BIOS 6612
Lecture 14
Repeated Measures ANOVA

Additional Reading:
KKMN Section 26.4.5

Review (Lecture 13)/ Current (Lecture 14)/ Preview (Lecture 15)

- Lecture 13: Linear Mixed Models

    - 2 time points per persons
        - Paired t-test
        - Linear regression
        - Random intercept model

    - Notation
    - Linear mixed models with a random intercept
    - Linear mixed models specifying the covariance structure

- Lecture 14: Repeated Measures ANOVA

    o ANOVA for repeated measurements

- Lecture 15: Modelling the Random Effects

$$Y = X\beta + Zb + \varepsilon \text{ and } V = Var(\mathbf{Y}) = \mathbf{ZGZ'} + \mathbf{R}$$

    o Specify the random effect b
    o Random intercept, random slope

RMANOVA

- Repeated measures ANOVA is the equivalent of the one-way ANOVA, but for <mark>related, not independent groups</mark>
    - o Test to detect any overall differences between related means

- ANOVA partitions total variability (SS_T) into between-groups variability (SS_b) and within-groups variability (SS_w)

- o In this design, <mark>within-group variability (SSw) is defined as the error variability (SSerror)</mark>
    - o F statistic= $MS_{model}/ MS_{error} = MS_b/MS_w$

- RMANOVA can <mark>further partition this error term,</mark> reducing its size

https://statistics.laerd.com/statistical-guides/repeated-measures-anova-statistical-guide.php
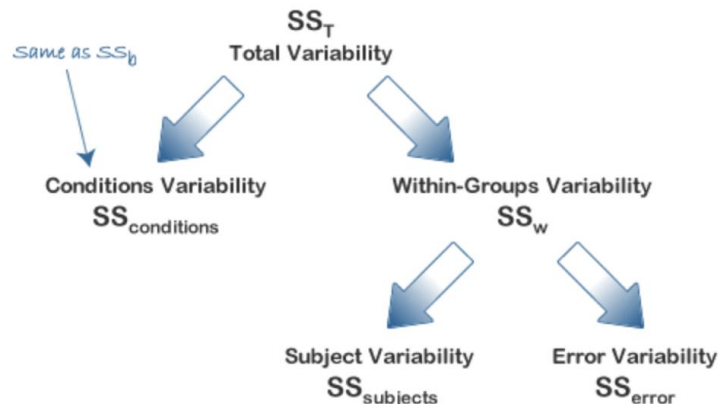
REVIEW: One-Way ANOVA

Respiratory Quotient (RQ), which measures the ratio between O_2 consumed and CO_2 produced, was measured for 15 participants after a week of consuming one of three diets of varying diet compositions.

	Standard Diet (n = 5)	High Fat Diet (n = 5)	Low Fat Diet (n = 5)
	0.80	0.77	0.83
	0.78	0.77	0.82
	0.82	0.80	0.87
	0.76	0.73	0.79
	0.83	0.83	0.86
Mean	0.798	0.780	0.834
Variance	0.00082	0.0014	0.00103

$\bar{Y} = 0.804$

$SD(Y) = 0.03832$

$SS_{Total} = 14 \times (0.03832)^2 = 0.02056$

$SS_{Diet} = 5 \times [(0.798\text{-}0.804)^2 + (0.780\text{-}0.804)^2 + (0.834\text{-}0.804)^2] = 0.00756$

$SS_{Error} = SS_{Total} - SS_{Diet} = 0.02056 - 0.00756 = 0.013$

$MS_{Error} = [(0.00082) + (0.0014) + (0.00103)] / 3 = 0.00108333 = s^2_p$

# diets-1=3-1=2	$df_{error}=df_{total}-df_{model}=14-2=12$	# subjects-1=15-1=14	$F= MS_{model}/MS_{Error}$

Source	Sum of Squares	d.f.	Mean Square	F	p-value
Model	0.00756	2	0.00378	3.489	0.0639
Error	0.013	12	0.00108333		
Total	0.02056	14			

When n are equal:

Estimate of MS_{Error} = $\overline{VAR}$
=(0.001030+.00082+0.0014)/3=0.00108333

For unequal n, MS_{Error} is a weighted average of the variances, with weights (n_k-1).

H_0: $\mu_{standard}$ = μ_{high} = μ_{low}
RQ does not differ significantly across the three diets.

$MS_{Error}=SS_{Error}/df_{Error}$

	Low Fat (n = 5)	Standard Fat (n = 5)	High Fat (n = 5)
Mean	0.834	0.798	0.780
Variance	0.00103	0.00082	0.0014

One-Way ANOVA Results

```
PROC GLM DATA=rq2;
 CLASS diet;
 MODEL rq = diet;
RUN;
```

The GLM Procedure

Class Level Information

Class	Levels	Values
diet	3	1 2 3

Number of Observations Read   15
Number of Observations Used   15

The GLM Procedure

Dependent Variable: rq

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	2	0.00756000	0.00378000	3.49	0.0639
Error	12	0.01300000	0.00108333		
Corrected Total	14	0.02056000			

R-Square	Coeff Var	Root MSE	rq Mean
0.367704	4.093785	0.032914	0.804000

Source	DF	Type I SS	Mean Square	F Value	Pr > F
diet	2	0.00756000	0.00378000	3.49	0.0639

Source	DF	Type III SS	Mean Square	F Value	Pr > F
diet	2	0.00756000	0.00378000	3.49	0.0639

H_0: $\mu_{standard} = \mu_{high} = \mu_{low}$
RQ does not differ significantly between the three diets.

One-way ANOVA: Results from R

```
respquot <- data.frame(subject=1:5,
                       standard=c(.8,.78,.82,.76,.83),
                       high.fat=c(.77,.77,.80,.73,.83),
                       low.fat=c(.83,.82,.87,.79,.86))
# put the data in "Long" format
respquot.long <- reshape(respquot,direction='long',
                       varying=2:4,
                       v.names='rq',
                       idvar='subject',
                       times=colnames(respquot)[-1],
                       timevar='diet')
# simple one-way ANOVA, ignoring repeated measures
mod1 <- lm(rq ~ diet,data=respquot.long)
anova(mod1)

## Analysis of Variance Table
##
## Response: rq
##            Df  Sum Sq   Mean Sq F value Pr(>F)
## diet        2 0.00756 0.0037800  3.4892 0.0639 .
## Residuals 12 0.01300 0.0010833
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Repeated Measures Data

Repeated Measures Data: The same outcome/response is measured on the same individual under multiple conditions (or at multiple times) or the same outcome/response is measured for clusters or groups of similar individuals.

Example: Respiratory Quotient (RQ), which measures the ratio between O_2 consumed and CO_2 produced, was measured for 5 subjects after a week of consuming one of three diets of varying diet compositions (with each diet separated by a week "washout" period).

Subject	Standard Diet	High Fat Diet	Low Fat Diet	Subject Mean
1	0.80	0.77	0.83	0.80
2	0.78	0.77	0.82	0.79
3	0.82	0.80	0.87	0.83
4	0.76	0.73	0.79	0.76
5	0.83	0.83	0.86	0.84
Diet Mean	0.798	0.780	0.834	0.804
Variance	0.00082	0.0014	0.00103	

Design: Rather than recruit 15 individuals (5 subjects for each diet), we could recruit 5 individuals and have each individual receive each of the three diets.

Benefits:
- Fewer participants needed
- Between-Subject variability is removed from error
  - More powerful

Drawbacks:
- Participants may be more likely to drop from the study
  - Missing values result in deletion of the subject when using traditional RM ANOVA approaches.
- Carry-over effects or order-effects possible.

Assumptions for Repeated Measures ANOVA

- **Normality**: Each population is normally distributed, and thus the errors follow a normal distribution.

- **Homogeneity of variances**: The variances of the k populations/treatments are the same.

- **Independence of experimental units**: Experimental units (e.g., individuals or clusters) are independent
  - Account for the correlation between measurements within individuals or clusters

- **Homogeneity of covariances**: Equal correlation between conditions

The join assumption of homogeneity of variances and of covariances is known as ***compound symmetry*** or ***sphericity***.

- **Mauchly's test** is one method for testing the assumption of sphericity.

- There are two common measures of sphericity:
  - Greehhouse-Geisser (conservative)
  - Huynh-Feldt (liberal)

Remedy: If the assumption of sphericity is violated:
1) The F statistic df can be corrected by multiplying by one of the sphericity estimates
2) Multivariate approach can be used which does not require this assumption

One-Way Repeated Measures ANOVA in Matrix Form

For i=1,..,5, $E[Y_i] = \beta_s \text{standard}_i + \beta_{HF}\text{highfat}_i + \beta_{LF}\text{lowfat}_i$ 📝

And $E[\mathbf{Y}] = \mathbf{X\beta}$ where

$$
\mathbf{Y} = \begin{bmatrix} Y_{11} \\ Y_{12} \\ Y_{13} \\ Y_{21} \\ Y_{22} \\ Y_{23} \\ Y_{31} \\ Y_{32} \\ Y_{33} \\ Y_{41} \\ Y_{42} \\ Y_{43} \\ Y_{51} \\ Y_{52} \\ Y_{53} \end{bmatrix} = \begin{bmatrix} 0.80 \\ 0.77 \\ 0.83 \\ 0.78 \\ 0.77 \\ 0.82 \\ 0.82 \\ 0.80 \\ 0.87 \\ 0.76 \\ 0.73 \\ 0.79 \\ 0.83 \\ 0.83 \\ 0.86 \end{bmatrix} \text{ and } \mathbf{X\beta} = \begin{bmatrix} 100 \\ 010 \\ 001 \\ 100 \\ 010 \\ 001 \\ 100 \\ 010 \\ 001 \\ 100 \\ 010 \\ 001 \\ 100 \\ 010 \\ 001 \end{bmatrix} \begin{bmatrix} \beta_S \\ \beta_{HF} \\ \beta_{Lf} \end{bmatrix} \text{ OR} = \begin{bmatrix} Y_{11} \\ Y_{12} \\ Y_{13} \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ Y_{51} \\ Y_{52} \\ Y_{53} \end{bmatrix} = \begin{bmatrix} 0.80 \\ 0.77 \\ 0.83 \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ 0.83 \\ 0.83 \\ 0.86 \end{bmatrix} \text{ and } \mathbf{X\beta} = \begin{bmatrix} 100 \\ 010 \\ 001 \\ \vdots\;\vdots\;\vdots \\ \vdots\;\vdots\;\vdots \\ \vdots\;\vdots\;\vdots \\ \vdots\;\vdots\;\vdots \\ \vdots\;\vdots\;\vdots \\ \vdots\;\vdots\;\vdots \\ \vdots\;\vdots\;\vdots \\ \vdots\;\vdots\;\vdots \\ \vdots\;\vdots\;\vdots \\ 100 \\ 010 \\ 001 \end{bmatrix} \begin{bmatrix} \beta_S \\ \beta_{HF} \\ \beta_{LF} \end{bmatrix}
$$

```
DATA RQ2;
INPUT id diet rq;
DATALINES;
1 1 .80
1 2 .77
1 3 .83
2 1 .78
2 2 .77
2 3 .82
3 1 .82
3 2 .80
3 3 .87
4 1 .76
4 2 .73
4 3 .79
5 1 .83
5 2 .83
5 3 .86
;
```

$\mathbf{X}$ is 15x3 matrix of full rank

Sphericity Assumption Implies: Var(Y) is a 15x15 matrix such that

$$Var(Y) = \begin{pmatrix}
\sigma^2+\sigma_\varepsilon^2 & \sigma^2 & \sigma^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\sigma^2 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\sigma^2 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & \sigma^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \sigma^2 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & \sigma^2 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \sigma^2 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & \sigma^2 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma^2 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & \sigma^2 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma^2 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2
\end{pmatrix}$$

$$Var(Y) = \begin{pmatrix}
\sigma^2+\sigma_\varepsilon^2 & \sigma^2 & \sigma^2 & & & & & 0 \\
\sigma^2 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & & & & & \\
\sigma^2 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & & & & & \\
& & & \ddots & & & & \\
& & & & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & \sigma^2 & \\
& & & & \sigma^2 & \sigma^2+\sigma_\varepsilon^2 & \sigma^2 & \\
0 & & & & \sigma^2 & \sigma^2 & \sigma^2+\sigma_\varepsilon^2
\end{pmatrix}$$

One-Way Repeated Measures ANOVA

	Standard Diet	*High Fat Diet*	*Low Fat Diet*	**Mean**
Subject				
1	0.80	0.77	0.83	0.80
2	0.78	0.77	0.82	0.79
3	0.82	0.80	0.87	0.83
4	0.76	0.73	0.79	0.76
5	0.83	0.83	0.86	0.84
Mean	0.798	0.780	0.834	0.804
Variance	0.00082	0.0014	0.00103	

Treat subject as a random factor. We now have a two-way ANOVA (with factors subject and diet).

$$SD(Y) = 0.03832$$

$$SS_{Total} = 14 \times (0.03832)^2 = 0.02056$$

$$SS_{Diet} = 5 \times [(0.798\text{-}0.804)^2 + (0.780\text{-}0.804)^2 + (0.834\text{-}0.804)^2] = 0.00756$$

SS_{Error} is also the Subject $\times$ Diet interaction. We must assume there is no interaction and this quantity is all error.

$$SS_{Subject} = 3 \times [(0.80\text{-}0.804)^2 + (0.79\text{-}0.804)^2 + (0.83\text{-}0.804)^2$$
$$+ (0.76\text{-}0.804)^2 + (0.84\text{-}0.804)^2] = 0.01236$$

$$SS_{Error} = (.80\text{-}.80\text{-}.798+.804)^2 + (.77\text{-}.80\text{-}.780+.804)^2 +$$
$$(.83\text{-}.80\text{-}.834+.804)^2 + \ldots + (.86\text{-}.84\text{-}.834+.804)^2 = 0.00064$$

$$SS_{Error} = SS_{Subject \times Diet}$$

$$SS_{Error} = SS_{Total} - SS_{Diet} - SS_{Subject} = 0.02056\text{-}0.00756\text{-}0.01236 = 0.00064$$

Variability between subjects is removed from the Error!

Repeated Measures ANOVA

Source	Sum of Squares	d.f.	Mean Square	F	p-value
Between Subjects	0.01236	4	0.00309	38.63	<.0001
Within Subjects	[0.0082]	[10]			
Diet	0.00756	2	0.00378	47.25	<.0001
Error	0.00064	8	0.00008		
Total	0.02056	14			

RQ differs significantly across the three diets.

$$MS_{Error} = \overline{VAR} - \overline{COV}$$

MSE has fewer d.f. for repeated measures design (8) compared to independent subjects design (12)

SS(Error) for independent subjects design is equal to SS(Between) + SS(Error) in RM design (0.013=0.01236+0.00064)

Repeated Measures ANOVA with R: Two-factor ANOVA

- Can treat subject as the second factor
- Two-way ANOVA
  - Factor subject varies between subjects
  - Factor diet varies within subjects (comparisons are made within independent units)
  - No interaction term included

```
mod2 <- lm(rq ~ as.factor(subject) + # between subjects
             diet, # within subjects
           data=respquot.long)
anova(mod2)

## Analysis of Variance Table
##
## Response: rq
##                    Df  Sum Sq Mean Sq F value    Pr(>F)
## as.factor(subject)  4 0.01236 0.00309  38.625 2.821e-05 ***
## diet                2 0.00756 0.00378  47.250 3.711e-05 ***
## Residuals           8 0.00064 0.00008
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Repeated Measures ANOVA with PROC GLM: Multivariate Layout

Multivariate Layout

id	RQ_standard	RQ_highfat	RQ_lowfat
1	0.80	0.77	0.83
2	0.78	0.77	0.82
3	0.82	0.80	0.87
4	0.76	0.73	0.79
5	0.83	0.83	0.86

```
DATA RQ;
INPUT id RQ_standard RQ_hifat RQ_lowfat;
DATALINES;
1 0.80  0.77  0.83
2 0.78  0.77  0.82
3 0.82  0.80  0.87
4 0.76  0.73  0.79
5 0.83  0.83  0.86
;


PROC GLM DATA=rq;
  MODEL RQ_standard RQ_hifat RQ_lowfat = /NOUNI;   %No univariate tests and output
  REPEATED diet 3;
RUN;
```

Repeated Measures ANOVA with PROC GLM: Multivariate Layout

```
                        The GLM Procedure
```

```
PROC GLM DATA=rq;
  MODEL RQ_standard RQ_hifat RQ_lowfat =;
  REPEATED diet 3;
RUN;
```

```
         Number of Observations Read          5
         Number of Observations Used          5

                        The GLM Procedure
              Repeated Measures Analysis of Variance


              Repeated Measures Level Information


     Dependent Variable      standard     hifat    lowfat
         Level of diet           1           2         3



Partial Correlation Coefficients from the Error SSCP Matrix / Prob > |r|


        DF = 4           standard          hifat          lowfat
        standard         1.000000       0.956650        0.962981
                                          0.0108          0.0085



        hifat            0.956650       1.000000        0.916031
                          0.0108                          0.0288



        lowfat           0.962981       0.916031        1.000000
                          0.0085          0.0288
```

Sphericity: assumes these correlations are equal.

```
                      Sphericity Tests


                            Mauchly's
Variables                 DF   Criterion   Chi-Square   Pr > ChiSq
Transformed Variates       2   0.5619147    1.7292158       0.4212
Orthogonal Components      2   0.703125     1.0566618       0.5896
```

Fail to reject. Assume sphericity.

GLM Repeated Measures Results

```
                         The GLM Procedure
                Repeated Measures Analysis of Variance
        Univariate Tests of Hypotheses for Within Subject Effects


   Source                  DF   Type III SS   Mean Square  F Value  Pr > F

   diet                     2   0.00756000    0.00378000    47.25  <.0001
   Error(diet)              8   0.00064000    0.00008000
```

RQ differs significantly across the three diets.

```
                                       Adj Pr > F
                  Source            G - G      H - F

                  diet              0.0002    <.0001
                  Error(diet)
```

Corrected for sphericity

Estimates used to correct d.f.

```
          Greenhouse-Geisser Epsilon      0.7711
          Huynh-Feldt Epsilon             1.1618
```

For G-G correction: df(diet): 2 × 0.7711 = 1.542
       df(error): 8 × 0.7711 = 6.1688

For H-F Correction: df(diet): 2 × 1 = 2
       df(error): 8 × 1 = 8

We do not increase or d.f. using these corrections. If the correction value is greater than 1 (e.g., 1.1618 for H-F), we use 1 and do not adjust our d.f.

NOTE that the other variance sources (e.g., the Between Subject SS) are not included by SAS in the multivariate layout.

Repeated Measures ANOVA with R 'car' package: Multivariate Layout

```
library(car)

mod3 <- lm(as.matrix(respquot[,-1]) ~ 1) # need data in "wide" form
diet <- factor(colnames(respquot)[-1])
results <- Anova(mod3, idata=data.frame(diet), idesign=~diet, type="III")
summary(results,multivariate=FALSE)

## Warning in summary.Anova.mlm(results, multivariate = FALSE): HF eps > 1
## treated as 1

##
## Univariate Type III Repeated-Measures ANOVA Assuming Sphericity
##
##               SS num Df Error SS den Df       F     Pr(>F)
## (Intercept) 9.6962      1  0.01236      4 3137.94 6.081e-07 ***
## diet        0.0076      2  0.00064      8   47.25 3.711e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## Mauchly Tests for Sphericity
##
##      Test statistic p-value
## diet        0.70313 0.58959
##
##
## Greenhouse-Geisser and Huynh-Feldt Corrections
##  for Departure from Sphericity
##
##      GG eps Pr(>F[GG])
## diet 0.77108  0.0002439 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##       HF eps   Pr(>F[HF])
## diet 1.161765 3.710774e-05
```

Repeated Measures ANOVA with PROC GLM: Univariate Layout

Univariate Layout

```
DATA RQ2;
INPUT id diet rq;
DATALINES;
1 1 .80
1 2 .77
1 3 .83
2 1 .78
2 2 .77
2 3 .82
3 1 .82
3 2 .80
3 3 .87
4 1 .76
4 2 .73
4 3 .79
5 1 .83
5 2 .83
5 3 .86
;

PROC GLM DATA=rq2;
  CLASS id diet;
  MODEL rq = diet id;
  RANDOM id /TEST;
RUN;
```

Univariate Layout

id	Diet	RQ
1	1	0.80
1	2	0.77
1	3	0.83
2	1	0.78
2	2	0.77
2	3	0.82
3	1	0.82
3	2	0.80
3	3	0.87
4	1	0.76
4	2	0.73
4	3	0.79
5	1	0.83
5	2	0.83
5	3	0.86

Repeated Measures ANOVA: Univariate Layout

The GLM Procedure

Source	Type III Expected Mean Square
diet	Var(Error) + Q(diet)
id	Var(Error) + 3 Var(id)

The GLM Procedure
Tests of Hypotheses for Mixed Model Analysis of Variance

Dependent Variable: rq

Source	DF	Type III SS	Mean Square	F Value	Pr > F
diet	2	0.007560	0.003780	47.25	<.0001
id	4	0.012360	0.003090	38.63	<.0001
Error: MS(Error)	8	0.000640	0.000080000		

RQ differs significantly across the three diets.

```
mod4 <- aov(rq ~ diet + Error(as.factor(subject)),data=respquot.long)
summary(mod4)

##
## Error: as.factor(subject)
##            Df  Sum Sq Mean Sq F value Pr(>F)
## Residuals   4 0.01236 0.00309
##
## Error: Within
##            Df  Sum Sq Mean Sq F value    Pr(>F)
## diet        2 0.00756 0.00378   47.25 3.71e-05 ***
## Residuals   8 0.00064 0.00008
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Review Repeated Measures Data

Repeated Measures Data:

1) The same outcome/response is measured on the same individual under multiple conditions or at multiple times

2) The same outcome/response is measured for clusters or groups of similar individuals

- Two sample t-test is to a paired t-test as an ANOVA is to a Repeated Measures ANOVA

Assumptions:

1) Normality: Each population is normally distributed (errors follow a normal distribution)

2) Sphericity: homogeneity of variances and of covariances

3) Independence of experimental units: Individuals or clusters are independent

- If sphericity is violated, then adjust the degrees of freedom or use **Mixed Models** approach

Note: two-sample *t* tests, paired *t* tests, ANOVA, Repeated Measures ANOVA do not easily account for confounders (Stratify but then reduce sample size)