

Biometry. Lecture 12

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- 1 One-dimensional data
 - One-dimensional tests
 - Normality and R functions



```
> setwd("<working folder>")  
or  
"Change dir"  
in menu!
```

On Mac, be sure that startup option is working: `getwd()`
(`getwd()` checks if R is in working folder, `dir()` checks the folder content)



One-dimensional data

One-dimensional tests



t-test and Wilcoxon test for one-dimensional data

- Statistical tests allow to check how well the general characteristic calculated from *sample* represents a *population*
- t-test (Student's) takes into account the normality of sample whereas Wilcoxon test do not consider the distribution, it is non-parametric
- Both give a *confidence interval* which is even more important because their hypotheses-related output is typically not interesting.



t-test for one variable

```
> salary <- c(21, 19, 27, 11, 102, 25, 21)
> t.test(salary, mu=mean(salary))
One Sample t-test

data:  salary
t = 0, df = 6, p-value = 1
alternative hypothesis: true mean is not equal to 32.28571
95 percent confidence interval:
 3.468127 61.103302
sample estimates:
mean of x
32.28571
```

As you see, p-value is high which is the strong argument to stay with a **null hypothesis: population mean is equal to sample mean** which is 32.28571.

Alternative hypothesis (**population mean is not equal to sample mean**) is not accepted.



Wilcoxon test for one variable

(At the moment, please ignore warnings)

```
> wilcox.test(salary, mu=median(salary), conf.int=TRUE)
```

Wilcoxon signed rank test with continuity correction

data: salary

V = 10, p-value = 0.5896

alternative hypothesis: true location is not equal to 21

80 percent confidence interval:

17.99999 63.50002

sample estimates:

(pseudo)median

24.99994

This will test median, not mean! Again, because p-value is much greater than 0.05, we must stay with our null hypothesis: population median is equal to sample median which is 21.

Alternative hypothesis (population median is not equal to sample median) is not accepted.



Understanding the test output: theory

This will be explained later, but it is probably better to look on it beforehand.

- Alternative hypothesis (“something”) and null hypothesis (“nothing”)
- Type I error (false alarm) is when nothing happens but you think that something happens. In other words, you accept alternative when null is true.
- Probability of the Type I error (probability to issue the false alarm), p-value, and significance level (matter of agreement) are related.
- More strictly, the **probability to have greater or equal effect (deviation) when null hypothesis is true (no deviation)** is a p-value.
- Type II error (carelessness) is when we accept null but alternative is true. Non-parametric tests are more careless (less powerful) than parametric so we always must check if parametric tests are applicable.
- In science, it is **agreed** that Type I error is more dangerous so we follow the “0.05 rule”: **if p-value is more than 0.05, we must stay with the null hypothesis**
- But look here: <http://www.nature.com/news/statisticians-issue-warning-over-misuse-of-p-values-1.19503>. There is a current movement to replace p-values with other measures like: (1) confidence intervals, (2) bootstrap support, (3) effect sizes and (4) likelihood.



Understanding the test output: quick and dirty

- Which hypothesis is null?
- Does p-value less than 0.05?
 - 1 No: accept the null hypothesis—"sit and relax"
 - 2 Yes: reject the null hypothesis—"jump and do something"

5% (0.05) criteria is accepted in science because "jumping" is much more costly so it is better to stay with null hypothesis until we 95% and more sure that we see something important.



How to understand which test to use? Normality.

- Normality tests will check if we can accept the normal distribution of our sample. If yes, we use parametric tests (like t-test), if not, we use non-parametric (like Wilcoxon test).
- It is widely accepted that the strict normality testing is not generally required, it is enough, for example, to test normality graphically



Quantile-quantile plot for normality

```
> qqnorm(salary); qqline(salary) # Bad!  
> # Good:  
> set.seed(1); qqnorm(rnorm(100)); qqline(rnorm(100))
```

`set.seed()` helps to maintain the same set of random numbers in the session.



Shapiro test for normality

```
> shapiro.test(salary) # What is a null hypothesis?!  
> set.seed(1); shapiro.test(rnorm(1000)) # Null is normality!
```



One-dimensional data

Normality and R functions



- `shapiro.test()` is good but it is hard to apply if for data frames, and output is not very helpful.
- We will create the user function which run Shapiro-Wilks test with better output.



Normality() function for human use

```
> Normality <- function(x, p=.05)
+ {
+   ifelse(shapiro.test(x)$p.value > p, "NORMAL", "NOT NORMAL")
+ }
> sapply(trees, Normality)
> sapply(log(trees+1), Normality)
```



Finishing...

Save your commands!

`(savehistory(<today's date>.r)` or File -> Save as... on
Mac)



Summary: most important commands

- `t.test()` — checks the reliability of mean (assuming that data distribution is normal)
- `wilcox.test()` — checks the reliability of median (non-parametric)
- `shapiro.test()` — Shapiro-Wilks test for normality
- `function() {}` — creates a function
- `ifelse(check, yes, no)` — selector



For Further Reading



A. Shipunov.

Biometry [Electronic resource].

2012—onwards.

Mode of access:

http://ashipunov.info/shipunov/school/biol_240



A. Shipunov, and many others.

Visual statistics. Use R!

2016—onwards.

Mode of access: http://ashipunov.info/shipunov/school/biol_240/en/visual_statistics.pdf

