

# A Tutorial for Linear Models and Linear Mixed Effects Models in R

Experimental Phonetics

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# T.O.C

- ① Instruction
- ② Example Description
- ③ Exercise 1: Pitch ~ Sex
- ④ Exercise 2: Pitch ~ Age
- ⑤ Assumption

# Outline

- 1 **Instruction**
- 2 Example Description
- 3 Exercise 1: Pitch ~ Sex
- 4 Exercise 2: Pitch ~ Age
- 5 Assumption

# Before beginning

## Source of this tutorial

- Bodo Winter homepage  
<http://www.bodowinter.com/tutorials.html>
- Linear models and linear mixed effects models in R  
<http://arxiv.org/pdf/1308.5499.pdf>

## Citation

- Winter, B. (2013). Linear models and linear mixed effects models in R with linguistic applications. arXiv:1308.5499.

## How to download this tutorial

- github page  
[https://github.com/HyuksuRyu/mixedLM\\_tutorial](https://github.com/HyuksuRyu/mixedLM_tutorial)

# Instruction

What we are dealing with?

- ① **Linear model** ←
- ② Linear mixed model

# Outline

- 1 Instruction
- 2 Example Description**
- 3 Exercise 1: Pitch ~ Sex
- 4 Exercise 2: Pitch ~ Age
- 5 Assumption

# Example description

## Question

- Assume you knew nothing about males and females
- you were interested in whether **voice pitch** of males and females differs, if so, by how much

## Experiment

- take a bunch of males and females
- ask them to say a single word
- measure the respective voice pitches

# Example description

Subject	Sex	Voice.Pitch(Hz)
1	female	233
2	female	204
3	female	242
4	male	130
5	male	112
6	male	142



# Example description

It looks like

- the female values seem to be about 100 Hz above the male ones
- females have higher voice pitch than males

But

- it could be the case that females and males have the same pitch
- you were just unlucky and happened to choose some exceptionally high-pitched females and some exceptionally low-pitched males

# Example description

We might want

- a more precise estimate of the difference between males and females
- an estimate about how likely (or unlikely) that difference in voice pitch could have arisen just because of drawing an unlucky sample

→ **The linear model** comes in

- give some value about voice pitch for males and females
- as well as **some probability values** as to how likely those values are

# Example description

## Basic idea

- relationship b/w sex and voice pitch as a simple formula
- $\text{pitch} \sim \text{sex}$
- This reads
  - pitch predicted by sex
  - pitch as a function of sex
- LEFT: pitch
  - response (dependent) variable
  - the thing you measure
- RIGHT: sex
  - explanatory (independent) variable
  - predictor

# Example Description

## Error term

- Problem: the world is not perfect.
- Pitch is not *completely* determined by sex
- a bunch of different factors such as language, dialect, etc
- We can never measure and control all of these things
- update our formula to capture the existence of these “random” factors.
- $\text{pitch} \sim \text{sex} + \epsilon$
- $\epsilon$ 
  - an error term
  - stands for all of the things that affect pitch that are not sex,
  - all of the stuff that is random or uncontrollable

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# Exercise

Let's create the dataset

```
pitch = c(233,204,242,130,112,142)
sex = c(rep("female",3),rep("male",3))
my.df = data.frame(sex, pitch)
```

```
my.df
```

```
##      sex pitch
## 1 female   233
## 2 female   204
## 3 female   242
## 4  male    130
## 5  male    112
## 6  male    142
```

# Exercise

Let's create the dataset

```
pitch = c(233,204,242,130,112,142)
sex = c(rep("female",3),rep("male",3))
my.df = data.frame(sex, pitch)
```

```
my.df
```

```
##      sex pitch
## 1 female  233
## 2 female  204
## 3 female  242
## 4  male   130
## 5  male   112
## 6  male   142
```

# Exercise

- `lm()`

```
xmdl = lm(pitch ~ sex, my.df)
```

- Generate the linear model
- Note that we omit the “ $\epsilon$ ” term
- we saved the model into an object `xmdl`



# Exercise

- `summary()`
  - To see what the linear model did

```
summary(xmdl)
```

# Exercise

```
##
## Call:
## lm(formula = pitch ~ sex, data = my.df)
##
## Residuals:
##      1      2      3      4      5      6
##  6.667 -22.333  15.667   2.000 -16.000  14.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   226.33      10.18   22.224 2.43e-05 ***
## sexmale       -98.33      14.40   -6.827  0.00241 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.64 on 4 degrees of freedom
## Multiple R-squared:  0.921, Adjusted R-squared:  0.9012
## F-statistic: 46.61 on 1 and 4 DF, p-value: 0.002407
```

← the model formula  
you entered

← the residuals

← the coefficients of  
the fixed effects

← the output prints  
some overall results of  
the model

# Output

## Multiple R-Squared

- $R^2$ 
  - variance explained
  - 0.921 (quite high) means 92.1% of the stuff is “explained” by our model
- In this case, we have only one independent variable (the fixed effect “sex”),
- $R^2$  reflects how much variance in our data is accounted for by differences b/w males and females

# Output

## Multiple R-Squared and Adjusted R-squared

- If you have two or more variables (fixed effect), you see Adjusted R-squared ( $R^2_{adj}$ ), instead of Multiple R-squared.
- $R^2$  has a property that it is increased when variables are added up, even though the variables are irrelevant.
- “Adjusted” R-squared are adjusted considering how many fixed effects you used.

# Output

## Meaning of p-value in the F-statistics

- **conditional probability**
  - a probability *under the condition that the  $H_0$  is true*
- $H_0$ : Explanatory variables (*sex*) have no effect on the response (*pitch*)
- “statistically significant” when the conditional probability is lower than a threshold, and the alternative hypothesis ( $H_1$ ) is more likely.
- Report
  - “We constructed a linear model of pitch as a function of sex. This model was significant ( $F(1,4)=46.61, p<0.01$ ).”
- Significance of the overall model
- How to distinguish b/w the significance of the overall model (considering all effects together) from the p-value of individual coefficients? → to be continue

# Output

## Coefficients table

- Significance of the individual coefficients

```
##              Estimate Std. Error   t value    Pr(>|t|)
## (Intercept) 226.33333   10.18441 22.223508 2.426952e-05
## sexmale     -98.33333   14.40293 -6.827314 2.406892e-03
```

- Why sexmale, rather than just sex?
- Estimate of intercept: mean of pitch of female
- Estimate of sexmale: difference of pitch b/w female and male  
 $\therefore \text{Pitch}(\text{male}) = \text{intercept} + \text{sexmale}$

	female	male	difference
mean	226.333	128	98.333

# Tips

## Tip 1 - calculate mean in terms of sex

### 1 Classic

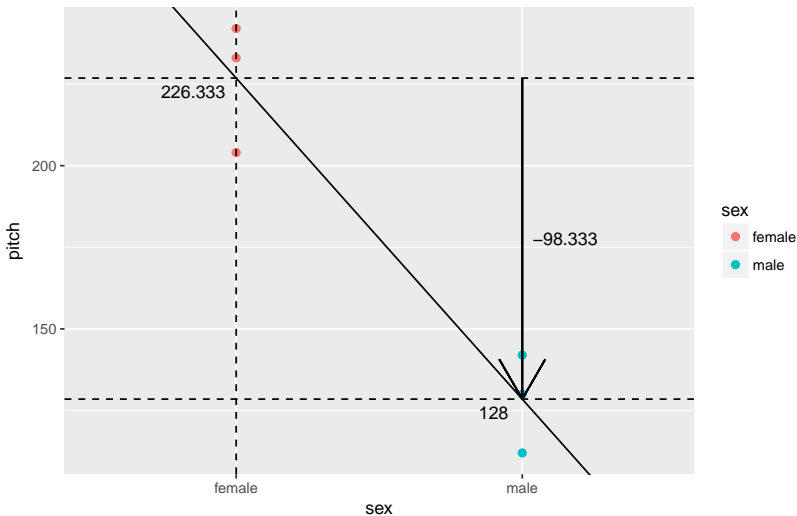
```
with(my.df, mean(pitch[sex=='female']))  
## [1] 226.3333  
  
with(my.df, mean(pitch[sex=='male']))  
## [1] 128
```

### 2 Using dplyr

```
library(dplyr)  
my.df %>%  
  group_by(sex) %>%  
  summarise(mean=mean(pitch))  
  
## # A tibble: 2 x 2  
##   sex      mean  
##   <fctr>   <dbl>  
## 1 female 226.3333  
## 2  male 128.0000
```

# Output

## Graphical interpretation





# Output

Secret of Intercept: Why did the model choose females to be the intercept?

∴ `lm()` function simply takes whatever comes first in **alphabet**  
“f” comes before “m”

# Output

Secret of Intercept: Why did the model choose females to be the intercept?

∴ `lm()` function simply takes whatever comes first in **alphabet**  
“f” comes before “m”

# Tips

## Tip 2 - How to change order of coefficients' level

```
my.df$sex = factor(my.df$sex, levels=c("male", "female"))
```

- Before (order: female-male)

##	Estimate	Std. Error	t value	Pr(> t )
## (Intercept)	226.33333	10.18441	22.223508	2.426952e-05
## sexmale	-98.33333	14.40293	-6.827314	2.406892e-03

- After (order: male-female)

##	Estimate	Std. Error	t value	Pr(> t )
## (Intercept)	128.00000	10.18441	12.568228	0.0002306453
## sexfemale	98.33333	14.40293	6.827314	0.0024068918

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# New model

Whether age predicts voice pitch

- continuous as explanatory
- $\text{pitch} \sim \text{age} + \epsilon$

Subject	Age	Pitch(Hz)
1	14	252
2	23	244
3	35	240
4	48	233
5	52	212
6	67	204

# Output

```
age = c(14,23,35,48,52,67)
pitch = c(252,244,240,233,212,204)
my.df = data.frame(age, pitch)
xmdl = lm(pitch~age, my.df)
summary(xmdl)

##
## Call:
## lm(formula = pitch ~ age, data = my.df)
##
## Residuals:
##      1      2      3      4      5      6
## -2.338 -2.149  4.769  9.597 -7.763 -2.115
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  267.0765     6.8522   38.98 2.59e-06 ***
## age         -0.9099     0.1569   -5.80 0.00439 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.886 on 4 degrees of freedom
## Multiple R-squared:  0.8937, Adjusted R-squared:  0.8672
## F-statistic: 33.64 on 1 and 4 DF, p-value: 0.004395
```

# Output

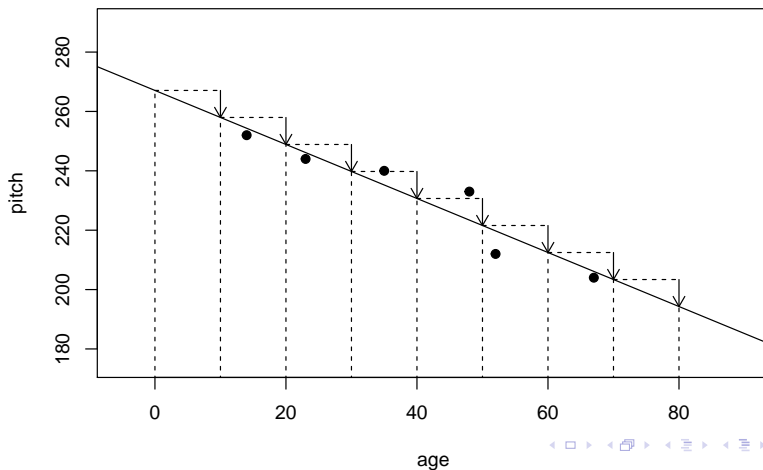
## Coefficient table

##		Estimate	Std. Error	t value	Pr(> t )
##	(Intercept)	267.0764640	6.8521942	38.976780	2.588356e-06
##	age	-0.9098694	0.1568771	-5.799888	4.394969e-03

- the significance of the intercept is NOT important
  - intercept means predicted pitch for people with age 0
- the significance of the age IS real interest.
  - every increase of age by 1 → decrease voice pitch by 0.9099

# Output

## Graphical interpretation





# Output

## Meaningful and meaningless intercepts

```
my.df$age.c = my.df$age - mean(my.df$age)
xmdl = lm(pitch~age.c, my.df)
```

- new column “age.c” → “centered” data

##	Estimate	Std. Error	t value	Pr(> t )
## (Intercept)	230.8333333	2.8112916	82.109353	1.318716e-07
## age.c	-0.9098694	0.1568771	-5.799888	4.394969e-03

- Same slope, but **different** intercept
- intercept here means pitch at mean age → mean pitch
- intercept becomes more meaningful than previous

# Tips

## Tip 3 - Manipulating data frame and add to a new column

### 1 Classic

```
my.df$age.c = my.df$age - mean(my.df$age)
```

### 2 Using dplyr

```
my.df %>%
  mutate(age.c = age-mean(age))

##   age pitch   age.c
## 1  14   252 -25.83333
## 2  23   244 -16.83333
## 3  35   240  -4.83333
## 4  48   233  8.166667
## 5  52   212 12.166667
## 6  67   204 27.166667
```

# Multiple regression

## Scaling up

- What if we measured two factors, such as age and sex?
- Multiple regression
  - a function of multiple predictor variables

$$pitch \sim sex + age + \epsilon$$

- But, same interpretation
  - Significance of overall model
  - Significance of each coefficient

# Multiple regression

## Example

```
##
## Call:
## lm(formula = pitch ~ sex + age, data = my.df)
##
## Residuals:
##      1      2      3      4      5      6
## -2.218 -7.103  9.321 13.846 -11.769 -2.077
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  202.2179    13.1658   15.359 0.000599 ***
## sexmale     -100.6603    10.3476   -9.728 0.002307 **
## age           0.6346     0.2887    2.198 0.115376
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.61 on 3 degrees of freedom
## Multiple R-squared:  0.9697, Adjusted R-squared:  0.9495
## F-statistic: 48.05 on 2 and 3 DF,  p-value: 0.005268
```

# The end of Linear model

The end of linear model!  
But one more thing!

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# Assumptions for LM

Assumptions for applying a linear model

- 1 Linearity
- 2 Absense of collinearity
- 3 Homoskedasticity
- 4 Normality of residuals
- 5 Absense of influential data points
- 6 Independence

# Linearity

## Linearity?

- linear what?
- linearity of residuals
- So, what is residuals?



# Linearity

Linearity?

- linear what?
- linearity of residuals
- So, what is residuals?

# Linearity

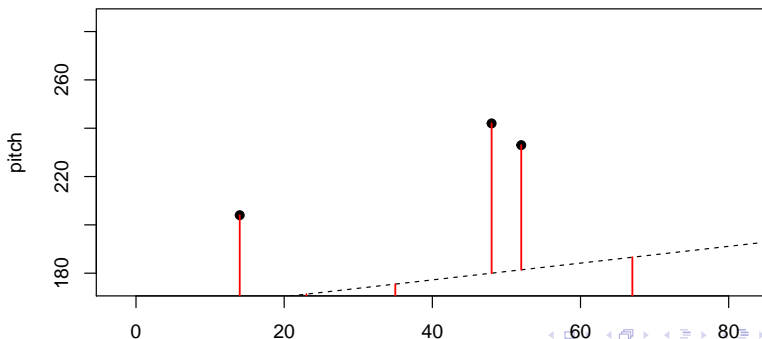
Linearity?

- linear what?
- linearity of residuals
- So, what is residuals?

# Linearity

## Residuals

- Deviations of the observed data points from the predicted values (fitted values)
- In this case, the residuals very small  $\rightarrow$  well predicted

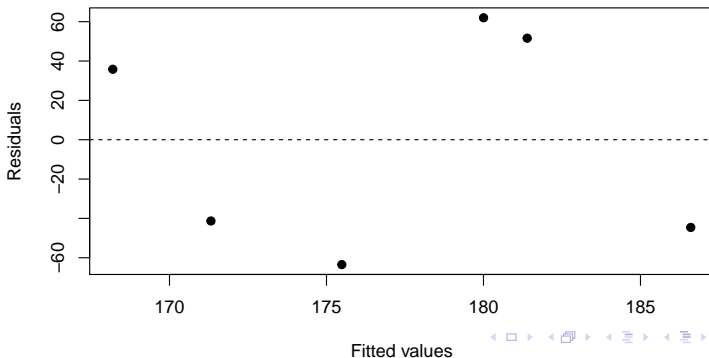


# Linearity

## Residuals

- Rotate the plot → Residual plot

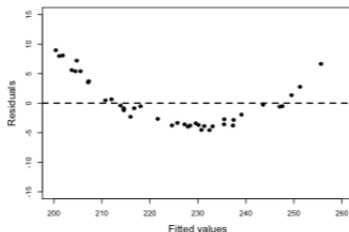
```
plot(fitted(xmdl), residuals(xmdl), pch=19,  
     xlab = 'Fitted values', ylab='Residuals' )
```



# Linearity

## Residual plot

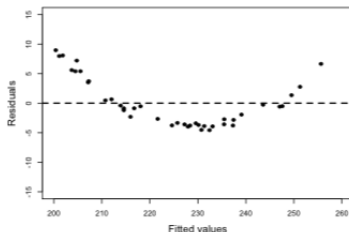
- The fitted values - on the horizontal line
- residuals - the vertical deviations from the line
- **No obvious pattern** in the residuals → **Linear**
- What if there were a nonlinear or curvy pattern?
- this would indicate a violation of the linearity assumption



# Linearity

## Residual plot

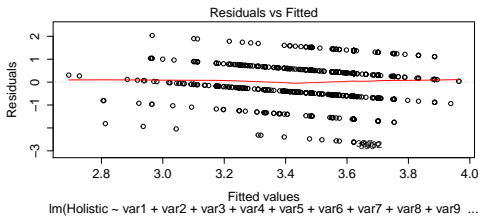
- The fitted values - on the horizontal line
- residuals - the vertical deviations from the line
- **No obvious pattern** in the residuals → **Linear**
- What if there were a nonlinear or curvy pattern?
- this would indicate a violation of the linearity assumption



# Linearity

What to do in case of non-linearity?

- ① You might miss an important fixed effects. Add them
- ② Perform a **nonlinear transformation** of your response, e.g., log-transform (*commonly chosen*)
- ③ Perform a nonlinear transformation of your fixed effects
  - if age showed in a U-shaped
  - add age and  $age^2$  as predictors
- ④ if stripes in residual plot, then you're most likely dealing with **categorical data** → different model such as logistic models



# Collinearity

What is collinearity?

- When two fixed effects (predictors) are **correlated with** each other,
- they are said to be **collinear**

Example

- you were interested in how average talking speed affects intelligence ratings

*intelligence ratings ~ talking speed*

- you measured several different indicators of talking speed
  - syllables/sec, words/sec, sentences/sec
- they are likely to be highly correlated with each other
- if you use all of them as predictors within the same model, there will be **collinearity problem**



# Collinearity

If there is collinearity

- the interpretation of the model becomes **unstable**
- the significance of these correlated or collinear fixed effects is not easily interpretable
  - $\therefore$  they might steal each other's **explanatory power**
- if multiple predictors are very similar to each other
  - it becomes very difficult to decide what, in fact, is playing a big role

# Collinearity

How to get rid of collinearity?

- ① pre-empt the problem in the design stage
  - focus on a few fixed effects that are not correlated with each other
- ② Or, think about which one is the most meaningful and drop the others
  - DO NOT base this dropping decision on the **significance** (circular logic problem)
- ③ Or, consider dimension-reduction techniques such as Principal Component Analysis
  - transform several correlated variables into a smaller set of variables which you can then use as new fixed effects.

# Homoskedasticity

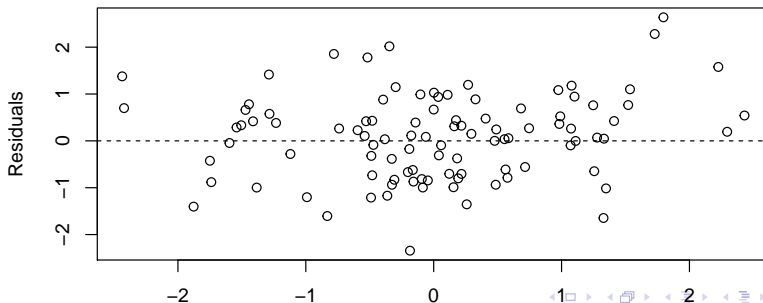
What is Homoskedasticity?

- The variance of your data should be approximately equal across the range of your predicted values
- it is **extremely important assumption**
- If homoscedasticity is violated → a problem with unequal variances

# Homoskedasticity

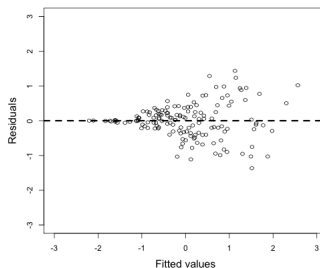
How to check whether homoscedasticity assumption were met?

- the **residuals** of your model need to roughly have a similar amount of deviation from the predicted values
- See Residual Plot
- Good residual plot essentially looks blob-like



# Homoskedasticity

## Example of **heteroskedasticity**



- higher fitted values have larger residuals

What to do?

- As mentioned earlier, consider a **log-transform**

# Normality of residuals

## Normality of residuals

- It is the one that is **least important**
- LM is relatively robust against violation of the normality assumption
- Gellman and Hill (2007), a famous book on LM and mixed models, DO NOT EVEN RECOMMEND diagnostics of the normality assumption

If you want to test the assumption

- Histogram

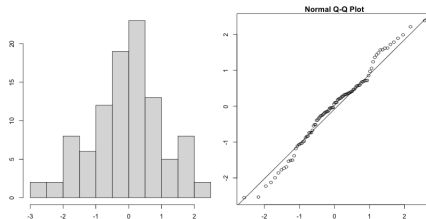
```
hist(residuals(xmdl))
```

- Q-Q plot

```
qqnorm(residuals(xmdl))
```

# Normality of residuals

## Example of normality



- These look good
- The histogram is relatively bell-shaped
- The Q-Q plot indicates that the data falls on a straight line
  - which means that it's similar to a normal distribution
- can conclude that there are no obvious violations of the normality assumption

# Absence of influential data points

What is the influential data point?

- If a particular data point is excluded, when values with which the coefficient is adjusted is large, it is an influential data point.
- Influential data points can drastically change the interpretation of the results, it can lead to instable results



# Absence of influential data points

How to check?

- Using `dfbeta()` function

```
dfbeta(xmdl)

##      (Intercept)          age
## 1  -5.7886394    0.4307550
## 2   51.5196947   -0.9857490
## 3   -0.1678502    0.3289864
## 4  -30.9878812    0.5260128
## 5  -20.6098951    0.1939283
## 6   39.1182640   -1.3964689
```

- DFbeta values are the values of coefficient as a result of *leave-one-out diagnostics*
- For example, if data point 1 is excluded, the coefficient for age has to be adjusted by 0.0644 from -0.9099, so -0.8455

# Absence of influential data points

What is the criteria for decision of influential data point

- There is no clear, sharp criteria
- One thing for sure
  - any value that changes the sign of the slope is **definitely** an influential point
  - be cautious to DFbeta value which is at least half of the absolute value of the slope (To author)

# Absence of influential data points

How to proceed if there are influential data points?

- DO NOT SIMPLY EXCLUDE those points and report only the results on the reduced set
  - The only case to exclude influential points is when
    - there is an obvious error (negative age)
    - or there is a value that obviously is the result due to a technical error (voice pitch value of 0)
- Run the analysis **with** the influential points and **without** the points, reports both analyses, state whether the interpretation of the results does or does not change

# Independence

What is independence?

- easy example - coin flip or roll of a dice
- each try is not influenced by another try
- each coin flip and each roll of a dice is absolutely independent from the outcome of the preceding coin flips or dice rolls
- The same should hold for your data points for LM analysis
- the data points should come from DIFFERENT SUBJECT
- Each subject should only contribute one data point
- Independence assumption is by far **the most important one**

# Independence

When you violate the indepenence assumption?

- may greatly inflate chance of finding a *spurious result*
- and it results in a p-value that is *completely meaningless*.

How can guarantee independence?

- Independence is a **question of the experimental design**
- by only collecting one data point per subject

# Independence

If you want to collect more data per subject?

- such as in repeated measures design
- need to resolve these non-independence at the analysis stage
- This is where **MIXED MODELS** comes in

Mixed models will be proceeded in  
Tutorial 2

# Independence

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Tutorial 2