Lecture 15 - Class Activity ANCOVA

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# Lecture 15: Analysis of Covariance (ANCOVA)

## What is ANCOVA?

ANCOVA (Analysis of Covariance) combines regression and ANOVA to: - Compare group means while adjusting for a continuous covariate - Increase statistical power by reducing residual error - Control for confounding variables

## When to Use ANCOVA

Use ANCOVA when you have: - **Response variable**: Continuous - **Predictor variable**: Categorical (factor/groups) - **Covariate**: Continuous variable that affects the response

## Key Assumptions of ANCOVA

1. **Independence** of observations
2. **Normality** of residuals
3. **Homogeneity of variances** across groups
4. **Linearity** between response and covariate within each group
5. **Homogeneity of slopes** (most critical!) - regression slopes must be equal across all groups

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| --- | --- |
|  | **Critical First Step**  Always test for **homogeneity of slopes** before proceeding with ANCOVA. If slopes differ significantly between groups, standard ANCOVA is inappropriate. |

# Part 1: Cricket Chirping Analysis

## Data Overview

We want to compare chirping rate of two cricket species: - *Oecanthus exclamationis* - *Oecanthus niveus*

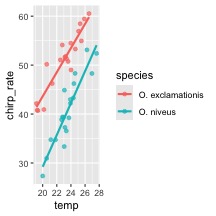
But we measured rates at different temperatures, and there’s a relationship between pulse rate and temperature. ANCOVA lets us adjust for temperature effect to get a more powerful test!

# Create simulated cricket data based on lecture example  
set.seed(456)  
n <- 40  
species <- rep(c("O. exclamationis", "O. niveus"), each = n/2)  
temp <- c(rnorm(n/2, mean = 22, sd = 2), rnorm(n/2, mean = 24, sd = 2))  
chirp\_rate <- 40 + 2.5 \* (temp - 23) + ifelse(species == "O. exclamationis", 10, 0) + rnorm(n, sd = 3)  
cricket\_data <- data.frame(species = species, temp = temp, chirp\_rate = chirp\_rate)  
  
# View data structure  
  
head(cricket\_data)

species temp chirp\_rate  
1 O. exclamationis 19.31296 40.69557  
2 O. exclamationis 23.24355 51.78799  
3 O. exclamationis 23.60175 50.75553  
4 O. exclamationis 19.22222 40.80589  
5 O. exclamationis 20.57129 50.16484  
6 O. exclamationis 21.35188 46.24225

# Plot with regression lines by species  
ggplot(cricket\_data, aes(x = temp, y = chirp\_rate, color = species)) +  
 geom\_point(alpha = 0.7) +  
 geom\_smooth(method = "lm", se = FALSE)

`geom\_smooth()` using formula = 'y ~ x'



## Step 1: Test Homogeneity of Slopes

This is the most critical assumption! We test if the regression slopes are equal across all groups.

# Test for homogeneity of slopes by including interaction term  
cricket\_slopes\_model <- lm(chirp\_rate ~ temp \* species, data = cricket\_data)  
Anova(cricket\_slopes\_model, type = 3)

Anova Table (Type III tests)  
  
Response: chirp\_rate  
 Sum Sq Df F value Pr(>F)   
(Intercept) 6.32 1 0.9393 0.338915   
temp 620.48 1 92.1572 0.00000000001828 \*\*\*  
species 69.76 1 10.3617 0.002724 \*\*   
temp:species 26.08 1 3.8734 0.056796 .   
Residuals 242.38 36   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Interpretation**: If p > 0.05, slopes are homogeneous and we can proceed with ANCOVA. If p < 0.05, slopes differ and standard ANCOVA is inappropriate.

## Step 2: Fit ANCOVA Model

Since slopes are homogeneous (p > 0.05), we can fit the ANCOVA model without the interaction term.

# Fit ANCOVA model (without interaction)  
cricket\_ancova <- lm(chirp\_rate ~ temp + species, data = cricket\_data)  
  
# Get model summary  
summary(cricket\_ancova)

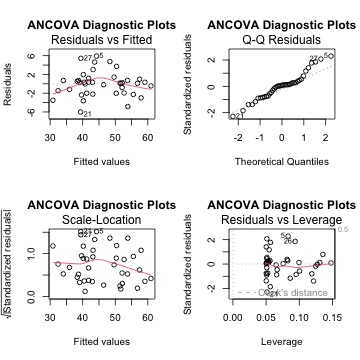
Call:  
lm(formula = chirp\_rate ~ temp + species, data = cricket\_data)  
  
Residuals:  
 Min 1Q Median 3Q Max   
-6.0065 -1.9653 0.1923 0.7886 5.9192   
  
Coefficients:  
 Estimate Std. Error t value Pr(>|t|)   
(Intercept) -13.2012 4.7423 -2.784 0.00842 \*\*   
temp 2.7926 0.2048 13.634 0.000000000000000530 \*\*\*  
speciesO. niveus -11.8005 0.8593 -13.733 0.000000000000000424 \*\*\*  
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
  
Residual standard error: 2.694 on 37 degrees of freedom  
Multiple R-squared: 0.8994, Adjusted R-squared: 0.894   
F-statistic: 165.4 on 2 and 37 DF, p-value: < 0.00000000000000022

# View ANOVA table  
Anova(cricket\_ancova)

Anova Table (Type II tests)  
  
Response: chirp\_rate  
 Sum Sq Df F value Pr(>F)   
temp 1348.81 1 185.90 0.0000000000000005296 \*\*\*  
species 1368.34 1 188.59 0.0000000000000004236 \*\*\*  
Residuals 268.46 37   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Step 3: Check Model Assumptions

# Create diagnostic plots  
par(mfrow = c(2, 2))  
plot(cricket\_ancova, main = "ANCOVA Diagnostic Plots")



par(mfrow = c(1, 1))

## Step 4: Calculate Adjusted Means

ANCOVA compares adjusted means - what each group’s mean would be at the overall mean of the covariate.

# Calculate adjusted means using emmeans  
cricket\_adjusted\_means <- emmeans(cricket\_ancova, "species")  
  
# Convert to dataframe for plotting  
cricket\_adj\_means\_df <- as.data.frame(cricket\_adjusted\_means)  
cricket\_adj\_means\_df

species emmean SE df lower.CL upper.CL  
 O. exclamationis 51.70513 0.6049702 37 50.47934 52.93091  
 O. niveus 39.90462 0.6049702 37 38.67883 41.13040  
  
Confidence level used: 0.95

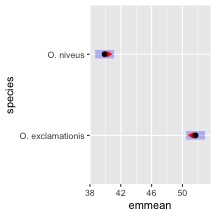
## Step 5: Pairwise Comparisons

# Pairwise comparisons of adjusted means  
pairs(cricket\_adjusted\_means, adjust = "sidak")

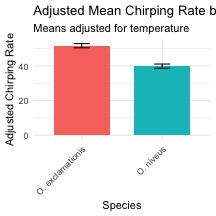
contrast estimate SE df t.ratio p.value  
 O. exclamationis - O. niveus 11.8 0.859 37 13.733 <.0001

## Step 6: Visualize Results

# Plot adjusted means with confidence intervals  
plot(cricket\_adjusted\_means, comparisons = TRUE)



# Bar chart of adjusted means  
ggplot(cricket\_adj\_means\_df, aes(x = species, y = emmean, fill = species)) +  
 geom\_bar(stat = "identity", width = 0.7) +  
 geom\_errorbar(aes(ymin = lower.CL, ymax = upper.CL), width = 0.2) +  
 labs(title = "Adjusted Mean Chirping Rate by Species",  
 subtitle = "Means adjusted for temperature",  
 x = "Species",  
 y = "Adjusted Chirping Rate") +  
 theme\_minimal() +  
 theme(legend.position = "none",  
 axis.text.x = element\_text(angle = 45, hjust = 1))



# Part 2: Partridge Longevity Analysis

## Data Overview

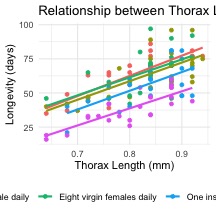
We’ll analyze the effect of mating strategy on male fruitfly longevity, using thorax length as a covariate.

# Load the partridge dataset  
partridge <- read.csv("data/partridge.csv")  
  
# Create better treatment names  
partridge$treatment <- factor(partridge$TREATMEN,  
 levels = 1:5,  
 labels = c("No females",   
 "One virgin female daily",  
 "Eight virgin females daily",  
 "One inseminated female daily",  
 "Eight inseminated females daily"))  
  
# View data structure  
head(partridge)

PARTNERS TYPE TREATMEN LONGEV LLONGEV THORAX RESID1 PREDICT1 RESID2  
1 8 0 1 35 1.544068 0.64 -5.868456 40.86846 -0.04743024  
2 8 0 1 37 1.568202 0.68 -9.301196 46.30120 -0.07105067  
3 8 0 1 49 1.690196 0.68 2.698804 46.30120 0.05094369  
4 8 0 1 46 1.662758 0.72 -5.733936 51.73394 -0.02424867  
5 8 0 1 63 1.799341 0.72 11.266064 51.73394 0.11233405  
6 8 0 1 39 1.591065 0.76 -18.166676 57.16668 -0.14369601  
 PREDICT2 treatment  
1 1.591498 No females  
2 1.639252 No females  
3 1.639252 No females  
4 1.687007 No females  
5 1.687007 No females  
6 1.734761 No females

# Visualize the relationship between thorax length and longevity by treatment  
ggplot(partridge, aes(x = THORAX, y = LONGEV, color = treatment)) +   
 geom\_point() +  
 geom\_smooth(method = "lm", se = FALSE) +  
 labs(title = "Relationship between Thorax Length and Longevity",  
 x = "Thorax Length (mm)",  
 y = "Longevity (days)",  
 color = "Treatment") +  
 theme\_minimal() +  
 theme(legend.position = "bottom")

`geom\_smooth()` using formula = 'y ~ x'



## Step 1: Test Homogeneity of Slopes

# Test for homogeneity of slopes  
homo\_slopes\_model <- lm(LONGEV ~ THORAX \* treatment, data = partridge)  
Anova(homo\_slopes\_model, type = 3)

Anova Table (Type III tests)  
  
Response: LONGEV  
 Sum Sq Df F value Pr(>F)   
(Intercept) 755.6 1 6.6320 0.01128 \*   
THORAX 3486.3 1 30.5999 0.0000002017 \*\*\*  
treatment 36.9 4 0.0810 0.98805   
THORAX:treatment 42.5 4 0.0933 0.98441   
Residuals 13102.1 115   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Step 2: Fit ANCOVA Model

# Fit the ANCOVA model (without interaction)  
ancova\_model <- lm(LONGEV ~ THORAX + treatment, data = partridge)  
  
  
  
# Get more detailed summary  
summary(ancova\_model)

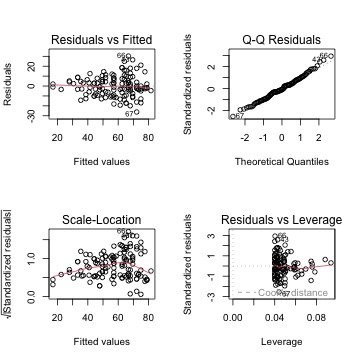
Call:  
lm(formula = LONGEV ~ THORAX + treatment, data = partridge)  
  
Residuals:  
 Min 1Q Median 3Q Max   
-26.189 -6.599 -0.989 6.408 30.244   
  
Coefficients:  
 Estimate Std. Error t value  
(Intercept) -46.055 10.239 -4.498  
THORAX 135.819 12.439 10.919  
treatmentOne virgin female daily -3.929 2.997 -1.311  
treatmentEight virgin females daily -1.276 2.983 -0.428  
treatmentOne inseminated female daily -10.946 2.999 -3.650  
treatmentEight inseminated females daily -23.879 2.973 -8.031  
 Pr(>|t|)   
(Intercept) 0.000016052501519 \*\*\*  
THORAX < 0.0000000000000002 \*\*\*  
treatmentOne virgin female daily 0.192347   
treatmentEight virgin females daily 0.669517   
treatmentOne inseminated female daily 0.000391 \*\*\*  
treatmentEight inseminated females daily 0.000000000000783 \*\*\*  
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
  
Residual standard error: 10.51 on 119 degrees of freedom  
Multiple R-squared: 0.6564, Adjusted R-squared: 0.6419   
F-statistic: 45.46 on 5 and 119 DF, p-value: < 0.00000000000000022

# View ANOVA table  
anova(ancova\_model)

Analysis of Variance Table  
  
Response: LONGEV  
 Df Sum Sq Mean Sq F value Pr(>F)   
THORAX 1 15496.6 15496.6 140.293 < 0.00000000000000022 \*\*\*  
treatment 4 9611.5 2402.9 21.753 0.0000000000001719 \*\*\*  
Residuals 119 13144.7 110.5   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Step 3: Check Assumptions

# Create diagnostic plots  
par(mfrow = c(2, 2))  
plot(ancova\_model)



## Step 4: Calculate Adjusted Means

# Get adjusted means using emmeans  
adjusted\_means <- emmeans(ancova\_model, "treatment")  
adjusted\_means

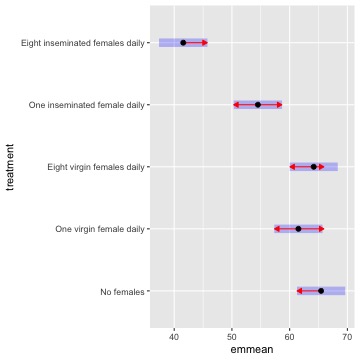
treatment emmean SE df lower.CL upper.CL  
 No females 65.4 2.11 119 61.3 69.6  
 One virgin female daily 61.5 2.11 119 57.3 65.7  
 Eight virgin females daily 64.2 2.10 119 60.0 68.3  
 One inseminated female daily 54.5 2.11 119 50.3 58.7  
 Eight inseminated females daily 41.6 2.12 119 37.4 45.8  
  
Confidence level used: 0.95

## Step 5: Pairwise Comparisons

# Pairwise comparisons of adjusted means  
pairs(adjusted\_means, adjust = "tukey")

contrast estimate SE  
 No females - One virgin female daily 3.93 3.00  
 No females - Eight virgin females daily 1.28 2.98  
 No females - One inseminated female daily 10.95 3.00  
 No females - Eight inseminated females daily 23.88 2.97  
 One virgin female daily - Eight virgin females daily -2.65 2.98  
 One virgin female daily - One inseminated female daily 7.02 2.97  
 One virgin female daily - Eight inseminated females daily 19.95 3.01  
 Eight virgin females daily - One inseminated female daily 9.67 2.98  
 Eight virgin females daily - Eight inseminated females daily 22.60 2.99  
 One inseminated female daily - Eight inseminated females daily 12.93 3.01  
 df t.ratio p.value  
 119 1.311 0.6849  
 119 0.428 0.9929  
 119 3.650 0.0035  
 119 8.031 <.0001  
 119 -0.891 0.8996  
 119 2.361 0.1336  
 119 6.636 <.0001  
 119 3.249 0.0129  
 119 7.560 <.0001  
 119 4.298 0.0003  
  
P value adjustment: tukey method for comparing a family of 5 estimates

# Plot adjusted means with confidence intervals  
plot(adjusted\_means, comparisons = TRUE)

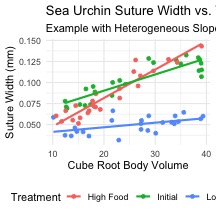


# Part 3: Example with Heterogeneous Slopes

Let’s look at an example where slopes are NOT homogeneous using sea urchin data.

# Create simulated sea urchin data with heterogeneous slopes  
set.seed(345)  
n <- 72 # 24 urchins per group  
  
# Create data frame  
treatments <- rep(c("Initial", "Low Food", "High Food"), each = n/3)  
volume <- c(  
 runif(n/3, 10, 40), # Initial  
 runif(n/3, 10, 40), # Low Food  
 runif(n/3, 10, 40) # High Food  
)  
  
# Create suture width with different slopes for each treatment  
suture\_width <- ifelse(  
 treatments == "Initial", 0.05 + 0.002 \* volume,  
 ifelse(  
 treatments == "Low Food", 0.04 + 0.0005 \* volume,  
 0.02 + 0.003 \* volume # High Food  
 )  
) + rnorm(n, 0, 0.01)  
  
urchin\_data <- data.frame(treatment = treatments, volume = volume, suture\_width = suture\_width)  
  
# Plot the data with regression lines  
ggplot(urchin\_data, aes(x = volume, y = suture\_width, color = treatment)) +  
 geom\_point() +  
 geom\_smooth(method = "lm", se = FALSE) +  
 labs(title = "Sea Urchin Suture Width vs. Volume",  
 subtitle = "Example with Heterogeneous Slopes",  
 x = "Cube Root Body Volume",  
 y = "Suture Width (mm)",  
 color = "Treatment") +  
 theme\_minimal() +  
 theme(legend.position = "bottom")

`geom\_smooth()` using formula = 'y ~ x'



## Test for Homogeneity of Slopes

# Fit model with interaction  
urchin\_model <- lm(suture\_width ~ volume \* treatment, data = urchin\_data)  
Anova(urchin\_model, type = 3)

Anova Table (Type III tests)  
  
Response: suture\_width  
 Sum Sq Df F value Pr(>F)   
(Intercept) 0.0005253 1 5.91 0.01778 \*   
volume 0.0151663 1 170.64 < 0.00000000000000022 \*\*\*  
treatment 0.0020070 2 11.29 0.00006064438398 \*\*\*  
volume:treatment 0.0062129 2 34.95 0.00000000004453 \*\*\*  
Residuals 0.0058662 66   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Result**: With p < 0.05, we have heterogeneous slopes! Standard ANCOVA would be inappropriate here.

## What to do with Heterogeneous Slopes

When slopes are not homogeneous, you have several options:

# Option: Analyze groups separately  
initial\_model <- lm(suture\_width ~ volume, data = filter(urchin\_data, treatment == "Initial"))  
low\_food\_model <- lm(suture\_width ~ volume, data = filter(urchin\_data, treatment == "Low Food"))  
high\_food\_model <- lm(suture\_width ~ volume, data = filter(urchin\_data, treatment == "High Food"))  
  
# Summary for each group  
initial\_model

Call:  
lm(formula = suture\_width ~ volume, data = filter(urchin\_data,   
 treatment == "Initial"))  
  
Coefficients:  
(Intercept) volume   
 0.051785 0.001926

low\_food\_model

Call:  
lm(formula = suture\_width ~ volume, data = filter(urchin\_data,   
 treatment == "Low Food"))  
  
Coefficients:  
(Intercept) volume   
 0.0359532 0.0005453

high\_food\_model

Call:  
lm(formula = suture\_width ~ volume, data = filter(urchin\_data,   
 treatment == "High Food"))  
  
Coefficients:  
(Intercept) volume   
 0.014077 0.003376

# Summary Checklist for ANCOVA

When conducting ANCOVA, always follow these steps:

|  |  |
| --- | --- |
|  | **ANCOVA Checklist**   1. **Visualize your data** - plot response vs covariate, colored by groups 2. **Test homogeneity of slopes** - fit model with interaction term    * If p > 0.05: proceed with ANCOVA    * If p < 0.05: use alternative approaches 3. **Fit ANCOVA model** - response ~ covariate + factor 4. **Check assumptions** - use diagnostic plots 5. **Interpret results** - focus on adjusted means, not raw means 6. **Conduct post-hoc tests** - pairwise comparisons if needed 7. **Visualize results** - show adjusted means with confidence intervals |

## Key Points to Remember

* **ANCOVA increases power** by accounting for covariate variation
* **Adjusted means** are what we compare, not raw group means
* **Homogeneity of slopes** is the most critical assumption
* **Parallel lines** in your plot suggest homogeneous slopes
* **Non-parallel lines** indicate heterogeneous slopes - use alternative methods

|  |  |
| --- | --- |
|  | **Key Points from ANCOVA Analysis**   1. **Test homogeneity of slopes first** - this is the most critical assumption 2. **ANCOVA compares adjusted means** at the mean value of the covariate 3. **Increases statistical power** by removing variation due to the covariate 4. **Choose appropriate methods** based on whether slopes are homogeneous 5. **Visualize your results** clearly showing the relationship between variables 6. **Check all assumptions** using diagnostic plots 7. **Interpret in biological context** - what do the adjusted means tell us?   Remember: The covariate should be measured independently of the treatment and should not be affected by the treatment itself! |