

Biometry. Lecture 21

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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)



Plan of the Exam 4

Morphometric data (plants or animals) with several species and several characters:

- Differences between two or more subgroups: two-sample tests or ANOVA-like methods
- Most correlated characters
- Linear model(s); possibly, compare them (ANCOVA)
- Classification of species or characters (clustering or similar)



Human genetic traits

Trait	Dominant	Recessive
Tongue rolling	yes	no
Earlobe attachment	free	attached
Pinky shape	bent (crooked)	straight
Arm folding	right on top	left on top
Cheek dimple	dimple	no dimple
Cleft chin	cleft	no cleft
Hitchhiker thumb	straight	hooked
Toe length	2nd toe longer	1st toe longer
Widow's peak	peak	no peak



Cluster analysis: training

```
> traits <- read.table("traits.txt", sep="\t", row.names=1, h=T)
> traits.d <- dist(traits, method="binary") # First
> plot(hclust(traits.d, method="ward"))
> library(vegan)
> traits.d2 <- vegdist(traits, method="jaccard") # Second
> plot(hclust(traits.d2))
> library(cluster)
> traits.d3 <- daisy(traits) # Third
> plot(hclust(traits.d3))
> traits.c <- cmdscale(traits.d) # Fourth
> plot(traits.c[,1:2], type="n")
> text(traits.c[,1:2], labels=row.names(traits))
```



Save your commands!

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



Short anonymous absolutely voluntary survey

- 1 What do you **like** most in biometrics course?
- 2 What do you **dislike** most in biometrics course?
- 3 **Which lab** do you remember most of all?
- 4 Please grade (1—bad, 5—excellent):
 - 1 Lectures
 - 2 Labs
 - 3 Final questions
 - 4 Exams
- 5 Please explain (1–3 sentences) how would you improve the textbook.

