# Quick Overview of Traditional Methods: Linear regression & hypothesis testing

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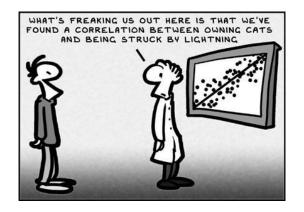
# What I will cover today

- Testing for associations between continuous variables
- 2 Testing for mean differences
- Within-subject designs: old school
- Within-subject designs extension





## Testing for associations between continuous variables



#### Correlations

## Pearson's $\rho$

- > x < c(165, 109, 132, 121, 115, 143, 119, 128, 132, 158)
- > y < c(124, 135, 119, 121, 139, 153, 101, 125, 106, 99)
- > cor(x, y)
- [1] -0.1790753

#### Spearman's r

- > cor(x, y, method="spearman")
- [1] -0.2553203

#### Kendall's au

- > cor(x, y, method="kendall")
- [1] -0.1797866

Neither cor() or cov produce tests of significance, although you can use\_the cor tast () function to test a single correlation coefficient Marijke Welvaert 22 February 2018





## General linear model: Overview

The general linear model is defined as

$$Y = \beta X + \varepsilon$$

with

- Y: Dependent variable (continuous)
- $\beta$ : Estimated coefficients
- X: Design matrix with 1 to p independent variables (continuous/categorical)
- $\varepsilon$ : Residual error

## Assumptions

- Linear relationship

Multiple regression, ANOVA and ANCOVA all belong under this umbrella!







#### Example data: Manatees in Florida

```
> speed <- c(447,460,481,498,513,512,526,559,585,614,
       645,675,711,719)
> seacow <- c(12,21,24,16,24,20,15,34,33,33,39,43,50,47)
> fit <- lm(seacow ~ speed)</pre>
> fit.
Call:
lm(formula = seacow ~ speed)
Coefficients:
(Intercept)
                    speed
    -42.125
                    0.126
> coef(fit)
(Intercept)
                   speed
 -42.124616
               0.125959
```



```
> summary(fit)
Call:
lm(formula = seacow ~ speed)
Residuals:
   Min 10 Median 30
                                Max
-9.1298 -2.2054 -0.0084 2.3027 5.7135
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) -42.12462 7.47213 -5.638 0.000109 ***
speed
            0.12596 0.01301 9.682 5.07e-07 ***
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
Residual standard error: 4.311 on 12 degrees of freedom
Multiple R-squared: 0.8865, Adjusted R-squared: 0.8771
F-statistic: 93.75 on 1 and 12 DF, p-value: 5.071e-07
> confint(fit)
                 2.5 % 97.5 %
(Intercept) -58.40498410 -25.8442488
speed 0.09761426 0.1543038
```

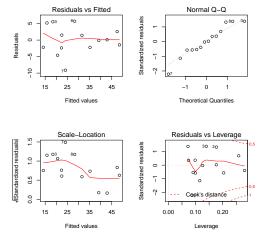






#### Diagnostic plots

- > par(mfrow=c(2,2))
- > plot(fit)







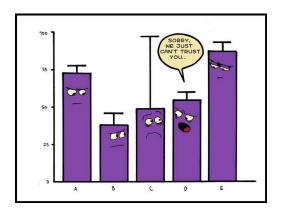


#### Predicting a new value

What is the expected number of killed Manatees if 800,000 speed boats are registered in a year?



## Testing for differences between means





```
Toy data:
```

```
> x <- c(165,109,132,121,115,143,119,128,132,158)
```

## One Sample t-test

```
> t.test(x, mu=120, alternative="two.sided",
+ conf.level=0.95)
```

One Sample t-test

```
data: x
t = 2.1097, df = 9, p-value = 0.0641
alternative hypothesis: true mean is not equal to 120
95 percent confidence interval:
   119.1185 145.2815
sample estimates:
mean of x
```





132.2

```
Toy data:
```

```
> x <- c(165,109,132,121,115,143,119,128,132,158)
> y <- c(124,135,119,121,139,153,101,125,106,99)
```

#### Two Sample t-test

```
> t.test(x, y, alternative="two.sided",
+ conf.level=0.95)
```

Welch Two Sample t-test

```
data: x and y
t = 1.2591, df = 17.935, p-value = 0.2241
alternative hypothesis: true difference in means is not equal
95 percent confidence interval:
-6.690478 26.690478
```

sample estimates:

mean of x mean of y

Equality of variances assumption:

1.128205

```
Two Sample t-test
```

```
> t.test(x, y, alternative="two.sided",
           var.equal=TRUE, conf.level=0.95)
       Two Sample t-test
data: x and y
t = 1.2591, df = 18, p-value = 0.2241
alternative hypothesis: true difference in means is not equal
95 percent confidence interval:
 -6.686136 26.686136
sample estimates:
mean of x mean of y
   132.2 122.2
```



```
Toy data:
```

```
> x1 \leftarrow c(165,109,132,121,115,143,119,128,132,158)
```

> x2 <- c(124,135,119,121,139,153,101,125,106,99)

## Paired Sample t-test

```
> t.test(x1, x2, alternative="greater",
                    paired=TRUE, conf.level=0.95)
```

Paired t-test

```
data: x1 and x2
```

$$t = 1.1597$$
,  $df = 9$ ,  $p$ -value = 0.138

alternative hypothesis: true difference in means is greater th 95 percent confidence interval:

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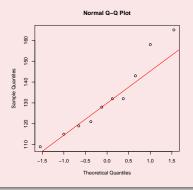
sample estimates:

mean of the differences

## Normality assumption

## QQ-plot

- > qqnorm(x)
- > qqline(x, col="red")





## Normality assumption

## Testing for normality

> shapiro.test(x)

Shapiro-Wilk normality test

data: x

W = 0.93085, p-value = 0.4563

Note: This test behaves badly with small sample sizes!

#### Non-parametric alternative

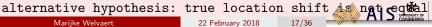
> wilcox.test(x1, x2, paired=TRUE)

Wilcoxon signed rank test with continuity correction

data: x1 and x2

V = 31.5, p-value = 0.3135

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#### **ANOVA**

#### Example data: Medicine trial in depressed patients





#### **ANOVA**

```
> summary(fit)
Call:
lm(formula = vertigo ~ fcond)
Residuals:
  Min 10 Median 30 Max
-5.875 -1.812 0.375 2.250 4.250
Coefficients:
          Estimate Std. Error t value Pr(>|t|)
            25.750 1.009 25.530 < 2e-16 ***
(Intercept)
fcond10mg 0.125 1.426 0.088 0.93079
fcond20mg -6.250 1.426 -4.382 0.00015 ***
fcond30mg -5.000 1.426 -3.505 0.00155 **
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
Residual standard error: 2.853 on 28 degrees of freedom
Multiple R-squared: 0.5377, Adjusted R-squared: 0.4882
F-statistic: 10.86 on 3 and 28 DF, p-value: 6.644e-05
```





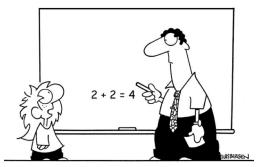


#### **ANOVA**





## Within-subject designs: old school



"How can I trust your information when you're using such outdated technology?"





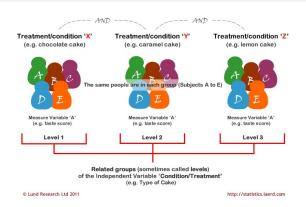
# Within-subject designs

- Repeated measures designs
- Longitudinal designs
- Cross-over designs

Any dataset in which you measured the same subject at least twice on a certain variable



## Repeated Measures ANOVA



#### Assumptions

- Balanced design
- Multivariate normal distribution
- **3** Sphericity ( $\approx$  variance homogeneity)



# Within-subject designs extension







# The linear mixed model as an extension of linear regression

## Standard linear regression

$$Y_i = \beta_0 + \beta_1 X_i + \varepsilon_i$$

with  $\varepsilon_i \stackrel{i.i.d}{\sim} N(0, \sigma_{\varepsilon})$ 

#### Linear mixed model

$$Y_i = \beta_0 + \beta_1 X_i + b_i + \varepsilon_i$$

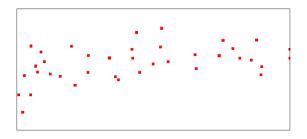
with  $b_i \sim N(0, \sigma_b)$  and  $\varepsilon_i \stackrel{i.i.d}{\sim} N(0, \sigma_{\varepsilon})$ 





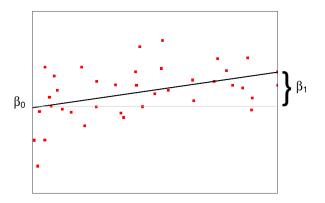


# The linear mixed model: Graphical interpretation



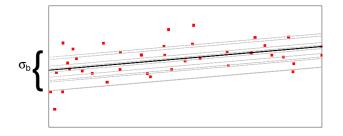


## The linear mixed model: Graphical interpretation





# The linear mixed model: Graphical interpretation





## When to consider a Linear Mixed Model?

- missing data
- unbalanced designs
- ullet more measurements than subject (n < p)
- control of "unwanted" variation
- . . .



# Example: Supernova 10K walking trials

Burke et al. (2017). Low Carbohydrate, High Fat diet impairs exercise economy and negates the performance benefit from intensified training in elite race walkers. *The Journal of Physiology*, 595(9), 2785–2807.



- Effect of diet on walking economy
- 3 diet interventions implemented over 2 camps
- Pre- and Post-camp 10K races
- Partial cross-over of subjects between camps
- Substantially different racing conditions within and between camps
- Missing data





## Example: Linear Mixed Model solution

Accounting for 3 sources of variation: Subject, Race and Camp

$$\begin{split} Y_i &= \beta_0 + \beta_1 \text{ Diet}_i + \beta_2 \text{ Race}_i + \beta_3 \text{ Camp}_i \\ &+ \beta_4 \text{ Diet}_i \times \text{Race}_i + \beta_5 \text{ Race}_i \times \text{Camp}_i \\ &+ b_{1i} + b_{2i} \text{ Race}_i + b_{3i^*} + b_{4i^*} \text{ Camp}_{i^*} + \varepsilon_i \end{split}$$



lme4

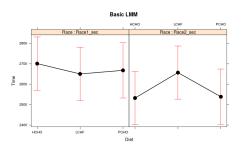
Bates et al. 2015, JSS

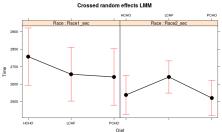






## Example: Results







```
> ## Load required packages
> library(lme4)
> library(reshape2)
> library(car)
> ## Read data
> data <- read.table("Diet_data_10Ktrial.csv",</pre>
          header=TRUE, sep=",", dec=".")
> data.trim <- data[, -c(4:5,7:8)]
> ## Transform data from wide format to long format
> data.long <- melt(data.trim,</pre>
+
            id.vars=c("subject", "camp", "Diet"),
            measure.vars=c("Race1_sec","Race2_sec"),
            variable.name="Race", value.name="Time")
> # convert camp into factor/make LCHF reference
> data.long$camp <- factor(data.long$camp)</pre>
> data.long$Diet <- relevel(data.long$Diet, ref="LCHF")
```



```
+ (Race|subject) + (camp|subject), data=data.long)
> print(fit, corr=FALSE)
Linear mixed model fit by REML ['lmerMod']
Formula:
Time ~ (Diet + Race + camp)^2 + (Race | subject) + (camp | subject)
Data: data.long
REML criterion at convergence: 558.5919
Random effects:
Groups Name Std.Dev. Corr
```

> fit <- lmer(Time ~ (Diet + Race + camp)^2 +

Residual 77.77

camp2

subject (Intercept) 249.64

subject.1 (Intercept) 192.87

Number of obs: 52, groups: subject, 18







170.97 -1.00

RaceRace2\_sec 180.95 -1.00

#### > summary(fit)\$coefficients

	Estimate	Std. Error	t value
(Intercept)	2749.87891	115.18479	23.8736291
DietHCHO	-162.25439	166.00956	-0.9773798
DietPCHO	-159.40113	152.26069	-1.0468962
RaceRace2_sec	70.28972	64.44298	1.0907272
camp2	-142.40756	111.90451	-1.2725810
DietHCHO:RaceRace2_sec	-203.37860	63.10971	-3.2226196
DietPCHO:RaceRace2_sec	-104.86568	63.21595	-1.6588484
DietHCHO:camp2	402.11982	185.88650	2.1632545
DietPCHO:camp2	219.99762	170.50420	1.2902768
RaceRace2_sec:camp2	-131.34933	49.79539	-2.6377809







```
> Anova(fit, test="F")
Analysis of Deviance Table (Type II Wald F tests with Kenward-
Response: Time
              F Df Df.res Pr(>F)
         1.3728 2 16.683 0.28059
Diet
       6.8797 1 24.011 0.01491 *
Race
camp 0.4602 1 12.199 0.51018
Diet:Race 4.3131 2 13.335 0.03592 *
Diet:camp 2.2025 2 15.468 0.14398
Race:camp 6.0796 1 10.109 0.03311 *
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' '
```