

One-way Analysis of Covariance (ANCOVA)

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Before we Begin

- Go to the github repo:
 - □ https://github.com/Mollinetti/Experiment-Design-R
 - Download the script for this class! (in the 'scripts' folder, class_4_5.r!)
- Run the first lines to load/install the required libraries

Agenda

- Introduction
- ANCOVA
- ANOVA review

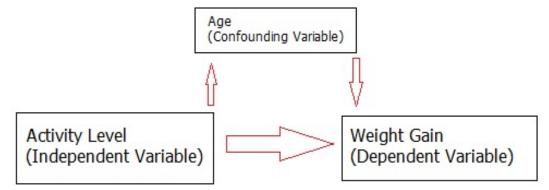
- Introduction
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- In clinical data, many confounding factors can compromise the test interpretation
- Example:
 - □ Fatigue
 - Motivation
 - □Age
 - Education



- Confounding factor: variable not accounted for
- Can suggest there is correlation when none
- Can introduce bias
- Absolute care must be taken to not include confounding variables





- If we are interested in comparison between groups, we must take the following into account:
 - □ Decide which variables are significant
 - Ensure that the chosen variables are able to generalize the model (i.e. confounding variables do not bias the experiment)

- Quality control of the experiments can be done in two ways:
 - Methodological
 - □ Statistically

- Methodological quality control
 - □ Sample choice
 - □ Randomization
 - □ Validity
 - ☐ Stratification
 - □ Cutoffs
- Problem: large sample size, hard to generalize, budget constraints

- Statistical quality control: if we can measure the covariant, it can be included in the regression model
- Error is now accounted
- Takes into account the inevitability of sample characteristics that cannot be factored out by design:
 - □ Age
 - □ Education
 - □ Intelligence



- Covariate: continuous uncontrollable variable directly related to dependent variable
- The relationship between variables may be clouded by the covariate
- If we can measure the covariates, ANCOVA is preferred over ANOVA

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- Purpose of ANCOVA:
 - □ Error reduction, especially if group sizes are small
 - □ Control for factors which cannot be randomized but which can be measured on an interval scale.
 - Remove the effects of variables which modify the relationship of the independent to the dependent variable

- Assumptions:
 - Linearity of regression
 - ☐ Homogeneity of error variances
 - Normality of residuals
 - □ Equality of groups on the covariate
 - □ equality of slopes—interaction

- Assumptions:
 - □ Linearity of regression: plot of slopes
 - □ Homogeneity of error variances: levene test
 - □ Normality of residuals: shapiro-wilk test
 - □ Equality of groups on the covariate: anova or t-test between covariate and independent variable
 - equality of slopes—interaction: t-test or anova between covariate and the variables

- Remember: just like ANOVA, ANCOVA can be:
 - □ Balanced/Unbalanced
 - One-way / Multiple (MANCOVA)
 - □ Fixed/ Random/ Mixed effects
- Usually, ANCOVA is fixed and balanced

- We will use the 'leprosy.dat' dataset
- Variables
 - □ Dependent: Drug
 - □ Independent: X
 - □ Covariate: Y
- Neither Tukey nor mmc are suitable for post-hoc tests
- Instead the general linear hypothesis will be used for analysis

Before conducting the ANCOVA, some assumptions must be tested:

```
#equality of slopes interaction
fitted.lepr <- aov(After ~ Drug * Before, data = lepr)</pre>
```



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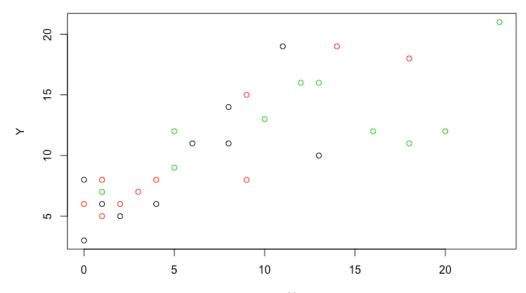
```
#equality of slopes interaction
fitted.lepr <- aov(After ~ Drug * Before, data = lepr)</pre>
```

```
Residuals 24 397.6 16.6
---
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```



Before conducting the ANCOVA, some assumptions must be tested:

```
#linearity of slopes (Eyeballing, just like Rick's neutrino bomb)
plot(After, Before, col = Drug, xlab = "Before", ylab = "After")
```



Pay attention to the pattern of each variable!



Before conducting the ANCOVA, some assumptions must be tested:

```
#Equality of the groups on the covariate
#Anova with the groups
fitted.eq<- aov(Before ~ Drug, data = lepr)
summary(fitted.eq)</pre>
```



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```

```
> summary(fitted.eq)

Df Sum Sq Mean Sq F value Pr(>F)

Drug 2 72.9 36.43 1.659 0.209

Residuals 27 593.0 21.96
```

*H*₀: No difference between variances

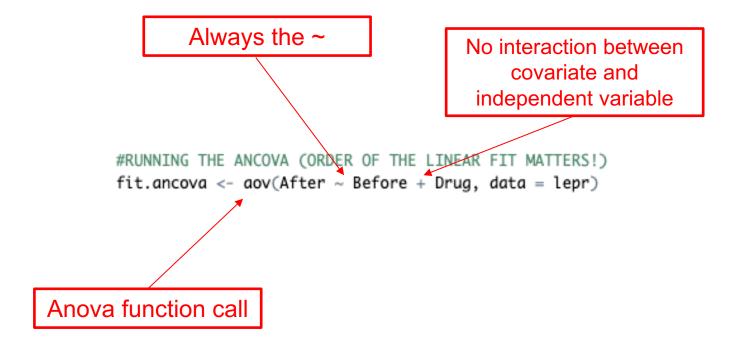


Clearing these assumptions, we call the ANCOVA

```
#RUNNING THE ANCOVA (ORDER OF THE LINEAR FIT MATTERS!)
fit.ancova <- aov(After ~ Before + Drug, data = lepr)
```



Clearing these assumptions, we call the ANCOVA





Posthoc is conducted by the glht function

```
# to get the 'real' p value and difference,
# uses the general linear hypothesis function
posthoc <- glht(fit.ancova, linfct = mcp(Drug = "Tukey"))</pre>
> summary(posthoc)
        Simultaneous Tests for General Linear Hypotheses
Multiple Comparisons of Means: Tukey Contrasts
Fit: aov(formula = After ~ Before + Drug, data = lepr)
Linear Hypotheses:
          Estimate Std. Error t value Pr(>|t|)
B - A == 0 0.109 1.795
                               0.061
                                        0.998
C - A == 0 3.446 1.887 1.826 0.181
C - B == 0 3.337 1.854 1.800
                                     0.189
(Adjusted p values reported -- single-step method)
```



Posthoc analysis is conducted by the glht function

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```

 H_0 : No significant differences of means



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ANOVA review

- We will use the Insect sprays dataset that comes with the 'car' library
- Script will be written now!
- Answers will be in the 'Class 4 5 ans.r' file



Next Episode

We will now proceed to fitting linear models with Linear regression



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