

5100 Methods Notes

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Key LM Results

A General Linear Model (GLM)

Suppose

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon},$$

where

- $\mathbf{y} \in \mathbb{R}^n$ is the response vector,
- \mathbf{X} is an $n \times p$ matrix of known (fixed) constants,
- $\boldsymbol{\beta} \in \mathbb{R}^p$ is an unknown parameter vector, and
- $\boldsymbol{\varepsilon}$ is a vector of unobserved random errors satisfying

$$\mathbb{E}(\boldsymbol{\varepsilon}) = \mathbf{0}, \quad \text{Cov}(\boldsymbol{\varepsilon}) = \boldsymbol{\Sigma}.$$

The model is called a *linear model* because the mean of the response vector is linear in the unknown parameter vector:

$$\mathbb{E}(\mathbf{y}) = \mathbf{X}\boldsymbol{\beta}.$$

Ordinary Least Squares (OLS) Estimation

Assume

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}, \quad \mathbb{E}(\boldsymbol{\varepsilon}) = \mathbf{0}, \quad \text{Cov}(\boldsymbol{\varepsilon}) = \sigma^2 \mathbf{I}.$$

Then

$$\mathbb{E}(\mathbf{y}) = \mathbf{X}\boldsymbol{\beta} \in \mathcal{C}(\mathbf{X}),$$

where $\mathcal{C}(\mathbf{X})$ denotes the column space of \mathbf{X} .

To estimate $\mathbb{E}(\mathbf{y})$, we consider vectors of the form $\mathbf{X}\hat{\boldsymbol{\beta}}$.

Thus, estimating $\mathbb{E}(\mathbf{y})$ amounts to finding the vector in $\mathcal{C}(\mathbf{X})$ that is closest to \mathbf{y} .

Let $\mathcal{N}(\mathbf{X}^\top)$ denote the null space of \mathbf{X}^\top .

Then $\mathcal{C}(\mathbf{X})$ and $\mathcal{N}(\mathbf{X}^\top)$ are orthogonal complements:

$$\mathcal{N}(\mathbf{X}^\top) \perp \mathcal{C}(\mathbf{X}).$$

The null space of a matrix \mathbf{A} is defined as

$$\mathcal{N}(\mathbf{A}) = \{\mathbf{x} : \mathbf{Ax} = \mathbf{0}\}.$$

Least Squares Estimate (LSE)

An estimate $\hat{\beta}$ is a *least squares estimate* (LSE) of β if $\mathbf{X}\hat{\beta}$ is the vector in $\mathcal{C}(\mathbf{X})$ that is closest to \mathbf{y} .

Equivalently,

$$\hat{\beta} = \arg \min_{\beta \in \mathbb{R}^p} (\mathbf{y} - \mathbf{X}\beta)^\top (\mathbf{y} - \mathbf{X}\beta).$$

Define the error sum of squares:

$$Q(\beta) = \|\mathbf{y} - \mathbf{X}\beta\|_2^2 = (\mathbf{y} - \mathbf{X}\beta)^\top (\mathbf{y} - \mathbf{X}\beta).$$

Identifying the LSE

There are two equivalent approaches:

- **Algebraic:** solving the normal equations
- **Geometric:** orthogonal projection of \mathbf{y} onto $\mathcal{C}(\mathbf{X})$

Normal Equations

Expand the objective function:

$$Q(\beta) = \mathbf{y}^\top \mathbf{y} - 2\beta^\top \mathbf{X}^\top \mathbf{y} + \beta^\top \mathbf{X}^\top \mathbf{X}\beta.$$

Taking derivatives and setting the gradient equal to zero yields

$$\nabla Q(\beta) = -2\mathbf{X}^\top \mathbf{y} + 2\mathbf{X}^\top \mathbf{X}\beta = \mathbf{0}.$$

This leads to the **normal equations**:

$$\mathbf{X}^\top \mathbf{X}\beta = \mathbf{X}^\top \mathbf{y}.$$

Solutions to the Normal Equations

If $\text{rank}(\mathbf{X}) = p$, then $\mathbf{X}^\top \mathbf{X}$ is invertible and the unique solution is

$$\hat{\beta} = (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{y}.$$

If $\text{rank}(\mathbf{X}) < p$, the normal equations have infinitely many solutions.

In this case, $\hat{\beta}$ may not be unique, but

$$\hat{\mathbf{y}} = \mathbf{X}\hat{\beta}$$

is unique.

Geometric Approach

Let \mathbf{P}_X denote the orthogonal projection matrix onto $\mathcal{C}(\mathbf{X})$:

$$\mathbf{P}_X = \mathbf{X}(\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top,$$

where $(\mathbf{X}^\top \mathbf{X})^{-1}$ is any generalized inverse.

Properties

- \mathbf{P}_X is idempotent:

$$\mathbf{P}_X^2 = \mathbf{P}_X.$$

- \mathbf{P}_X projects onto $\mathcal{C}(\mathbf{X})$.
- \mathbf{P}_X is symmetric:

$$\mathbf{P}_X^\top = \mathbf{P}_X.$$

- $\mathbf{P}_X \mathbf{X} = \mathbf{X}$ and $\mathbf{X}^\top \mathbf{P}_X = \mathbf{X}^\top$.
- $\text{rank}(\mathbf{X}) = \text{rank}(\mathbf{P}_X) = \text{tr}(\mathbf{P}_X)$.

Fitted Values and Residuals

An estimate $\hat{\beta}$ is a least squares estimate if and only if

$$\mathbf{X}\hat{\beta} = \mathbf{P}_X \mathbf{y}.$$

The OLS estimator of $\mathbb{E}(\mathbf{y})$ is

$$\hat{\mathbf{y}} = \mathbf{P}_X \mathbf{y}.$$

The residual vector is

$$\hat{\mathbf{e}} = \mathbf{y} - \hat{\mathbf{y}} = (\mathbf{I} - \mathbf{P}_X)\mathbf{y}.$$

Note that

$$\hat{\mathbf{e}} \in \mathcal{N}(\mathbf{X}^\top).$$

Since $\mathcal{C}(\mathbf{X})$ and $\mathcal{N}(\mathbf{X}^\top)$ are orthogonal complements, we obtain the unique decomposition

$$\mathbf{y} = \hat{\mathbf{y}} + \hat{\mathbf{e}}.$$

ANOVA Decomposition for the Linear Model

Suppose y is $n \times 1$, X is $n \times p$ with rank $r \leq p$, β is $p \times 1$, and ε is $n \times 1$. We assume the model given in (1):

$$y = X\beta + \varepsilon.$$

Then, the ANOVA table is:

Source	df	Sum of Squares
Model	r	$\hat{y}^\top \hat{y} = y^\top P_X y$
Residual	$n - r$	$\hat{e}^\top \hat{e} = y^\top (I - P_X) y$
Total	$n - 1$	$y^\top y = y^\top I y$

Starting on estimability

For any $q \times n$ matrix A , $AE(y)$ is a linear function of $E(y)$.

For any $q \times n$ matrix A , the OLS estimator of

$$AE(y) = AX\beta$$

is

$$A[\text{OLS Estimator of } E(y)] = A\hat{y} = AP_X y = AX(X^\top X)^{-1}X^\top y.$$

Note that

$$AE(y) = AX\beta$$

is automatically a linear function of β of the form

$$C\beta,$$

where

$$C = AX.$$

If C is any $q \times p$ matrix, we say that the linear function of β given by $C\beta$ is **estimable** if and only if

$$C = AX$$

for some $q \times n$ matrix A .

The OLS estimator of an estimable linear function $C\beta$ is

$$C(X^\top X)^{-1}X^\top y.$$

Uniqueness of the OLS Estimator of an Estimable $C\beta$

If $C\beta$ is estimable, then $C\hat{\beta}$ is the same for all solutions $\hat{\beta}$ to the normal equations.

In particular, the unique OLS estimator of $C\beta$ is

$$C\hat{\beta} = C(X^\top X)^{-1}X^\top y = AX(X^\top X)^{-1}X^\top y = AP_X y,$$

where $C = AX$.

Furthermore, if $C\beta$ is estimable, then $C\hat{\beta}$ is a **linear unbiased estimator** of $C\beta$.

The OLS estimator is linear because it is a linear function of y :

$$C\hat{\beta} = C(X^\top X)^{-1}X^\top y = My,$$

where

$$M = C(X^\top X)^{-1}X^\top.$$

The OLS estimator is unbiased because, for all $\beta \in \mathbb{R}^p$,

$$\begin{aligned} E(C\hat{\beta}) &= E(C(X^\top X)^{-1}X^\top y) \\ &= C(X^\top X)^{-1}X^\top E(y) \\ &= AX(X^\top X)^{-1}X^\top X\beta \\ &= AP_X X\beta \\ &= AX\beta \\ &= C\beta. \end{aligned}$$

Gauss–Markov Model (GMM)

Suppose

$$y = X\beta + \varepsilon,$$

where

- $y \in \mathbb{R}^n$ is the response vector,
- X is an $n \times p$ matrix of known constants,
- $\beta \in \mathbb{R}^p$ is an unknown parameter vector, and
- ε is a vector of random errors satisfying

$$E(\varepsilon) = 0, \quad \text{Var}(\varepsilon) = \sigma^2 I,$$

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

Gauss–Markov Theorem.

The OLS estimator of an estimable function $C\beta$ is the **Best Linear Unbiased Estimator (BLUE)** of $C\beta$, in the sense that it has the smallest variance among all linear unbiased estimators of $C\beta$.

Gauss–Markov Model with Normal Errors (GMMNE)

Suppose

$$y = X\beta + \varepsilon,$$

where

- $y \in \mathbb{R}^n$,
- X is an $n \times p$ matrix of known constants,
- $\beta \in \mathbb{R}^p$ is unknown, and
- $\varepsilon \sim \mathcal{N}(0, \sigma^2 I)$.

Distribution of $C\hat{\beta}$ and $\hat{\sigma}^2$

In the GMMNE model, the distribution of $C\hat{\beta}$ is

$$C\hat{\beta} \sim \mathcal{N}(C\beta, \sigma^2 C(X^\top X)^{-1} C^\top).$$

The distribution of $\hat{\sigma}^2$ is a scaled chi-square distribution:

$$\frac{(n-r)\hat{\sigma}^2}{\sigma^2} \sim \chi_{n-r}^2,$$

equivalently,

$$\hat{\sigma}^2 \sim \frac{\sigma^2}{n-r} \chi_{n-r}^2.$$

Moreover,

$C\hat{\beta}$ and $\hat{\sigma}^2$ are independent.

F-Test

For $H_0 : C\beta = d$

To test

$$H_0 : C\beta = d,$$

use the statistic

$$F = \frac{(C\hat{\beta} - d)^\top \left[\text{Var}(C\hat{\beta}) \right]^{-1} (C\hat{\beta} - d)}{q}.$$

Since

$$\text{Var}(C\hat{\beta}) = \sigma^2 C(X^\top X)^{-1} C^\top,$$

this becomes

$$F = \frac{(C\hat{\beta} - d)^\top [C(X^\top X)^{-1} C^\top]^{-1} (C\hat{\beta} - d)/q}{\hat{\sigma}^2}.$$

Under H_0 , F follows an F distribution with

$$q \quad \text{and} \quad n - r$$

degrees of freedom.

Under the alternative, F has a noncentral F distribution with noncentrality parameter

$$\theta = \frac{(C\beta - d)^\top [C(X^\top X)^{-1} C^\top]^{-1} (C\beta - d)}{2\sigma^2}.$$

The non-negative non-centrality parameter

$$\frac{(C\beta - d)^\top [C(X^\top X)^{-1} C^\top]^{-1} (C\beta - d)}{2\sigma^2}$$

is equal to zero if and only if $H_0 : C\beta = d$ is true.

If $H_0 : C\beta = d$ is true, the statistic F has a **central** F -distribution with

$$q \quad \text{and} \quad n - r$$

degrees of freedom, denoted $F_{q,n-r}$.

t-Test

For $(H_0 : c^\top \beta = d)$ for Estimable $c^\top \beta$

Here, c^\top is a row vector and d is a scalar ($q = 1$).

The test statistic is

$$t \equiv \frac{c^\top \hat{\beta} - d}{\sqrt{\widehat{\text{Var}}(c^\top \hat{\beta})}} = \frac{c^\top \hat{\beta} - d}{\sqrt{\hat{\sigma}^2 c^\top (X^\top X)^{-1} c}}.$$

The statistic t has a non-central t -distribution with noncentrality parameter

$$\frac{c^\top \beta - d}{\sqrt{\sigma^2 c^\top (X^\top X)^{-1} c}},$$

and degrees of freedom

$$n - r.$$

The non-centrality parameter

$$\frac{c^\top \beta - d}{\sqrt{\sigma^2 c^\top (X^\top X)^{-1} c}}$$

is equal to zero if and only if $H_0 : c^\top \beta = d$ is true.

If $H_0 : c^\top \beta = d$ is true, the statistic t has a **central** t -distribution with

$$n - r$$

degrees of freedom, denoted t_{n-r} .

Confidence Interval

For Estimable $c^\top \beta$, a $100(1 - \alpha)\%$ confidence interval for estimable $c^\top \beta$ is given by

$$c^\top \hat{\beta} \pm t_{n-r, 1-\alpha/2} \sqrt{\hat{\sigma}^2 c^\top (X^\top X)^{-1} c}.$$

That is,

estimate \pm (distribution quantile) \times (estimated standard error).

Reduced vs. Full

Model and Hypotheses

Assume the Gauss–Markov model with normal errors:

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

Suppose $\mathcal{C}(X_0) \subset \mathcal{C}(X)$ and we wish to test

$$H_0 : E(y) \in \mathcal{C}(X_0) \quad \text{vs.} \quad H_A : E(y) \in \mathcal{C}(X) \setminus \mathcal{C}(X_0).$$

- The *reduced* model corresponds to the null hypothesis and states that

$$E(y) \in \mathcal{C}(X_0),$$

a specified subspace of $\mathcal{C}(X)$.

- The *full* model states that $E(y)$ can be anywhere in $\mathcal{C}(X)$.

Example

Suppose a reduced model is that every group has the same mean, and suppose the full model has every group has a unique mean.

Given:

$$X_0 = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}$$

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

Model Interpretation:

- The **reduced model** says we assume the same mean for all observations:

$$E(y) = \mu$$

This corresponds to the design matrix X_0 .

- The **full model** says there are 3 distinct means: each group (of size 2) has its own mean.
This corresponds to the design matrix X , which is a 4×3 matrix (though it codes for 3 groups).

Test Statistic

For the general case, consider the test statistic

$$F = \frac{y^\top (P_X - P_{X_0})y / [\text{rank}(X) - \text{rank}(X_0)]}{y^\top (I - P_X)y / [n - \text{rank}(X)]}.$$

- When the reduced model is correct, the numerator and denominator of the F statistic are both unbiased estimators of σ^2 , so F should be close to 1.
- When the reduced model is not correct, the numerator of the F statistic estimates something larger than σ^2 , so F should be larger than 1. Thus, values of F much larger than 1 are not consistent with the reduced model being correct.

Deriving the Distribution of F

Our main assumption about the model is

$$\varepsilon \sim \mathcal{N}(0, \sigma^2 I) \implies y \sim \mathcal{N}(X\beta, \sigma^2 I).$$

Recall the following result:

- Suppose Σ is an $n \times n$ positive definite matrix.
- Suppose A is an $n \times n$ symmetric matrix of rank m such that $A\Sigma$ is idempotent (i.e., $A\Sigma A\Sigma = A\Sigma$).

Then, if $y \sim \mathcal{N}(\mu, \Sigma)$,

$$y^\top A y \sim \chi_m^2 \left(\frac{\mu^\top A \mu}{2} \right).$$

Distribution of the Numerator

For the numerator of our F statistic, we have

$$\mu = X\beta, \quad \Sigma = \sigma^2 I, \quad A = \frac{P_X - P_{X_0}}{\sigma^2}.$$

The rank is

$$\begin{aligned} m &= \text{rank}(A) = \text{rank}\left(\frac{P_X - P_{X_0}}{\sigma^2}\right) = \text{rank}(P_X - P_{X_0}) \\ &= \text{tr}(P_X - P_{X_0}) = \text{tr}(P_X) - \text{tr}(P_{X_0}) \\ &= \text{rank}(P_X) - \text{rank}(P_{X_0}) = \text{rank}(X) - \text{rank}(X_0). \end{aligned}$$

Therefore,

$$\frac{y^\top (P_X - P_{X_0}) y}{\sigma^2} \sim \chi_{\text{rank}(X) - \text{rank}(X_0)}^2(\theta),$$

where

$$\theta = \frac{1}{2} \beta^\top X^\top \left(\frac{P_X - P_{X_0}}{\sigma^2} \right) X \beta.$$

Distribution of the Denominator

The denominator (mean squared error) is

$$\text{MSE} = \frac{y^\top (I - P_X) y}{n - \text{rank}(X)}.$$

Its distribution is

$$\frac{y^\top (I - P_X) y}{\sigma^2} \sim \chi_{n - \text{rank}(X)}^2.$$

This distributional result holds regardless of whether or not the reduced model is correct.

Independence of Numerator and Denominator

We can show that

$$\frac{y^\top (P_X - P_{X_0})y}{\sigma^2} \perp \frac{y^\top (I - P_X)y}{\sigma^2},$$

because

$$\left(\frac{P_X - P_{X_0}}{\sigma^2} \right) (\sigma^2 I) \left(\frac{I - P_X}{\sigma^2} \right) = 0.$$

Indeed,

$$\begin{aligned} \frac{1}{\sigma^2} (P_X - P_X P_X - P_{X_0} + P_{X_0} P_X) &= \frac{1}{\sigma^2} (P_X - P_X - P_{X_0} + P_{X_0}) \\ &= 0. \end{aligned}$$

Distribution of F

Thus, it follows that

$$F = \frac{y^\top (P_X - P_{X_0})y / [\text{rank}(X) - \text{rank}(X_0)]}{y^\top (I - P_X)y / [n - \text{rank}(X)]} \sim F_{\text{rank}(X) - \text{rank}(X_0), n - \text{rank}(X)}(\theta),$$

where

$$\theta = \frac{\beta^\top X^\top (P_X - P_{X_0}) X \beta}{2\sigma^2}.$$

Noncentrality Parameter

- If H_0 is true, i.e., if $E(y) = X\beta \in \mathcal{C}(X_0)$, then the noncentrality parameter θ is 0 because

$$(P_X - P_{X_0})X\beta = P_X X\beta - P_{X_0} X\beta = X\beta - X\beta = 0.$$

Hence,

$$\frac{y^\top (P_X - P_{X_0})y}{\sigma^2} \sim \chi^2_{\text{rank}(X) - \text{rank}(X_0)},$$

a central χ^2 distribution.

- If H_0 is false and $E(y) = X\beta \notin \mathcal{C}(X_0)$, then $(P_X - P_{X_0})X\beta \neq 0$ and $\theta > 0$. Hence,

$$\frac{y^\top (P_X - P_{X_0})y}{\sigma^2} \sim \chi^2_{\text{rank}(X) - \text{rank}(X_0)}(\theta).$$

In general, the noncentrality parameter quantifies how far the mean of y is from $\mathcal{C}(X_0)$ because

$$\begin{aligned}\beta^\top X^\top (P_X - P_{X_0})X\beta &= \beta^\top X^\top (P_X - P_{X_0})^\top (P_X - P_{X_0})X\beta \\ &= \|(P_X - P_{X_0})X\beta\|^2 = \|P_X X\beta - P_{X_0} X\beta\|^2 \\ &= \|X\beta - P_{X_0} X\beta\|^2 = \|E(y) - P_{X_0} E(y)\|^2.\end{aligned}$$

If $E(y)$ indeed lies in $\mathcal{C}(X_0)$, then $P_{X_0} E(y) = E(y)$.

Useful Identities

Note that

$$\begin{aligned}y^\top (P_X - P_{X_0})y &= y^\top [(I - P_{X_0}) - (I - P_X)]y \\ &= y^\top (I - P_{X_0})y - y^\top (I - P_X)y \\ &= \text{SSE}_{\text{REDUCED}} - \text{SSE}_{\text{FULL}}.\end{aligned}$$

Also,

$$\begin{aligned}\text{rank}(X) - \text{rank}(X_0) &= [n - \text{rank}(X_0)] - [n - \text{rank}(X)] \\ &= \text{DFE}_{\text{REDUCED}} - \text{DFE}_{\text{FULL}},\end{aligned}$$

where DFE denotes degrees of freedom for error.

Result

Thus, the F statistic has the familiar form

$$F = \frac{(\text{SSE}_{\text{REDUCED}} - \text{SSE}_{\text{FULL}})/(\text{DFE}_{\text{REDUCED}} - \text{DFE}_{\text{FULL}})}{\text{SSE}_{\text{FULL}}/\text{DFE}_{\text{FULL}}}.$$

Equivalence of F -Tests

It turns out that this reduced vs. full model F -test is equivalent to the F -test for testing

$$H_0 : C\beta = d \quad \text{vs.} \quad H_A : C\beta \neq d,$$

with an appropriately chosen C and d .

Two-Factor Cell-Means Models

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 \times 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.

Factors, Levels, Design

This experiment involves 2 factors: **Diet** and **Drug**.

- The factor **Diet** has 2 levels: low fiber and high fiber.
- The factor **Drug** has 3 levels: D1, D2, and D3.

Treatment Design vs. Experimental Design

- A combination of one level from each factor forms a *treatment*.
- The *treatment design* used in this experiment is known as a **full-factorial treatment design** because each possible combination of one level from each factor was applied to at least one experimental unit.
- The *experimental design* is a balanced **completely randomized design (CRD)** because all possible balanced assignments of the 12 pigs to the 6 treatment groups were equally likely.

The Cell-Means Model

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

$$y_{ijk} = \mu_{ij} + \varepsilon_{ijk}, \quad \varepsilon_{ijk} \stackrel{\text{iid}}{\sim} \mathcal{N}(0, \sigma^2).$$

Here,

$$(\mu_{11}, \mu_{12}, \mu_{13}, \mu_{21}, \mu_{22}, \mu_{23}) \in \mathbb{R} \quad \text{and} \quad \sigma^2 \in \mathbb{R}^+$$

are unknown parameters. The μ_{ij} represent the *treatment (cell) means*.

A cell-means table is given by

	Drug 1	Drug 2	Drug 3
Diet 1	μ_{11}	μ_{12}	μ_{13}
Diet 2	μ_{21}	μ_{22}	μ_{23}

Estimability of β

For the General Linear Model, the parameter vector β is estimable whenever X has full column rank, i.e.,

$$\text{rank}(X) = p.$$

Least Squares Means (LSMEANS) in SAS

SAS can be used to compute LSMEANS.

LSMEANS are simply OLS estimators of cell or marginal means.

Each LSMEAN has the form

$$c^\top \hat{\beta}$$

for an appropriate vector c .

For example, the LSMEAN for Diet 1 is $c^\top \hat{\beta}$ with

$$c^\top = \left[\frac{1}{3}, \frac{1}{3}, \frac{1}{3}, 0, 0, 0 \right], \quad \hat{\beta} = [\bar{y}_{11.}, \bar{y}_{12.}, \bar{y}_{13.}, \bar{y}_{21.}, \bar{y}_{22.}, \bar{y}_{23.}]^\top.$$

Thus, the LSMEAN for Diet 1 is

$$\frac{\bar{y}_{11.} + \bar{y}_{12.} + \bar{y}_{13.}}{3},$$

an estimator of the marginal mean $\mu_{1..}$.

Note that the LSMEAN for Diet 1 is simply an average of the estimated means for treatments involving Diet 1.

When data are balanced, the LSMEAN for Diet 1 is also just the average of responses for all pigs that were fed Diet 1.

When data are unbalanced, the LSMEAN for Diet 1 may not equal the average of responses for all pigs that were fed Diet 1.

Standard Error

A *standard error* is the estimated standard deviation of a statistic.

A standard error is usually found by estimating the variance of a statistic and then taking the square root of the estimate.

Because each LSMEAN has the form $c^\top \hat{\beta}$ for an appropriate vector c , the standard error for an LSMEAN is given by

$$\sqrt{\widehat{\text{Var}}(c^\top \hat{\beta})} = \sqrt{\hat{\sigma}^2 c^\top (X^\top X)^{-1} c}.$$

Effects We Can Estimate

- Simple effects
- Main effects
- Interactions

Simple Effects

A **simple effect** is the difference between cell means that differ in level for only one factor.

In our two-factor example, simple effects are differences between cell means within any row or within any column.

Consider a two-factor layout:

- **Simple effect of diet within drug 1** compares μ_{11} (diet 1, drug 1) and μ_{21} (diet 2, drug 1).
- Similarly, **simple effect of drug** can be examined within a fixed diet level.

For example: - Drug 1, Diet 1 vs. Diet 2 → Simple effect of Diet within Drug 1 - Diet 1, Drug 2 vs. Drug 3 → Simple effect of Drug within Diet 1

Note: A contrast such as $\mu_{22} - \mu_{13}$ is **not** a simple effect, because it differs in both factors (diet and drug).

Continued

The simple effect of **Diet for Drug 1** is:

$$\mu_{11} - \mu_{21}$$

The simple effect of **Drug 2 vs. Drug 3 for Diet 2** is:

$$\mu_{22} - \mu_{23}$$

Where μ_{ij} denotes the mean response for diet i and drug j .

Main Effects

A *main effect* is the difference between marginal means associated with two levels of a factor.

In our two-factor example, the *main effect* of Diet is

$$\bar{\mu}_{1\cdot} - \bar{\mu}_{2\cdot}$$

In our two-factor example, the *main effects* of Drug involve the differences

$$\bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 2}, \quad \bar{\mu}_{\cdot 1} - \bar{\mu}_{\cdot 3}, \quad \text{and} \quad \bar{\mu}_{\cdot 2} - \bar{\mu}_{\cdot 3}.$$

If

$$\bar{\mu}_{1\cdot} = \bar{\mu}_{2\cdot},$$

it would be customary to say, “There is no Diet main effect.”

If

$$\bar{\mu}_{\cdot 1} = \bar{\mu}_{\cdot 2} = \bar{\mu}_{\cdot 3},$$

it would be customary to say, “There are no Drug main effects.”

Interaction Effects

The linear combination

$$\mu_{ij} - \mu_{ij'} - \mu_{i'j} + \mu_{i'j'}$$

for $i \neq i'$ and $j \neq j'$ is an interaction effect.

Every interaction can be expressed using this format.

For example,

$$\mu_{11} - \mu_{12} - \mu_{21} + \mu_{22} = (\mu_{11} - \mu_{12}) - (\mu_{21} - \mu_{22}) = (\mu_{11} - \mu_{21}) - (\mu_{12} - \mu_{22})$$

is an interaction effect.

These contrasts are equal if there is no interaction.

Continued

When all interaction effects are zero, we may say there are “no interactions” between the factors, or that the two factors do not interact.

When there are no interactions between factors, the simple effects of either factor are the same across all levels of the other factor.

For example, when there are no interactions between the factors Diet and Drug, the simple effect of Diet is the same for each level of Drug.

Likewise, any simple effect of Drug is the same for both diets.

Testing for Non-Zero Effects

We can test whether simple effects, main effects, or interaction effects are zero versus non-zero using tests of the form

$$H_0 : C\beta = \mathbf{0} \quad \text{vs.} \quad H_A : C\beta \neq \mathbf{0}.$$

To properly set up C , look at β and how the parameters are arranged in β .

Alternative Parametrization of Two-Factor Cell-Means Models

An alternative parameterization of the cell-means model is

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

Here, $-\mu$ is the intercept (overall mean), $-\alpha_i$ is the effect associated with Diet, $-\beta_j$ is the effect associated with Drug, $-\gamma_{ij}$ is the interaction between Diet and Drug.

The parameters

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

are unknown real-valued parameters, and

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

are independent and identically distributed with

$$\varepsilon_{ijk} \stackrel{\text{iid}}{\sim} \mathcal{N}(0, \sigma^2),$$

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

Cell and Marginal Means

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

The cell means are

$$\mu + \alpha_i + \beta_j + \gamma_{ij}.$$

The Diet marginal means are

$$\bar{\mu}_{1\cdot} = \mu + \alpha_1 + \bar{\beta}_+ + \bar{\gamma}_{1\cdot}, \quad \bar{\mu}_{2\cdot} = \mu + \alpha_2 + \bar{\beta}_+ + \bar{\gamma}_{2\cdot}.$$

Thus, the main effect of Diet is

$$\bar{\mu}_{1\cdot} - \bar{\mu}_{2\cdot} = \alpha_1 - \alpha_2 + \bar{\gamma}_{1\cdot} - \bar{\gamma}_{2\cdot}.$$

An example of a simple effect of Drug within Diet 1 is

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

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:

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

which simplifies to

$$\gamma_{11} - \gamma_{13} - \gamma_{21} + \gamma_{23}.$$

Estimation and Testing

As before, estimation or testing involves finding an appropriate matrix C to estimate $C\beta$ or test

$$H_0 : C\beta = 0.$$

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

$$F = \frac{\mathbf{y}^\top (P_X - P_{X_0})\mathbf{y} / [\text{rank}(X) - \text{rank}(X_0)]}{\mathbf{y}^\top (I - P_X)\mathbf{y} / [n - \text{rank}(X)]},$$

for an appropriate reduced model matrix X_0 .

It is not always easy to specify an appropriate matrix X_0 .

Misc

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.”

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*.

Missing Cells

Consider the following layout with a missing cell (no data for Diet 2 with Drug 2):

	Drug 1	Drug 2	Drug 3
Diet 1	μ_{11}	μ_{12}	μ_{13}
Diet 2	μ_{21}	Missing	μ_{23}

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:

$$\mu_{11}, \mu_{12}, \mu_{13}, \mu_{21}, \text{ and } \mu_{23}.$$

We could estimate any linear combination of these 5 means.

However, linear combinations involving μ_{22} are **not estimable** because there is no data for that treatment combination.

Two Factor Additive Models

When factors do not interact, it makes sense to consider the *additive model*:

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

Here, - $\mu, \alpha_1, \alpha_2, \beta_1, \beta_2, \beta_3$ are unknown real-valued parameters, and -

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

are independent and identically distributed with

$$\varepsilon_{ijk} \stackrel{\text{iid}}{\sim} \mathcal{N}(0, \sigma^2),$$

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

Cell Means for the Additive Model

- All interactions are zero for the additive model.
- The simple effect of Diet is $\alpha_1 - \alpha_2$ for all levels of Drug.
- The simple effect of Drug j vs. Drug j' is $\beta_j - \beta_{j'}$, regardless of Diet.

The table of cell means is:

	Drug 1	Drug 2	Drug 3
Diet 1	$\mu + \alpha_1 + \beta_1$	$\mu + \alpha_1 + \beta_2$	$\mu + \alpha_1 + \beta_3$
Diet 2	$\mu + \alpha_2 + \beta_1$	$\mu + \alpha_2 + \beta_2$	$\mu + \alpha_2 + \beta_3$

The marginal mean difference for Diet is

$$\bar{\mu}_{1\cdot} - \bar{\mu}_{2\cdot} = \alpha_1 - \alpha_2.$$

Estimation of α_1 and α_2 uses all available data across all three levels of Drug.

Marginal Means for the Additive Model

Averaging over Drug yields the Diet marginal means:

$$\mu + \alpha_1 + \bar{\beta}, \quad \mu + \alpha_2 + \bar{\beta},$$

where

$$\bar{\beta} = \frac{\beta_1 + \beta_2 + \beta_3}{3}.$$

Thus, the difference between Diet marginal means is

$$(\mu + \alpha_1 + \bar{\beta}) - (\mu + \alpha_2 + \bar{\beta}) = \alpha_1 - \alpha_2.$$

Averaging over Diet yields the Drug marginal means:

$$\mu + \bar{\alpha} + \beta_j,$$

where

$$\bar{\alpha} = \frac{\alpha_1 + \alpha_2}{2}.$$

Differences such as $\beta_1 - \beta_2$ or $\beta_2 - \beta_3$ represent main effects of Drug.

Tests for Main Effects in the Additive Model

No Diet main effect is equivalent to

$$\alpha_1 = \alpha_2.$$

No Drug main effects is equivalent to

$$\beta_1 = \beta_2 = \beta_3.$$

LSMEANS for the Additive Model

LSMEANS are OLS estimators of the quantities in the margins below.

The Diet marginal LSMEANS are

$$\mu + \alpha_1 + \bar{\beta}, \quad \mu + \alpha_2 + \bar{\beta}.$$

The Drug marginal LSMEANS are

$$\mu + \bar{\alpha} + \beta_1, \quad \mu + \bar{\alpha} + \beta_2, \quad \mu + \bar{\alpha} + \beta_3.$$

For example, the LSMEAN for Diet 1 can be written as

$$c^\top \hat{\beta} = [1 \ 1 \ 0 \ \frac{1}{3} \ \frac{1}{3} \ \frac{1}{3}] \begin{bmatrix} \hat{\mu} \\ \hat{\alpha}_1 \\ \hat{\alpha}_2 \\ \hat{\beta}_1 \\ \hat{\beta}_2 \\ \hat{\beta}_3 \end{bmatrix} = \hat{\mu} + \hat{\alpha}_1 + \frac{\hat{\beta}_1 + \hat{\beta}_2 + \hat{\beta}_3}{3}.$$

Here, $\hat{\beta}$ is any solution to the Normal Equations.

Although $\hat{\beta}$ depends on which of infinitely many solutions is used, the quantity $c^\top \hat{\beta}$ is the same for all solutions.

R Full-Rank Formulation

Under the R full-rank (treatment-coded) formulation for the additive model, the table of means is:

	Drug 1	Drug 2	Drug 3	Diet Marginal
Diet 1	μ	$\mu + \beta_2$	$\mu + \beta_3$	$\mu + \frac{\beta_2 + \beta_3}{3}$
Diet 2	$\mu + \alpha_2$	$\mu + \alpha_2 + \beta_2$	$\mu + \alpha_2 + \beta_3$	$\mu + \alpha_2 + \frac{\beta_2 + \beta_3}{3}$
Drug Marginal	$\mu + \frac{\alpha_2}{2}$	$\mu + \frac{\alpha_2}{2} + \beta_2$	$\mu + \frac{\alpha_2}{2} + \beta_3$	$\mu + \frac{\alpha_2}{2} + \frac{\beta_2 + \beta_3}{3}$

Main Effects

This parameterization differs from the earlier sum-to-zero setup and instead uses a full-rank model matrix.

No Diet main effect is equivalent to

$$\alpha_2 = 0.$$

No Drug main effects is equivalent to

$$\beta_2 = \beta_3 = 0.$$

Under $\beta_2 = \beta_3 = 0$, all Drug marginal means collapse to the same value.

Diet Main Effect

The null hypothesis of no Diet main effect is

$$H_0 : \alpha_2 = 0.$$

This can be written in matrix form as

$$C^\top \beta = 0,$$

where

$$C^\top = [0 \ 1 \ 0 \ 0], \quad \beta = \begin{bmatrix} \mu \\ \alpha_2 \\ \beta_2 \\ \beta_3 \end{bmatrix}.$$

Drug Main Effects

The null hypothesis of no Drug main effects is

$$H_0 : \beta_2 = \beta_3 = 0.$$

This can be written as

$$C\beta = \begin{bmatrix} 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \mu \\ \alpha_2 \\ \beta_2 \\ \beta_3 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}.$$

ANOVA

Setup and Notation

We consider the general linear model

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

Let

$$\mathbf{X}_1 = \mathbf{1}, \quad \mathbf{X}_m = \mathbf{X}, \quad \mathbf{X}_{m+1} = \mathbf{I}.$$

Suppose $\mathbf{X}_2, \dots, \mathbf{X}_m$ are matrices satisfying the nested column space condition

$$\mathcal{C}(\mathbf{X}_1) \subset \mathcal{C}(\mathbf{X}_2) \subset \dots \subset \mathcal{C}(\mathbf{X}_m).$$

Let

$$\mathbf{P}_j = \mathbf{P}_{\mathbf{X}_j}, \quad r_j = \text{rank}(\mathbf{X}_j), \quad j = 1, \dots, m+1.$$

The Total Sum of Squares

The **total sum of squares** (also called the corrected total sum of squares) is

$$\sum_{i=1}^n (y_i - \bar{y})^2.$$

In matrix form,

$$\sum_{i=1}^n (y_i - \bar{y})^2 = (\mathbf{y} - \bar{y}\mathbf{1})^\top (\mathbf{y} - \bar{y}\mathbf{1}) = (\mathbf{y} - \mathbf{P}_1\mathbf{y})^\top (\mathbf{y} - \mathbf{P}_1\mathbf{y}).$$

Since \mathbf{P}_1 is symmetric and idempotent,

$$\sum_{i=1}^n (y_i - \bar{y})^2 = \mathbf{y}^\top (\mathbf{I} - \mathbf{P}_1)\mathbf{y}.$$

Partitioning the Total Sum of Squares

Recall that $\mathbf{X}_{m+1} = \mathbf{I}$, so $\mathbf{P}_{m+1} = \mathbf{I}$. Then

$$\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_1)\mathbf{y} = \mathbf{y}^\top (\mathbf{P}_{m+1} - \mathbf{P}_1)\mathbf{y}.$$

Insert intermediate projections:

$$\mathbf{y}^\top (\mathbf{P}_{m+1} - \mathbf{P}_1)\mathbf{y} = \mathbf{y}^\top \left(\sum_{j=2}^{m+1} \mathbf{P}_j - \sum_{j=1}^m \mathbf{P}_j \right) \mathbf{y}.$$

Rearranging,

$$\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_1) \mathbf{y} = \mathbf{y}^\top (\mathbf{P}_{m+1} - \mathbf{P}_m) \mathbf{y} + \cdots + \mathbf{y}^\top (\mathbf{P}_2 - \mathbf{P}_1) \mathbf{y}.$$

Equivalently,

$$\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_1) \mathbf{y} = \sum_{j=1}^m \mathbf{y}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{y}.$$

Sums of Squares Representation

The quantities in

$$\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_1) \mathbf{y} = \sum_{j=1}^m \mathbf{y}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{y}$$

are often arranged in an ANOVA table.

We define

$$\text{SS}(j+1 | j) = \mathbf{y}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{y}.$$

In particular,

$$\text{SSE} = \mathbf{y}^\top (\mathbf{I} - \mathbf{P}_X) \mathbf{y}.$$

Interpretation of Sequential Sums of Squares

Note that

$$\begin{aligned} \text{SS}(j+1 | j) &= \mathbf{y}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{y} \\ &= \mathbf{y}^\top (\mathbf{I} - \mathbf{P}_j) \mathbf{y} - \mathbf{y}^\top (\mathbf{I} - \mathbf{P}_{j+1}) \mathbf{y} \\ &= \text{SSE}_j - \text{SSE}_{j+1}. \end{aligned}$$

Thus, $\text{SS}(j+1 | j)$ is the **reduction in error sum of squares** when projecting \mathbf{y} onto

$$\mathcal{C}(\mathbf{X}_{j+1}) \quad \text{instead of} \quad \mathcal{C}(\mathbf{X}_j).$$

Sequential (Type I) Sums of Squares

The quantities

$$\text{SS}(j+1 | j), \quad j = 1, \dots, m-1,$$

are called **Sequential Sums of Squares**.

In SAS terminology, these are known as **Type I Sums of Squares**.

Generally, the Type (I, II, III, IV) will refer to what elements of the ANOVA table are being conditioned on, particularly the first element of the table.

Properties of the Matrices of the Quadratic Forms

The matrices of the quadratic forms in the ANOVA table have several useful properties:

- **Symmetry**

$$A = A^T$$

- **Idempotency**

$$A^2 = A$$

- **Rank relationship**

$$\text{rank}(P_{j+1} - P_j) = r_{j+1} - r_j$$

- **Zero Cross-Products**

$$(P_{j+1} - P_j)(P_{k+1} - P_k) = 0 \text{ for } j \neq k$$

Distribution of Scaled ANOVA Sums of Squares

Given $y \sim N(X\beta, \sigma^2 I)$ and an idempotent matrix A :

$$y^T A y \sim \sigma^2 \chi_{\text{rank}(A)}^2 \left(\frac{\beta^T X^T A X \beta}{2\sigma^2} \right)$$

Specifically, for the projection matrices P_j in the nested sequence:

Because

$$\frac{P_{j+1} - P_j}{\sigma^2} \cdot \sigma^2 I = P_{j+1} - P_j$$

is idempotent,

we have:

$$y^T (P_{j+1} - P_j) y \sim \sigma^2 \chi_{r_{j+1}-r_j}^2 \left(\frac{\beta^T X^T (P_{j+1} - P_j) X \beta}{2\sigma^2} \right)$$

for all $j = 1, \dots, m$.

ANOVA Tables

ANOVA with Degrees of Freedom

Consider the sequential sums of squares

$$\mathbf{y}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{y}, \quad j = 1, \dots, m.$$

Each line in the ANOVA table corresponds to a number of degrees of freedom equal to the increase in rank when moving from \mathbf{X}_j to \mathbf{X}_{j+1} .

ANOVA Table with degrees of freedom is:

Sum of Squares	Degrees of Freedom	DF
$\mathbf{y}^\top (\mathbf{P}_2 - \mathbf{P}_1) \mathbf{y}$	$\text{rank}(\mathbf{X}_2) - \text{rank}(\mathbf{X}_1)$	$r_2 - 1$
$\mathbf{y}^\top (\mathbf{P}_3 - \mathbf{P}_2) \mathbf{y}$	$\text{rank}(\mathbf{X}_3) - \text{rank}(\mathbf{X}_2)$	$r_3 - r_2$
\vdots	\vdots	\vdots
$\mathbf{y}^\top (\mathbf{P}_m - \mathbf{P}_{m-1}) \mathbf{y}$	$\text{rank}(\mathbf{X}_m) - \text{rank}(\mathbf{X}_{m-1})$	$r - r_{m-1}$
$\mathbf{y}^\top (\mathbf{P}_{m+1} - \mathbf{P}_m) \mathbf{y}$	$\text{rank}(\mathbf{X}_{m+1}) - \text{rank}(\mathbf{X}_m)$	$n - r$
$\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_1) \mathbf{y}$	$\text{rank}(\mathbf{X}_{m+1}) - \text{rank}(\mathbf{X}_1)$	$n - 1$

ANOVA Table with Mean Squares

Dividing each sum of squares by its corresponding degrees of freedom yields the mean squares.

Sum of Squares	Degrees of Freedom	Mean Square
$\text{SS}(2 1)$	$r_2 - 1$	$\text{MS}(2 1)$
$\text{SS}(3 2)$	$r_3 - r_2$	$\text{MS}(3 2)$
\vdots	\vdots	\vdots
$\text{SS}(m m - 1)$	$r - r_{m-1}$	$\text{MS}(m m - 1)$
SSE	$n - r$	$\text{MSE} = \hat{\sigma}^2$
SST_0	$n - 1$	

Independence of ANOVA Sums of Squares

Because

$$(\mathbf{P}_{j+1} - \mathbf{P}_j)(\sigma^2 \mathbf{I})(\mathbf{P}_{\ell+1} - \mathbf{P}_\ell) = \mathbf{0} \quad \text{for } j \neq \ell,$$

any two ANOVA sums of squares (not including SST_0) are independent.

It is also true that the ANOVA sums of squares (not including SST_0) are *mutually independent* by Cochran's Theorem, although this stronger result is not usually needed.

ANOVA F Statistics

For $j = 1, \dots, m - 1$, define the ANOVA F statistic

$$F_j = \frac{\text{MS}(j+1 | j)}{\text{MSE}} = \frac{\mathbf{y}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{y} / (r_{j+1} - r_j)}{\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_x) \mathbf{y} / (n - r)}.$$

Under the general linear model,

$$F_j \sim F_{r_{j+1} - r_j, n-r}(\delta_j),$$

where the non-centrality parameter is

$$\delta_j = \frac{\beta^\top \mathbf{X}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{X} \beta}{2\sigma^2}.$$

Relationship with Reduced vs. Full Model F Statistic

The sequential ANOVA F_j statistic can be written as

$$F_j = \frac{\mathbf{y}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{y} / (r_{j+1} - r_j)}{\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_X) \mathbf{y} / (n - r)} = \frac{\text{MS}(j+1 | j)}{\text{MSE}}.$$

This matches the reduced vs. full model F statistic

$$F = \frac{\mathbf{y}^\top (\mathbf{P}_X - \mathbf{P}_{X_0}) \mathbf{y} / (r - r_0)}{\mathbf{y}^\top (\mathbf{I} - \mathbf{P}_X) \mathbf{y} / (n - r)}.$$

What Do ANOVA F -Statistics Test?

In general, an F statistic tests

$$H_0 : \text{the non-centrality parameter is } 0 \quad \text{vs.} \quad H_A : \text{the non-centrality parameter is not } 0.$$

For the sequential ANOVA statistic F_j , the non-centrality parameter is

$$\delta_j = \frac{\boldsymbol{\beta}^\top \mathbf{X}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{X} \boldsymbol{\beta}}{2\sigma^2}.$$

Thus, F_j can be used to test

$$H_{0j} : \boldsymbol{\beta}^\top \mathbf{X}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{X} \boldsymbol{\beta} = 0 \quad \text{vs.} \quad H_{Aj} : \boldsymbol{\beta}^\top \mathbf{X}^\top (\mathbf{P}_{j+1} - \mathbf{P}_j) \mathbf{X} \boldsymbol{\beta} \neq 0.$$

What Do ANOVA F -Statistics Test Pt. II?

Estimability does not necessarily imply testability.

In general, for the j -th sequential test we have:

$$H_{0j} : (P_{j+1} - P_j) X \boldsymbol{\beta} = 0 \quad \text{vs.} \quad H_{Aj} : (P_{j+1} - P_j) X \boldsymbol{\beta} \neq 0$$

which, in testable form, is:

$$H_{0j} : C_j \boldsymbol{\beta} = 0 \quad \text{vs.} \quad H_{Aj} : C_j \boldsymbol{\beta} \neq 0,$$

where C_j is any matrix whose $q = r_{j+1} - r_j$ rows form a basis for the row space of $(P_{j+1} - P_j) X$.

Hypothesis Testing Interpretation

Recall that $C \boldsymbol{\beta}$ is estimable if and only if

$$C = A \mathbf{X}$$

for some matrix A .

The hypotheses above can be written as

$$H_{0j} : (\mathbf{P}_{j+1} - \mathbf{P}_j)\mathbf{X}\beta = 0 \quad \text{vs.} \quad H_{Aj} : (\mathbf{P}_{j+1} - \mathbf{P}_j)\mathbf{X}\beta \neq 0.$$

This is of the form

$$H_{0j} : C_j^* \beta = 0 \quad \text{vs.} \quad H_{Aj} : C_j^* \beta \neq 0,$$

where

$$C_j^* = (\mathbf{P}_{j+1} - \mathbf{P}_j)\mathbf{X}.$$

As written, H_{0j} is not directly testable because C_j^* has n rows but rank

$$\text{rank}(C_j^*) = r_{j+1} - r_j < n.$$

We can rewrite H_{0j} as a testable hypothesis by replacing C_j^* with any matrix C_j whose

$$q = r_{j+1} - r_j$$

rows form a basis for the row space of C_j^* .

Example: Multiple Regression

In multiple linear regression, we consider a sequence of nested models:

$$X_1 = 1$$

$$X_2 = [1, x_1]$$

$$X_3 = [1, x_1, x_2]$$

⋮

$$X_m = [1, x_1, \dots, x_{m-1}]$$

Here, $SS(j+1|j)$ is the decrease in SSE that results when the explanatory variable x_j is added to a model containing an intercept and explanatory variables x_1, \dots, x_{j-1} .

Example: Polynomial Regression

For polynomial regression, the sequence is:

$$X_1 = 1$$

$$X_2 = [1, x]$$

$$X_3 = [1, x, x^2]$$

⋮

$$X_m = [1, x, x^2, \dots, x^{m-1}]$$

Here, $SS(j+1|j)$ is the decrease in SSE that results when the term x^j is added to a model containing an intercept and the lower-order terms x, x^2, \dots, x^{j-1} .

Aside: Centering and Standardizing for Numerical Stability

It is typically best for numerical stability to center and scale a quantitative explanatory variable prior to computing higher-order terms.

In the plant density example, we could replace x by

$$\frac{x - 30}{10}$$

and work with the transformed matrices.

Because these matrices have the same column spaces as the original matrices, the ANOVA table entries are **mathematically identical** for either set of matrices.

ANOVA Balanced Two Factor