# Biometry. Lecture 16

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1. Two-dimensional statistics
   - Hypotheses and tests
   - Test for tables: chi-squared
   - The anatomy of two-sample test: sign test
   - Multiple comparisons
   - Concordance and Cohen kappa

> 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)

# Two-dimensional statistics
## Hypotheses and tests

# Null and alternative for two numeric samples

- Null: difference equal to $0 \approx$ similar $\approx$ related $\approx$ samples came from same population
- Alternative: difference not equal to $0 \approx$ different $\approx$ non-related $\approx$ samples came from different populations

# Null and alternative for chi-squared

- Null: independent distribution $\approx$ equal counts in each cell $\approx$ no pattern
- Alternative: concerted distribution $\approx$ non-equal counts in each cell $\approx$ pattern

## p-value

- p-value is the probability to have equal or greater effect in case if null hypothesis is true
- p-value is related with the accepted level of Type I statistical error (false alarm): the bigger is the significance level of p-value, the more false alarms we accept and at the same time, the more sensitive is our research
- In biology, the most common level of significance is 0.05
- As a rule, if p-value is equal or less then 0.05, we reject the null hypothesis, if more – we stay with null hypothesis

# Two main questions

- Normal?
  `t.test()` or `wilcox.test()`
- Paired?
  `(..., paired=T)` or `(...)`

# Two-dimensional statistics
## Test for tables: chi-squared

# Food intoxication example

- The poisoning took place on the party of Epidemiology Statistics association
- 13 food choices and 45 persons
- Data file `tox.txt`: ILL $= 1$ (poisoned), $= 2$ (not poisoned)

```
> tox <- read.table("http://ashipunov.info/data/tox.txt",
+ h=TRUE)
> str(tox)
> head(tox)
> for (m in 2:ncol(tox))
+ {
+ tmp <- chisq.test(tox$ILL, tox[,m])
+ print(paste(names(tox)[m], tmp$p.value))
+ }
> assocplot(table(ILL=tox$ILL, CAESAR=tox$CAESAR))
> assocplot(table(ILL=tox$ILL, TOMATO=tox$TOMATO))
```

# Two-dimensional statistics
## The anatomy of two-sample test: sign test

# Sign test

- Idea is simple: to calculate differences between all pairs of values (paired test!)
- Then take only positive differences
- If two samples came from a same distribution, approximately 50% of differences should be positive—we can test with with, e.g., binomial test

## Making the sign test

These are points from the first and second exam in one small class.
Both exams were equivalent. Are second exam results better?

```
> first <- c(63, 72, 77, 76, 67, 56, 55, 51, 77, 64)
> second <- c(87, 86, 76, 79, 54, 60, 97, 80, 73, 97)
> dif <- second - first
> pos.dif <- dif[dif > 0]
> binom.test(length(pos.dif), length(dif))
```

# Two-dimensional statistics
## Multiple comparisons

## Multiple comparisons

- If we apply multiple tests to one component (e.g., test several samples against one), probability to obtain incorrect answer will grow
- To keep the error rate low, one should apply the so-called *Bonferroni correction*, in other words—increase p-values to avoid the growing error

# Seedling example

Which fungus terminates the germination?

```
> pr <- read.table(
+ "http://ashipunov.info/data/seedlings.txt", h=TRUE)
> head(pr)
> unique(pr$CID)
# correct only for one comparison!
> chisq.test(table(subset(pr, CID==c(0,105))))
> p105 <- chisq.test(table(subset(pr,
+ CID==c(0,105))))$p.value
> p63 <- chisq.test(table(subset(pr,
+ CID==c(0,63))))$p.value
> p80 <- chisq.test(table(subset(pr,
+ CID==c(0,80))))$p.value
> all.p <- c(p105, p63, p80)
> p.adjust(all.p)
```

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## Toxicity with correction

```
> tox <- read.table("http://ashipunov.info/data/tox.txt",
+ h=TRUE)
> answer <- data.frame(FOOD=NA, CHISQ.P=NA)
> for (m in 2:ncol(tox))
+ {
+ tmp <- chisq.test(tox$ILL, tox[,m])
+ answer[m-1,] <- c(names(tox)[m], tmp$p.value)
+ }
> answer[,2] <- p.adjust(answer[,2])
> answer
```

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# Two-dimensional statistics
## Concordance and Cohen kappa

- Concordance is a measure of "agreement" between two expert answer sheets
- The most common application are psychological tests
- Cohen kappa test is frequently used for understanding the degree of concordance; **the null hypothesis for Cohen kappa is that two answer sheets are non-concordant**

# Cohen kappa and island flora

```
> source("http://ashipunov.info/data/concordance.r")
> isl <- read.table(
+ "http://ashipunov.info/data/pokorm_03.dat",
+ h=TRUE, sep=";")
> str(isl); head(isl)
> cohen.kappa(as.matrix(isl))
```

## Finishing...

Save your commands!

(savehistory(<todaysdate>.r) or File -> Save as... on Mac)

# Summary: most important commands

- `chisq.test()`—test for independence of rows and columns

# For Further Reading

A. Shipunov.
*Biometry* [Electronic resource].
2012—onwards.
Mode of access:
http://ashipunov.info/shipunov/school/biol_240

A. Shipunov, and others.
*Visual statistics. Use R!*
Ongoing translation from Russian.