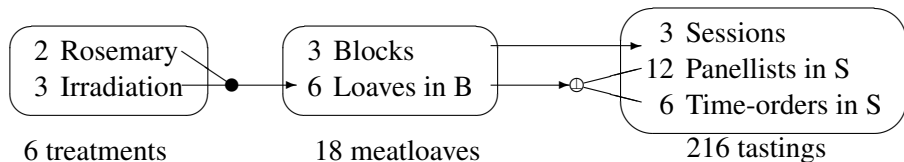
$$\xi_0 \mathbf{P}_0 + \xi_S \mathbf{P}_S + \xi_{SP} \mathbf{P}_{SP} + \xi_{ST} \mathbf{P}_{ST} + \xi_{SPT} \mathbf{P}_{SPT}.$$

Because the design at Phase II has equal replication 12, the overall covariance matrix for the 216 responses on tastings is

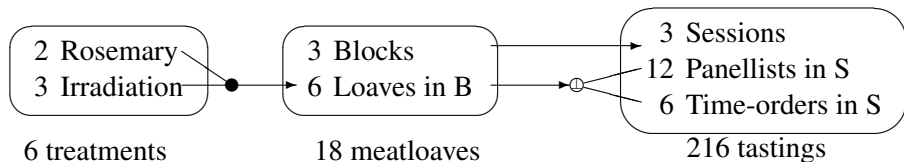
$$\xi_0 \mathbf{P}_0 + \xi_S \mathbf{P}_S + \xi_{SP} \mathbf{P}_{SP} + \xi_{ST} \mathbf{P}_{ST} + \xi_{SPT} \mathbf{P}_{SPT} + 12\eta_0 \tilde{\mathbf{Q}}_0 + 12\eta_B \tilde{\mathbf{Q}}_B + 12\eta_{BL} \tilde{\mathbf{Q}}_{BL}$$



# Meatloaves: skeleton anova

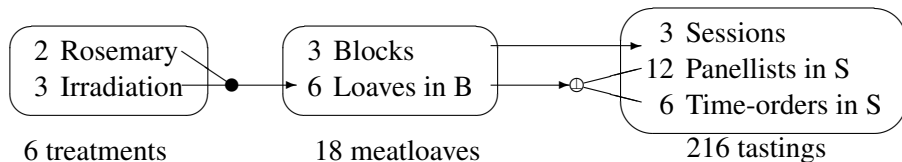


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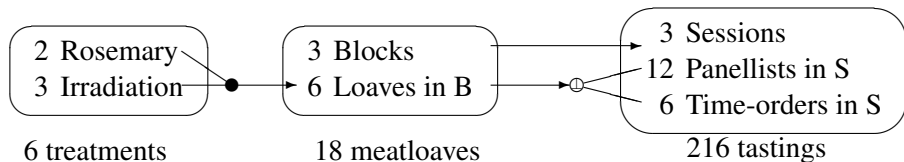
tastings				
source	df			
Mean	1			
Sessions	2			
Panellists[S]	33			
Time-orders[S]	15			
P#T[S]	165			

# Meatloaves: skeleton anova



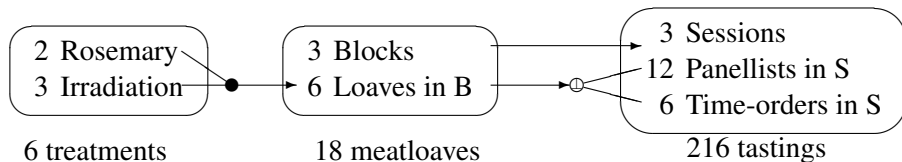
tastings				
source	df			EMS
Mean	1			$\xi_0$
Sessions	2			$\xi_S$
Panellists[S]	33			$\xi_{SP}$
Time-orders[S]	15			$\xi_{ST}$
P#T[S]	165			$\xi_{SPT}$
				$\xi_{SPT}$
				$\xi_{SPT}$
				$\xi_{SPT}$
				$\xi_{SPT}$

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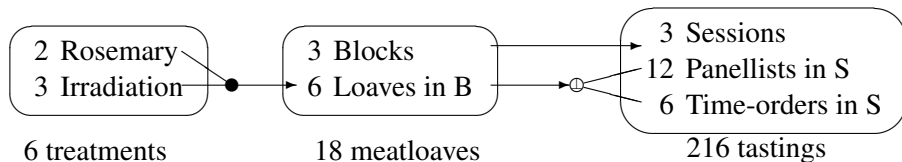
tastings		meatloaves			
source	df	source	df		EMS
Mean	1				$\xi_0$
Sessions	2				$\xi_S$
Panellists[S]	33				$\xi_{SP}$
Time-orders[S]	15				$\xi_{ST}$
P#T[S]	165				$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$

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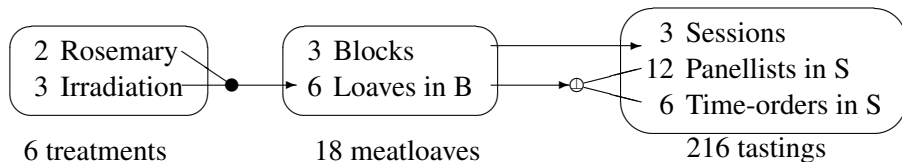
tastings		meatloaves			
source	df	source	df		EMS
Mean	1	Mean	1		$\xi_0$
Sessions	2				$\xi_S$
Panellists[S]	33				$\xi_{SP}$
Time-orders[S]	15				$\xi_{ST}$
P#T[S]	165				$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$

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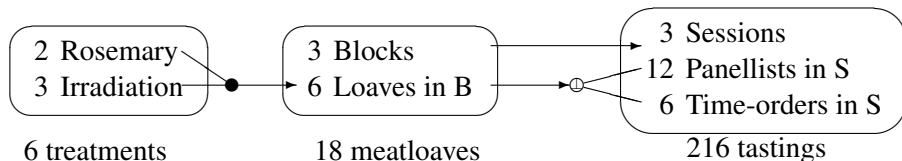
tastings		meatloaves			
source	df	source	df		EMS
Mean	1	Mean	1		$\xi_0$
Sessions	2	Blocks	2		$\xi_S$
Panellists[S]	33				$\xi_{SP}$
Time-orders[S]	15				$\xi_{ST}$
P#T[S]	165				$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$

# Meatloaves: skeleton anova



tastings		meatloaves			
source	df	source	df		EMS
Mean	1	Mean	1		$\xi_0$
Sessions	2	Blocks	2		$\xi_S$
Panellists[S]	33				$\xi_{SP}$
Time-orders[S]	15				$\xi_{ST}$
P#T[S]	165	Loaves[B]	15		$\xi_{SPT}$
					$\xi_{SPT}^r$
					$\xi_{SPT}^r$
					$\xi_{SPT}^r$
					$\xi_{SPT}$

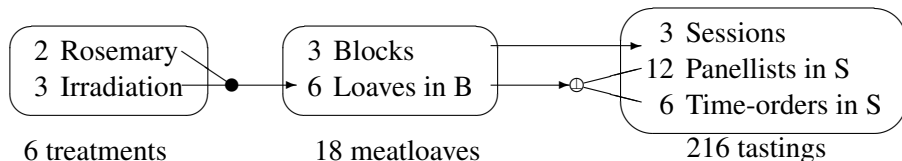
# Meatloaves: skeleton anova



tastings		meatloaves			
source	df	source	df		EMS
Mean	1	Mean	1		$\xi_0$
Sessions	2	Blocks	2		$\xi_S$
Panellists[S]	33				$\xi_{SP}$
Time-orders[S]	15				$\xi_{ST}$
P#T[S]	165	Loaves[B]	15		$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$
					$\xi_{SPT}$
		Residual	150		$\xi_{SPT}$

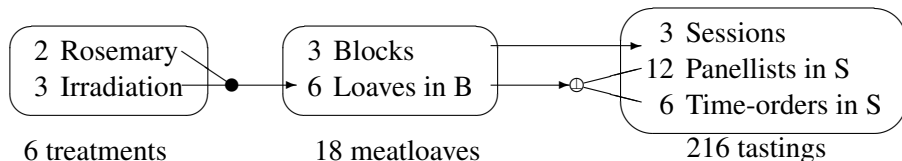


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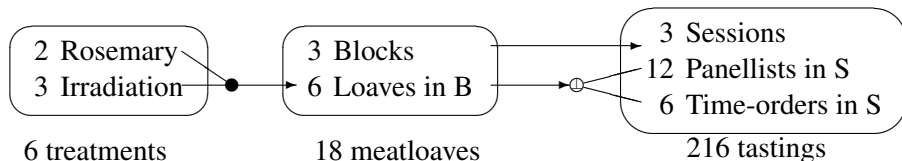
tastings		meatloaves			
source	df	source	df		EMS
Mean	1	Mean	1		$\xi_0 + 12\eta_0$
Sessions	2	Blocks	2		$\xi_S + 12\eta_B$
Panellists[S]	33				$\xi_{SP}$
Time-orders[S]	15				$\xi_{ST}$
P#T[S]	165	Loaves[B]	15		$\xi_{SPT} + 12\eta_{BL}$
					$\xi_{SPT} + 12\eta_{BL}$
					$\xi_{SPT} + 12\eta_{BL}$
					$\xi_{SPT} + 12\eta_{BL}$
		Residual	150		$\xi_{SPT}$

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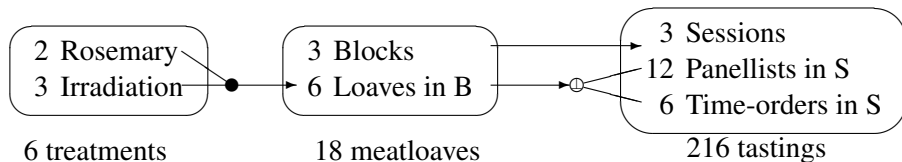
tastings		meatloaves		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1			$\xi_0 + 12\eta_0$
Sessions	2	Blocks	2			$\xi_S + 12\eta_B$
Panellists[S]	33					$\xi_{SP}$
Time-orders[S]	15					$\xi_{ST}$
P#T[S]	165	Loaves[B]	15			$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
		Residual	150			$\xi_{SPT}$

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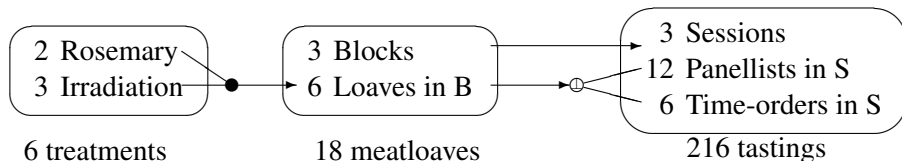
tastings		meatloaves		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 12\eta_0$
Sessions	2	Blocks	2			$\xi_S + 12\eta_B$
Panellists[S]	33					$\xi_{SP}$
Time-orders[S]	15					$\xi_{ST}$
P#T[S]	165	Loaves[B]	15			$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
		Residual	150			$\xi_{SPT}$

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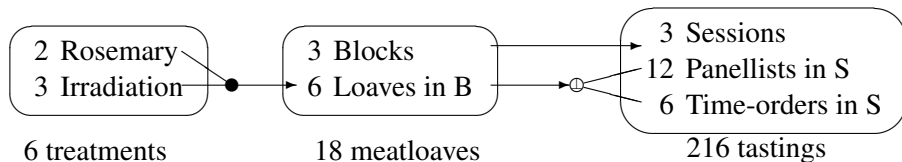
tastings		meatloaves		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 12\eta_0$
Sessions	2	Blocks	2			$\xi_S + 12\eta_B$
Panellists[S]	33					$\xi_{SP}$
Time-orders[S]	15					$\xi_{ST}$
P#T[S]	165	Loaves[B]	15	Rosemary	1	$\xi_{SPT} + 12\eta_{BL} + q(R)$
						$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
		Residual	150			$\xi_{SPT}$

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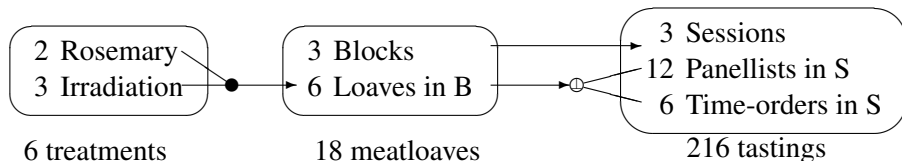
tastings		meatloaves		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 12\eta_0$
Sessions	2	Blocks	2			$\xi_S + 12\eta_B$
Panellists[S]	33					$\xi_{SP}$
Time-orders[S]	15					$\xi_{ST}$
P#T[S]	165	Loaves[B]	15	Rosemary	1	$\xi_{SPT} + 12\eta_{BL} + q(R)$
				Irradiation	2	$\xi_{SPT} + 12\eta_{BL} + q(I)$
						$\xi_{SPT} + 12\eta_{BL}$
						$\xi_{SPT} + 12\eta_{BL}$
		Residual	150			$\xi_{SPT}$

# Meatloaves: skeleton anova



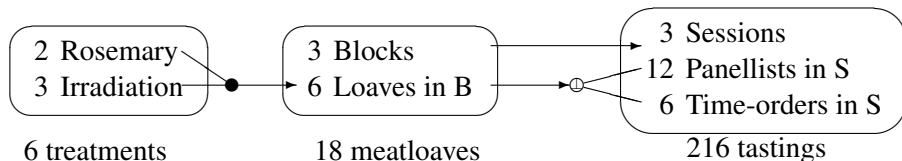
tastings		meatloaves		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 12\eta_0$
Sessions	2	Blocks	2			$\xi_S + 12\eta_B$
Panellists[S]	33					$\xi_{SP}$
Time-orders[S]	15					$\xi_{ST}$
P#T[S]	165	Loaves[B]	15	Rosemary	1	$\xi_{SPT} + 12\eta_{BL} + q(R)$
				Irradiation	2	$\xi_{SPT} + 12\eta_{BL} + q(I)$
				R# I	2	$\xi_{SPT} + 12\eta_{BL} + q(RI)$
						$\xi_{SPT} + 12\eta_{BL}$
		Residual	150			$\xi_{SPT}$

# Meatloaves: skeleton anova



tastings		meatloaves		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 12\eta_0$
Sessions	2	Blocks	2			$\xi_S + 12\eta_B$
Panellists[S]	33					$\xi_{SP}$
Time-orders[S]	15					$\xi_{ST}$
P#T[S]	165	Loaves[B]	15	Rosemary	1	$\xi_{SPT} + 12\eta_{BL} + q(R)$
				Irradiation	2	$\xi_{SPT} + 12\eta_{BL} + q(I)$
				R# I	2	$\xi_{SPT} + 12\eta_{BL} + q(RI)$
				Residual	10	$\xi_{SPT} + 12\eta_{BL}$
		Residual	150			$\xi_{SPT}$

# Meatloaves: skeleton anova



tastings		meatloaves		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 12\eta_0$
Sessions	2	Blocks	2			$\xi_S + 12\eta_B$
Panellists[S]	33					$\xi_{SP}$
Time-orders[S]	15					$\xi_{ST}$
P#T[S]	165	Loaves[B]	15	Rosemary	1	$\xi_{SPT} + 12\eta_{BL} + q(R)$
				Irradiation	2	$\xi_{SPT} + 12\eta_{BL} + q(I)$
				R# I	2	$\xi_{SPT} + 12\eta_{BL} + q(RI)$
				<b>Residual</b>	<b>10</b>	<b><math>\xi_{SPT} + 12\eta_{BL}</math></b>
		Residual	150			$\xi_{SPT}$



# Residual degrees of freedom

## Lesson

*If treatments are applied in Phase I,  
the number of degrees of freedom for the relevant residual  
cannot increase in Phase II.*

# Residual degrees of freedom

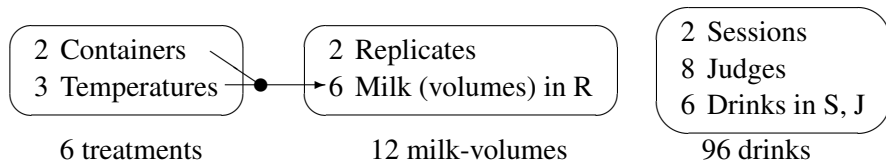
## Lesson

*If treatments are applied in Phase I,  
the number of degrees of freedom for the relevant residual  
**cannot increase** in Phase II.*

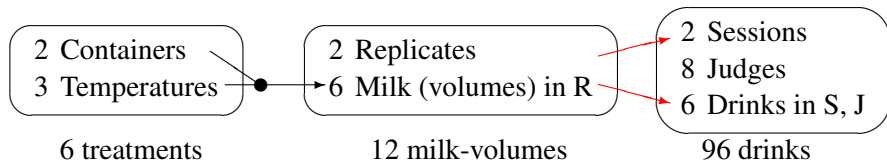
## Principle

*If treatments are orthogonal to ‘large blocks’ in Phase I,  
then those large blocks should be confounded with  
“large blocks” in Phase II.*

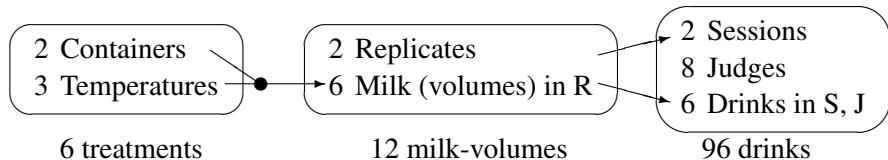
# Milk storage (Wood, Willams and Speed)



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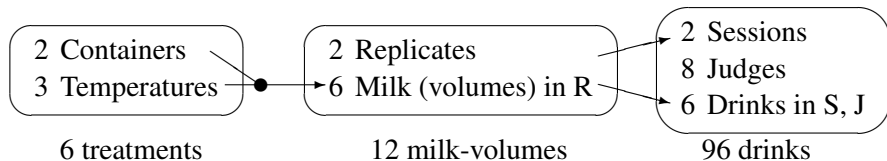


# Milk storage (Wood, Willams and Speed)



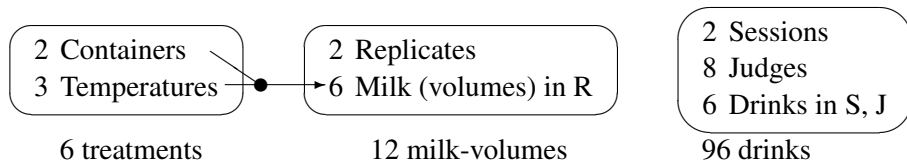
drinks		milk-volumes		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Sessions	1	Replicates	1			$\xi_S + 8\eta_R$
Judges	7					$\xi_J$
S# J	7					$\xi_{SJ}$
Drinks[S $\wedge$ J] 80		Milk[R] 10		Containers	1	$\xi_{SJD} + 8\eta_{RM} + q(C)$
				Temperatures	2	$\xi_{SJD} + 8\eta_{RM} + q(T)$
				C#T	2	$\xi_{SJD} + 8\eta_{RM} + q(CT)$
				Residual	5	$\xi_{SJD} + 8\eta_{RM}$
		Residual	70			$\xi_{SJD}$

# Milk storage (Wood, Willams and Speed)

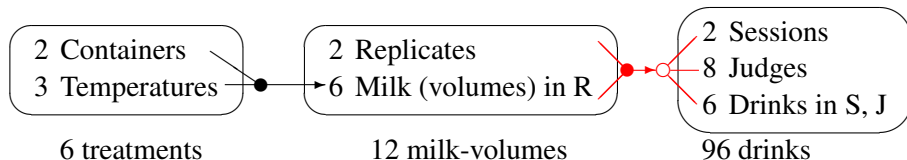


drinks		milk-volumes		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Sessions	1	Replicates	1			$\xi_S + 8\eta_R$
Judges	7					$\xi_J$
S# J	7					$\xi_{SJ}$
Drinks[S $\wedge$ J] 80		Milk[R] 10		Containers 1		$\xi_{SJD} + 8\eta_{RM} + q(C)$
				Temperatures 2		$\xi_{SJD} + 8\eta_{RM} + q(T)$
				C#T 2		$\xi_{SJD} + 8\eta_{RM} + q(CT)$
				<b>Residual 5</b>		<b><math>\xi_{SJD} + 8\eta_{RM}</math></b>
		Residual 70				$\xi_{SJD}$

# Milk storage (Wood, Willams and Speed): design 2



# Milk storage (Wood, Willams and Speed): design 2





# Milk storage (Wood, Willams and Speed): anova 2

drinks		milk-volumes		treatments			
source	df	eff	source	df	source	df	EMS
Mean	1	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Sessions	1						$\xi_S$
Judges	7						$\xi_J$
S#J	7	$\frac{1}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJ} + \frac{8}{3}\eta_{RM}$
			Residual	4			$\xi_{SJ}$
Drinks[S^J]	80	1	Replicates	1			$\xi_{SJD} + 8\eta_R$
		$\frac{2}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJD} + \frac{16}{3}\eta_{RM}$
		1	Milk[R] <sub>2</sub>	7	Containers	1	$\xi_{SJD} + 8\eta_{RM} + q(C)$
					Temperatures	2	$\xi_{SJD} + 8\eta_{RM} + q(T)$
					C#T	2	$\xi_{SJD} + 8\eta_{RM} + q(CT)$
					Residual	2	$\xi_{SJD} + 8\eta_{RM}$
			Residual	69			$\xi_{SJD}$

# Milk storage (Wood, Willams and Speed): anova 2

drinks		milk-volumes		treatments			
source	df	eff	source	df	source	df	EMS
Mean	1	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Sessions	1						$\xi_S$
Judges	7						$\xi_J$
S#J	7	$\frac{1}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJ} + \frac{8}{3}\eta_{RM}$
			Residual	4			$\xi_{SJ}$
Drinks[S^J]	80	1	Replicates	1			$\xi_{SJD} + 8\eta_R$
		$\frac{2}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJD} + \frac{16}{3}\eta_{RM}$
		1	Milk[R] <sub>2</sub>	7	Containers	1	$\xi_{SJD} + 8\eta_{RM} + q(C)$
					Temperatures	2	$\xi_{SJD} + 8\eta_{RM} + q(T)$
					C#T	2	$\xi_{SJD} + 8\eta_{RM} + q(CT)$
					Residual	2	$\xi_{SJD} + 8\eta_{RM}$
			Residual	69			$\xi_{SJD}$

# Milk storage (Wood, Willams and Speed): anova 2

drinks		milk-volumes		treatments			
source	df	eff	source	df	source	df	EMS
Mean	1	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Sessions	1						$\xi_S$
Judges	7						$\xi_J$
S#J	7	$\frac{1}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJ} + \frac{8}{3}\eta_{RM}$
			Residual	4			$\xi_{SJ}$
Drinks[S^J]	80	1	Replicates	1			$\xi_{SJD} + 8\eta_R$
		$\frac{2}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJD} + \frac{16}{3}\eta_{RM}$
		1	Milk[R] <sub>2</sub>	7	Containers	1	$\xi_{SJD} + 8\eta_{RM} + q(C)$
					Temperatures	2	$\xi_{SJD} + 8\eta_{RM} + q(T)$
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					Residual	2	$\xi_{SJD} + 8\eta_{RM}$
			Residual	69			$\xi_{SJD}$

# Milk storage (Wood, Willams and Speed): anova 2

drinks		milk-volumes		treatments			
source	df	eff	source	df	source	df	EMS
Mean	1	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Sessions	1						$\xi_S$
Judges	7						$\xi_J$
S#J	7	$\frac{1}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJ} + \frac{8}{3}\eta_{RM}$
			Residual	4			$\xi_{SJ}$
Drinks[S^J]	80	1	Replicates	1			$\xi_{SJD} + 8\eta_R$
		$\frac{2}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJD} + \frac{16}{3}\eta_{RM}$
		1	Milk[R] <sub>2</sub>	7	Containers	1	$\xi_{SJD} + 8\eta_{RM} + q(C)$
					Temperatures	2	$\xi_{SJD} + 8\eta_{RM} + q(T)$
					C#T	2	$\xi_{SJD} + 8\eta_{RM} + q(CT)$
					Residual	2	$\xi_{SJD} + 8\eta_{RM}$
			Residual	69			$\xi_{SJD}$

efficiency factor

# Milk storage (Wood, Willams and Speed): anova 2

drinks		milk-volumes		treatments			
source	df	eff	source	df	source	df	EMS
Mean	1	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Sessions	1						$\xi_S$
Judges	7						$\xi_J$
S#J	7	$\frac{1}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJ} + \frac{8}{3}\eta_{RM}$
			Residual	4			$\xi_{SJ}$
Drinks[S^J]	80	1	Replicates	1			$\xi_{SJD} + 8\eta_R$
		$\frac{2}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJD} + \frac{16}{3}\eta_{RM}$
		1	Milk[R] <sub>2</sub>	7	Containers	1	$\xi_{SJD} + 8\eta_{RM} + q(C)$
					Temperatures	2	$\xi_{SJD} + 8\eta_{RM} + q(T)$
					C#T	2	$\xi_{SJD} + 8\eta_{RM} + q(CT)$
					Residual	2	$\xi_{SJD} + 8\eta_{RM}$
			Residual	69			$\xi_{SJD}$

efficiency factor

# Milk storage (Wood, Willams and Speed): anova 2

drinks		milk-volumes		treatments			
source	df	eff	source	df	source	df	EMS
Mean	1	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Sessions	1						$\xi_S$
Judges	7						$\xi_J$
S#J	7	$\frac{1}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJ} + \frac{8}{3}\eta_{RM}$
			Residual	4			$\xi_{SJ}$
Drinks[S^J]	80	1	Replicates	1			$\xi_{SJD} + 8\eta_R$
		$\frac{2}{3}$	Milk[R] <sub>1</sub>	3			$\xi_{SJD} + \frac{16}{3}\eta_{RM}$
		1	Milk[R] <sub>2</sub>	7	Containers	1	$\xi_{SJD} + 8\eta_{RM} + q(C)$
					Temperatures	2	$\xi_{SJD} + 8\eta_{RM} + q(T)$
					C#T	2	$\xi_{SJD} + 8\eta_{RM} + q(CT)$
					Residual	2	$\xi_{SJD} + 8\eta_{RM}$
			Residual	69			$\xi_{SJD}$

efficiency factor

# Factors which are 'hard to set' or which must be applied to large areas

## Lesson

*If a treatment factor is 'hard to set' in Phase I,  
then it is probably in a Phase I stratum with large variance.  
Stratum variances from the two phases are added.*

# Factors which are 'hard to set' or which must be applied to large areas

## Lesson

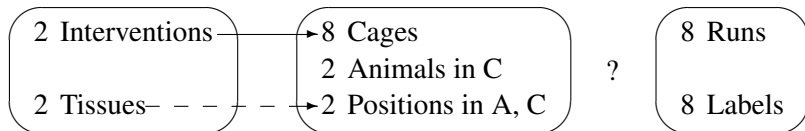
*If a treatment factor is 'hard to set' in Phase I, then it is probably in a Phase I stratum with large variance. Stratum variances from the two phases are added.*

## Principle

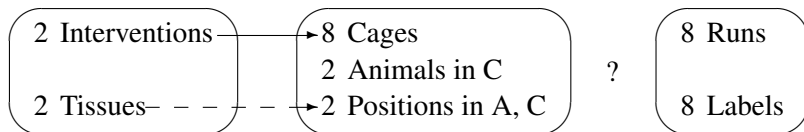
*If a treatment factor is 'hard to set' in Phase I, then it should be allocated to a Phase II stratum with small variance.*



# Proteomics (Ruggiero)

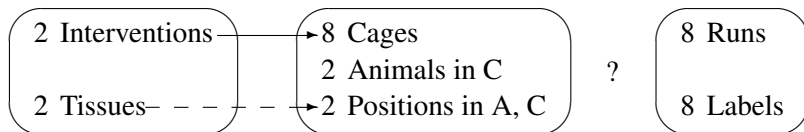


# Proteomics (Ruggiero)



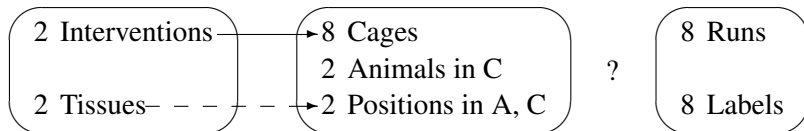
- Interventions probably has the biggest variance from Phase I, so try to confound this with a low-variance term in Phase II.

# Proteomics (Ruggiero)



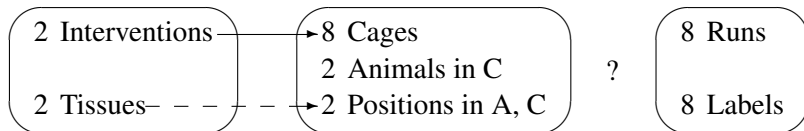
- ▶ Interventions probably has the biggest variance from Phase I, so try to confound this with a low-variance term in Phase II.
- ▶ If possible, confound the rest of Cages with the same term, to avoid losing degrees of freedom for the residual.

# Proteomics (Ruggiero)



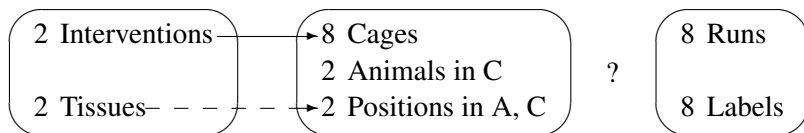
- ▶ Interventions probably has the biggest variance from Phase I, so try to confound this with a low-variance term in Phase II.
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- ▶ If possible, make Tissues and I#T orthogonal to Runs and Labels.

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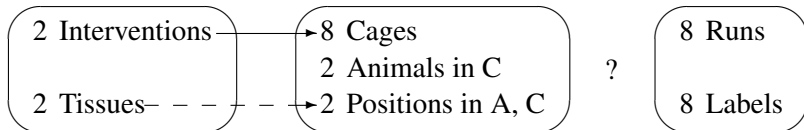
# Proteomics (Ruggiero)



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Use 2-level pseudofactors and Patterson's **design key**.

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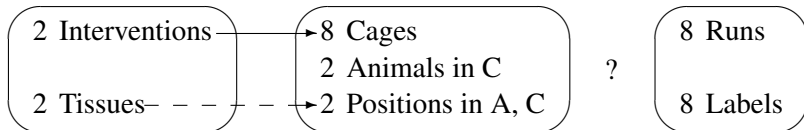


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Use 2-level pseudofactors and Patterson's **design key**.

$I$	$C_1 \ C_2 \ C_3$	$R_1 \ R_2 \ R_3$
	$A$	
$T$	$P$	$L_1 \ L_2 \ L_3$

## Proteomics (Ruggiero)



- ▶ Interventions probably has the biggest variance from Phase I, so try to confound this with a low-variance term in Phase II.
- ▶ If possible, confound the rest of Cages with the same term, to avoid losing degrees of freedom for the residual.
- ▶ If possible, make Tissues and I#T orthogonal to Runs and Labels.

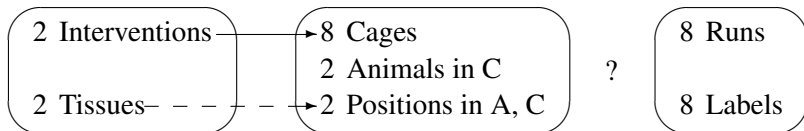
Use 2-level pseudofactors and Patterson's **design key**.

$$\begin{array}{ccccc} I & I \equiv C_1 & C_1 & C_2 & C_3 \\ & & & A & \\ T & & & P & \end{array}$$

$$\begin{array}{ccc} R_1 & R_2 & R_3 \\ L_1 & L_2 & L_3 \end{array}$$



# Proteomics (Ruggiero)

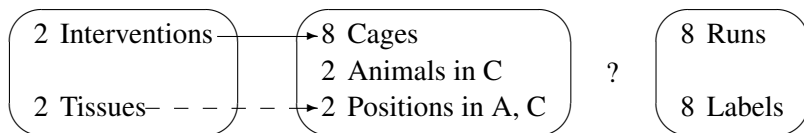


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Use 2-level pseudofactors and Patterson's **design key**.

$$\begin{array}{ccccccc}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & & & & \\
 T & & & P & & & L_1 & L_2 & L_3
 \end{array}$$

# Proteomics (Ruggiero)

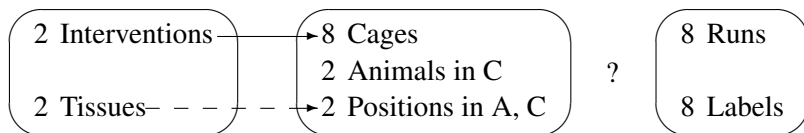


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$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & & & P & & & L_1 & L_2 & L_3
 \end{array}$$

# Proteomics (Ruggiero)

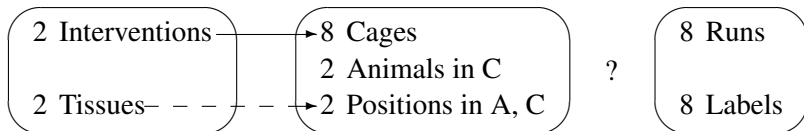


- ▶ Interventions probably has the biggest variance from Phase I, so try to confound this with a low-variance term in Phase II.
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$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & & & P & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

# Proteomics (Ruggiero)

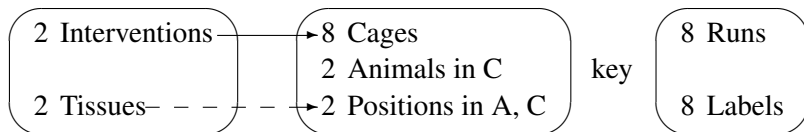


- ▶ Interventions probably has the biggest variance from Phase I, so try to confound this with a low-variance term in Phase II.
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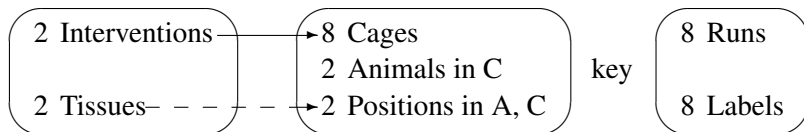
$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & T \equiv P + C_3 & P & & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

# Calculations using the design key



$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & T \equiv P + C_3 & P & & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

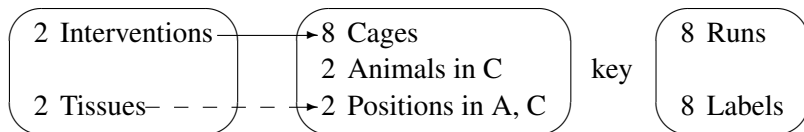
# Calculations using the design key



$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & T \equiv P + C_3 & P & & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

$$P + C_2 = R_2$$

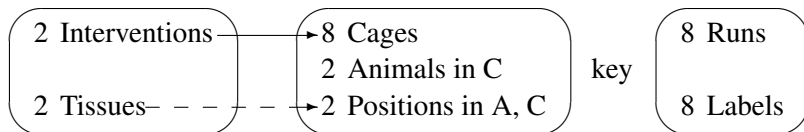
# Calculations using the design key



$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & T \equiv P + C_3 & P & & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

$$P + C_2 = R_2 \quad \text{Positions}[A, C], \text{Runs}$$

# Calculations using the design key



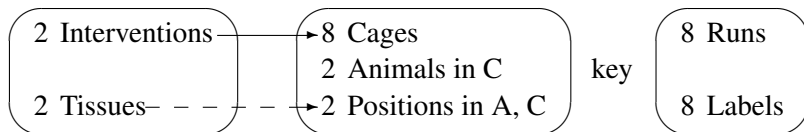
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 T & T \equiv P + C_3 & P & & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

$$P + C_2 = R_2 \quad \text{Positions}[A, C], \text{Runs}$$

$$T \equiv P + C_3 \equiv L_2 + R_3 + L_3$$



# Calculations using the design key

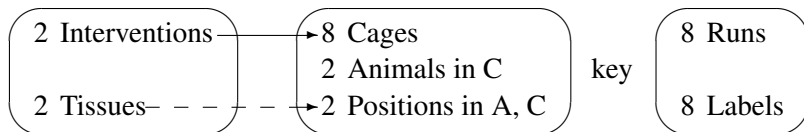


$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & T \equiv P + C_3 & P & & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

$$P + C_2 = R_2 \quad \text{Positions}[A, C], \text{Runs}$$

$$T \equiv P + C_3 \equiv L_2 + R_3 + L_3 \quad \text{T, P}[A, C], \text{R\#L}$$

# Calculations using the design key



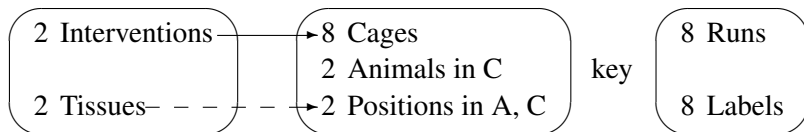
$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & T \equiv P + C_3 & P & & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

$$P + C_2 = R_2 \quad \text{Positions}[A, C], \text{Runs}$$

$$T \equiv P + C_3 \equiv L_2 + R_3 + L_3 \quad \text{T, P}[A, C], \text{R}\#L$$

$$I + T = C_1 + P + C_3 = R_1 + L_1 + L_2 + R_3 + L_3$$

# Calculations using the design key



$$\begin{array}{llllll}
 I & I \equiv C_1 & C_1 & C_2 & C_3 & C_i \equiv R_i + L_i & R_1 & R_2 & R_3 \\
 & & & A & & A \equiv R_1 & & & \\
 T & T \equiv P + C_3 & P & & & P \equiv L_2 & L_1 & L_2 & L_3
 \end{array}$$

$$P + C_2 = R_2 \quad \text{Positions}[A, C], \text{Runs}$$

$$T \equiv P + C_3 \equiv L_2 + R_3 + L_3 \quad T, P[A, C], R \# L$$

$$I + T = C_1 + P + C_3 = R_1 + L_1 + L_2 + R_3 + L_3 \quad I \# T, P[A, C], R \# L$$

# Proteomics: skeleton anova

units		animal-bits		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Runs	7	Animals[C] <sub>1</sub>	1			$\xi_R + 2\eta_{CA}$
		Positions[A,C] <sub>1</sub>	2			$\xi_R + 2\eta_{CAP}$
		Residual	4			$\xi_R$
Labels	7	Animals[C] <sub>2</sub>	1			$\xi_L + 2\eta_{CA}$
		Positions[A,C] <sub>2</sub>	2			$\xi_L + 2\eta_{CAP}$
		Residual	4			$\xi_L$
R#L	49	Cages	7	Interventions	1	$\xi_{RL} + 2\eta_C + q(I)$
				Residual	6	$\xi_{RL} + 2\eta_C$
		Animals[C] <sub>3</sub>	6			$\xi_{RL} + 2\eta_{CA}$
		Positions[A,C] <sub>3</sub>	12	Tissues	1	$\xi_{RL} + 2\eta_{CAP} + q(T)$
				I#T	1	$\xi_{RL} + 2\eta_{CAP} + q(IT)$
				Residual	10	$\xi_{RL} + 2\eta_{CAP}$
		Residual	24			$\xi_{RL}$

# Proteomics: skeleton anova

units		animal-bits		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Runs	7	Animals[C] <sub>1</sub>	1			$\xi_R + 2\eta_{CA}$
		Positions[A,C] <sub>1</sub>	2			$\xi_R + 2\eta_{CAP}$
		Residual	4			$\xi_R$
Labels	7	Animals[C] <sub>2</sub>	1			$\xi_L + 2\eta_{CA}$
		Positions[A,C] <sub>2</sub>	2			$\xi_L + 2\eta_{CAP}$
		Residual	4			$\xi_L$
R#L	49	Cages	7	Interventions	1	$\xi_{RL} + 2\eta_C + q(I)$
				Residual	6	$\xi_{RL} + 2\eta_C$
		Animals[C] <sub>3</sub>	6			$\xi_{RL} + 2\eta_{CA}$
		Positions[A,C] <sub>3</sub>	12	Tissues	1	$\xi_{RL} + 2\eta_{CAP} + q(T)$
				I#T	1	$\xi_{RL} + 2\eta_{CAP} + q(IT)$
				Residual	10	$\xi_{RL} + 2\eta_{CAP}$
		Residual	24			$\xi_{RL}$

# Proteomics: skeleton anova

units		animal-bits		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Runs	7	Animals[C] <sub>1</sub>	1			$\xi_R + 2\eta_{CA}$
		Positions[A,C] <sub>1</sub>	2			$\xi_R + 2\eta_{CAP}$
		Residual	4			$\xi_R$
Labels	7	Animals[C] <sub>2</sub>	1			$\xi_L + 2\eta_{CA}$
		Positions[A,C] <sub>2</sub>	2			$\xi_L + 2\eta_{CAP}$
		Residual	4			$\xi_L$
R#L	49	Cages	7	Interventions	1	$\xi_{RL} + 2\eta_C + q(I)$
				Residual	6	$\xi_{RL} + 2\eta_C$
		Animals[C] <sub>3</sub>	6			$\xi_{RL} + 2\eta_{CA}$
		Positions[A,C] <sub>3</sub>	12	Tissues	1	$\xi_{RL} + 2\eta_{CAP} + q(T)$
				I#T	1	$\xi_{RL} + 2\eta_{CAP} + q(IT)$
				Residual	10	$\xi_{RL} + 2\eta_{CAP}$
		Residual	24			$\xi_{RL}$

# Proteomics: skeleton anova

units		animal-bits		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Runs	7	Animals[C] <sub>1</sub>	1			$\xi_R + 2\eta_{CA}$
		Positions[A,C] <sub>1</sub>	2			$\xi_R + 2\eta_{CAP}$
		Residual	4			$\xi_R$
Labels	7	Animals[C] <sub>2</sub>	1			$\xi_L + 2\eta_{CA}$
		Positions[A,C] <sub>2</sub>	2			$\xi_L + 2\eta_{CAP}$
		Residual	4			$\xi_L$
R#L	49	Cages	7	Interventions	1	$\xi_{RL} + 2\eta_C + q(I)$
				Residual	6	$\xi_{RL} + 2\eta_C$
		Animals[C] <sub>3</sub>	6			$\xi_{RL} + 2\eta_{CA}$
		Positions[A,C] <sub>3</sub>	12	Tissues	1	$\xi_{RL} + 2\eta_{CAP} + q(T)$
				I#T	1	$\xi_{RL} + 2\eta_{CAP} + q(IT)$
				Residual	10	$\xi_{RL} + 2\eta_{CAP}$
		Residual	24			$\xi_{RL}$

# Proteomics: skeleton anova

units		animal-bits		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Runs	7	Animals[C] <sub>1</sub>	1			$\xi_R + 2\eta_{CA}$
		Positions[A,C] <sub>1</sub>	2			$\xi_R + 2\eta_{CAP}$
		Residual	4			$\xi_R$
Labels	7	Animals[C] <sub>2</sub>	1			$\xi_L + 2\eta_{CA}$
		Positions[A,C] <sub>2</sub>	2			$\xi_L + 2\eta_{CAP}$
		Residual	4			$\xi_L$
R#L	49	Cages	7	Interventions	1	$\xi_{RL} + 2\eta_C + q(I)$
				Residual	6	$\xi_{RL} + 2\eta_C$
		Animals[C] <sub>3</sub>	6			$\xi_{RL} + 2\eta_{CA}$
		Positions[A,C] <sub>3</sub>	12	Tissues	1	$\xi_{RL} + 2\eta_{CAP} + q(T)$
				I#T	1	$\xi_{RL} + 2\eta_{CAP} + q(IT)$
				Residual	10	$\xi_{RL} + 2\eta_{CAP}$
		Residual	24			$\xi_{RL}$



# Proteomics: skeleton anova

units		animal-bits		treatments		
source	df	source	df	source	df	EMS
Mean	1	Mean	1	Mean	1	$\xi_0 + 8\eta_0$
Runs	7	Animals[C] <sub>1</sub>	1			$\xi_R + 2\eta_{CA}$
		Positions[A,C] <sub>1</sub>	2			$\xi_R + 2\eta_{CAP}$
		Residual	4			$\xi_R$
Labels	7	Animals[C] <sub>2</sub>	1			$\xi_L + 2\eta_{CA}$
		Positions[A,C] <sub>2</sub>	2			$\xi_L + 2\eta_{CAP}$
		Residual	4			$\xi_L$
R#L	49	Cages	7	Interventions	1	$\xi_{RL} + 2\eta_C + q(I)$
				Residual	6	$\xi_{RL} + 2\eta_C$
		Animals[C] <sub>3</sub>	6			$\xi_{RL} + 2\eta_{CA}$
		Positions[A,C] <sub>3</sub>	12	Tissues	1	$\xi_{RL} + 2\eta_{CAP} + q(T)$
				I#T	1	$\xi_{RL} + 2\eta_{CAP} + q(IT)$
				Residual	10	$\xi_{RL} + 2\eta_{CAP}$
		Residual	24			$\xi_{RL}$

# Some lessons

## Lesson

*If the design in both phases is orthogonal,  
the using the design key gives a simple method of establishing the  
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*The skeleton anova (decomposition table) shows EMS for treatment terms and for residual terms, as well as residual degrees of freedom, so it is a useful tool for evaluating designs.*

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*If the design in both phases is orthogonal, the using the design key gives a simple method of establishing the confounding.*

## Lesson

*The skeleton anova (decomposition table) shows EMS for treatment terms and for residual terms, as well as residual degrees of freedom, so it is a useful tool for evaluating designs.*

## Lesson

*Equating mean squares to their expectations may give several inconsistent estimators of the  $\xi_i$  and  $\eta_j$ , each with potentially few degrees of freedom.*

# Data analysis after Phase II

## Query

*Is it better to analyse the data with*

- ▶ *ANOVA (for three tiers)*
- ▶ *REML*  
*(but beware!—small degrees of freedom can lead to silly results)*
- ▶ *other mixed model software*  
*(can it cope with the confounding?)*  
*(For example, the single degree of freedom for  $R_1$  is part of both*  
*Runs and Animals[Cages]—*  
*does the software give the same result regardless of which is*  
*written down first in the list of random effects?)*

?

# Field then laboratory (Butler)

27 Varieties

3 Rows  
3 Columns  
9 Plots in R, C

9 Batches  
9 Samples in B

# Field then laboratory (Butler)

27 Varieties

$V_1$   $V_2$   $V_3$

3 Rows  
3 Columns  
9 Plots in R, C

$R$   
 $C$   
 $P_1$   $P_2$

9 Batches

9 Samples in B

$B_1$   $B_2$

$S_1$   $S_2$

# Field then laboratory (Butler)

27 Varieties

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$V_1$   $V_2$   $V_3$

$V_3 \equiv R + C$

$R$

$V_1 \equiv P_1$

$C$

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$P_1$   $P_2$

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$V_1 \equiv P_1$

$C$

$C \equiv B_2$

$V_2 \equiv P_2$

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$P_i \equiv S_i$

$S_1$   $S_2$

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$V_3 \equiv R + C$

$R$

$R \equiv B_1$

$B_1 \ B_2$

$V_1 \equiv P_1$

$C$

$C \equiv B_2$

$V_2 \equiv P_2$

$P_1 \ P_2$

$P_i \equiv S_i$

$S_1 \ S_2$

samples		plots		varieties		
source	df	source	df	source	df	EMS
Batches	8	Rows	2			$\xi_B + \eta_R$
		Columns	2			$\xi_B + \eta_C$
		R#C	4	$V_3$	2	$\xi_B + \eta_{RC} + q(V_3)$
				Residual	2	$\xi_B + \eta_{RC}$

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9 Samples in B

$V_1 \ V_2 \ V_3$

$V_3 \equiv R + C$

$R$

$R \equiv B_1$

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$V_1 \equiv P_1$

$C$

$C \equiv B_2$

$V_2 \equiv P_2$

$P_1 \ P_2$

$P_i \equiv S_i$

$S_1 \ S_2$

samples		plots		varieties		
source	df	source	df	source	df	EMS
Batches	8	Rows	2			$\xi_B + \eta_R$
		Columns	2			$\xi_B + \eta_C$
		R#C	4	$V_3$	2	$\xi_B + \eta_{RC} + q(V_3)$
				Residual	2	$\xi_B + \eta_{RC}$

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$V_1 \ V_2 \ V_3$

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source	df	source	df	source	df	EMS
Batches	8	Rows	2			$\xi_B + \eta_R$
		Columns	2			$\xi_B + \eta_C$
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$R$

$B_1$   $B_2$

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$C$

$V_2 \equiv P_2$

$P_1$   $P_2$

$S_1$   $S_2$

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9 Samples in B

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$V_3 \equiv R + C$

$R$

$R \equiv B_1$

$B_1$   $B_2$

$V_1 \equiv P_1$

$C$

$P_1 \equiv B_2$

$V_2 \equiv P_2$

$P_1$   $P_2$

$C \equiv S_1, P_2 \equiv S_2$

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$B_1 \ B_2$

$V_1 \equiv P_1$

$C$

$P_1 \equiv B_2$

$V_2 \equiv P_2$

$P_1 \ P_2$

$C \equiv S_1, P_2 \equiv S_2$

$S_1 \ S_2$

samples		plots		varieties		
source	df	source	df	source	df	EMS
Batches	8	Rows	2			$\xi_B + \eta_R$
		Plots[R,C] <sub>1</sub>	6	$V_1$	2	$\xi_B + \eta_{RCP} + q(V_1)$
				Residual	4	$\xi_B + \eta_{RCP}$

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$V_1 \ V_2 \ V_3$        $V_3 \equiv R + C$        $R$        $R \equiv B_1$        $B_1 \ B_2$   
 $V_1 \equiv P_1$        $C$        $P_1 \equiv B_2$   
 $V_2 \equiv P_2$        $P_1 \ P_2 \ C \equiv S_1, P_2 \equiv S_2$        $S_1 \ S_2$

samples		plots		varieties		
source	df	source	df	source	df	EMS
Batches	8	Rows	2			$\xi_B + \eta_R$
		Plots[R,C] <sub>1</sub>	6	$V_1$	2	$\xi_B + \eta_{RCP} + q(V_1)$
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 $V_2 \equiv P_2$        $P_1 \ P_2$        $C \equiv S_1, P_2 \equiv S_2$        $S_1 \ S_2$

samples		plots		varieties		
source	df	source	df	source	df	EMS
Batches	8	Rows	2			$\xi_B + \eta_R$
		Plots[R,C] <sub>1</sub>	6	$V_1$	2	$\xi_B + \eta_{RCP} + q(V_1)$
				Residual	4	$\xi_B + \eta_{RCP}$

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$B_1$   $B_2$

$S_1$   $S_2$

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9 Batches

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$V_1$   $V_2$   $V_3$

$V_3 \equiv R + C$

$R$

$R \equiv B_1 + S_2$

$B_1$   $B_2$

$V_1 \equiv P_1$

$C$

$P_1 \equiv B_2$

$V_2 \equiv P_2$

$P_1$   $P_2$

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$S_1$   $S_2$

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9 Batches  
9 Samples in B

$V_1 \ V_2 \ V_3$        $V_3 \equiv R + C$        $R$        $R \equiv B_1 + S_2$        $B_1 \ B_2$   
 $V_1 \equiv P_1$        $C$        $P_1 \equiv B_2$   
 $V_2 \equiv P_2$        $P_1 \ P_2$        $C \equiv S_1, P_2 \equiv S_2$        $S_1 \ S_2$

samples		plots		varieties		
source	df	source	df	source	df	EMS
Batches	8	Plots[R,C] <sub>1</sub>	8	$V_1$	2	$\xi_B + \eta_{RCP} + q(V_1)$
				Residual	6	$\xi_B + \eta_{RCP}$

# Field then laboratory (Butler)

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3 Rows  
3 Columns  
9 Plots in R, C

9 Batches  
9 Samples in B

$V_1 \ V_2 \ V_3$        $V_3 \equiv R + C$        $R$        $R \equiv B_1 + S_2$        $B_1 \ B_2$   
 $V_1 \equiv P_1$        $C$        $P_1 \equiv B_2$   
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samples		plots		varieties		
source	df	source	df	source	df	EMS
Batches	8	Plots[R,C] <sub>1</sub>	8	$V_1$	2	$\xi_B + \eta_{RCP} + q(V_1)$
				Residual	6	$\xi_B + \eta_{RCP}$

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samples		plots		varieties		
source	df	source	df	source	df	EMS
Batches	8	Plots[R,C] <sub>1</sub>	8	$V_1$	2	$\xi_B + \eta_{RCP} + q(V_1)$
				<b>Residual</b>	<b>6</b>	$\xi_B + \eta_{RCP}$

## Principle

*If a treatment term is in a Phase I stratum with large variance, then it should be allocated to a Phase II stratum with small variance.*

## Lesson

- ▶ *This may force sacrificing some information on another treatment term at Phase II.*
- ▶ *This may not be practicable.*

# Nonorthogonality in Phase I

## Query

*What should we do if the design used in Phase I is not orthogonal (in the sense that there are efficiency factors other than 0 and 1)?*



# Two-colour microarrays (Mead; Ruggiero; Lynch)

6 Treatments

6 treatments

4 Litters  
3 Animals in L

12 animals

12 Slides  
2 Colours

24 spots

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24 spots

Litter 1 | Litter 2 | Litter 3 | Litter 4

1 2 3 | 1 4 5 | 2 4 6 | 2 5 6

Treatments form three groups of size two:  $\{1,6\}$ ,  $\{2,5\}$ ,  $\{3,4\}$

Groups are orthogonal to litters;

treatments-within-groups have efficiency factor  $\frac{1}{3}$  in litters.

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24 spots

	Litter 1			Litter 2			Litter 3			Litter 4		
Slide	1	2	3	4	5	6	7	8	9	10	11	12
	1	2	3	1	4	5	2	4	6	2	5	6

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	Litter 1			Litter 2			Litter 3			Litter 4		
Slide	1	2	3	4	5	6	7	8	9	10	11	12
Red	1	2	3	1	4	5	2	4	6	2	5	6
Green												

Treatments form three groups of size two:  $\{1,6\}$ ,  $\{2,5\}$ ,  $\{3,4\}$

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Slide	1	2	3	4	5	6	7	8	9	10	11	12
Red	1	2	3	1	4	5	2	4	6	2	5	6
Green	2	3	1									

Treatments form three groups of size two:  $\{1,6\}$ ,  $\{2,5\}$ ,  $\{3,4\}$

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Green	2	3	1	4	5	1	4	6	2	5	6	2

Treatments form three groups of size two:  $\{1,6\}$ ,  $\{2,5\}$ ,  $\{3,4\}$

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12 animals

12 Slides  
2 Colours

24 spots

	Litter 1			Litter 2			Litter 3			Litter 4			
Slide	1	2	3	4	5	6	7	8	9	10	11	12	
Red	1	2	3	1	4	5	2	4	6	2	5	6	
Green	2	3	1	4	5	1	4	6	2	5	6	2	same animal

Treatments form three groups of size two:  $\{1,6\}$ ,  $\{2,5\}$ ,  $\{3,4\}$

Groups are orthogonal to litters;

treatments-within-groups have efficiency factor  $\frac{1}{3}$  in litters.

# Two-colour microarrays: skeleton anova

	Litter 1			Litter 2			Litter 3			Litter 4		
Slide	1	2	3	4	5	6	7	8	9	10	11	12
Red	1	2	3	1	4	5	2	4	6	2	5	6
Green	2	3	1	4	5	1	4	6	2	5	6	2

spots		animals		treatments				
source	df	eff	source	df	eff	source	df	EMS
Mean	1	1	Mean	1	1	Mean	1	$\xi_0$
Slides	11	1	Litters	3	$1 \times \frac{1}{3}$	Tmts[G]	3	$\xi_S + 2\eta_L + \frac{1}{3}q(T[G])$
		$\frac{1}{4}$	Animals[L]	8	$\frac{1}{4} \times \frac{2}{3}$	Tmts[G]	3	$\xi_S + \frac{2}{4}2\eta_{LA} + \frac{1}{6}q(T[G])$
					$\frac{1}{4} \times 1$	Groups	2	$\xi_S + \frac{2}{4}2\eta_{LA} + \frac{1}{4}q(G)$
						Residual	3	$\xi_S + \frac{2}{4}2\eta_{LA}$
Colours	1							$\xi_C$
S#C	11	$\frac{3}{4}$	Animals[L]	8	$\frac{3}{4} \times \frac{2}{3}$	Tmts[G]	3	$\xi_{SC} + \frac{6}{4}2\eta_{LA} + \frac{1}{2}q(T[G])$
					$\frac{3}{4} \times 1$	Groups	2	$\xi_{SC} + \frac{6}{4}2\eta_{LA} + \frac{3}{4}q(G)$
						Residual	3	$\xi_{SC} + \frac{6}{4}2\eta_{LA}$
			Residual	3				$\xi_{SC}$



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Slide	1	2	3	4	5	6	7	8	9	10	11	12
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spots		animals		treatments				
source	df	eff	source	df	eff	source	df	EMS
Mean	1	1	Mean	1	1	Mean	1	$\xi_0$
Slides	11	1	Litters	3	$1 \times \frac{1}{3}$	Tmts[G]	3	$\xi_S + 2\eta_L + \frac{1}{3}q(T[G])$
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		$\frac{1}{4} \times 1$			Groups	2	$\xi_S + \frac{2}{4}2\eta_{LA} + \frac{1}{4}q(G)$	
					Residual	3	$\xi_S + \frac{2}{4}2\eta_{LA}$	
Colours	1						$\xi_C$	
S#C	11	$\frac{3}{4}$	Animals[L]	8	$\frac{3}{4} \times \frac{2}{3}$	Tmts[G]	3	$\xi_{SC} + \frac{6}{4}2\eta_{LA} + \frac{1}{2}q(T[G])$
		$\frac{3}{4} \times 1$			Groups	2	$\xi_{SC} + \frac{6}{4}2\eta_{LA} + \frac{3}{4}q(G)$	
					Residual	3	$\xi_{SC} + \frac{6}{4}2\eta_{LA}$	
			Residual	3			$\xi_{SC}$	

# Nonorthogonality in Phase I: revisited

## Query

*Suppose that, in Phase I, treatment term  $i$  is partially confounded, with a small efficiency factor  $\lambda_{ij}$ , with stratum  $j$ , which has a large variance  $\eta_j$ .*

# Nonorthogonality in Phase I: revisited

## Query

*Suppose that, in Phase I, treatment term  $i$  is partially confounded, with a small efficiency factor  $\lambda_{ij}$ , with stratum  $j$ , which has a large variance  $\eta_j$ .*

*At Phase II, should we*

- ▶ *try to confound stratum  $j$  with a Phase II stratum with small variance, or*
- ▶ *cut our losses on this part of the information about treatment term  $i$ ?*

# Nonorthogonality in Phase I: a special case

Suppose that,

- ▶ in Phase I, there is a treatment term that has efficiency factors

$$\begin{array}{ll} p & \text{in stratum 1 with variance } \eta_1 \\ q & \text{in stratum 2 with variance } \eta_2, \end{array}$$

where  $p + q = 1$  and  $\eta_1 > \eta_2$ ;

- ▶ the design for Phase II has replication  $r$ , there are two Phase II strata where these Phase I strata might be confounded, but they cannot both go in the one with the smaller variance.

Label the Phase I strata 1, 2 so that

$$\begin{array}{lll} p & \eta_1 & \xi_1 \\ q & \eta_2 & \xi_2. \end{array}$$

## Query

*Should we do this so that  $\xi_1 > \xi_2$  or  $\xi_2 > \xi_1$ ?*

# How to confound two pairs of strata from the two phases

tmt efficiency factor	Phase I variance	Phase II variance
$p$	$\eta_1(> \eta_2)$	$\xi_1$
$q$	$\eta_2$	$\xi_2$

# How to confound two pairs of strata from the two phases

tmt efficiency factor	Phase I variance	Phase II variance
$p$	$\eta_1 (> \eta_2)$	$\xi_1$
$q$	$\eta_2$	$\xi_2$

## Theorem

*Smaller variance is obtained if the Phase II strata are labelled so that*

$$\xi_1 > \xi_2 \quad \text{if} \quad \frac{q}{p} > \frac{(r\eta_2 + \xi_1)(r\eta_2 + \xi_2)}{(r\eta_1 + \xi_1)(r\eta_1 + \xi_2)};$$

*in particular, if*  $\frac{q}{p} > 1$ ;

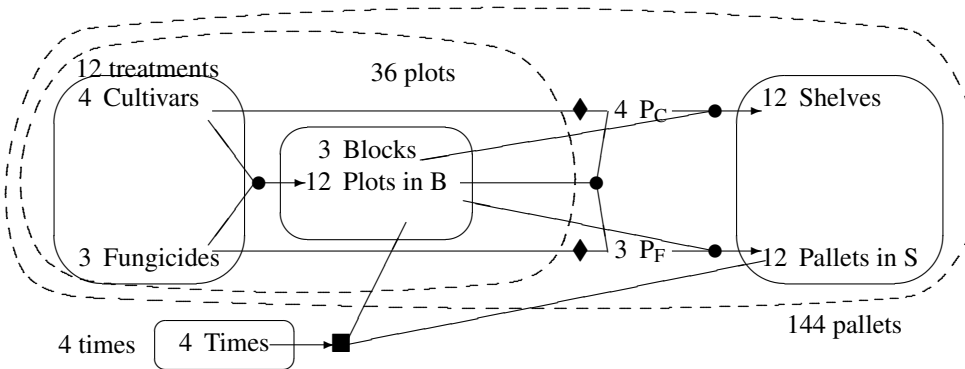
$$\xi_1 < \xi_2 \quad \text{if} \quad \frac{q}{p} < \frac{(r\eta_2 + \xi_1)(r\eta_2 + \xi_2)}{(r\eta_1 + \xi_1)(r\eta_1 + \xi_2)}.$$

# Some treatment factors may be applied only in Phase II

## Principle

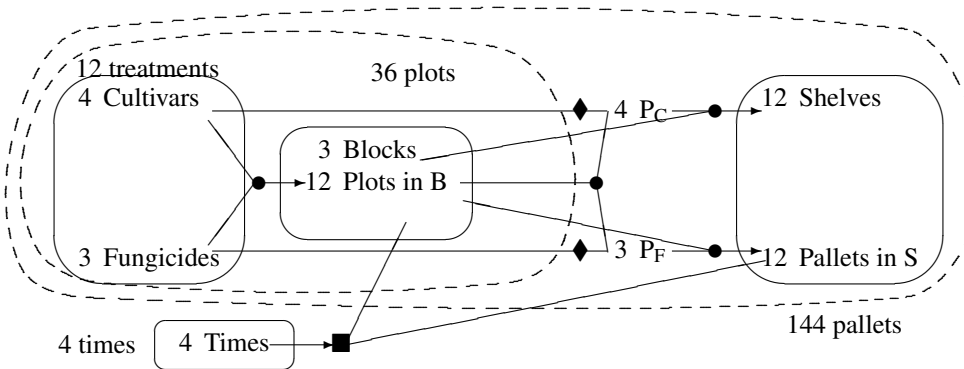
*Plan the whole experiment in advance,  
especially if you want to estimate interactions  
between the Phase I treatments and the Phase II treatments.*

# Potato storage (Payne)





# Potato storage (Payne)



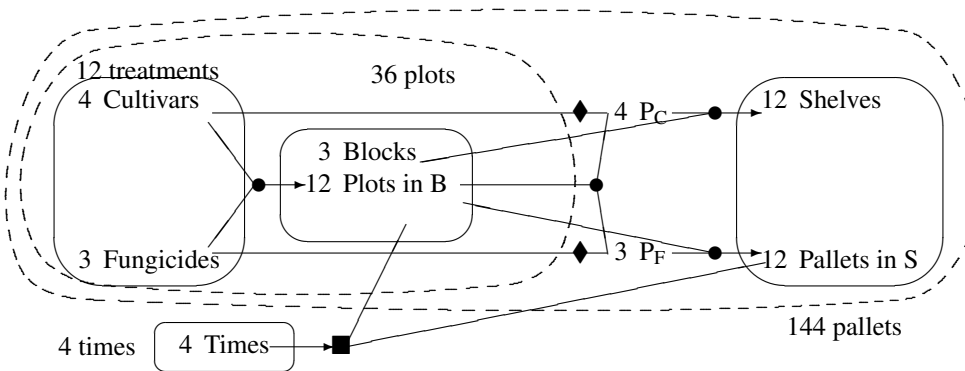
levels tmts  
4  $C$   
3  $F$

plots  
 $P_2$   
 $B, P_1$

pallets  
 $S_2, Q_2$   
 $S_1, Q_1$

times  
 $T$

# Potato storage (Payne)



levels tmts

4  $C$

3  $F$

plots

$P_2$

$B, P_1$

pallets

$S_2, Q_2$

$S_1, Q_1$

times

$T$

$C \equiv P_2$

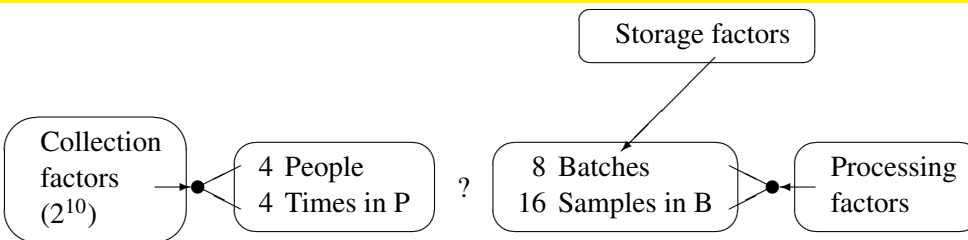
$F \equiv P_1$

$P_2 \equiv S_2$

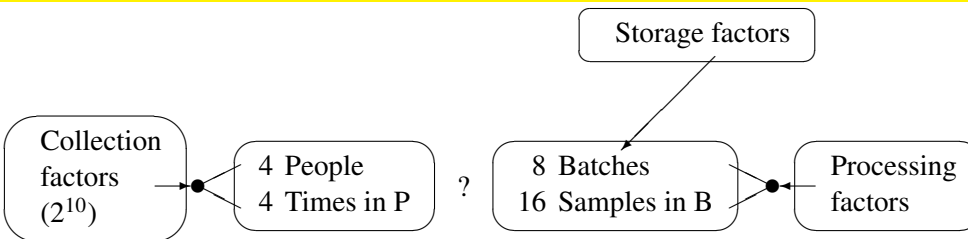
$B \equiv S_1, P_1 \equiv Q_1$

$T \equiv Q_2$

# Blood (Speed)

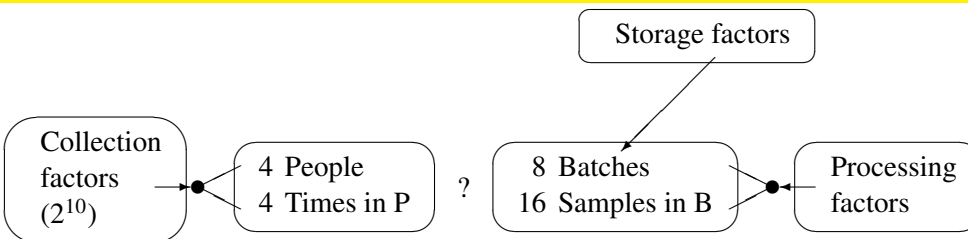


# Blood (Speed)



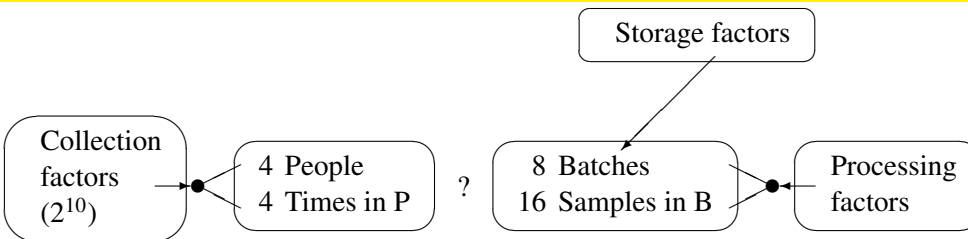
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# Blood (Speed)



- ▶ Confounding People with Batches increases the variance for some Storage factors.
- ▶ Making People orthogonal to Batches uses up more degrees of freedom.

# Blood (Speed)



- ▶ Confounding People with Batches increases the variance for some Storage factors.
- ▶ Making People orthogonal to Batches uses up more degrees of freedom.
- ▶ The compromise has a single df for People  $\vee$  Batches, with a variance which is large and different from all other variances (Cheng; Vivacqua).

# Conclusions: I

When designing a two-phase experiment  
(or a multi-stage batch reprocessing experiment)

- ▶ design the whole thing in advance;
- ▶ pay attention to making variance small;
- ▶ pay attention to residual degrees of freedom;
- ▶ if treatments are orthogonal to ‘large blocks’ in Phase I, then those large blocks should be confounded with “large blocks” in Phase II;
- ▶ if a treatment term is in a Phase I stratum with large variance (in particular, if a treatment factor is ‘hard to set’ in Phase I), then it should be allocated to a Phase II stratum with small variance.
- ▶ if a treatment term is partially confounded with more than one Phase I stratum, and cannot be wholly allocated to a ‘small variance’ stratum in Phase II, then the best design depends on the ratios of the stratum variances and on the efficiency factors from Phase I.

# Conclusions: II

When designing a two-phase experiment (or a multi-stage batch reprocessing experiment), the following are useful concepts and tools.

- ▶ diagrams with panels to show tiers;
- ▶ Hasse diagrams to elucidate strata and degrees of freedom;
- ▶ the design key method of construction, which can also be used to elucidate the confounding;
- ▶ decomposition tables (skeleton anova) to assess the qualities of the design.