# Day 14: Comparing Means with ANOVA (Section 5.5)

BSTA 511/611

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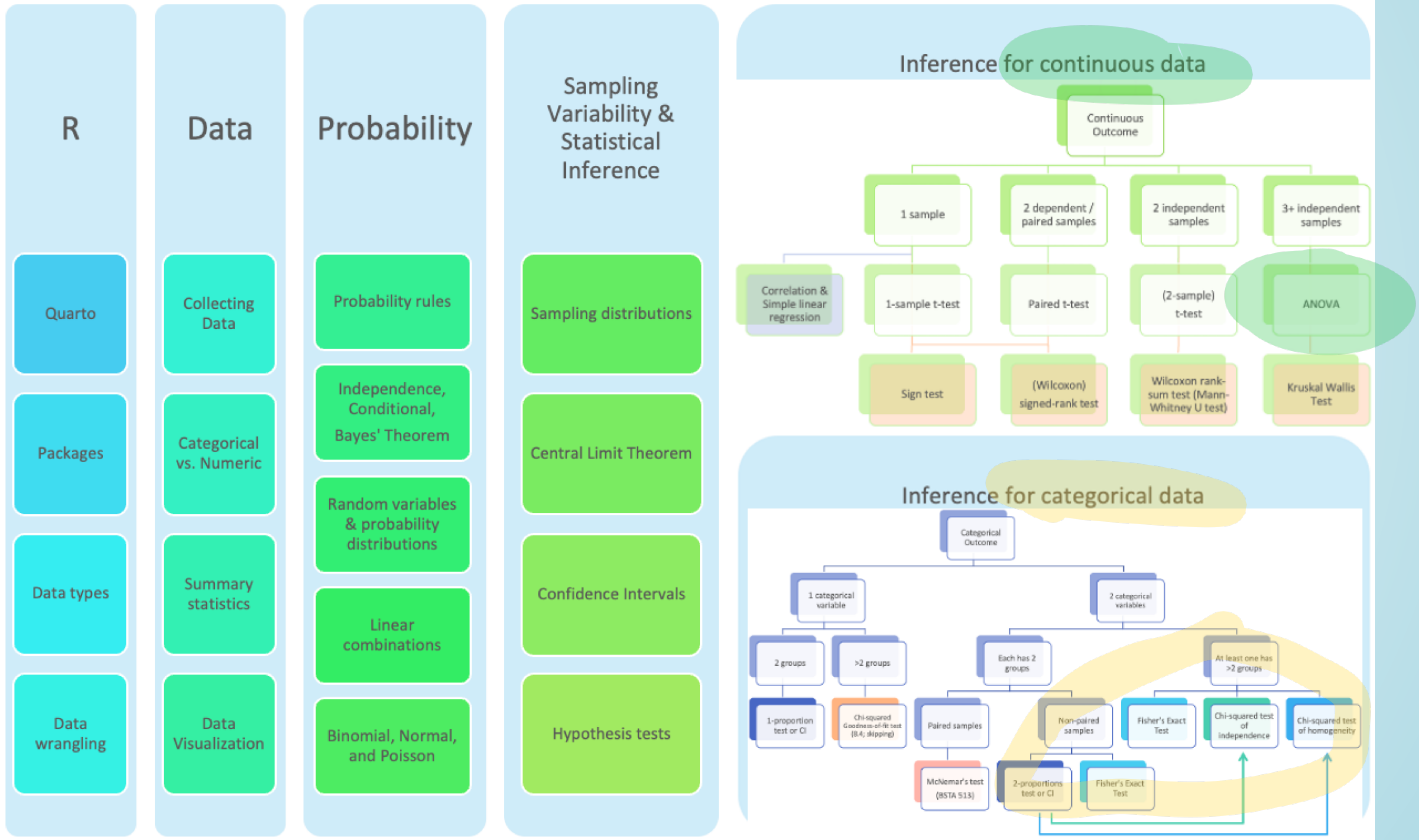
2023-11-20

# Where are we?



## R

- Quarto
- Packages
- Data types
- Data wrangling

## Data

- Collecting Data
- Categorical vs. Numeric
- Summary statistics
- Data Visualization

## Probability

- Probability rules
- Independence, Conditional, Bayes' Theorem
- Random variables & probability distributions
- Linear combinations
- Binomial, Normal, and Poisson

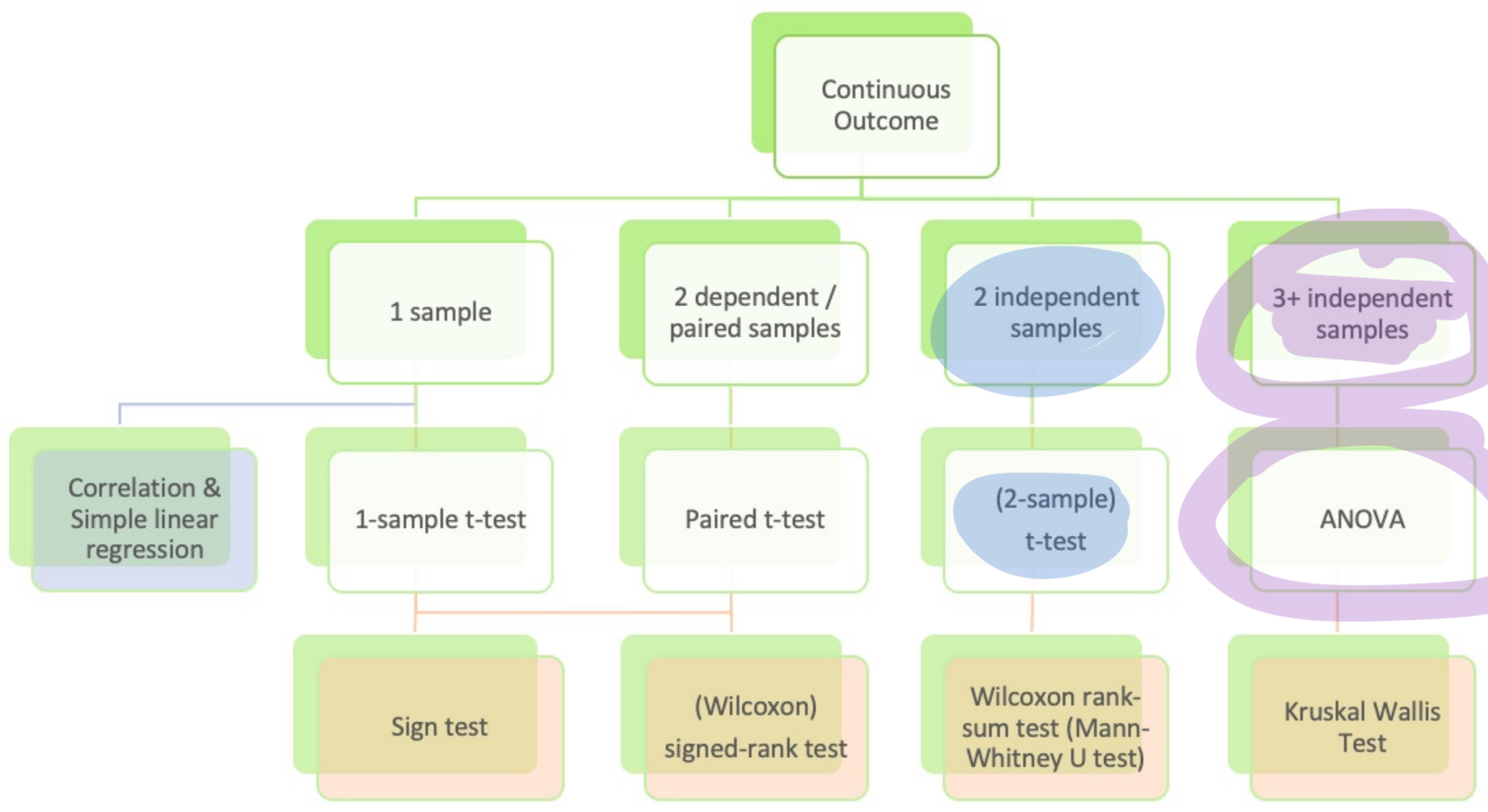
## Sampling Variability & Statistical Inference

- Sampling distributions
- Central Limit Theorem
- Confidence Intervals
- Hypothesis tests

## Inference for continuous data

## Inference for categorical data

# Where are we? Continuous outcome zoomed in



Continuous Outcome

1 sample

2 dependent / paired samples

2 independent samples

3+ independent samples

Correlation & Simple linear regression

1-sample t-test

Paired t-test

(2-sample) t-test

ANOVA

Sign test

(Wilcoxon) signed-rank test

Wilcoxon rank-sum test (Mann-Whitney U test)

Kruskal Wallis Test

# Goals for today (Section 5.5)

- Analysis of Variance (ANOVA)
- When to use an ANOVA
- Hypotheses
- ANOVA table
- Different sources of variation in ANOVA
- ANOVA conditions
- F-distribution
- Post-hoc testing of differences in means
- Running an ANOVA in R

# Disability Discrimination Example

- The U.S. Rehabilitation Act of 1973 prohibited discrimination against people with physical disabilities.
  - The act defined a disabled person as any individual who has a physical or mental impairment that limits the person's major life activities.
- A 1980's study examined whether physical disabilities affect people's perceptions of employment qualifications
  - (Cesare, Tannenbaum, & Dalessio, 1990).
- Researchers prepared recorded job interviews, using *same actors and script each time*.
- Only difference: job applicant appeared with different disabilities.
  - *No disability*
  - *Leg amputation*
  - *Crutches*
  - *Hearing impairment*
  - *Wheelchair confinement*
- 70 undergrad students were randomly assigned to view one of the videotapes,
  - then **rated** the candidate's qualifications on a **1-10 scale**.

- The research question: **are qualifications evaluated differently depending on the applicant's presented disability?**

# Load interview data from `.txt` file

- `.txt` (text) files are usually tab-deliminated files
  - `.csv` files are comma-separated files
- `read_delim` is from the `readr` package, just like `read_csv`, and loads with other `tidyverse` packages

```r
employ <- read_delim(
  file = here::here("data", "DisabilityEmployment.txt"),
  delim = "\t",     # tab delimited
  trim_ws = TRUE)
```

`trim_ws`: specify whether leading and trailing white space should be trimmed from each field before parsing it

```r
glimpse(employ)
```

```
Rows: 70
Columns: 2
$ disability <chr> "none", "none", "none", "none", "none", "none", "none", "no…
$ score      <dbl> 1.9, 2.5, 3.0, 3.6, 4.1, 4.2, 4.9, 5.1, 5.4, 5.9, 6.1, 6.7,…
```

```r
summary(employ)
```

```
  disability            score      
 Length:70          Min.   :1.400  
 Class :character   1st Qu.:3.700  
 Mode  :character   Median :5.050  
                    Mean   :4.929  
                    3rd Qu.:6.100  
                    Max.   :8.500  
```

```r
employ %>% tabyl(disability)
```

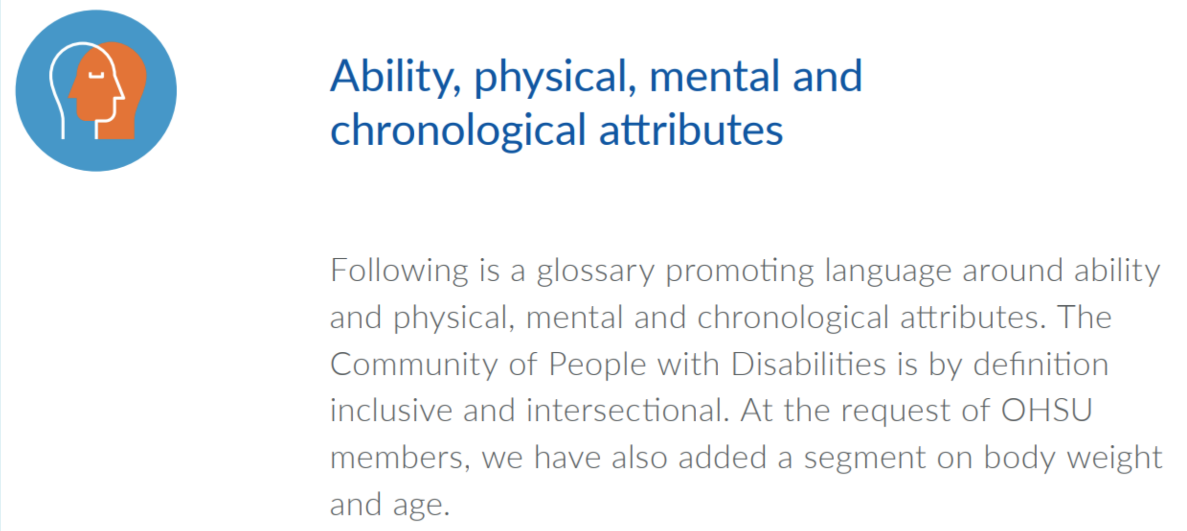
```
 disability  n percent
    amputee 14     0.2
   crutches 14     0.2
    hearing 14     0.2
       none 14     0.2
 wheelchair 14     0.2
```

# MoRitz's tip of the day

Read OHSU's Inclusive Language Guide (below is from pgs. 22-25)

"… an evolving tool to help OHSU members learn about and use inclusive language…"

Sections on: Race and ethnicity, Immigration status, Gender and sexual orientation, and Ability (including physical, mental and chronological attributes)

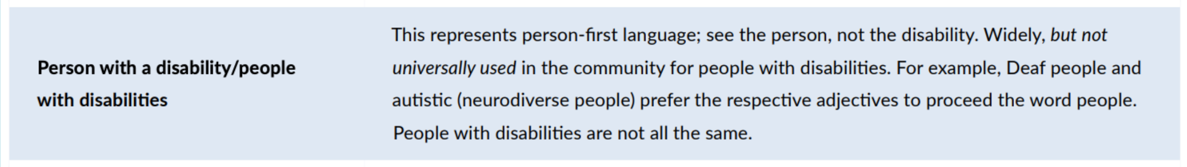


## Ability, physical, mental and chronological attributes

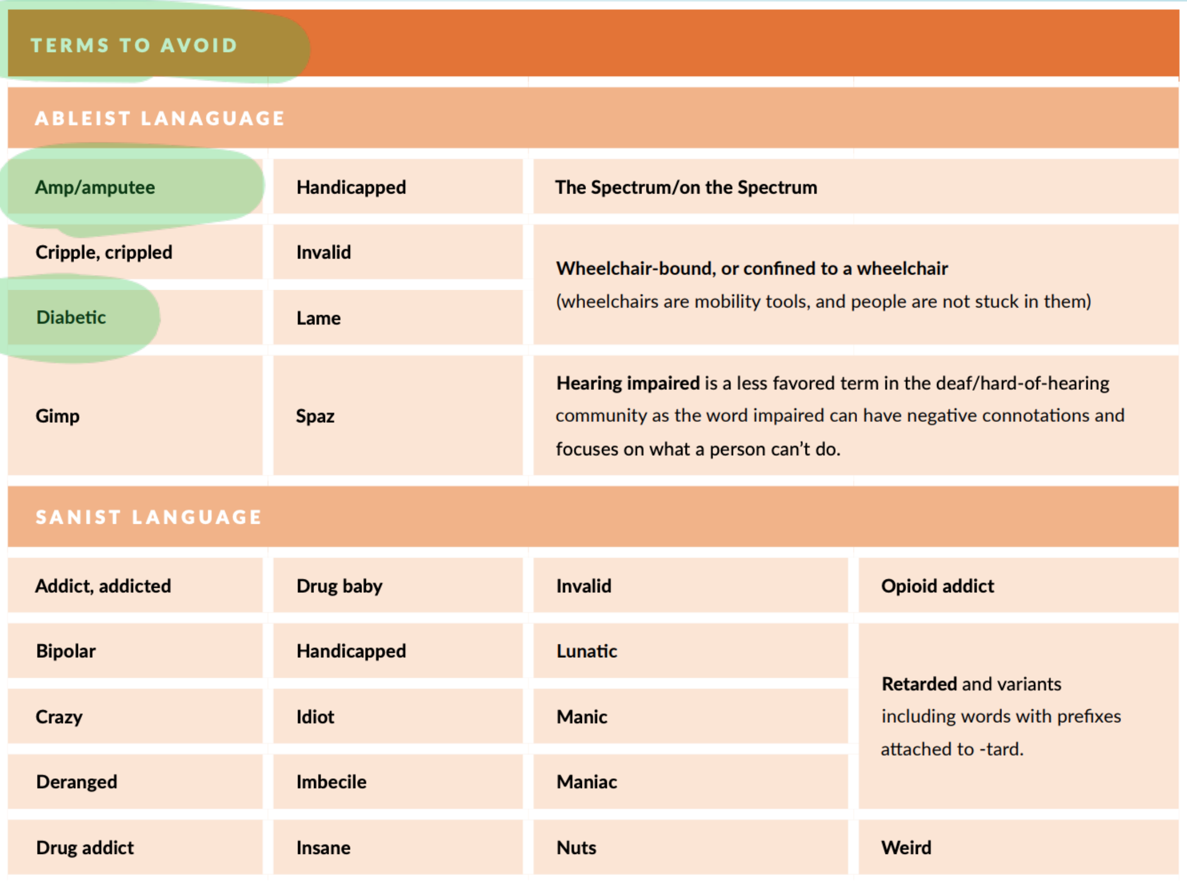
Following is a glossary promoting language around ability and physical, mental and chronological attributes. The Community of People with Disabilities is by definition inclusive and intersectional. At the request of OHSU members, we have also added a segment on body weight and age.

**RESPECTFUL LANGUAGE**

| TERM | DEFINITION |
|---|---|



| | |
|---|---|
| **Person with a disability/people with disabilities** | This represents person-first language; see the person, not the disability. Widely, *but not universally used* in the community for people with disabilities. For example, Deaf people and autistic (neurodiverse people) prefer the respective adjectives to proceed the word people. People with disabilities are not all the same. |



**TERMS TO AVOID**

**ABLEIST LANAGUAGE**

| | | |
|---|---|---|
| **Amp/amputee** | **Handicapped** | **The Spectrum/on the Spectrum** |
| **Cripple, crippled** | **Invalid** | **Wheelchair-bound, or confined to a wheelchair**<br>(wheelchairs are mobility tools, and people are not stuck in them) |
| **Diabetic** | **Lame** | |
| **Gimp** | **Spaz** | **Hearing impaired** is a less favored term in the deaf/hard-of-hearing community as the word impaired can have negative connotations and focuses on what a person can't do. |

**SANIST LANGUAGE**

| | | | |
|---|---|---|---|
| **Addict, addicted** | **Drug baby** | **Invalid** | **Opioid addict** |
| **Bipolar** | **Handicapped** | **Lunatic** | **Retarded** and variants including words with prefixes attached to -tard. |
| **Crazy** | **Idiot** | **Manic** | |
| **Deranged** | **Imbecile** | **Maniac** | |
| **Drug addict** | **Insane** | **Nuts** | **Weird** |

# Factor variable: Make disability a factor variable

```r
glimpse(employ)
```

```
Rows: 70
Columns: 2
$ disability <chr> "none", "none", "none", "none", "none", "none", "none", "no…
$ score      <dbl> 1.9, 2.5, 3.0, 3.6, 4.1, 4.2, 4.9, 5.1, 5.4, 5.9, 6.1, 6.7,…
```

```r
summary(employ)
```

```
  disability            score      
 Length:70          Min.   :1.400  
 Class :character   1st Qu.:3.700  
 Mode  :character   Median :5.050  
                    Mean   :4.929  
                    3rd Qu.:6.100  
                    Max.   :8.500  
```

## Make disability a factor variable:

```r
employ <- employ %>%
  mutate(disability = factor(disability))
```

## What’s different now?

```r
glimpse(employ)
```

```
Rows: 70
Columns: 2
$ disability <fct> none, none, none, none, none, none, none, none, none, none,…
$ score      <dbl> 1.9, 2.5, 3.0, 3.6, 4.1, 4.2, 4.9, 5.1, 5.4, 5.9, 6.1, 6.7,…
```

```r
summary(employ)
```

```
     disability     score      
 amputee   :14   Min.   :1.400  
 crutches  :14   1st Qu.:3.700  
 hearing   :14   Median :5.050  
 none      :14   Mean   :4.929  
 wheelchair:14   3rd Qu.:6.100  
                 Max.   :8.500  
```

# Factor variable: Change order & name of disability levels

## What are the current level names and order?

```
levels(employ$disability)
```

```
[1] "amputee"    "crutches"   "hearing"    "none"       "wheelchair"
```

## What changes are being made below?

```
employ <- employ %>%
  mutate(
    # make "none" the first level
    # by only listing the level none, all other levels will be in original order
    disability = fct_relevel(disability, "none"),
    # change the level name amputee to amputation
    disability = fct_recode(disability, amputation = "amputee")
    )
```

new old

- `fct_relevel()` and `fct_recode()` are from the `forcats` package: https://forcats.tidyverse.org/index.html.
- `forcats` is loaded with `library(tidyverse)`.

## New order & names:

```
levels(employ$disability) # note the new order and new name
```

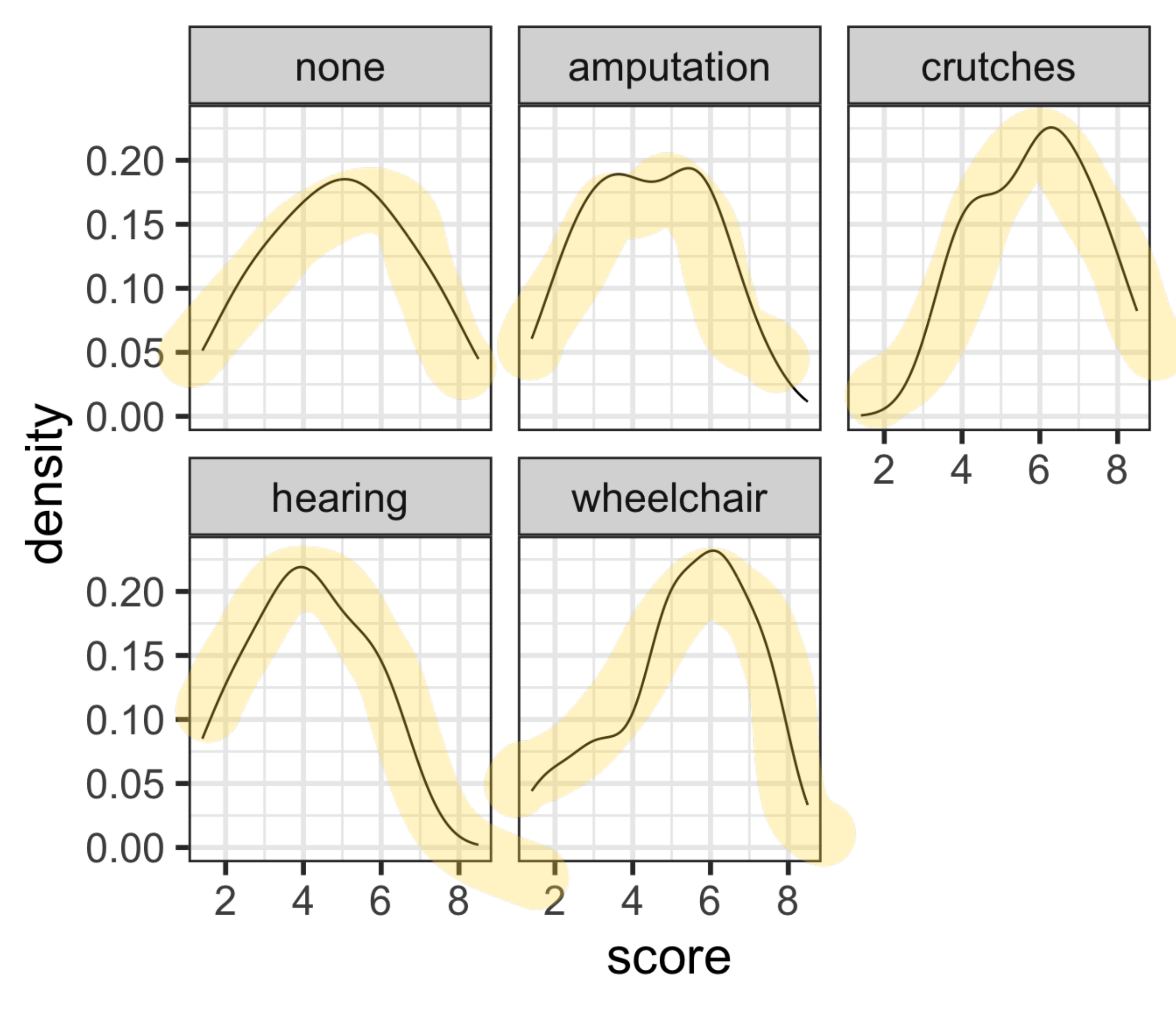
```
[1] "none"       "amputation" "crutches"   "hearing"    "wheelchair"
```

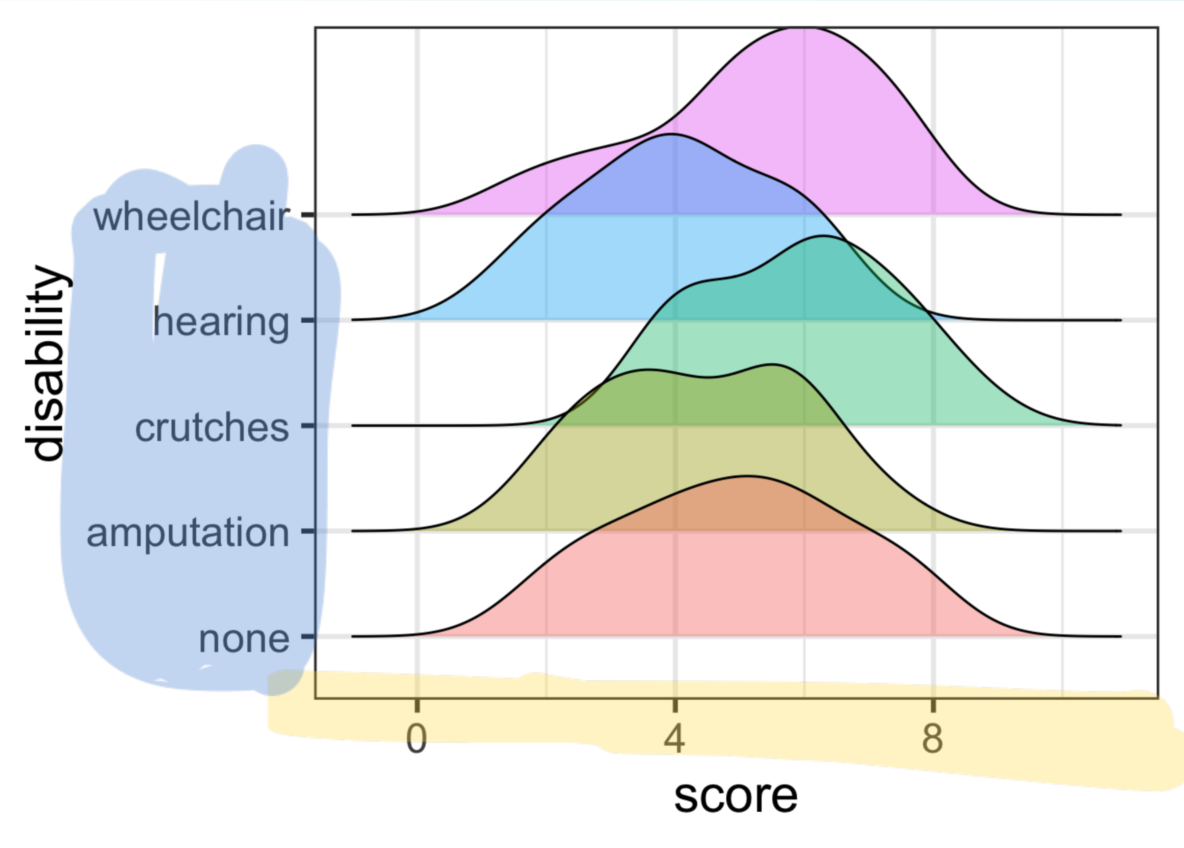
# Data viz (1/2)

- What are the `score` distribution shapes within each group?
- Any unusual values?

```r
ggplot(employ, aes(x=score)) +
  geom_density() +
  facet_wrap(~ disability)
```

```r
library(ggridges)
ggplot(employ,
       aes(x=score,
           y = disability,
           fill = disability)) +
  geom_density_ridges(alpha = 0.4) +
  theme(legend.position="none")
```



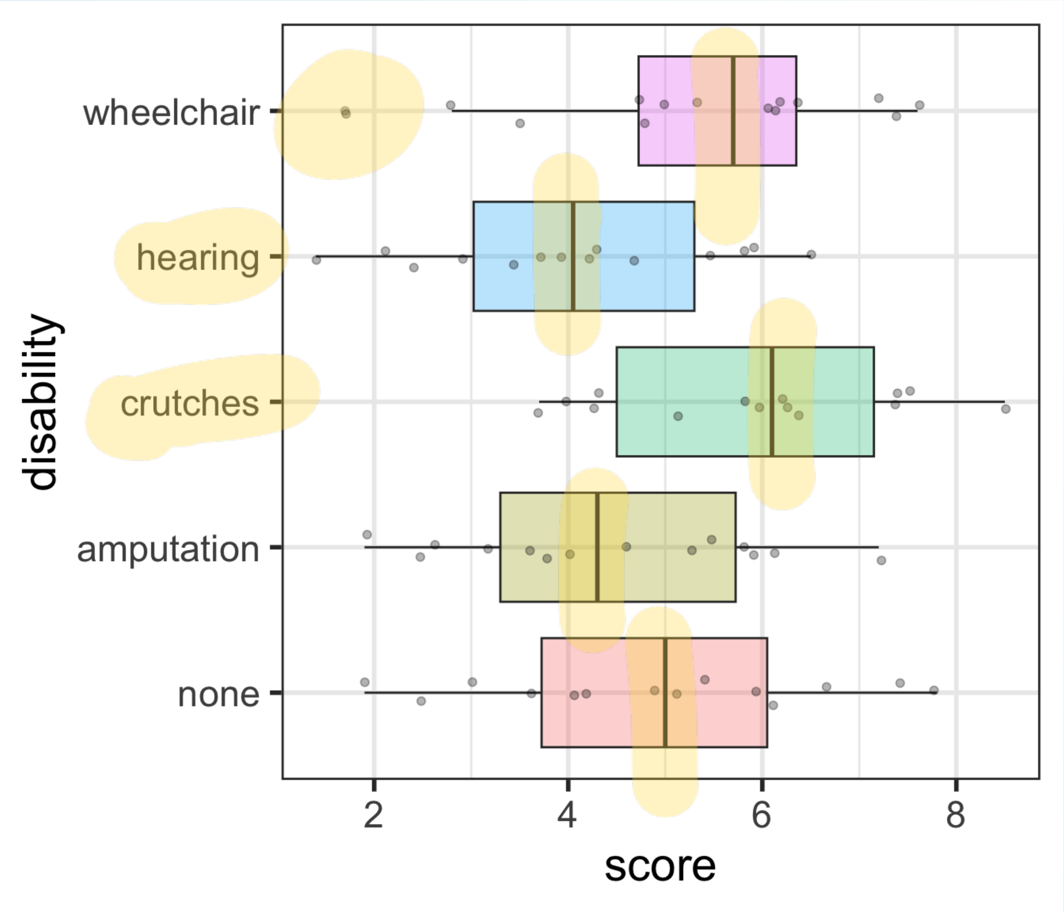


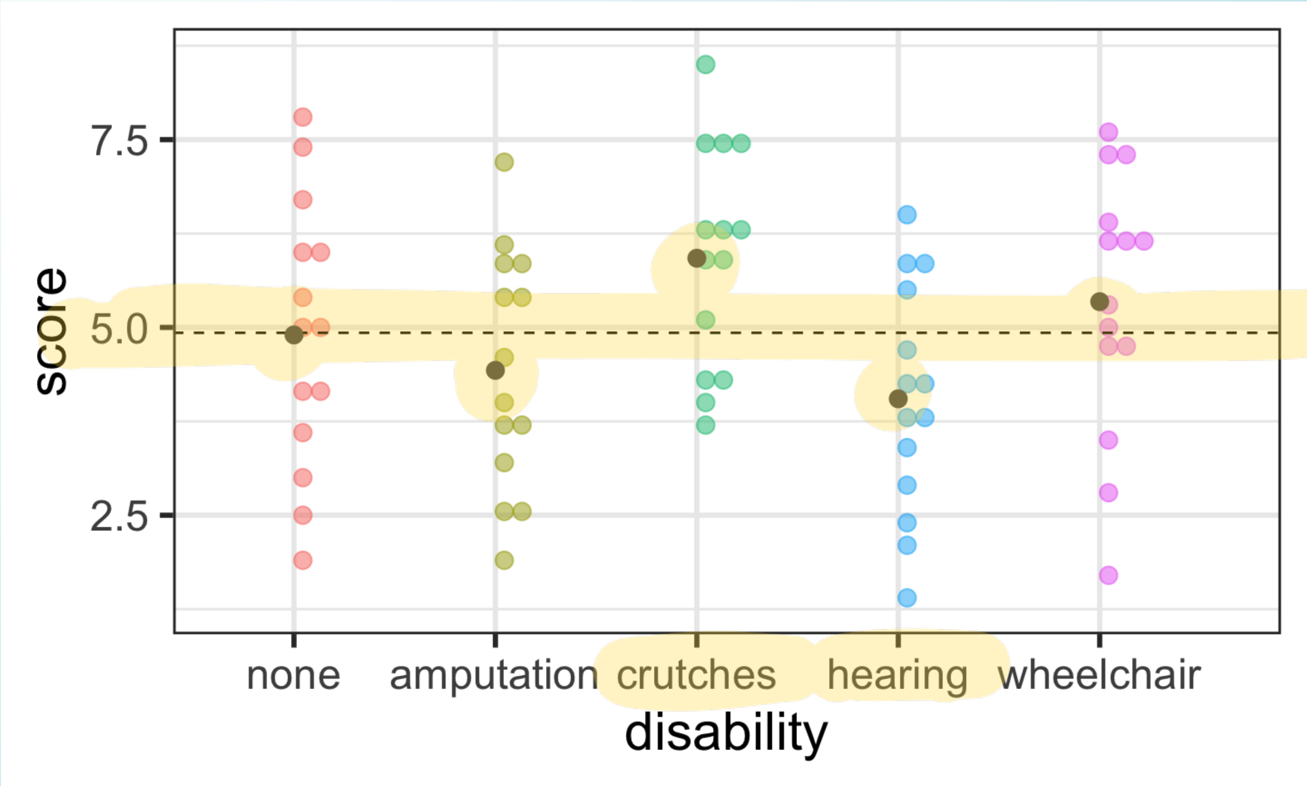
# Data viz (2/2)

- Compare the `score` measures of **center** and **spread** between the groups

```r
ggplot(employ,
       aes(y=score,
           x = disability,
           fill = disability)) +
  geom_boxplot(alpha = 0.3) +
  coord_flip() +
  geom_jitter(width = 0.1,
              alpha = 0.3) +
  theme(legend.position = "none")
```

```r
ggplot(employ,
       aes(x = disability,
           y=score,
           fill=disability,
           color=disability)) +
  geom_dotplot(binaxis = "y", alpha = 0.5) +
  geom_hline(aes(yintercept = mean(score)),
             lty = "dashed") +
  stat_summary(fun ="mean", geom="point",
    size = 3, color = "grey33", alpha = 1) +
  theme(legend.position = "none")
```





# Hypotheses

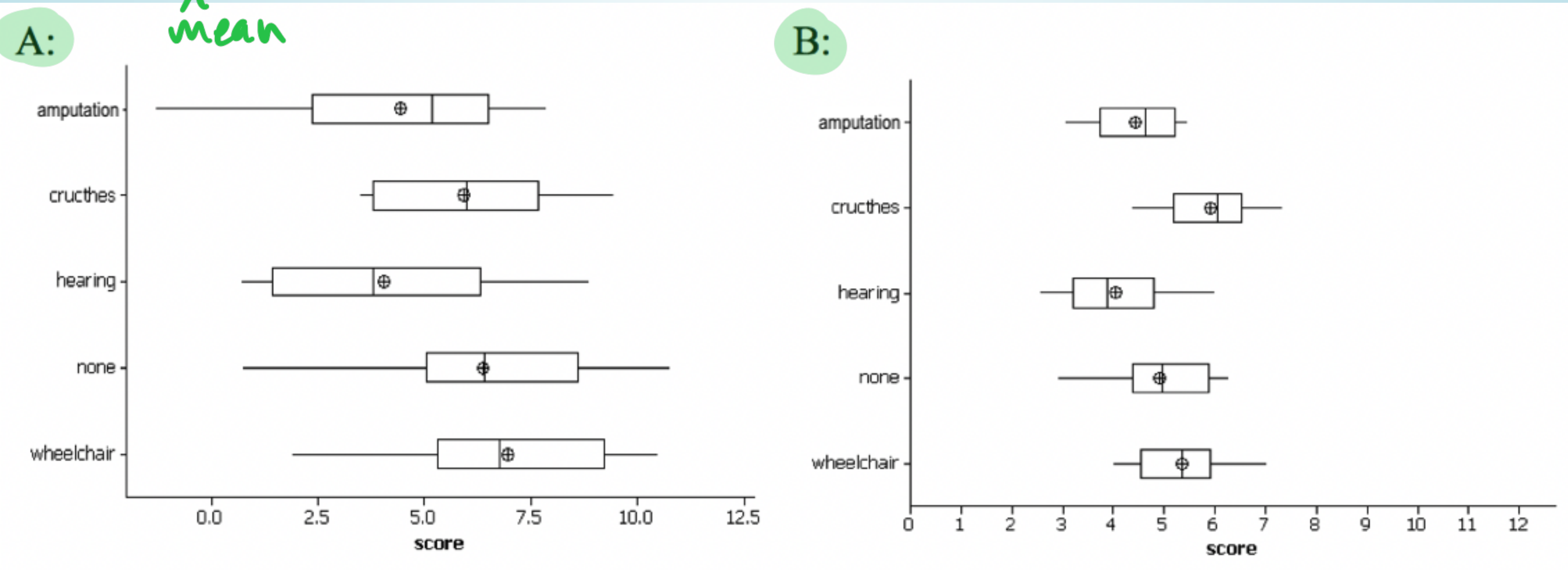
To test for a difference in means across *k* groups:

$$H_0 : \mu_1 = \mu_2 = \ldots = \mu_k$$
$$\text{vs. } H_A : \text{At least one pair } \mu_i \neq \mu_j \text{ for } i \neq j$$

**Hypothetical examples:**

Class discussion

In which set (A or B) do you believe the evidence will be stronger that at least one population mean differs from the others?



# Comparing means

Whether or not two means are significantly different depends on:

- How far apart the **means** are
- How much **variability** there is within each group

**Questions:**

- How to measure variability **between** groups?
- How to measure variability **within** groups?
- How to compare the two measures of variability?
- How to determine significance?

# ANOVA in base R

- There are several options to run an ANOVA model in R
- Two most common are `lm` and `aov`
  - `lm` = linear model; will be using frequently in BSTA 512

```
lm(score ~ disability, data = employ) %>% anova()
```

y ~ x

```
Analysis of Variance Table

Response: score
           Df  Sum Sq Mean Sq F value  Pr(>F)  
disability  4  30.521  7.6304  2.8616 0.03013 *
Residuals  65 173.321  2.6665                  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

<.05

```
aov(score ~ disability, data = employ) %>% summary()
```

```
            Df Sum Sq Mean Sq F value Pr(>F)  
disability   4  30.52   7.630   2.862 0.0301 *
Residuals   65 173.32   2.666                 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hypotheses:

$$H_0: \mu_{none} = \mu_{amputation} = \mu_{crutches} = \mu_{hearing} = \mu_{wheelchair}$$

$$\text{vs. } H_A: \text{At least one pair } \mu_i \neq \mu_j \text{ for } i \neq j$$

Do we reject or fail to reject $H_0$?

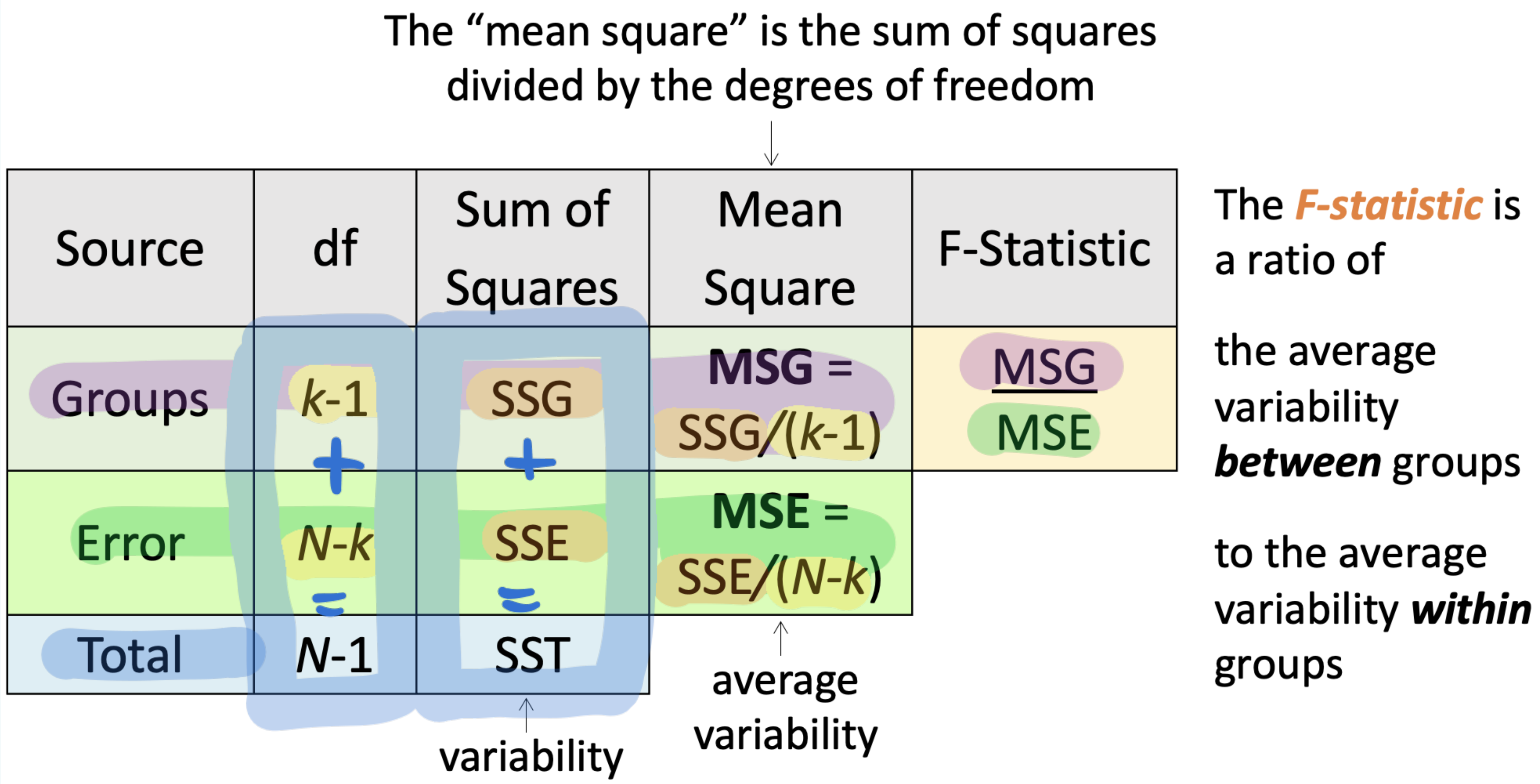
# ANOVA tables

## Disability example ANOVA table from R:

```r
lm(score ~ disability, data = employ) %>% anova()
```

```
Analysis of Variance Table

Response: score
           Df  Sum Sq Mean Sq F value  Pr(>F)
disability  4  30.521  7.6304  2.8616 0.03013 *
Residuals  65 173.321  2.6665
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Generic ANOVA table:



The “mean square” is the sum of squares divided by the degrees of freedom

| Source | df | Sum of Squares | Mean Square | F-Statistic |
|---|---|---|---|---|
| Groups | $k$-1 | SSG | **MSG** = SSG/($k$-1) | $\frac{\text{MSG}}{\text{MSE}}$ |
| | + | + | | |
| Error | $N$-$k$ | SSE | **MSE** = SSE/($N$-$k$) | |
| | = | = | | |
| Total | $N$-1 | SST | | |

variability

average variability

The ***F-statistic*** is a ratio of

the average variability ***between*** groups

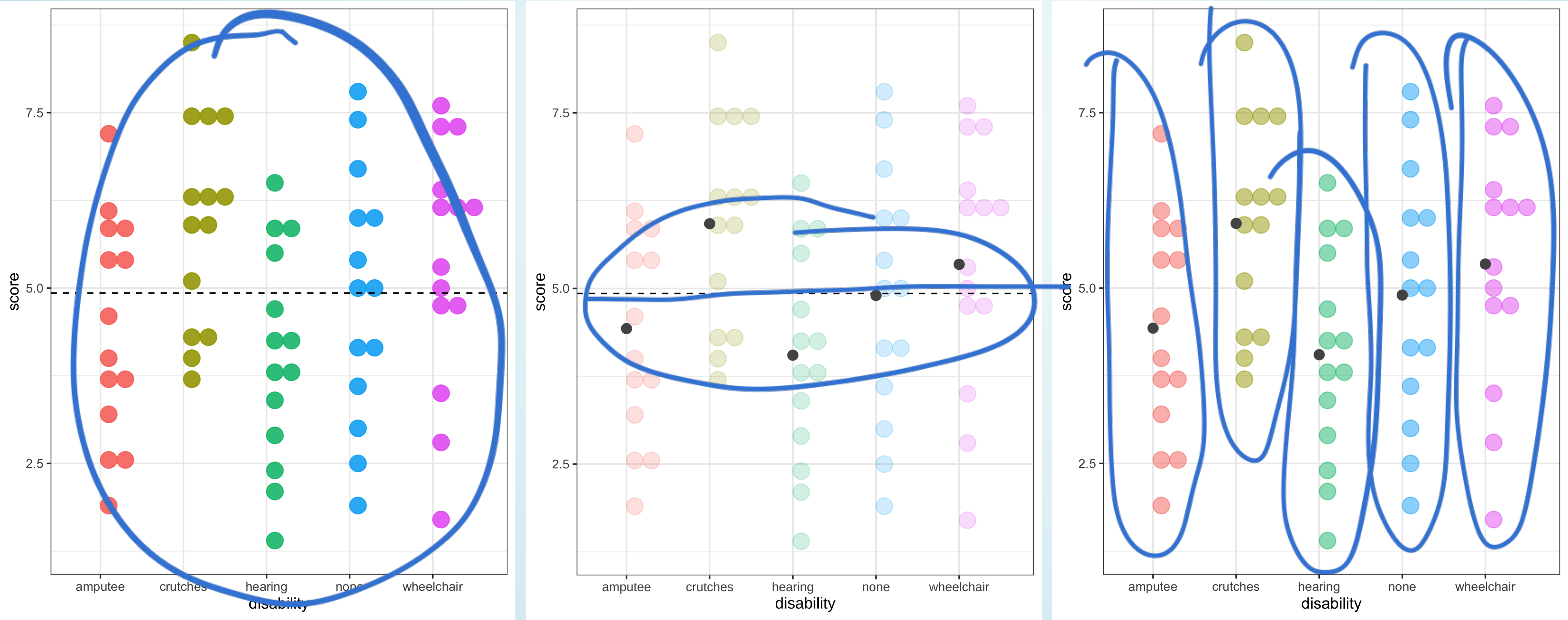
to the average variability ***within*** groups

# ANOVA: Analysis of Variance

**ANOVA** compares the variability between groups to the variability within groups

Total variability = Variability between groups + Variability within groups

$$SST = SSG + SSE$$



# ANOVA: Analysis of Variance

**Analysis of Variance (ANOVA)** compares the variability between groups to the variability within groups

**Total variability** = **Variability between groups** + **Variability within groups**

$$\sum_{i=1}^{k}\sum_{j=1}^{n_i}(x_{ij}-\bar{x})^2 = \sum_{i=1}^{k} n_i(\bar{x}_i-\bar{x})^2 + \sum_{i=1}^{k}\sum_{j=1}^{n_i}(x_{ij}-\bar{x}_i)^2$$

**SST** (Total sum of squares) = **SSG** (sum of squares due to groups) + **SSE** (Error sum of squares)

# Notation

- $k$ groups
- $n_i$ observations in each of the $k$ groups
- Total sample size is $N = \sum_{i=1}^{k} n_i$
- $\bar{x}_i$ = mean of observations in group $i$
- $\bar{x}$ = mean of *all* observations

Groups 1 to k (i)

| Observation | $i = 1$ | $i = 2$ | $i = 3$ | . . . | $i = k$ | overall |
|---|---|---|---|---|---|---|
| $j = 1$ | $x_{11}$ | $x_{21}$ | $x_{31}$ | . . . | $x_{k1}$ | |
| $j = 2$ | $x_{12}$ | $x_{22}$ | $x_{32}$ | . . . | $x_{k2}$ | |
| $j = 3$ | $x_{13}$ | $x_{23}$ | $x_{33}$ | . . . | $x_{k3}$ | |
| $j = 4$ | $x_{14}$ | $x_{24}$ | $x_{34}$ | . . . | $x_{k4}$ | |
| $\vdots$ | $\vdots$ | $\vdots$ | $\vdots$ | $\ddots$ | $\vdots$ | |
| $j = n_i$ | $x_{1n_1}$ | $x_{2n_2}$ | $x_{3n_3}$ | . . . | $x_{kn_k}$ | |
| Means | $\bar{x}_1$ | $\bar{x}_2$ | $\bar{x}_3$ | . . . | $\bar{x}_k$ | $\bar{x}$ |
| Variance | $s_1^2$ | $s_2^2$ | $s_3^2$ | . . . | $s_k^2$ | $s^2$ |

Observations within each group

$x_{ij}$

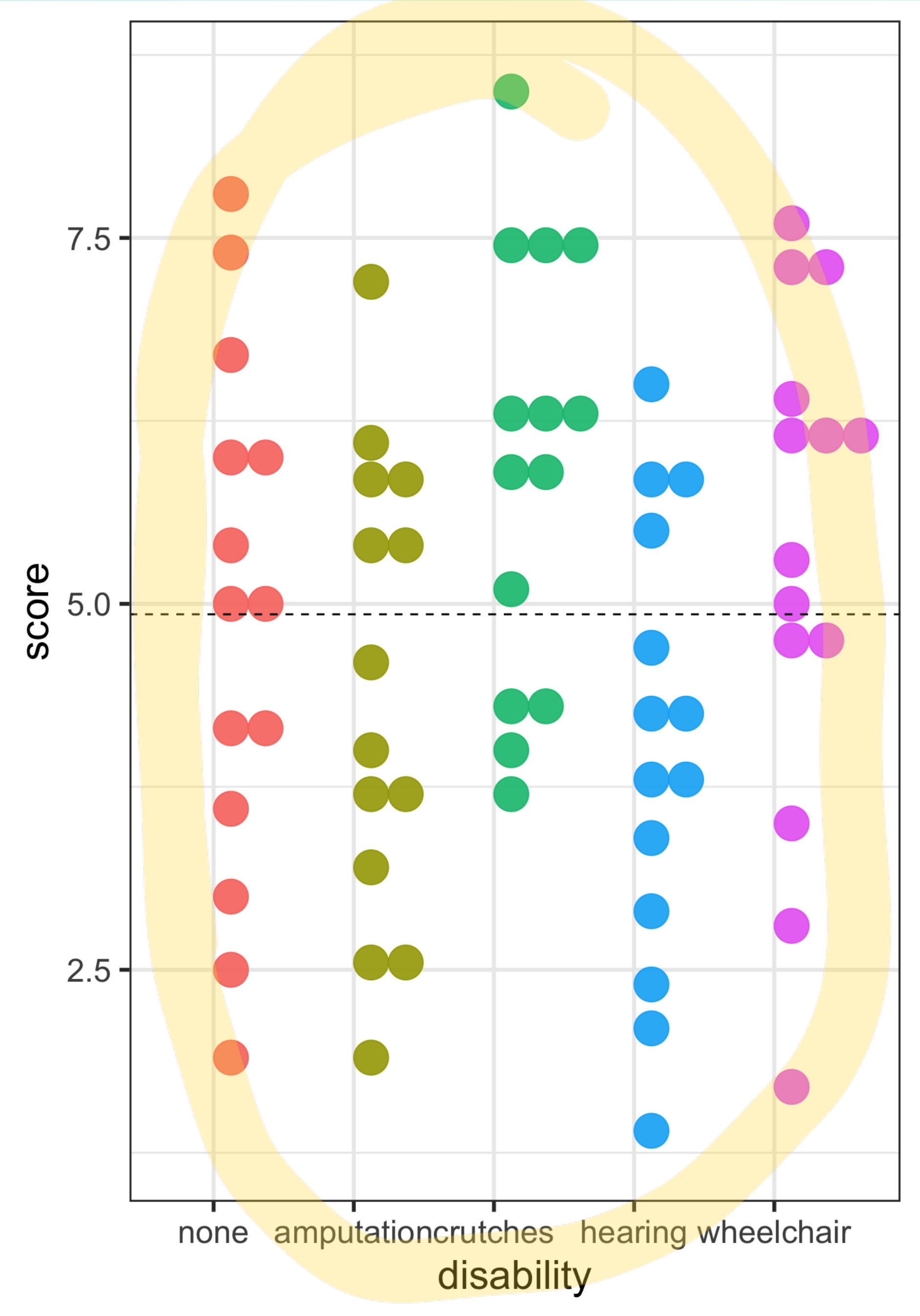
group i

observation j

# Total Sums of Squares Visually

Previously:

$$\text{variance} = s^2 = \frac{\sum_{i=1}^{n} (x_i - \bar{x})^2}{n-1}$$



Total Sums of Squares:

$$SST = \sum_{i=1}^{k} \left[ \sum_{j=1}^{n_i} (x_{ij} - \bar{x})^2 \right] = (N-1)s^2$$

sum over groups

sum over observations in group i

- where
  - $N = \sum_{i=1}^{k} n_i$ is the total sample size and
  - $s^2$ is the grand standard deviation of all the observations
- This is the sum of the squared differences between each observed $x_{ij}$ value and the *grand mean*, $\bar{x}$.
- That is, it is the total deviation of the $x_{ij}$'s from the grand mean.

# Calculate Total Sums of Squares

Total Sums of Squares:

$$SST = \sum_{i=1}^{k}\sum_{j=1}^{n_i}(x_{ij} - \bar{x})^2 = (N - 1)s^2$$

- where
  - $N = \sum_{i=1}^{k} n_i$ is the total sample size and
  - $s^2$ is the grand standard deviation of all the observations

Total sample size $N$:

```r
(Ns <- employ %>% group_by(disability) %>% count())
```

```
# A tibble: 5 × 2
# Groups:   disability [5]
  disability     n
  <fct>      <int>
1 none          14
2 amputation    14
3 crutches      14
4 hearing       14
5 wheelchair    14
```

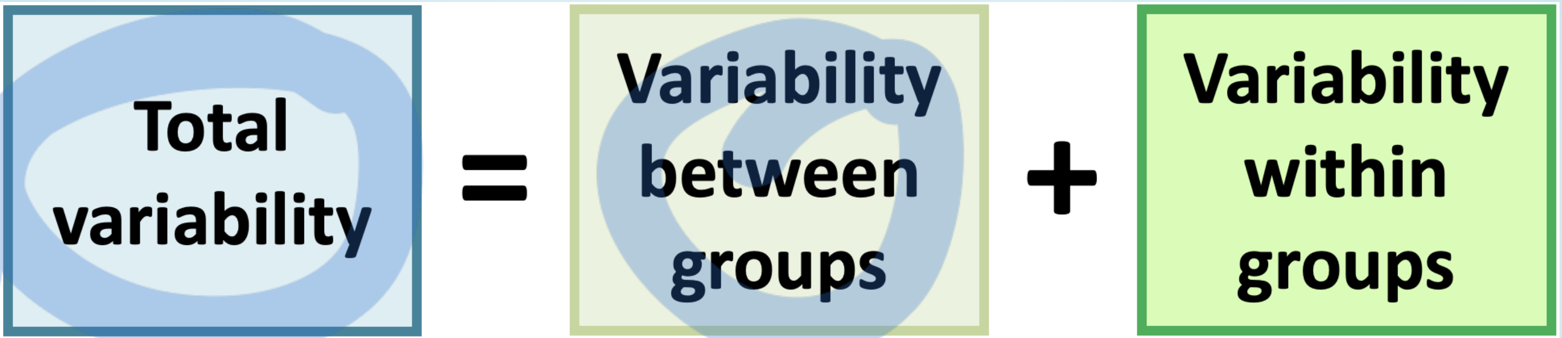
$SST$:

```r
(SST <- (sum(Ns$n) - 1) * sd(employ$score)^2)
```

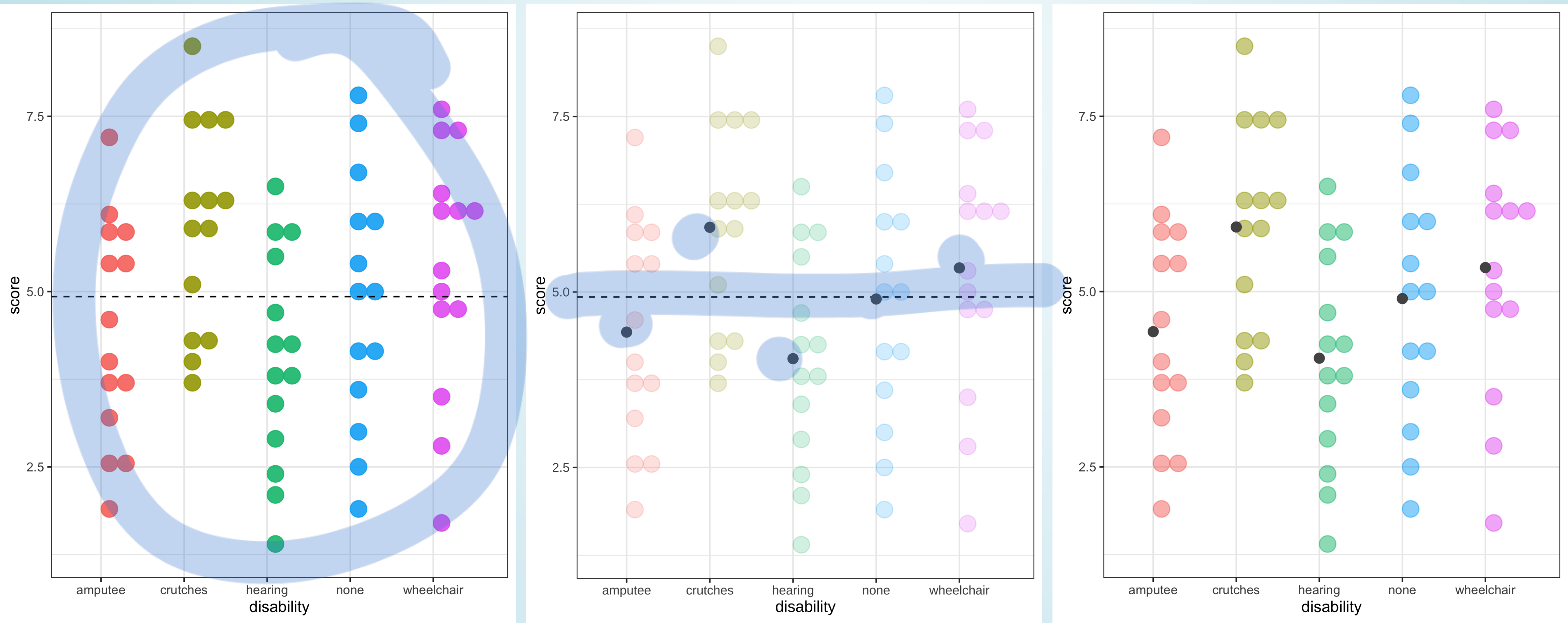
```
[1] 203.8429
```

# ANOVA: Analysis of Variance

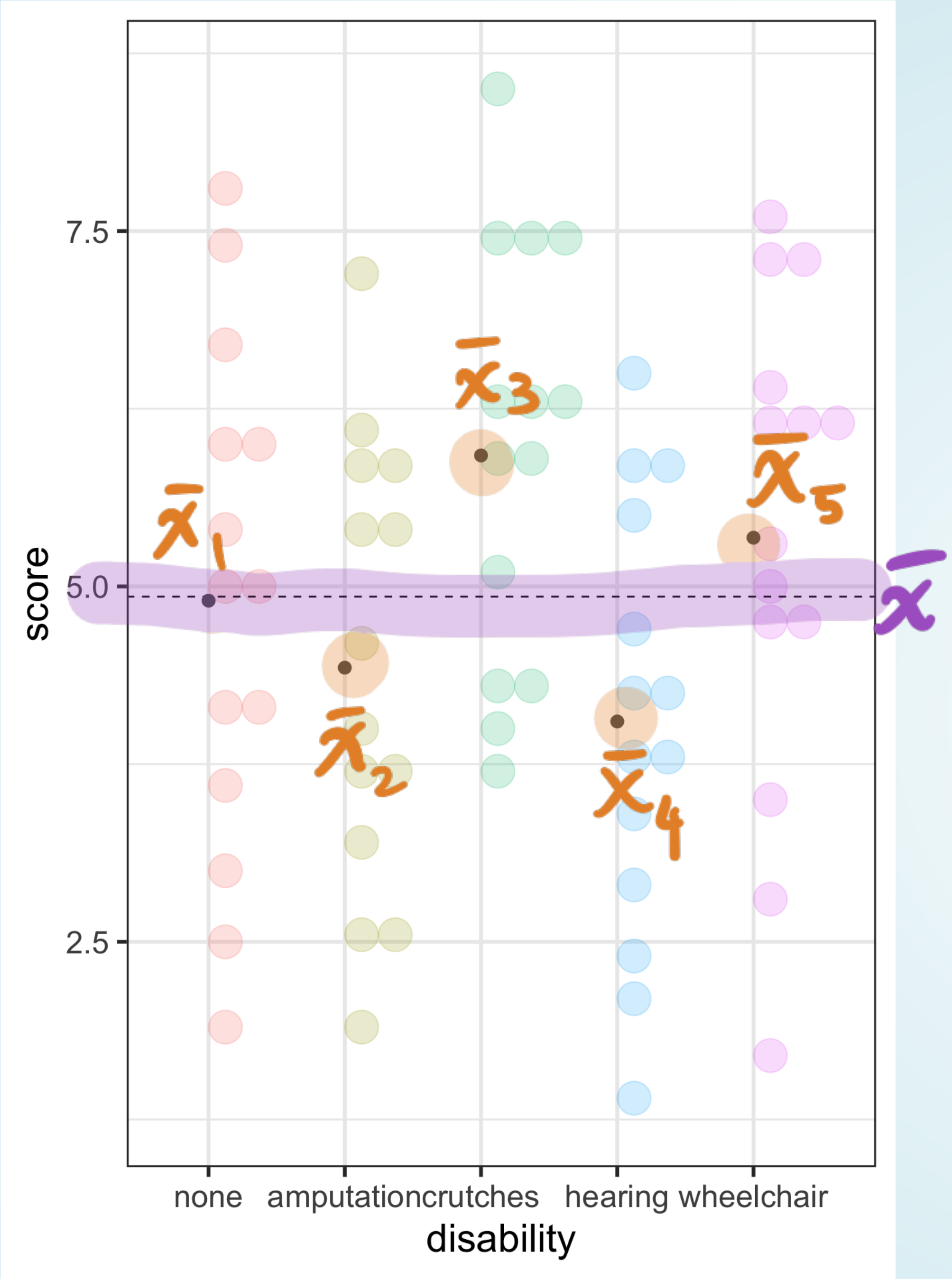
**ANOVA** compares the variability between groups to the variability within groups



**Total variability** = **Variability between groups** + **Variability within groups**



# Sums of Squares due to Groups Visually ("between" groups)



Sums of Squares due to Groups:

$$SSG = \sum_{i=1}^{k} n_i(\bar{x}_i - \bar{x})^2$$

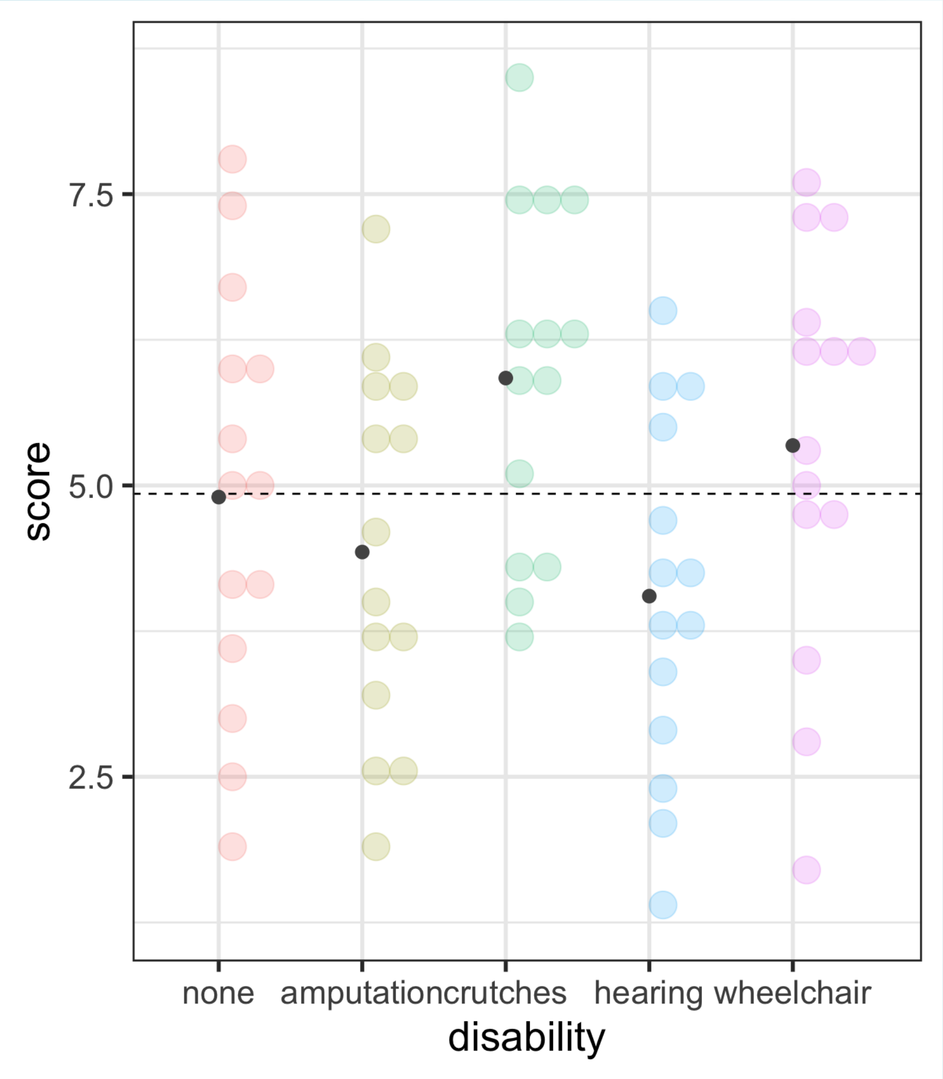
- This is the sum of the squared differences between each *group mean*, $\bar{x}_i$, and the *grand mean*, $\bar{x}$.
- That is, it is the deviation of the group means from the grand mean.
- Also called the Model SS, or $SS_{model}$.

Usual variance:

$$s^2 = \frac{\sum_{i=1}^{n}(x_i - \bar{x})^2}{n}$$

# Calculate Sums of Squares due to Groups (“between” groups)

$$SSG = \sum_{i=1}^{k} n_i(\bar{x}_i - \bar{x})^2$$



Calculate means $\bar{x}_i$ for each group:

```r
xbar_groups <- employ %>%
  group_by(disability) %>%
  summarise(mean = mean(score))
xbar_groups
```

```
# A tibble: 5 × 2
  disability  mean
  <fct>      <dbl>
1 none        4.9 
2 amputation  4.43
3 crutches    5.92
4 hearing     4.05
5 wheelchair  5.34
```

Calculate $SSG$:

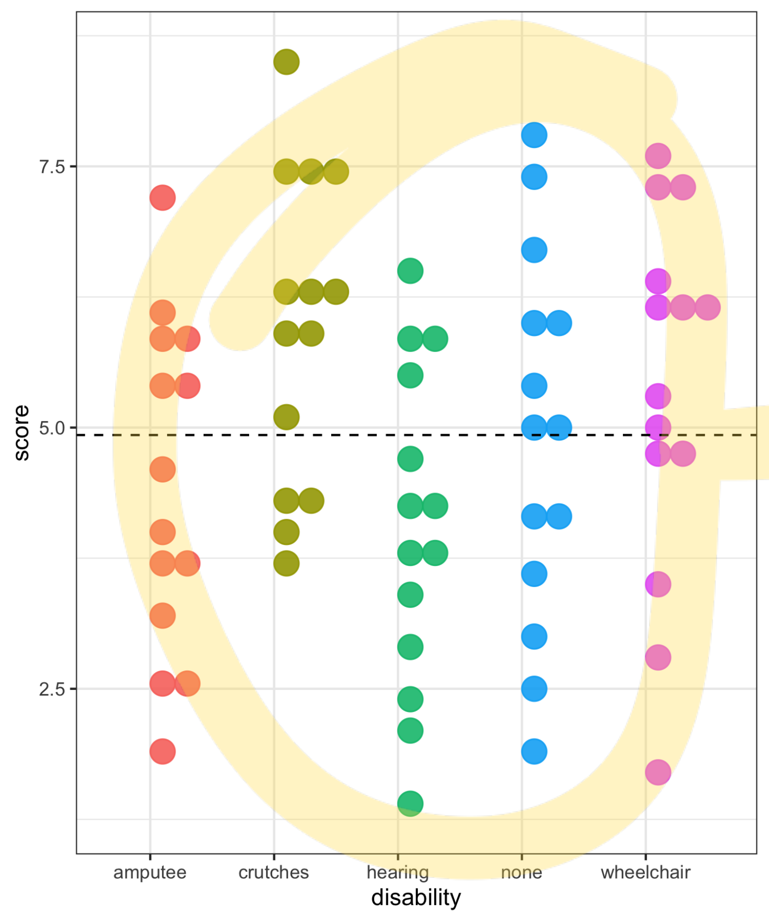
```r
(SSG <- sum(Ns$n *
  (xbar_groups$mean - mean(employ$score))^2))
```

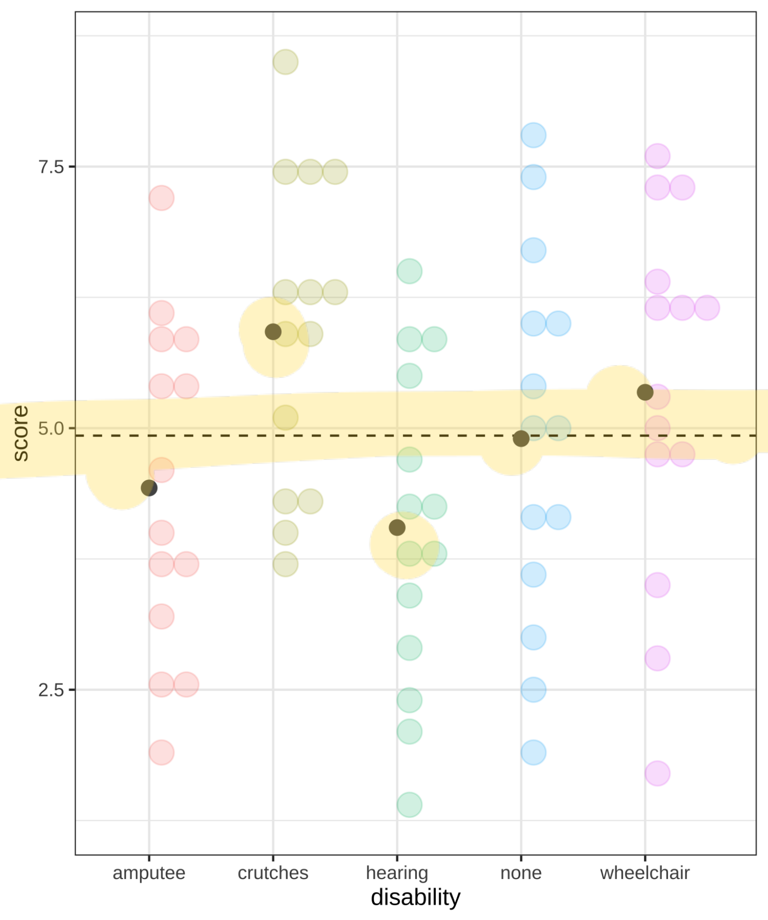
```
[1] 30.52143
```

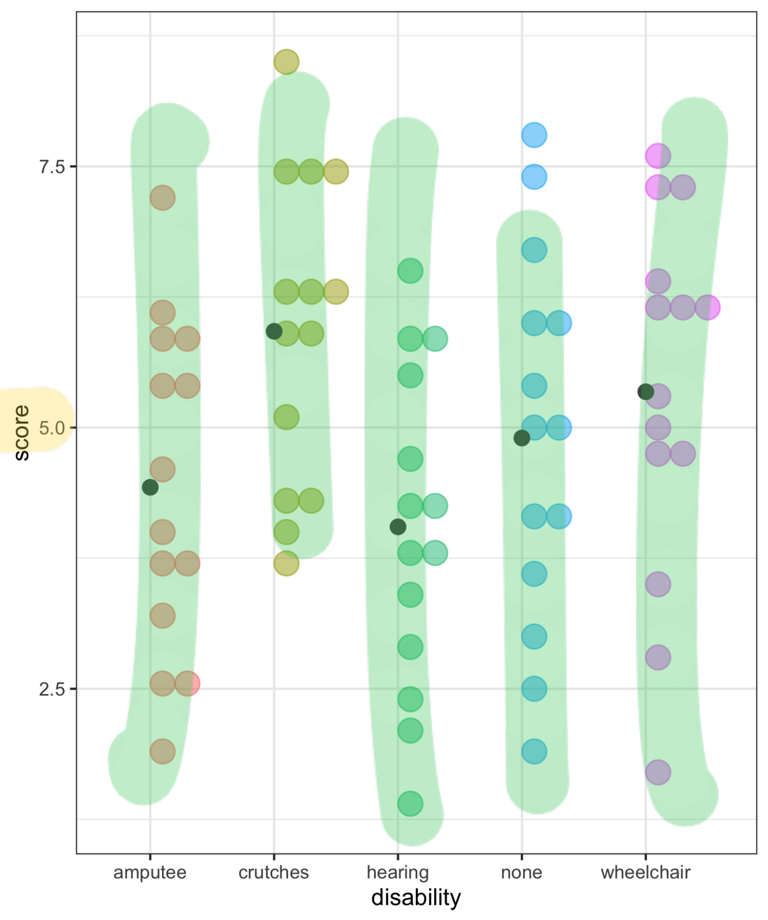
# ANOVA: Analysis of Variance

**ANOVA** compares the variability between groups to the variability within groups

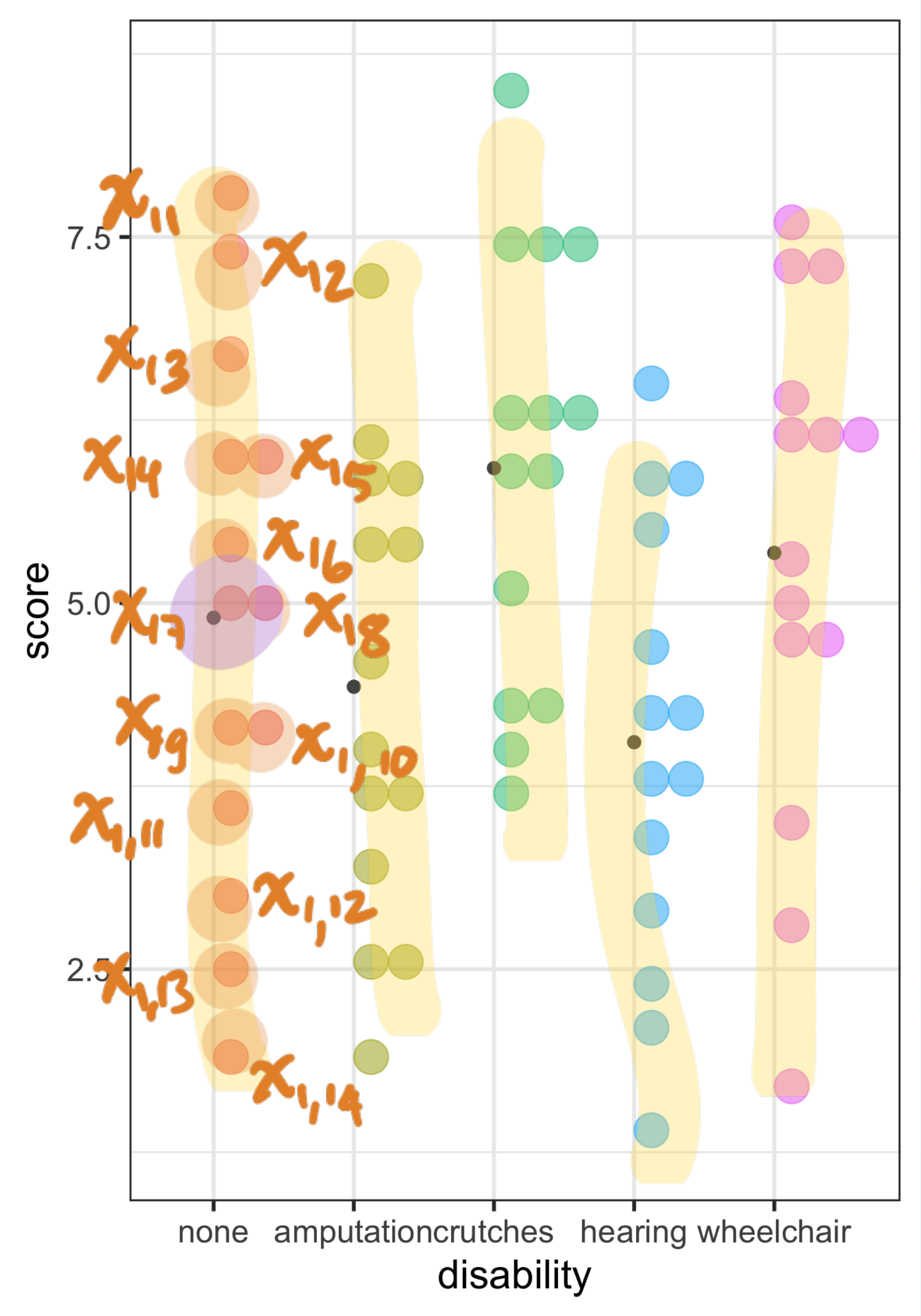
**Total variability** = **Variability between groups** + **Variability within groups**







# Sums of Squares Error Visually (within groups)



Sums of Squares Error:

add up SS for group i

$$SSE = \sum_{i=1}^{k}\left[\sum_{j=1}^{n_i}(x_{ij}-\bar{x}_i)^2\right] = \sum_{i=1}^{k}(n_i-1)s_i^2$$

Add up for each group

where $s_i$ is the standard deviation of the $i^{th}$ group

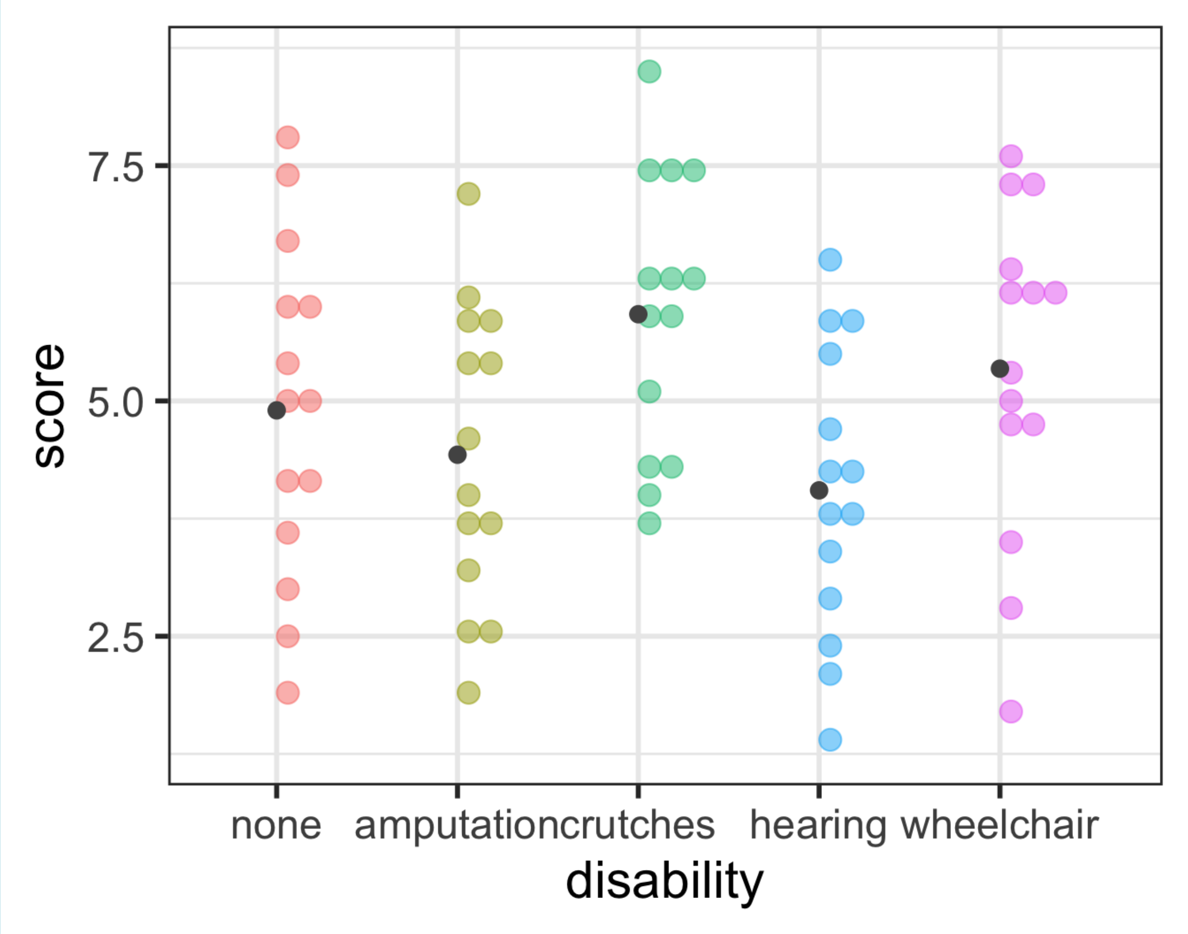
- This is the sum of the squared differences between each observed $x_{ij}$ value and its group mean $\bar{x}_i$.
- That is, it is the deviation of the $x_{ij}$'s from the predicted score by group.
- Also called the residual sums of squares, or $SS_{residual}$.

usual variance $= s^2 = \dfrac{\sum_{i=1}^{n}(x_i-\bar{x})^2}{n-1}$

# Calculate Sums of Squares Error (within groups)

$$SSE = \sum_{i=1}^{k}\sum_{j=1}^{n_i}(x_{ij} - \bar{x}_i)^2 = \sum_{i=1}^{k}(n_i - 1)s_i^2$$

where $s_i$ is the standard deviation of the $i^{th}$ group



## Calculate sd's $s_i$ for each group:

```
sd_groups <- employ %>%
  group_by(disability) %>%
  summarise(SD = sd(score))
sd_groups
```

```
# A tibble: 5 × 2
  disability    SD
  <fct>      <dbl>
1 none        1.79
2 amputation  1.59
3 crutches    1.48
4 hearing     1.53
5 wheelchair  1.75
```

## Calculate $SSE$:

```
(SSE <- sum(
  (Ns$n-1)*sd_groups$SD^2))
```

```
[1] 173.3214
```

# Verify *SST = SSG + SSE*

**ANOVA** compares the variability between groups to the variability within groups

**Total variability** **=** **Variability between groups** **+** **Variability within groups**

$x_{ij} - \bar{x} = x_{ij} - \bar{x}_i + \bar{x}_i - \bar{x}$

$$\sum_{i=1}^{k}\sum_{j=1}^{n_i}(x_{ij}-\bar{x})^2 = n_i\sum_{i=1}^{k}(\bar{x}_i-\bar{x})^2 + \sum_{i=1}^{k}\sum_{j=1}^{n_i}(x_{ij}-\bar{x}_i)^2$$

$$(N-1)s^2 = \sum_{i=1}^{k} n_i(\bar{x}_i-\bar{x})^2 + \sum_{i=1}^{k}(n_i-1)s_i^2$$

**SST** (Total sum of squares) **=** **SSG** (sum of squares due to groups) **+** **SSE** (Error sum of squares)

```
SST
```

```
[1] 203.8429
```

```
SSG + SSE
```

```
[1] 203.8429
```

# ANOVA table

score
disability
7.5
5.0
2.5
amputee
crutches
hearing
none
wheelchair

The “mean square” is the sum of squares divided by the degrees of freedom

| Source | df | Sum of Squares | Mean Square | F-Statistic |
|---|---|---|---|---|
| Groups | *k*-1 | SSG | **MSG** = SSG/(*k*-1) | $\frac{\text{MSG}}{\text{MSE}}$ |
| Error | *N*-*k* | SSE | **MSE** = SSE/(*N*-*k*) | |
| Total | *N*-1 | SST | | |

variability

average variability

The ***F-statistic*** is a ratio of

the average variability ***between*** groups

to the average variability ***within*** groups

# Thinking about the F-statistic

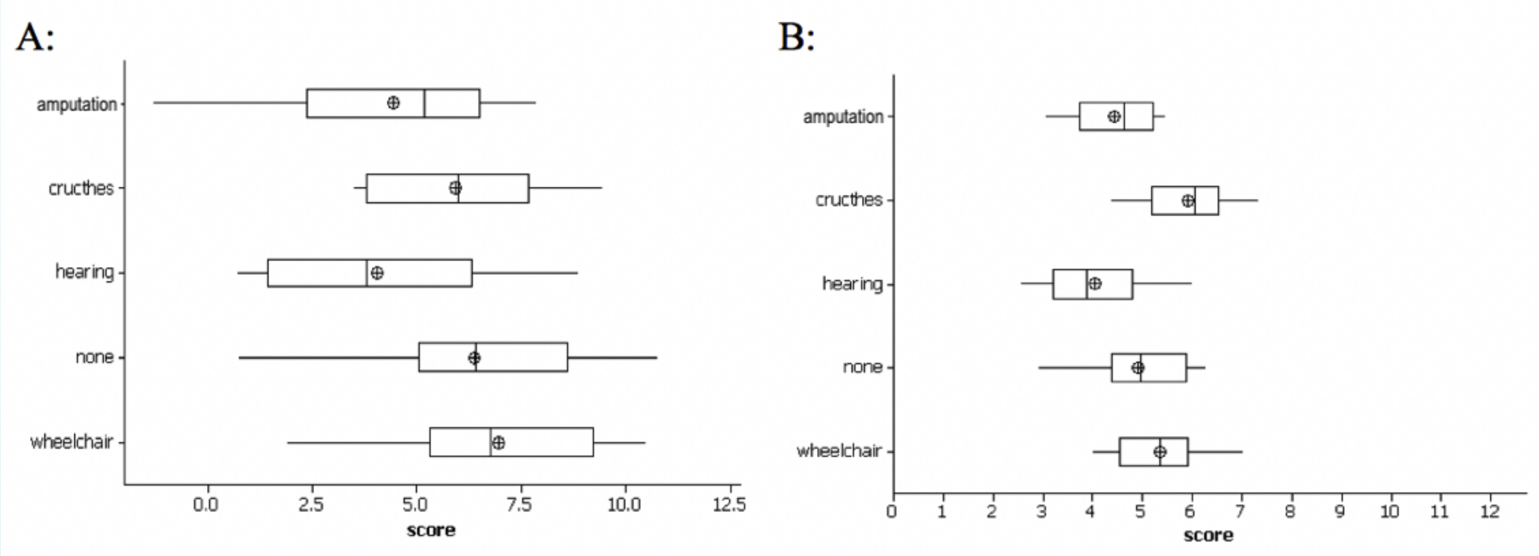
**If the groups are actually different, then which of these is more accurate?**

1. The variability between groups should be higher than the variability within groups
2. The variability within groups should be higher than the variability between groups

**If there really is a difference between the groups, we would expect the F-statistic to be which of these:**

1. Higher than we would observe by random chance
2. Lower than we would observe by random chance

$$F = \frac{MSG}{MSE}$$



# ANOVA in base R

```r
# Note that I'm saving the tidy anova table
# Will be pulling p-value from this on future slide

empl_lm <- lm(score ~ disability, data = employ) %>%
  anova() %>%
  tidy()

empl_lm %>% gt()
```

| term | df | sumsq | meansq | statistic | p.value |
|---|---|---|---|---|---|
| disability | 4 | 30.52143 | 7.630357 | 2.86158 | 0.03012686 |
| Residuals | 65 | 173.32143 | 2.666484 | NA | NA |

$< .05$

Hypotheses:

$$H_0 : \mu_{none} = \mu_{amputation} = \mu_{crutches} = \mu_{hearing} = \mu_{wheelchair}$$
$$\text{vs. } H_A : \underline{\text{At least one pair } \mu_i \neq \mu_j \text{ for } i \neq j}$$

Do we [✓ reject] or fail to reject $\underline{H_0}$?

# Conclusion to hypothesis test

$$H_0 : \mu_{none} = \mu_{amputation} = \mu_{crutches} = \mu_{hearing} = \mu_{wheelchair}$$
$$\text{vs. } H_A : \text{At least one pair } \mu_i \neq \mu_j \text{ for } i \neq j$$

```
empl_lm # tidy anova output
```

```
# A tibble: 2 × 6
  term          df sumsq meansq statistic p.value
  <chr>      <int> <dbl>  <dbl>     <dbl>   <dbl>
1 disability     4  30.5   7.63      2.86  0.0301
2 Residuals     65 173.    2.67     NA    NA
```

```
# Note that this is a vector:
empl_lm$p.value
```

```
[1] 0.03012686         NA
```

Pull the p-value using base R:

```
round(empl_lm$p.value[1],2)
```

```
[1] 0.03
```

Pull the p-value using tidyverse:

```
empl_lm %>%
  filter(term == "disability") %>%
  pull(p.value) %>%
  round(2)
```

```
[1] 0.03
```

- Use $\alpha$ = 0.05.
- Do we reject or fail to reject $H_0$?

**Conclusion statement**:

- There is sufficient evidence that at least one of the disability groups has a mean employment score statistically different from the other groups. ( $p$-value = 0.03).

# Conditions for ANOVA

**IF** ALL of the following conditions hold:

1. Observations are independent and groups are independent

(1. The null hypothesis is true)

2. Sample sizes in each group group are large (each $n \geq 30$)
   - OR the data are relatively normally distributed in each group

→ we have $n = 14$

3. Variability is "similar" in all group groups:
   - Is the within group variability about the same for each group?
   - As a rough rule of thumb, this condition is *violated if the standard deviation of one group is more than double the standard deviation of another group*

Checking the **equal variance** condition:

```
sd_groups # previously defined
```

```
# A tibble: 5 × 2
  disability    SD
  <fct>      <dbl>
1 none        1.79
2 amputation  1.59
3 crutches    1.48
4 hearing     1.53
5 wheelchair  1.75
```

```
max(sd_groups$SD) / min(sd_groups$SD)
```

```
[1] 1.210425
```

**THEN** the sampling distribution of the **F-statistic** is an **F-distribution**

$$\frac{S_{max}}{S_{min}} < 2$$

# Testing variances (Condition 3)

## Bartlett’s test for equal variances

- $H_0$ : population variances of group levels are equal
- $H_A$ : population variances of group levels are NOT equal

*Note: $H_A$ is same as saying that at least one of the group levels has a different variance*

**Caution**

- Bartlett’s test assumes the data in each group are normally distributed.
- Do not use if data do not satisfy the normality condition.

```r
bartlett.test(score ~ disability, data = employ)
```

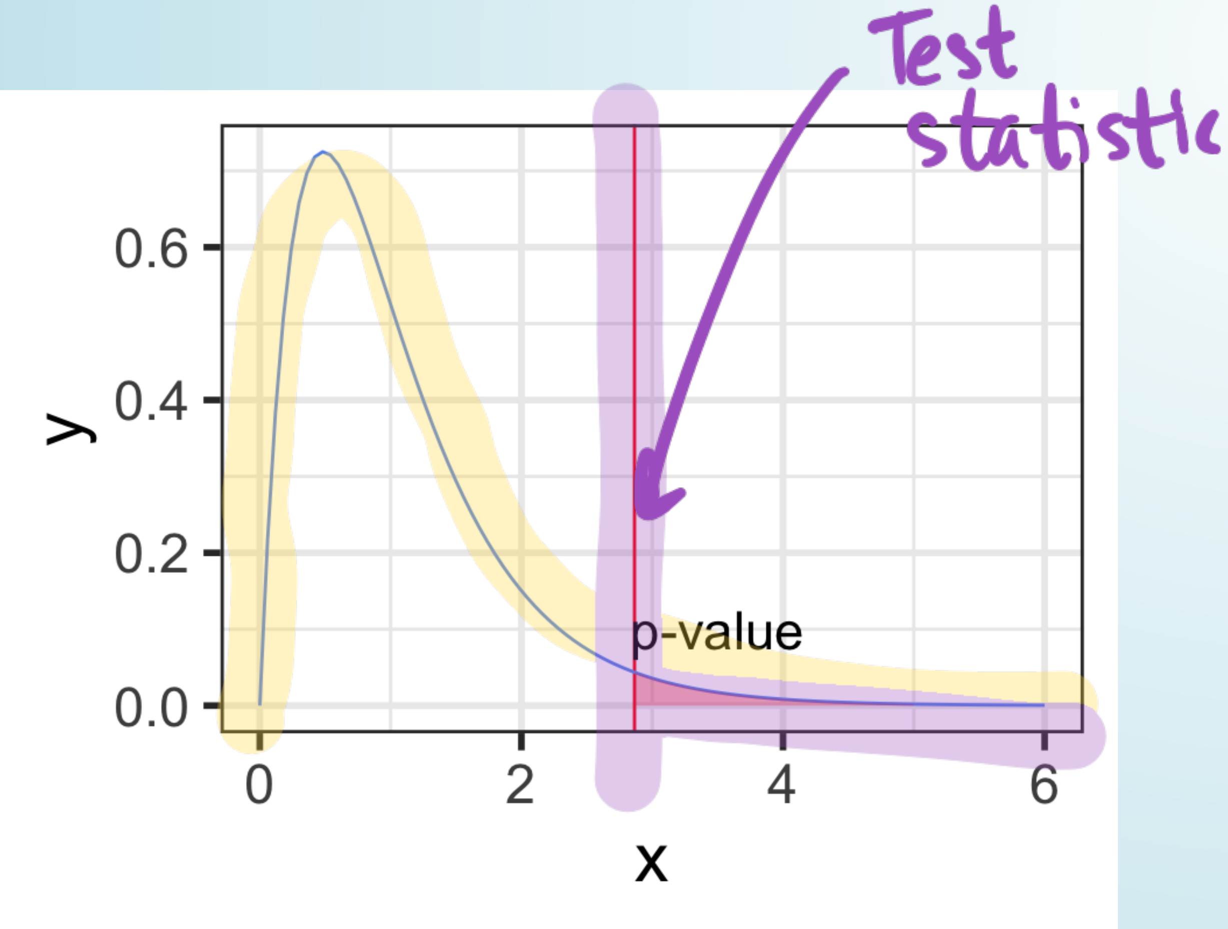
```
	Bartlett test of homogeneity of variances

data:  score by disability
Bartlett's K-squared = 0.7016, df = 4, p-value = 0.9511
```

**Tip**

Levene’s test for equality of variances is not as restrictive: see https://www.statology.org/levenes-test-r/

# The F-distribution

- The F-distribution is skewed right.
- The F-distribution has **two different degrees of freedom**:
  - one for the numerator of the ratio (k – 1) and df1
  - one for the denominator (N – k) df 2
- *p*-**value**
  - is always the **upper tail**
  - (the area as extreme or more extreme)



```r
empl_lm %>% gt()
```

| term | df | sumsq | meansq | statistic | p.value |
|---|---|---|---|---|---|
| disability | 4 | 30.52143 | 7.630357 | 2.86158 | 0.03012686 |
| Residuals | 65 | 173.32143 | 2.666484 | NA | NA |

```r
# p-value using F-distribution

pf(2.86158, df1=5-1, df2=70-5,
   lower.tail = FALSE)
```

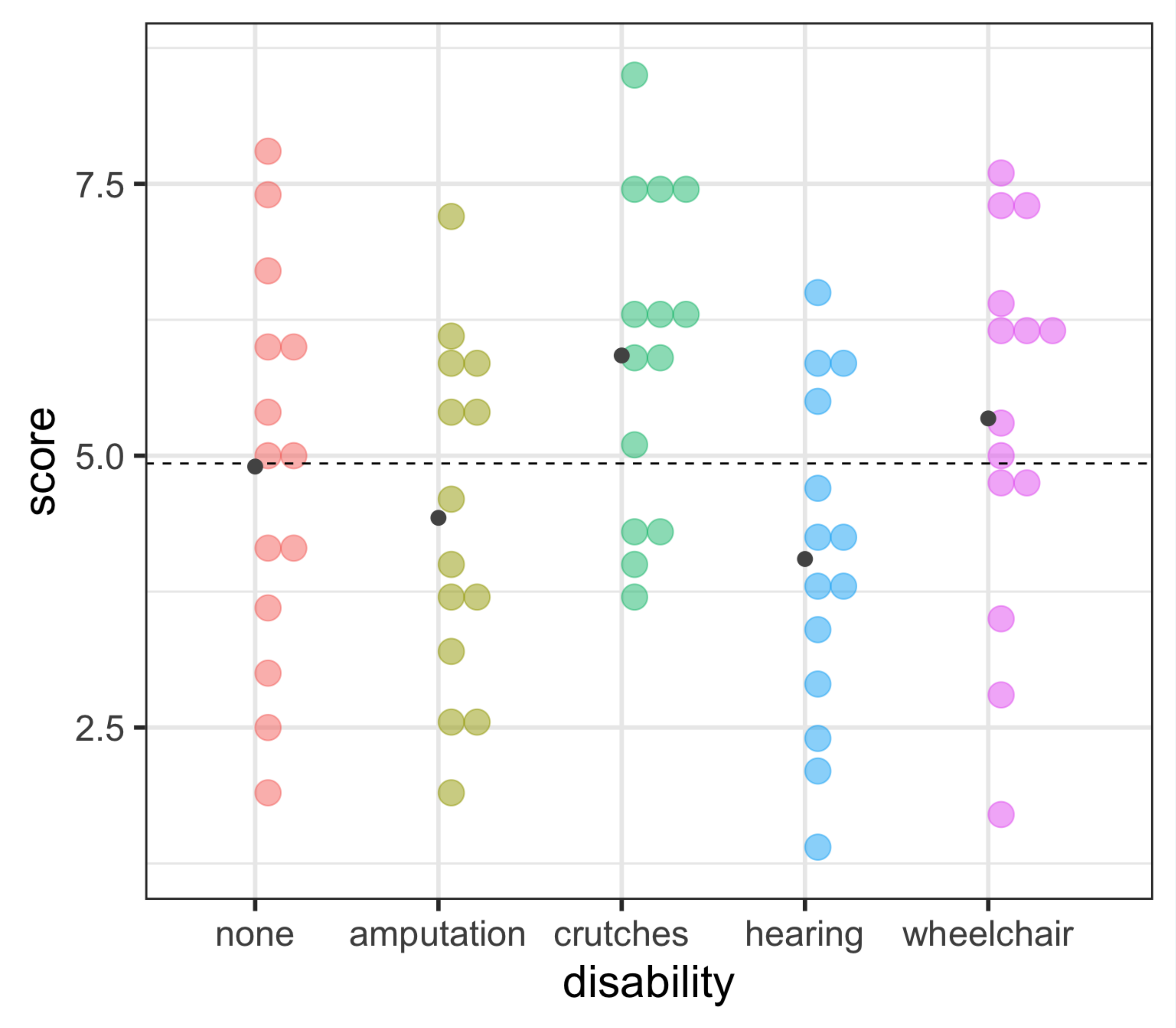
```
[1] 0.03012688
```

= 1 − pf ( ~ , lower.tail = TRUE)

# Which groups are statistically different?

- So far we've only determined that *at least one of the groups is different* from the others,
  - but we don't know which.

- What's your guess?



# Post-hoc testing for ANOVA

*determining which groups are statistically different*

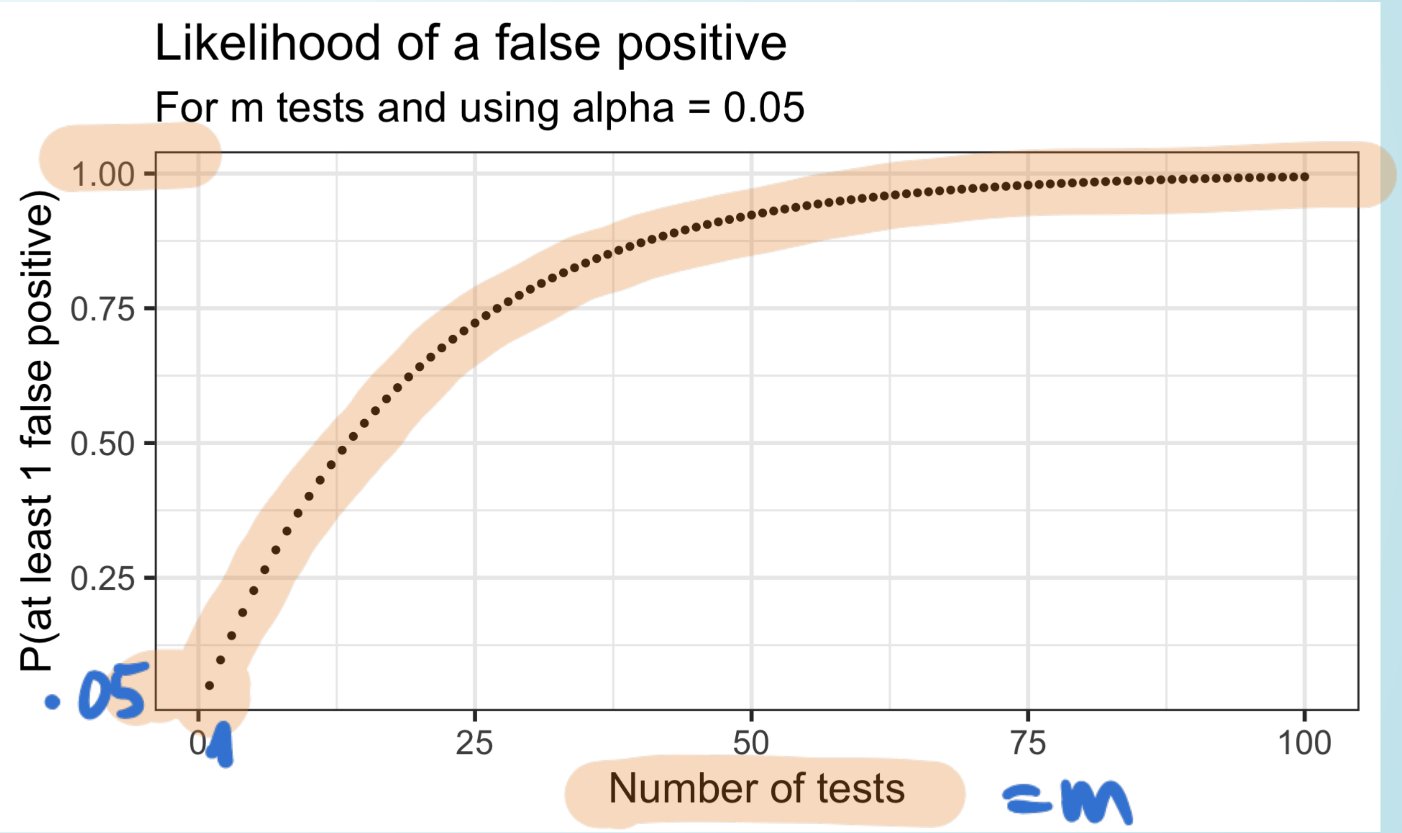
# Post-hoc testing: pairwise t-tests

- In post-hoc testing we **run all the pairwise t-tests** comparing the means from each pair of groups.
- With 5 groups, this involves doing $\binom{5}{2} = \frac{5!}{2!3!} = \frac{5\cdot 4}{2} = 10$ different pairwise tests.

$$
\begin{aligned}
P(\text{making an error}) &= \alpha \\
P(\text{not making an error}) &= 1 - \alpha \\
P(\text{not making an error in m tests}) &= (1-\alpha)^m \\
P(\text{making at least 1 error in m tests}) &= 1 - (1-\alpha)^m
\end{aligned}
$$

**Problem:**

- Although the ANOVA test has an $\alpha$ chance of a Type I error (finding a difference between a pair that aren't different),
- the overall Type I error rate will be much higher when running many tests simultaneously.



# The Bonferroni Correction (1/2)

A very conservative (but very popular) approach is to divide the $\alpha$ level by how many tests $m$ are being done:

$$\alpha_{Bonf} = \frac{\alpha}{m}$$

$$\frac{.05}{10} = 0.005$$

- This is equivalent to multiplying the *p*-values by m:

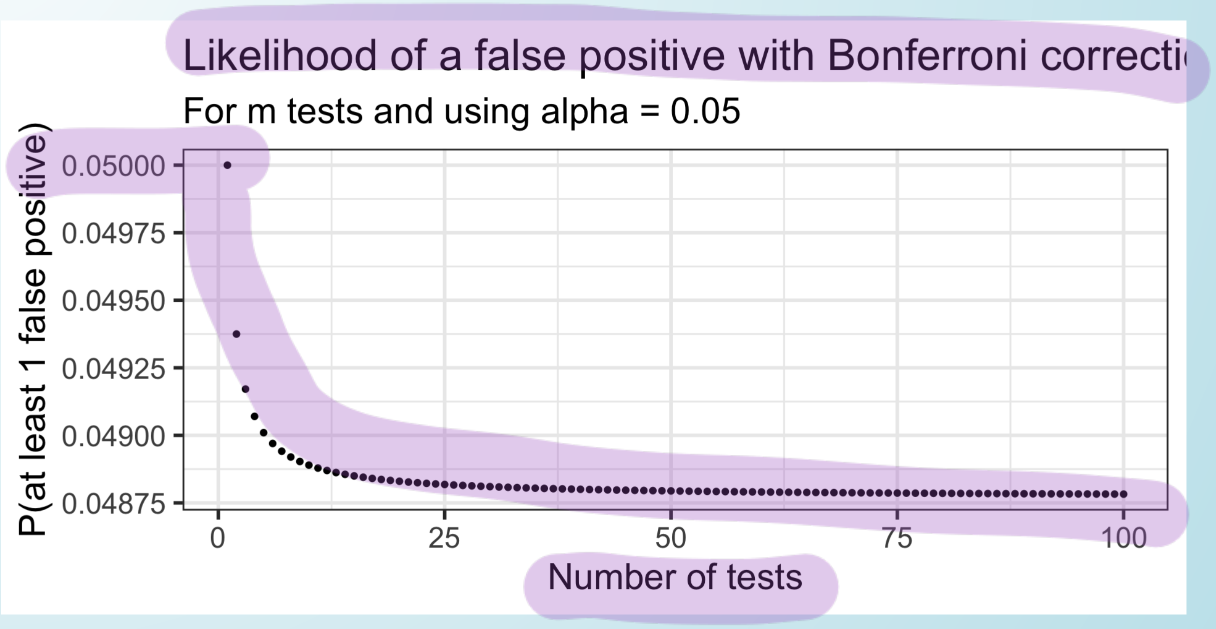
$$p\text{-value} < \alpha_{Bonf} = \frac{\alpha}{m}$$

is the same as

$$m \cdot (p\text{-value}) < \alpha$$

The Bonferroni correction is popular since it's very easy to implement.

- The **plot below** shows the **likelihood of making at least one Type I error** depending on how may tests are done.
- Notice the likelihood decreases very quickly
  - Unfortunately the likelihood of a Type II error is increasing as well
  - It becomes "harder" and harder to reject $H_0$ if doing many tests.



# The Bonferroni Correction (2/2)

Pairwise t-tests without any *p*-value adjustments:

```r
pairwise.t.test(employ$score,
                employ$disability,
                p.adj="none")
```

```
    Pairwise comparisons using t tests with pooled SD

data:  employ$score and employ$disability

           none   amputation crutches hearing
amputation 0.4477 -          -        -
crutches   0.1028 0.0184     -        -
hearing    0.1732 0.5418     0.0035   -
wheelchair 0.4756 0.1433     0.3520   0.0401

P value adjustment method: none
```

Pairwise t-tests **with Bonferroni *p*-value adjustments**:

```r
pairwise.t.test(employ$score,
                employ$disability,
                p.adj="bonferroni")
```

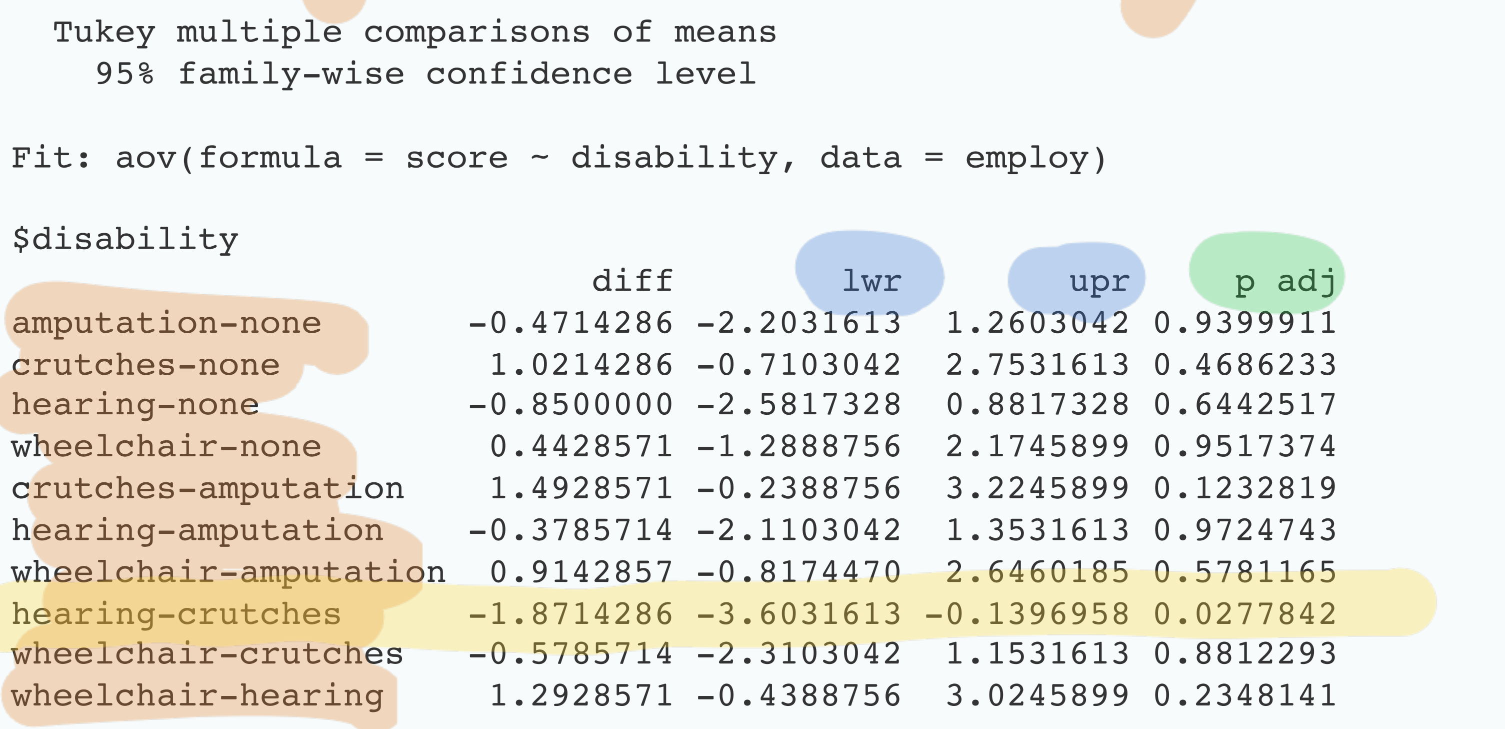
```
    Pairwise comparisons using t tests with pooled SD

data:  employ$score and employ$disability

           none  amputation crutches hearing
amputation 1.000 -          -        -
crutches   1.000 0.184      -        -
hearing    1.000 1.000      0.035    -
wheelchair 1.000 1.000      1.000    0.401

P value adjustment method: bonferroni
```

- Since there were 10 tests, all the *p*-values were multiplied by 10.
- Are there any significant pairwise differences?

# Tukey's Honest Significance Test (HSD)

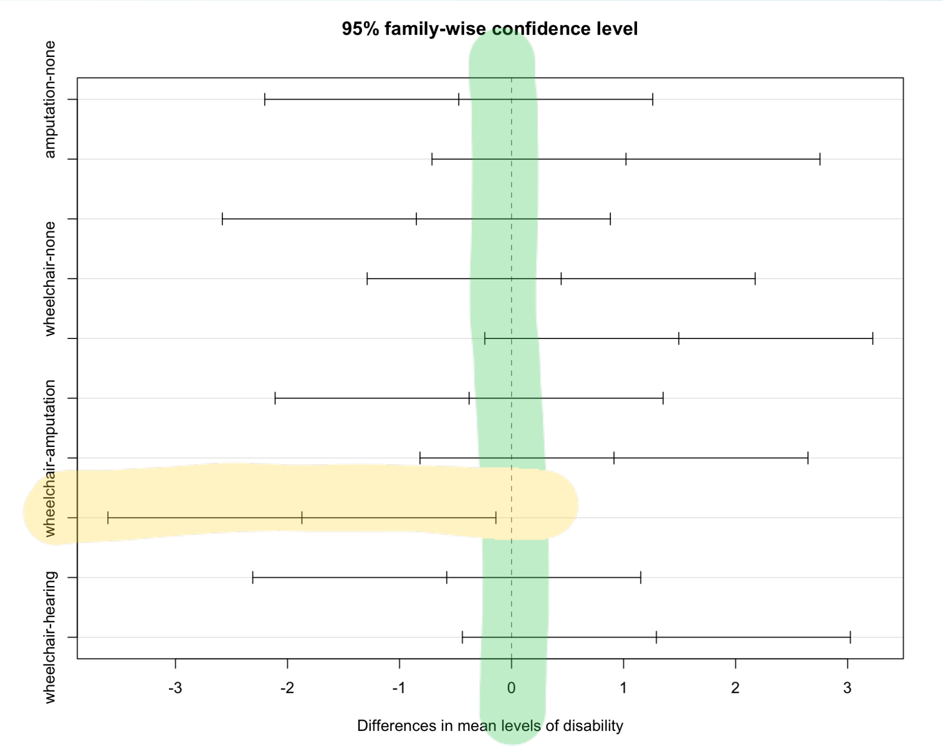
- Tukey's Honest Significance Test (HSD) controls the "family-wise probability" of making a Type I error using a much less conservative method than Bonferroni
  - **It is specific to ANOVA**
- In addition to adjusted *p*-values, it also calculates Tukey adjusted CI's for all pairwise differences
- The function `TukeyHSD()` creates a **set of confidence intervals** of the differences between means with the specified **family-wise probability of coverage**.

```r
# need to run the model using `aov` instead of `lm`
empl_aov <- aov(score ~ disability, data = employ)

TukeyHSD(x=empl_aov, conf.level = 0.95)
```



```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = score ~ disability, data = employ)

$disability
                            diff        lwr        upr     p adj
amputation-none       -0.4714286 -2.2031613  1.2603042 0.9399911
crutches-none          1.0214286 -0.7103042  2.7531613 0.4686233
hearing-none          -0.8500000 -2.5817328  0.8817328 0.6442517
wheelchair-none        0.4428571 -1.2888756  2.1745899 0.9517374
crutches-amputation    1.4928571 -0.2388756  3.2245899 0.1232819
hearing-amputation    -0.3785714 -2.1103042  1.3531613 0.9724743
wheelchair-amputation  0.9142857 -0.8174470  2.6460185 0.5781165
hearing-crutches      -1.8714286 -3.6031613 -0.1396958 0.0277842
wheelchair-crutches   -0.5785714 -2.3103042  1.1531613 0.8812293
wheelchair-hearing     1.2928571 -0.4388756  3.0245899 0.2348141
```

```r
plot(TukeyHSD(x=empl_aov,
         conf.level = 0.95))
```



# There are many more multiple testing adjustment procedures

- Bonferroni is popular because it’s so easy to apply
- Tukey’s HSD is usually used for ANOVA
- Code below used Holm’s adjustment

```r
# default is Holm's adjustments
pairwise.t.test(employ$score,
                employ$disability)
```

```

	Pairwise comparisons using t tests with pooled SD 

data:  employ$score and employ$disability 

           none  amputation crutches hearing
amputation 1.000 -          -        -      
crutches   0.719 0.165      -        -      
hearing    0.866 1.000      0.035    -      
wheelchair 1.000 0.860      1.000    0.321  

P value adjustment method: holm 
```

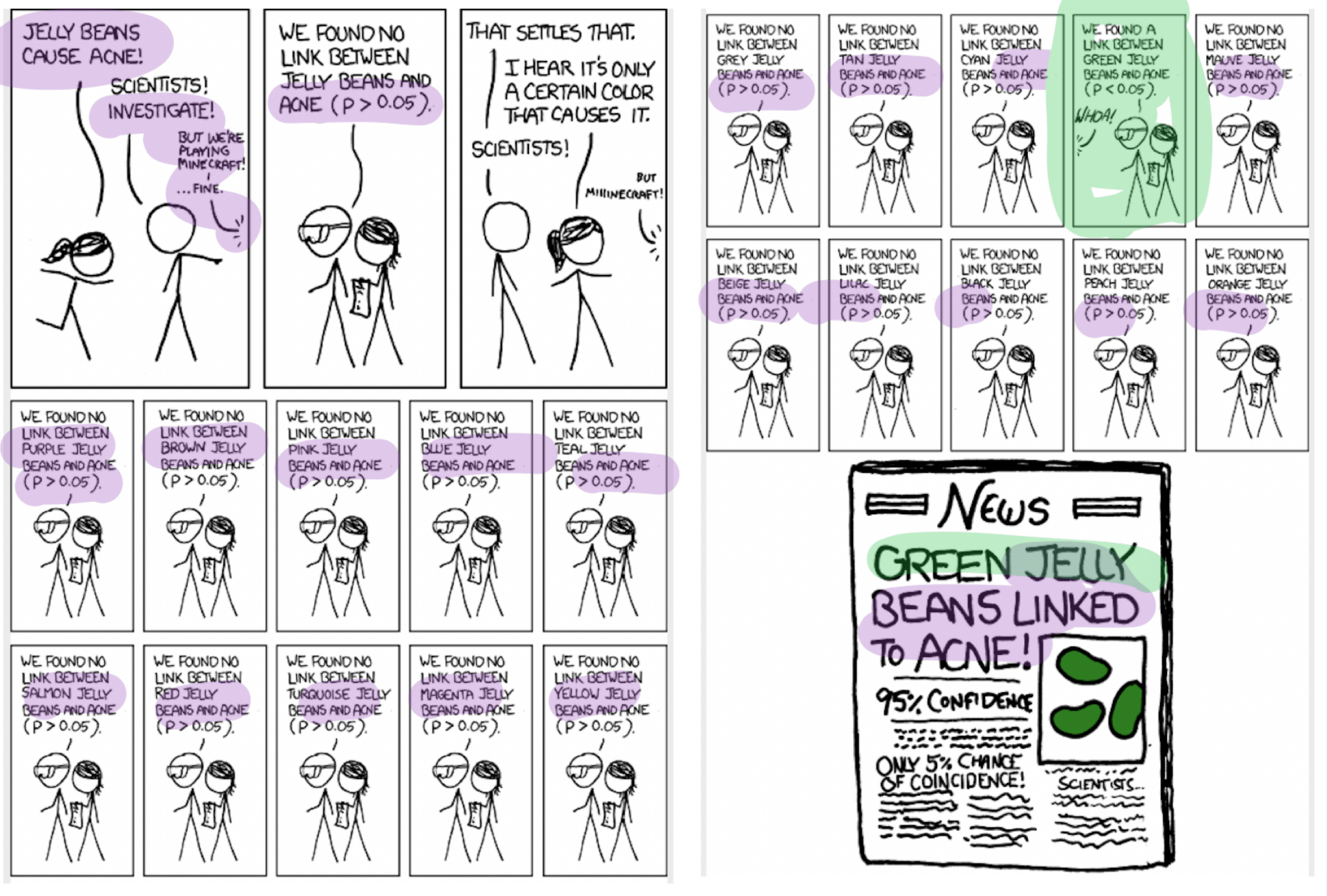
- **False discovery rate (fdr)** *p*-value adjustments are popular in omics, or whenever there are *many* tests being run:

```r
pairwise.t.test(employ$score,
                employ$disability,
                p.adj="fdr")
```

```

	Pairwise comparisons using t tests with pooled SD 

data:  employ$score and employ$disability 

           none  amputation crutches hearing
amputation 0.528 -          -        -      
crutches   0.257 0.092      -        -      
hearing    0.289 0.542      0.035    -      
wheelchair 0.528 0.287      0.503    0.134  

P value adjustment method: fdr 
```

# Multiple testing

*post-hoc testing* vs. *testing many outcomes*

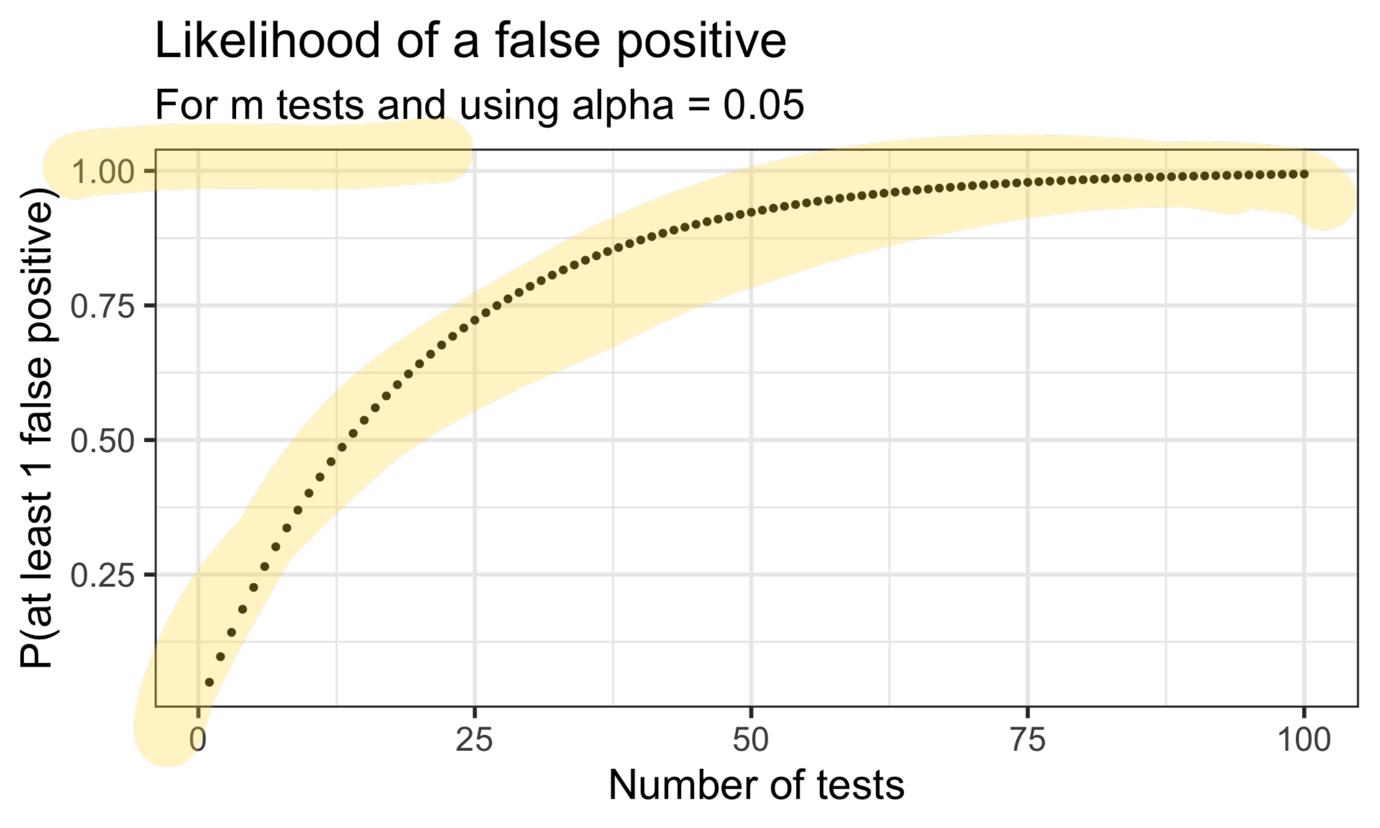

JELLY BEANS CAUSE ACNE!
SCIENTISTS! INVESTIGATE!
BUT WE'RE PLAYING MINECRAFT!
... FINE.
WE FOUND NO LINK BETWEEN JELLY BEANS AND ACNE (P > 0.05).
THAT SETTLES THAT.
I HEAR IT'S ONLY A CERTAIN COLOR THAT CAUSES IT.
SCIENTISTS!
BUT MIIINECRAFT!
WE FOUND NO LINK BETWEEN PURPLE JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN BROWN JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN PINK JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN BLUE JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN TEAL JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN SALMON JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN RED JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN TURQUOISE JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN MAGENTA JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN YELLOW JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN GREY JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN TAN JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN CYAN JELLY BEANS AND ACNE (P > 0.05).
WE FOUND A LINK BETWEEN GREEN JELLY BEANS AND ACNE (P < 0.05).
WHOA!
WE FOUND NO LINK BETWEEN MAUVE JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN BEIGE JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN LILAC JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN BLACK JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN PEACH JELLY BEANS AND ACNE (P > 0.05).
WE FOUND NO LINK BETWEEN ORANGE JELLY BEANS AND ACNE (P > 0.05).
NEWS
GREEN JELLY BEANS LINKED TO ACNE!
95% CONFIDENCE
ONLY 5% CHANCE OF COINCIDENCE!
SCIENTISTS...

https://xkcd.com/882/

# Multiple testing: controlling the Type I error rate

- The multiple testing issue is not unique to ANOVA post-hoc testing.
- It is also a concern when running separate tests for many related outcomes.
- **Beware of *p*-hacking!**

$$
\begin{aligned}
P(\text{making an error}) &= \alpha \\
P(\text{not making an error}) &= 1-\alpha \\
P(\text{not making an error in m tests}) &= (1-\alpha)^m \\
P(\text{making at least 1 error in m tests}) &= 1-(1-\alpha)^m
\end{aligned}
$$



**Problem:**

- Although one test has an $\alpha$ chance of a Type I error (finding a difference between a pair that aren't different),
- the **overall Type I error rate will be much higher when running many tests simultaneously**.

# ANOVA Summary

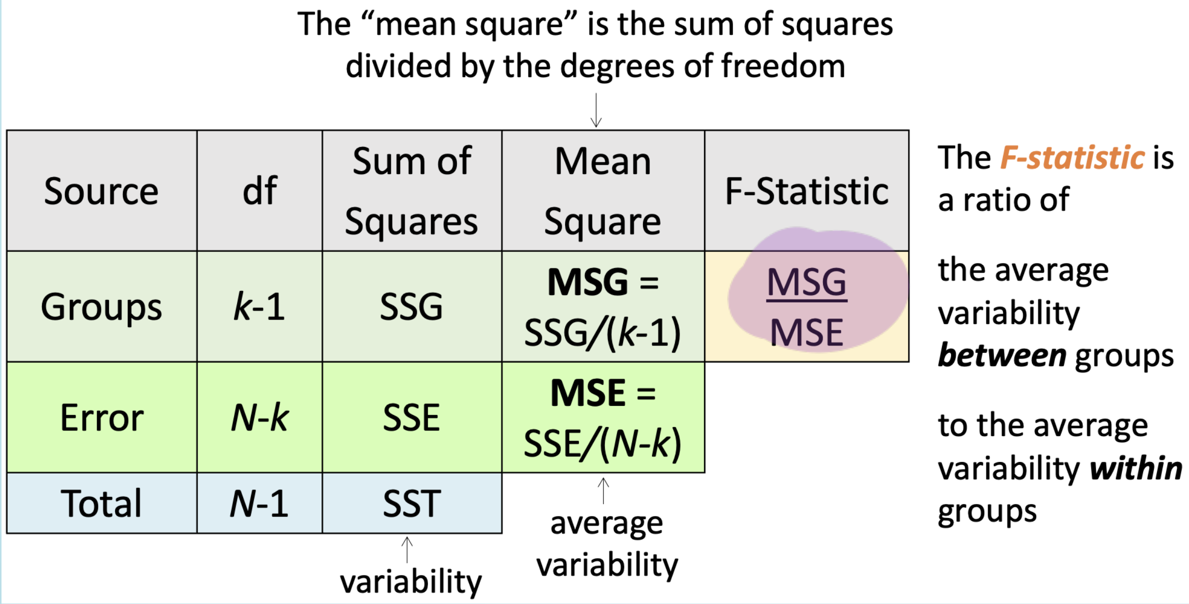
$$H_0 : \mu_1 = \mu_2 = \ldots = \mu_k$$
$$\text{vs. } H_A : \text{At least one pair } \mu_i \neq \mu_j \text{ for } i \neq j$$

## ANOVA table in R:

```r
lm(score ~ disability, data = employ) %>% anova()
```

```
Analysis of Variance Table

Response: score
          Df  Sum Sq Mean Sq F value  Pr(>F)  
disability  4  30.521  7.6304  2.8616 0.03013 *
Residuals  65 173.321  2.6665                  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## ANOVA table



The “mean square” is the sum of squares divided by the degrees of freedom

| Source | df | Sum of Squares | Mean Square | F-Statistic |
|---|---|---|---|---|
| Groups | *k*-1 | SSG | **MSG** = SSG/(*k*-1) | $\frac{MSG}{MSE}$ |
| Error | *N*-*k* | SSE | **MSE** = SSE/(*N*-*k*) | |
| Total | *N*-1 | SST | | |

variability

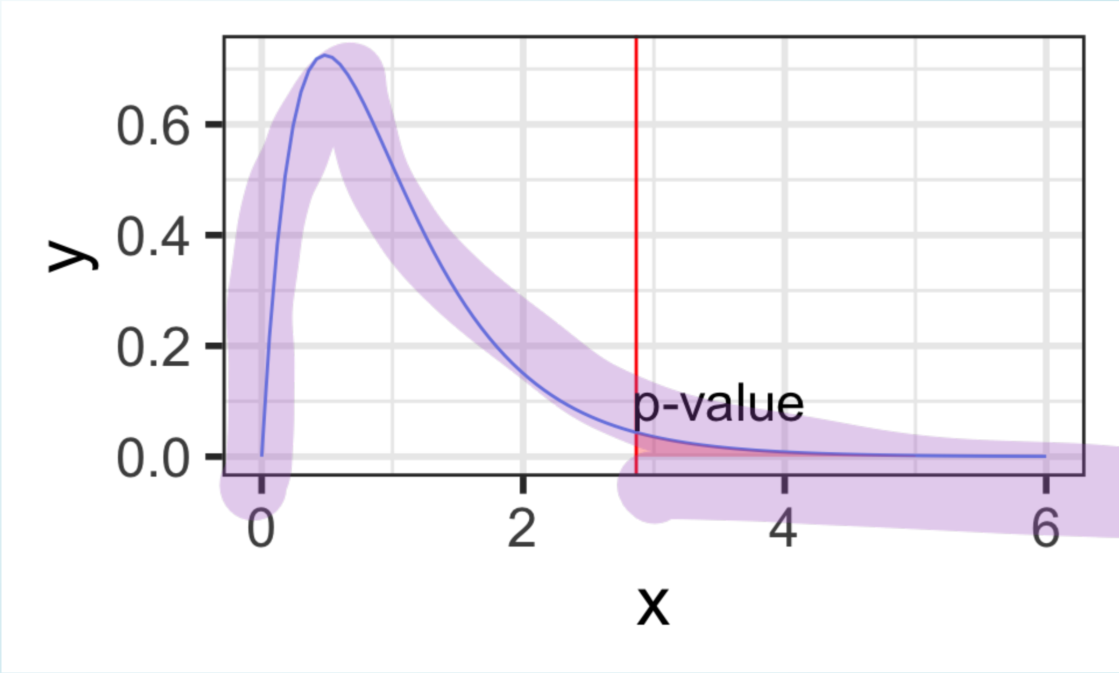
average variability

The ***F-statistic*** is a ratio of

the average variability ***between*** groups

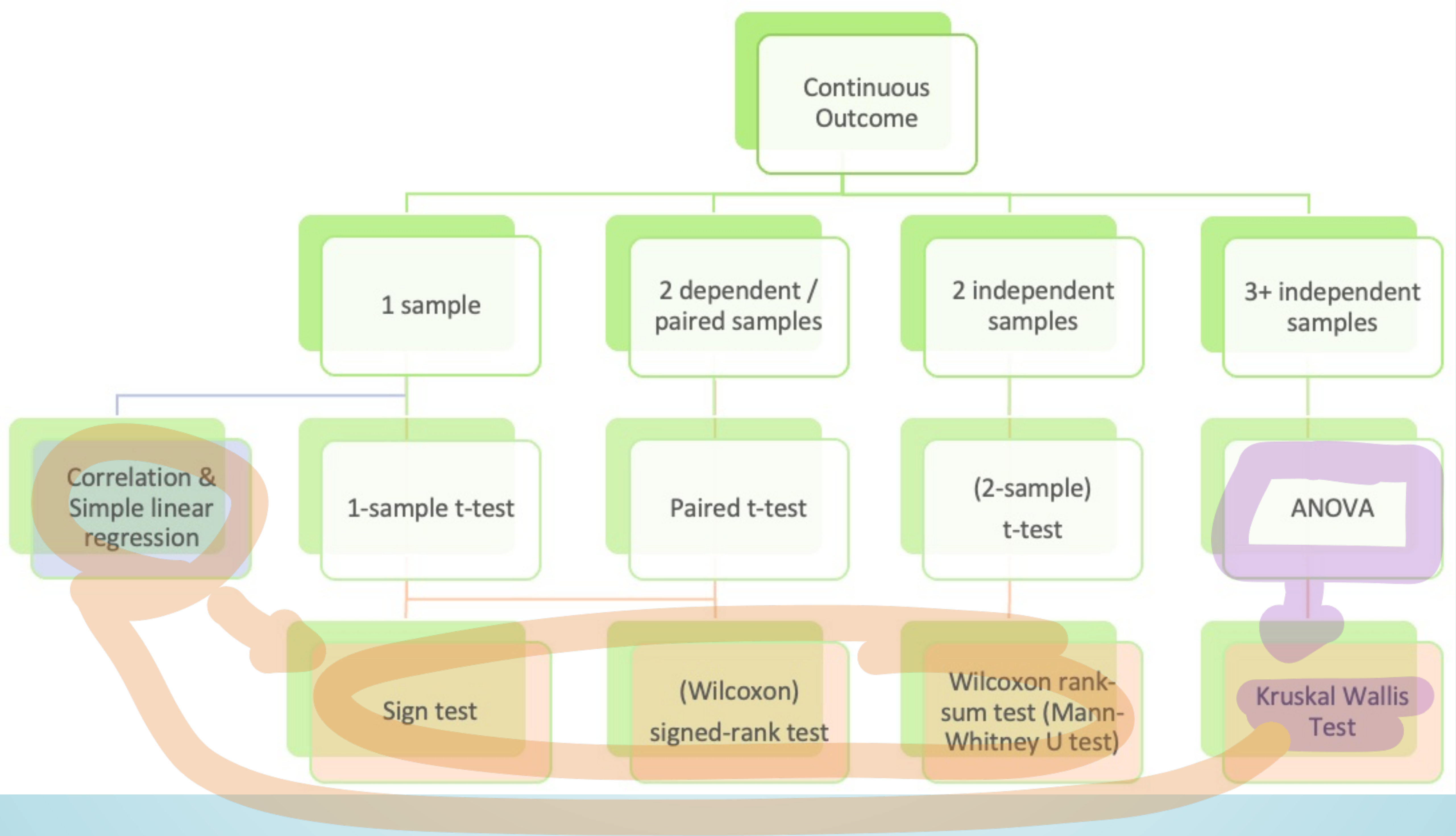
to the average variability ***within*** groups

## F-distribution & p-value



## Post-hoc testing

# What’s next?


Continuous Outcome
1 sample
2 dependent / paired samples
2 independent samples
3+ independent samples
Correlation & Simple linear regression
1-sample t-test
Paired t-test
(2-sample) t-test
ANOVA
Sign test
(Wilcoxon) signed-rank test
Wilcoxon rank-sum test (Mann-Whitney U test)
Kruskal Wallis Test