

# Biometry. Lecture 16

Alexey Shipunov

Minot State University

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```
> 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)



# 2D 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



# 2D statistics

## Exact and approximate tests



# Chi-squared and Fisher exact

- Chi-squared proportion tests will **estimate** the p-value from theoretical distribution. As a consequence, it may say “*Chi-squared approximation may be incorrect*”.
- Fisher exact and binomial tests will **calculate** p-value directly. That is why they are sometimes preferable.





# Fisher's tea drinker

A British woman claimed to be able to distinguish whether milk or tea was added to the cup first. To test, she was given 8 cups of tea, in four of which milk was added first.

```
> tea <- matrix(c(3,1,1,3), nrow=2)
> colnames(tea) <- row.names(tea) <- c("Milk", "Tea")
> tea
> chisq.test(tea) # warning!
> fisher.test(tea) # note odds ratio
```



# How to avoid the approximation with simulation

```
> chisq.test(tea, simulate.p.value=T) # no warning!
```

When some cells contain less than 5 items, `simulate.p.value=T` is recommended.



# 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))
```

As it was said above, here is better to use `simulate.p.value=T` for chi-squared test.



# 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 *Bonferroni* or another p-value correction, in other words—increase p-values to avoid the growing error



# 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
```



# 2D statistics

## 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))
```



# 2D 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/r/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(<today's date>.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](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](http://ashipunov.info/shipunov/school/biol_240/en/visual_statistics.pdf)

