

## 7. Analysis of Variance for Balanced Two-Factor Experiments

# An Example Two-Factor Experiment

Researchers were interested in studying the effects of 2 diets (low fiber, high fiber) and 3 drugs (D1, D2, D3) on weight gained by Yorkshire pigs. A total of 12 pigs were assigned to the 6 diet-drug combinations using a balanced and completely randomized experimental design. Pigs were housed in individual pens, injected with their assigned drugs once per week, and fed their assigned diets for a 6-week period. The amount of weight gained during the 6-week period was recorded for each pig.



# A Model for the Data

Always begin by writing out the model

For  $i = 1, 2$ ;  $j = 1, 2, 3$ ; and  $k = 1, 2$ ; let  $y_{ijk}$  denote the weight gain of the  $k^{\text{th}}$  pig that received diet  $i$  and drug  $j$ , and suppose

$(\alpha\beta)_{ij}$   
↑

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \epsilon_{ijk} \quad (i = 1, 2; j = 1, 2, 3; k = 1, 2) \quad \text{where}$$

$$\mu, \alpha_1, \alpha_2, \beta_1, \beta_2, \beta_3, \gamma_{11}, \gamma_{12}, \gamma_{13}, \gamma_{21}, \gamma_{22}, \gamma_{23}$$

are unknown real-valued parameters and

$$\epsilon_{111}, \epsilon_{112}, \epsilon_{121}, \epsilon_{122}, \epsilon_{131}, \epsilon_{132}, \epsilon_{211}, \epsilon_{212}, \epsilon_{221}, \epsilon_{222}, \epsilon_{231}, \epsilon_{232} \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma^2)$$

for some unknown  $\sigma^2 > 0$ .

# Model in Matrix and Vector Form

*less than full rank model matrix*

$$\begin{bmatrix} y_{111} \\ y_{112} \\ y_{121} \\ y_{122} \\ y_{131} \\ y_{132} \\ y_{211} \\ y_{212} \\ y_{221} \\ y_{222} \\ y_{231} \\ y_{232} \end{bmatrix} = \begin{bmatrix} 1 & 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \mu \\ \alpha_1 \\ \alpha_2 \\ \beta_1 \\ \beta_2 \\ \beta_3 \\ \gamma_{11} \\ \gamma_{12} \\ \gamma_{13} \\ \gamma_{21} \\ \gamma_{22} \\ \gamma_{23} \end{bmatrix} + \begin{bmatrix} \epsilon_{111} \\ \epsilon_{112} \\ \epsilon_{121} \\ \epsilon_{122} \\ \epsilon_{131} \\ \epsilon_{132} \\ \epsilon_{211} \\ \epsilon_{212} \\ \epsilon_{221} \\ \epsilon_{222} \\ \epsilon_{231} \\ \epsilon_{232} \end{bmatrix}$$

$$y = X\beta + \epsilon, \quad \epsilon \sim \mathcal{N}(0, \sigma^2 I)$$

## Same Model with Cell Means Parameterization

$$\begin{bmatrix} y_{111} \\ y_{112} \\ y_{121} \\ y_{122} \\ y_{131} \\ y_{132} \\ y_{211} \\ y_{212} \\ y_{221} \\ y_{222} \\ y_{231} \\ y_{232} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \mu_{11} \\ \mu_{12} \\ \mu_{13} \\ \mu_{21} \\ \mu_{22} \\ \mu_{23} \end{bmatrix} + \begin{bmatrix} \epsilon_{111} \\ \epsilon_{112} \\ \epsilon_{121} \\ \epsilon_{122} \\ \epsilon_{131} \\ \epsilon_{132} \\ \epsilon_{211} \\ \epsilon_{212} \\ \epsilon_{221} \\ \epsilon_{222} \\ \epsilon_{231} \\ \epsilon_{232} \end{bmatrix}$$

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}, \quad \boldsymbol{\epsilon} \sim \mathcal{N}(\mathbf{0}, \sigma^2 \mathbf{I})$$

We could consider a sequence of progressively more complex models for the response mean that lead up to our full cell means model.

- 1  $E(y_{ijk}) = \mu + \underbrace{\alpha_i + \beta_j + \gamma_{ij}}_{=0}$  *intercept only*
- 2  $E(y_{ijk}) = \mu + \underline{\alpha_i}$
- 3  $E(y_{ijk}) = \mu + \alpha_i + \underline{\beta_j}$
- 4  $E(y_{ijk}) = \mu + \alpha_i + \beta_j + \gamma_{ij} \iff E(y_{ijk}) = \mu_{ij}$
- we could also start out by modeling drug first and then add diet*

# Matrices with Nested Column Spaces

$$\begin{array}{c} \mu \\ \mathbf{X}_1 = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}, \quad \begin{array}{c} \mu \quad \alpha_1 \quad \alpha_2 \\ \mathbf{X}_2 = \begin{bmatrix} 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \end{bmatrix}, \quad \begin{array}{c} \mu \quad \alpha_1 \quad \alpha_2 \\ \mathbf{X}_3 = \begin{bmatrix} 1 & 1 & 0 & 1 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 \\ 1 & 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 0 & 1 \end{bmatrix} \end{array} \quad \& \end{array}$$

$\beta_1 \quad \beta_2 \quad \beta_3$

# Matrices with Nested Column Spaces

less than full rank

$$X_4 = \begin{bmatrix} 1 & 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \quad \text{or}$$

$\delta_{ij}$ 's



# Matrices with Nested Column Spaces

*cell-means model matrix*

$$\mathbf{X}_4 = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} .$$

*full rank*

# ANOVA Table for Our Two-Factor Example

by how much does SSE decrease when adding diet into model?

end  
lecture 15  
2-24-25

Source	Sum of Squares	DF
Diets 1	$\mathbf{y}^\top (\mathbf{P}_2 - \mathbf{P}_1) \mathbf{y}$	$2 - 1 = 1$
Drugs 1, Diets	$\mathbf{y}^\top (\mathbf{P}_3 - \mathbf{P}_2) \mathbf{y}$	$4 - 2 = 2$
Diets $\times$ Drugs 1, Diets, Drugs	$\mathbf{y}^\top (\mathbf{P}_4 - \mathbf{P}_3) \mathbf{y}$	$6 - 4 = 2$
Error	$\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_4) \mathbf{y}$	$12 - 6 = 6$
C. Total	$\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_1) \mathbf{y}$	$12 - 1 = 11$

given intercept & diet, how much more variability can we explain by adding drug?