HW3: Question 1g) reference is to slide 26 not 20

4. Analysis of Two-Factor Experiments Based on Cell-Means Models –

Alternative Parameterization

useful, e.g., when we have no interactions

The Cell-Means Model

Earlier, we introduced the cell-means model as follows:

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

$$\begin{aligned} y_{ijk} &= \mu_{ij} + \epsilon_{ijk}, \\ \epsilon_{ijk} &\overset{iid}{\sim} \mathcal{N}(0, \sigma^2), \end{aligned}$$

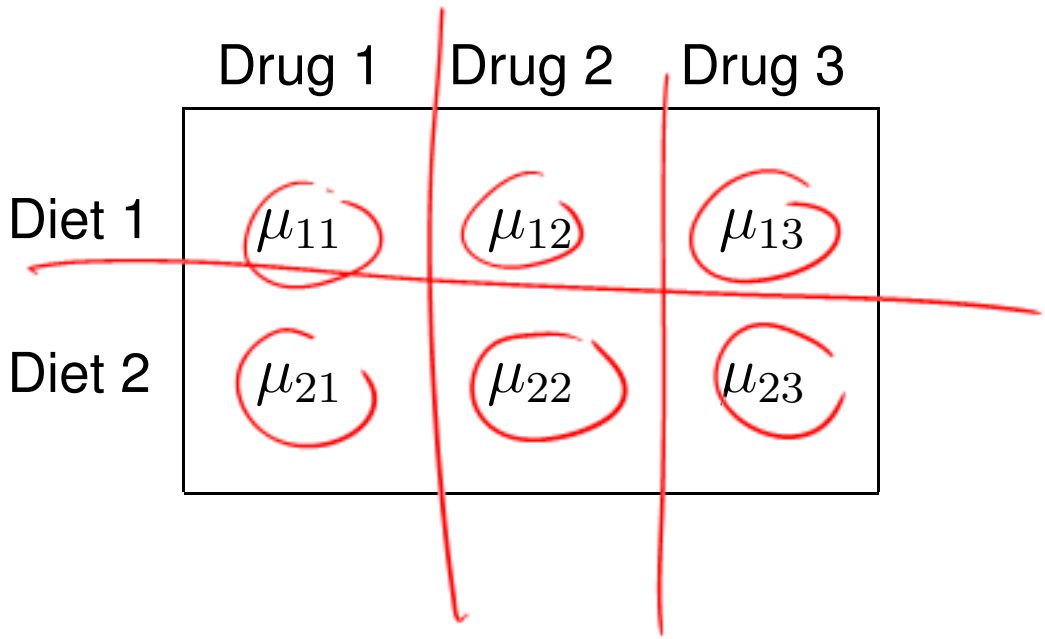
where $\mu_{11}, \mu_{12}, \mu_{13}, \mu_{21}, \mu_{22}, \mu_{23} \in \mathbb{R}$ and $\sigma^2 \in \mathbb{R}^+$ are unknown parameters.

Table of Treatments and Means for Cell-Means Model

Treatment	Diet	Drug	Mean
1	1	1	μ_{11}
2	1	2	μ_{12}
3	1	3	μ_{13}
4	2	1	μ_{21}
5	2	2	μ_{22}
6	2	3	μ_{23}

Diet 1 = Low Fiber,
Diet 2 = High Fiber

Drug 1 = D1, Drug 2 = D2,
Drug 3 = D3



An Alternative Parameterization

An alternative parameterization of the cell-means model is

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

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

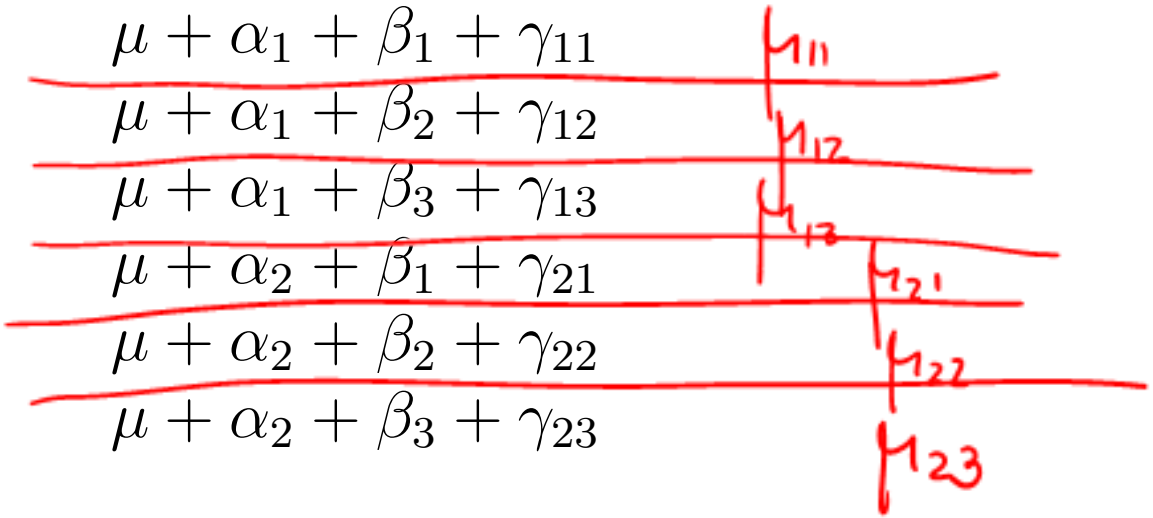
$$\epsilon_{111}, \epsilon_{112}, \epsilon_{121}, \epsilon_{122}, \epsilon_{131}, \epsilon_{132}, \epsilon_{211}, \epsilon_{212}, \epsilon_{221}, \epsilon_{222}, \epsilon_{231}, \epsilon_{232}$$

$$\overset{iid}{\sim} \mathcal{N}(0, \sigma^2)$$

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

Table of Treatments and Means

Treatment	Diet	Drug	Mean
1	1	1	$\mu + \alpha_1 + \beta_1 + \gamma_{11}$
2	1	2	$\mu + \alpha_1 + \beta_2 + \gamma_{12}$
3	1	3	$\mu + \alpha_1 + \beta_3 + \gamma_{13}$
4	2	1	$\mu + \alpha_2 + \beta_1 + \gamma_{21}$
5	2	2	$\mu + \alpha_2 + \beta_2 + \gamma_{22}$
6	2	3	$\mu + \alpha_2 + \beta_3 + \gamma_{23}$



Diet 1 = Low Fiber, Diet 2 = High Fiber

Drug 1 = D1, Drug 2 = D2, Drug 3 = D3

Model in Matrix and Vector Form

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

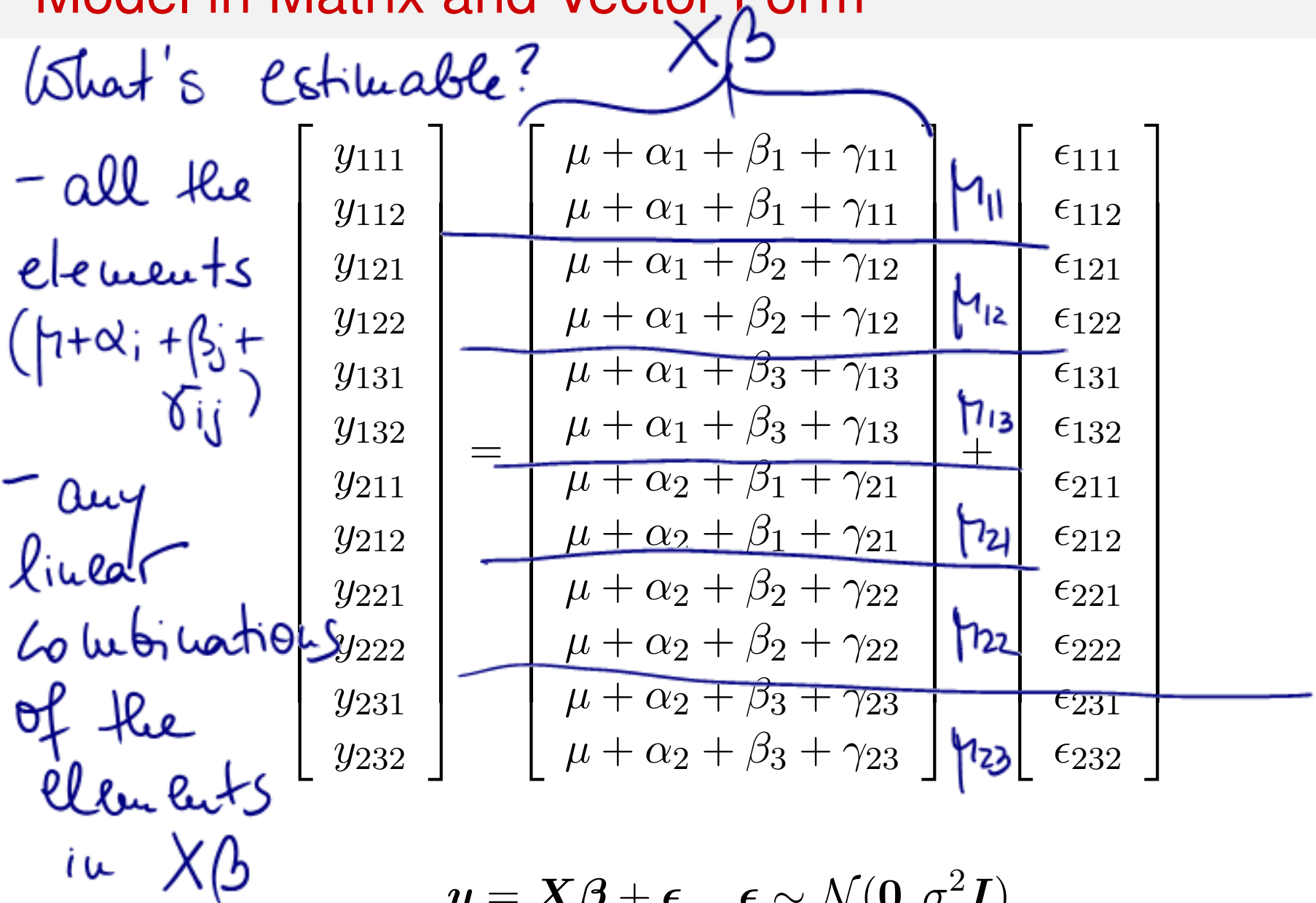
X which is no longer full rank

β

identical to full rank X under previous parameters.

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

Model in Matrix and Vector Form



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

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

Table of Cell and Marginal Means

main diet effect: $\bar{\mu}_{1\cdot} - \bar{\mu}_{2\cdot} = (\mu + \alpha_1 + \bar{\beta}_\cdot + \bar{\gamma}_{1\cdot}) - (\mu + \alpha_2 + \bar{\beta}_\cdot + \bar{\gamma}_{2\cdot}) = \alpha_1 - \alpha_2 + \bar{\gamma}_{1\cdot} - \bar{\gamma}_{2\cdot}$

Any linear combination of the entries in this table is estimable.

	Drug 1	Drug 2	Drug 3	
D1	$\mu + \alpha_1 + \beta_1 + \gamma_{11}$	$\mu + \alpha_1 + \beta_2 + \gamma_{12}$	$\mu + \alpha_1 + \beta_3 + \gamma_{13}$	$\mu + \alpha_1 + \bar{\beta}_\cdot + \bar{\gamma}_{1\cdot}$
D2	$\mu + \alpha_2 + \beta_1 + \gamma_{21}$	$\mu + \alpha_2 + \beta_2 + \gamma_{22}$	$\mu + \alpha_2 + \beta_3 + \gamma_{23}$	$\mu + \alpha_2 + \bar{\beta}_\cdot + \bar{\gamma}_{2\cdot}$
	$\mu + \bar{\alpha}_\cdot + \beta_1 + \bar{\gamma}_{\cdot 1}$	$\mu + \bar{\alpha}_\cdot + \beta_2 + \bar{\gamma}_{\cdot 2}$	$\mu + \bar{\alpha}_\cdot + \beta_3 + \bar{\gamma}_{\cdot 3}$	$\mu + \bar{\alpha}_\cdot + \bar{\beta}_\cdot + \bar{\gamma}_{\cdot\cdot}$

Simple effect of Drug 1 - Drug 2 within Diet 1:

$(\mu + \alpha_1 + \beta_1 + \gamma_{11}) - (\mu + \alpha_1 + \beta_2 + \gamma_{12}) = \beta_1 - \beta_2 + \gamma_{11} - \gamma_{12}$

Example Estimable Functions

- Simple effect of Diet for Drug 1: $\alpha_1 - \alpha_2 + \gamma_{11} - \gamma_{21}$ 
- Simple effect of Drug 1 vs. Drug 3 for Diet 2:
  $\beta_1 - \beta_3 + \gamma_{21} - \gamma_{23}$
- Main effect of Diet: $\alpha_1 - \alpha_2 + \bar{\gamma}_{1\cdot} - \bar{\gamma}_{2\cdot}$
- Interaction effect involving Diets 1 and 2 and Drugs 1 and 3:

$$
\begin{aligned}
&[(\mu + \alpha_1 + \beta_1 + \gamma_{11}) - (\mu + \alpha_2 + \beta_1 + \gamma_{21})] \\
-&[(\mu + \alpha_1 + \beta_3 + \gamma_{13}) - (\mu + \alpha_2 + \beta_3 + \gamma_{23})] \\
=&\ \gamma_{11} - \gamma_{13} - \gamma_{21} + \gamma_{23}
\end{aligned}
$$

Estimation and Testing

Recall set-up of $\beta = (\mu \; \alpha_1 \; \alpha_2 \ldots)^\top$

As before, estimation or testing involves finding an appropriate matrix C to estimate $C\beta$ or test $H_0 : C\beta = 0$.

For example, the Diet main effect is estimated by $C\hat{\beta}$, where

$$C = \begin{bmatrix} 0 & 1 & -1 & 0 & 0 & 0 & \frac{1}{3} & \frac{1}{3} & \frac{1}{3} & -\frac{1}{3} & -\frac{1}{3} & -\frac{1}{3} \end{bmatrix}$$

(-1: α_2; $\frac{1}{3}$: α_1; $\bar{y}_{1\cdot}$; $-\bar{y}_{2\cdot}$)

and

$$\hat{\beta} = \begin{bmatrix} \hat{\mu} & \hat{\alpha}_1 & \hat{\alpha}_2 & \hat{\beta}_1 & \hat{\beta}_2 & \hat{\beta}_3 & \hat{\gamma}_{11} & \hat{\gamma}_{12} & \hat{\gamma}_{13} & \hat{\gamma}_{21} & \hat{\gamma}_{22} & \hat{\gamma}_{23} \end{bmatrix}^\top$$

is any solution to the Normal Equations involving the new matrix X.

Estimation and Testing (continued)

As another example, the test for Drug main effects can be carried out as a test of $H_0 : \boldsymbol{C\beta} = \mathbf{0}$, where

$$\boldsymbol{C} = \begin{bmatrix} 0 & 0 & 0 & 1 & -1 & 0 & \frac{1}{2} & -\frac{1}{2} & 0 & \frac{1}{2} & -\frac{1}{2} & 0 \\ 0 & 0 & 0 & 1 & 0 & -1 & \frac{1}{2} & 0 & -\frac{1}{2} & \frac{1}{2} & 0 & -\frac{1}{2} \end{bmatrix}$$

so that

$$\boldsymbol{C\beta} = \begin{bmatrix} \beta_1 - \beta_2 + \bar{\gamma}_{\cdot 1} - \bar{\gamma}_{\cdot 2} \\ \beta_1 - \beta_3 + \bar{\gamma}_{\cdot 1} - \bar{\gamma}_{\cdot 3} \end{bmatrix}.$$

The model matrix $\boldsymbol{X}$ is not full-column rank.

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

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

The Alternative Parameterization in R

The `lm` function in R uses a full-rank model matrix.

The code

```
o=lm(weightgain~diet+drug+diet:drug,data=d)
```

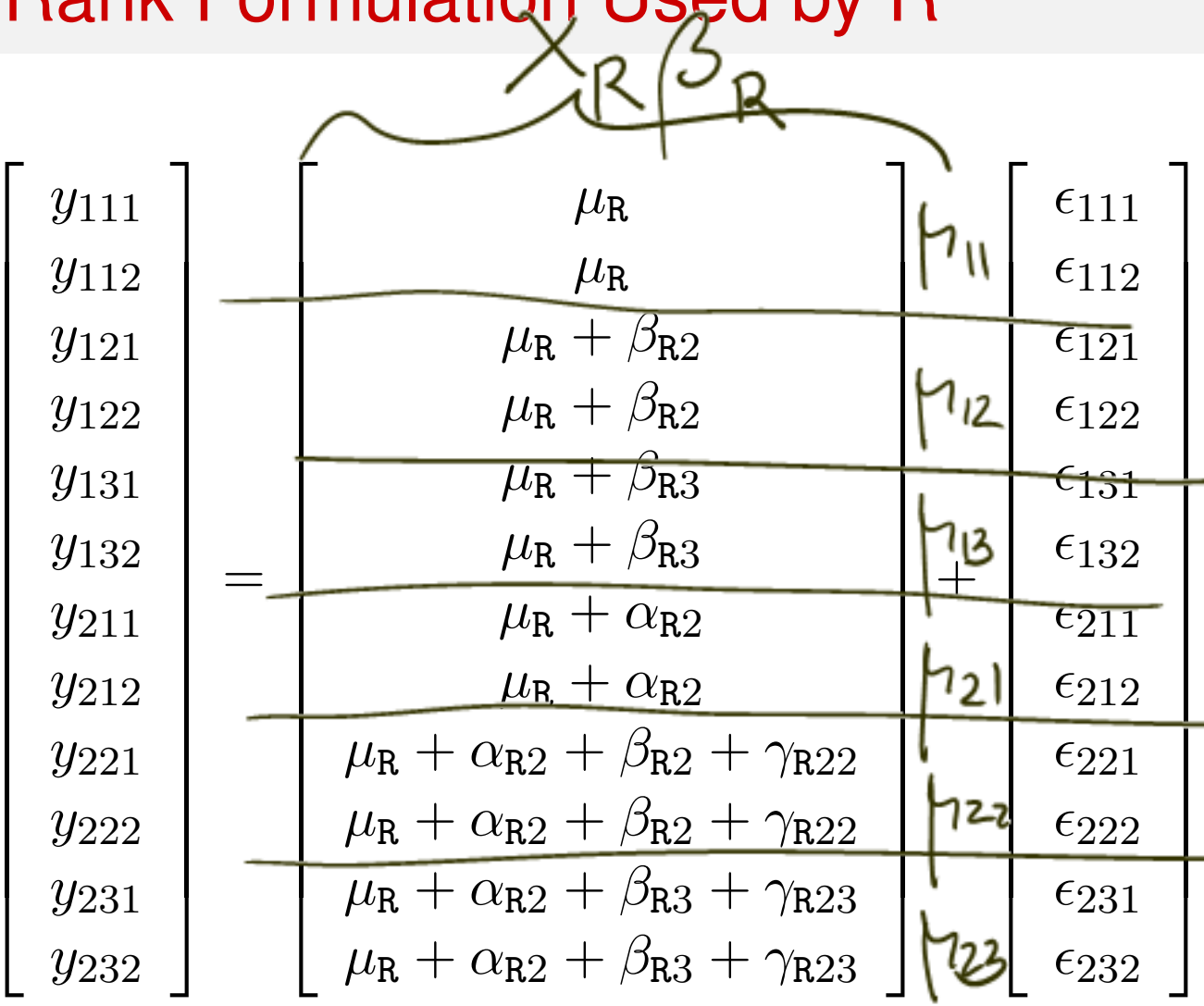
will fit the following full-rank version of the cell-means model.

The Full-Rank Formulation Used by R

$$\begin{bmatrix} y_{111} \\ y_{112} \\ y_{121} \\ y_{122} \\ y_{131} \\ y_{132} \\ y_{211} \\ y_{212} \\ y_{221} \\ y_{222} \\ y_{231} \\ y_{232} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 1 & 0 & 1 \end{bmatrix} \begin{bmatrix} \mu_{\mathrm{R}} \\ \alpha_{\mathrm{R}2} \\ \beta_{\mathrm{R}2} \\ \beta_{\mathrm{R}3} \\ \gamma_{\mathrm{R}22} \\ \gamma_{\mathrm{R}23} \end{bmatrix} + \begin{bmatrix} \epsilon_{111} \\ \epsilon_{112} \\ \epsilon_{121} \\ \epsilon_{122} \\ \epsilon_{131} \\ \epsilon_{132} \\ \epsilon_{211} \\ \epsilon_{212} \\ \epsilon_{221} \\ \epsilon_{222} \\ \epsilon_{231} \\ \epsilon_{232} \end{bmatrix}$$

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

The Full-Rank Formulation Used by R



$$\begin{bmatrix} y_{111} \\ y_{112} \\ y_{121} \\ y_{122} \\ y_{131} \\ y_{132} \\ y_{211} \\ y_{212} \\ y_{221} \\ y_{222} \\ y_{231} \\ y_{232} \end{bmatrix} = \begin{bmatrix} \mu_R \\ \mu_R \\ \mu_R + \beta_{R2} \\ \mu_R + \beta_{R2} \\ \mu_R + \beta_{R3} \\ \mu_R + \beta_{R3} \\ \mu_R + \alpha_{R2} \\ \mu_R + \alpha_{R2} \\ \mu_R + \alpha_{R2} + \beta_{R2} + \gamma_{R22} \\ \mu_R + \alpha_{R2} + \beta_{R2} + \gamma_{R22} \\ \mu_R + \alpha_{R2} + \beta_{R3} + \gamma_{R23} \\ \mu_R + \alpha_{R2} + \beta_{R3} + \gamma_{R23} \end{bmatrix} + \begin{bmatrix} \epsilon_{111} \\ \epsilon_{112} \\ \epsilon_{121} \\ \epsilon_{122} \\ \epsilon_{131} \\ \epsilon_{132} \\ \epsilon_{211} \\ \epsilon_{212} \\ \epsilon_{221} \\ \epsilon_{222} \\ \epsilon_{231} \\ \epsilon_{232} \end{bmatrix}$$

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

Table of Means for the R Full-Rank Formulation

$$\bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 2} = \left(\mu_R + \frac{\alpha_{R2}}{2}\right) - \left(\mu_R + \frac{\alpha_{R2}}{2} + \beta_{R2} + \frac{\gamma_{R22}}{2}\right)$$

$$= -\beta_{R2} - \frac{\gamma_{R22}}{2}$$

	Drug 1	Drug 2	Drug 3	
D1	μ_R	$\mu_R + \beta_{R2}$	$\mu_R + \beta_{R3}$	$\mu_R + \frac{\beta_{R2}+\beta_{R3}}{3} = \bar{\mu}_{1\cdot}$
D2	$\mu_R + \alpha_{R2}$	$\mu_R + \alpha_{R2} + \beta_{R2} + \gamma_{R22}$	$\mu_R + \alpha_{R2} + \beta_{R3} + \gamma_{R23}$	$\mu_R + \alpha_{R2} + \frac{\beta_{R2}+\beta_{R3}}{3} + \frac{\gamma_{R22}+\gamma_{R23}}{3} = \bar{\mu}_{2\cdot}$
	$\mu_R + \frac{\alpha_{R2}}{2}$	$\mu_R + \frac{\alpha_{R2}}{2} + \beta_{R2} + \frac{\gamma_{R22}}{2}$	$\mu_R + \frac{\alpha_{R2}}{2} + \beta_{R3} + \frac{\gamma_{R23}}{2}$	$\mu_R + \frac{\alpha_{R2}}{2} + \frac{\beta_{R2}+\beta_{R3}}{3} + \frac{\gamma_{R22}+\gamma_{R23}}{6}$
	$\bar{\mu}_{\cdot 1}$	$\bar{\mu}_{\cdot 2}$	$\bar{\mu}_{\cdot 3}$	

Parameter Interpretation for R Full-Rank Formulation

- μ_{R} is the mean for the Diet 1 Drug 1 treatment.
- α_{R2} is the simple effect of Diet 2 vs. Diet 1 for Drug 1.
- β_{R2} is the simple effect of Drug 2 vs. Drug 1 for Diet 1.
- β_{R3} is the simple effect of Drug 3 vs. Drug 1 for Diet 1.
- γ_{R22} is an interaction effect involving Diets 1 and 2 and Drugs 1 and 2. It tells how much bigger the Diet 2 $-$ Diet 1 mean difference is for Drug 2 than it is for Drug 1.
- γ_{R23} is an interaction effect involving Diets 1 and 2 and Drugs 1 and 3. It tells how much bigger the Diet 2 $-$ Diet 1 mean difference is for Drug 3 than it is for Drug 1.

Estimation and Testing in R

As before, estimation or testing involves finding an appropriate matrix $\boldsymbol{C}$ to estimate $\boldsymbol{C\beta}_{\mathrm{R}}$ or test $H_0 : \boldsymbol{C\beta}_{\mathrm{R}} = \boldsymbol{0}$.

For example, the Diet main effect is estimated by

$$\boldsymbol{C}\widehat{\boldsymbol{\beta}}_{\mathrm{R}} = \begin{bmatrix} 0 & -1 & 0 & 0 & -\frac{1}{3} & -\frac{1}{3} \end{bmatrix} \begin{bmatrix} \widehat{\mu}_{\mathrm{R}} \\ \widehat{\alpha}_{\mathrm{R}2} \\ \widehat{\beta}_{\mathrm{R}2} \\ \widehat{\beta}_{\mathrm{R}3} \\ \widehat{\gamma}_{\mathrm{R}22} \\ \widehat{\gamma}_{\mathrm{R}23} \end{bmatrix} = -\widehat{\alpha}_{\mathrm{R}2} - \frac{\widehat{\gamma}_{\mathrm{R}22} + \widehat{\gamma}_{\mathrm{R}23}}{3},$$

where $\widehat{\boldsymbol{\beta}}_{\mathrm{R}} = (\boldsymbol{X}_{\mathrm{R}}^{\top}\boldsymbol{X}_{\mathrm{R}})^{-1}\boldsymbol{X}_{\mathrm{R}}^{\top}\boldsymbol{y}$.

reflecting average of the 3 levels of drug!

Estimation and Testing in R (continued)

As another example, the test for Drug main effects can be carried out as a test of $H_0 : \boldsymbol{C}\boldsymbol{\beta}_{\mathrm{R}} = \mathbf{0}$, where

$$\boldsymbol{C} = \begin{bmatrix} 0 & 0 & 1 & 0 & \frac{1}{2} & 0 \\ 0 & 0 & 0 & 1 & 0 & \frac{1}{2} \end{bmatrix}$$

reflecting the average of diet 1 & diet 2

so that

end lecture 9
2-10-25

$$\boldsymbol{C}\boldsymbol{\beta}_{\mathrm{R}} = \begin{bmatrix} \beta_{\mathrm{R}2} + \frac{\gamma_{\mathrm{R}22}}{2} \\ \beta_{\mathrm{R}3} + \frac{\gamma_{\mathrm{R}23}}{2} \end{bmatrix}.$$

Tests Based on Reduced vs. Full Model Comparison

Any of the tests we have discussed could alternatively be carried out using a statistic of the form

$$F = \frac{\boldsymbol{y}^\top(\boldsymbol{P}_{\boldsymbol{X}} - \boldsymbol{P}_{\boldsymbol{X}_0})\boldsymbol{y}/\left[\text{rank}(\boldsymbol{X}) - \text{rank}(\boldsymbol{X}_0)\right]}{\boldsymbol{y}^\top(\boldsymbol{I} - \boldsymbol{P}_{\boldsymbol{X}})\boldsymbol{y}/\left[n - \text{rank}(\boldsymbol{X})\right]}$$

for an appropriate reduced model matrix $\boldsymbol{X}_0$.

It is not always easy to specify an appropriate matrix $\boldsymbol{X}_0$.

We will discuss specification of $\boldsymbol{X}_0$ in subsequent slide sets.

Testing for Main Effects When Factors Interact

Some statisticians argue against testing for main effects when there are interactions between factors.

Others believe that, depending on the scientific questions of interest, any contrasts of treatment means may be worth examining.

Be aware that "no main effects" does not necessarily mean "no effects."

	Drug 1	Drug 2	Drug 3	
Diet 1	$\mu_{11} = 42$	$\mu_{12} = 40$	$\mu_{13} = 38$	$\bar{\mu}_{1\cdot} = 40$
Diet 2	$\mu_{21} = 38$	$\mu_{22} = 40$	$\mu_{23} = 42$	$\bar{\mu}_{2\cdot} = 40$
	$\bar{\mu}_{\cdot 1} = 40$	$\bar{\mu}_{\cdot 2} = 40$	$\bar{\mu}_{\cdot 3} = 40$	$\bar{\mu}_{\cdot\cdot} = 40$

diet here is effective for weight gain, however which diet we assign does not matter!

Unbalanced Data and Missing Cells

Although we have focused on a balanced two-factor experiment with 2 experimental units per treatment, the techniques presented in these slides work the same way whether data are balanced or not, as long as each treatment has a response for at least one experimental unit and some treatments have more than one.

If there are no experimental units for one or more treatments, then the treatment design may not be a full-factorial treatment design, and we may have a *missing cell* or *missing cells*.

Example with Missing Cells

	Drug 1	Drug 2	Drug 3	
Diet 1	μ_{11}	μ_{12}	μ_{13}	$\bar{\mu}_{1\cdot}$
Diet 2	μ_{21}	-	μ_{23}	-
	$\bar{\mu}_{\cdot 1}$	-	$\bar{\mu}_{\cdot 3}$	-

Example with Missing Cells

In this example, we have no data for the treatment combination Diet 2 with Drug 2.

In this case, we could fit a model with the 5 means μ_{11}, μ_{12}, μ_{13}, μ_{21}, and μ_{23}.

We could estimate any linear combination of the 5 means μ_{11}, μ_{12}, μ_{13}, μ_{21}, and μ_{23}.

Linear combinations involving μ_{22} are not estimable.

Finished at the beginning of Lecture 10