

# Exercises in Marine Ecological Genetics

## 02. Hardy-Weinberg equilibrium

- Calculate allele and genotype frequencies
- Test for Hardy-Weinberg equilibrium
- Work with data in Genepop format
- Learn to interpret HW test results

Martin Helmkamp



# Working with the command line / bash

## Windows

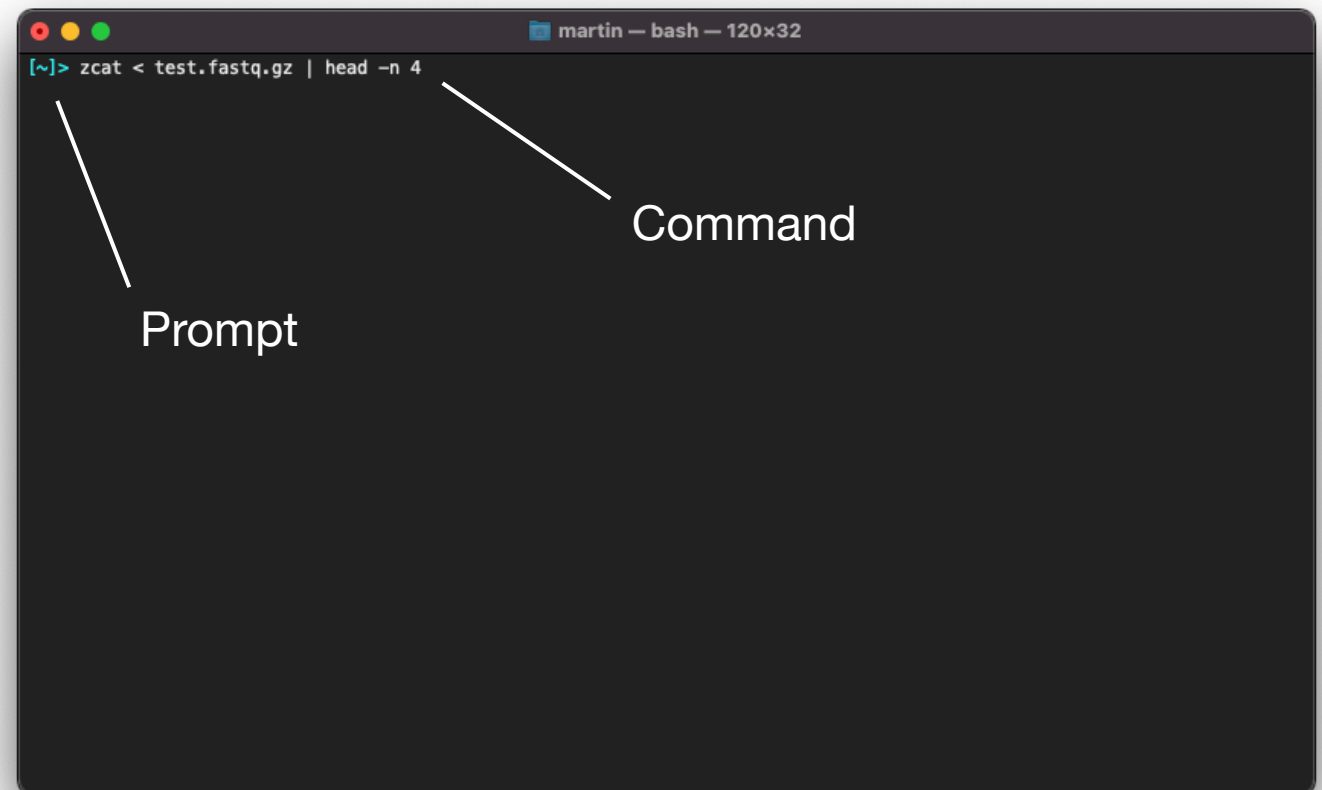
- Launch git bash from Start menu
- Alternatively, install Windows Subsystem for Linux (WSL) on Windows 10 or above (see <https://learn.microsoft.com/en-us/windows/wsl/install>)

## macOS

- Open Terminal app in /Applications/Utilities, type and execute “bash”

## Typical usage

`command [-options] [file]`



# Recap: basic bash commands

See also [other/bash\\_cheatsheet\\_?.pdf](#)

<code>ls -l</code>	<code># List directory contents in long format</code>
<code>cd <i>dir</i></code>	<code># Change into directory</code>
<code>cd ..</code>	<code># Move up one directory</code>
<code>pwd</code>	<code># Print current directory</code>
<code>mkdir <i>dir</i></code>	<code># Create new directory</code>
<code>mv <i>file/dir1 file/dir2</i></code>	<code># Move or rename file or directory</code>
<code>cp <i>file/dir1 file/dir2</i></code>	<code># Copy file or directory</code>
<code>rm <i>file</i></code>	<code># Delete file</code>

<code>tab key</code>	<code># Autocomplete file or directory name</code>
<code>up arrow key</code>	<code># Cycle through previous commands</code>

# Download course materials using git

Go to project directory and check contents

```
cd dir          # e.g. Documents/meg23_exercises  
ls -l            # -l: long format
```





# Download course materials using git

Go to project directory and check contents

```
cd dir          # e.g. Documents/meg23_exercises  
ls -l            # -l: long format
```

Update course repository

```
cd meg23_repo  
git pull
```



Please do not save over files in the course repository. Instead, save your own scripts to the local subdirectory (including copies of course scripts you would like to edit), e.g with

```
cp code/02_hwe.R ../local/02_hwe_lc.R          # cp [source] [destination]
```

# In case of an error message ...

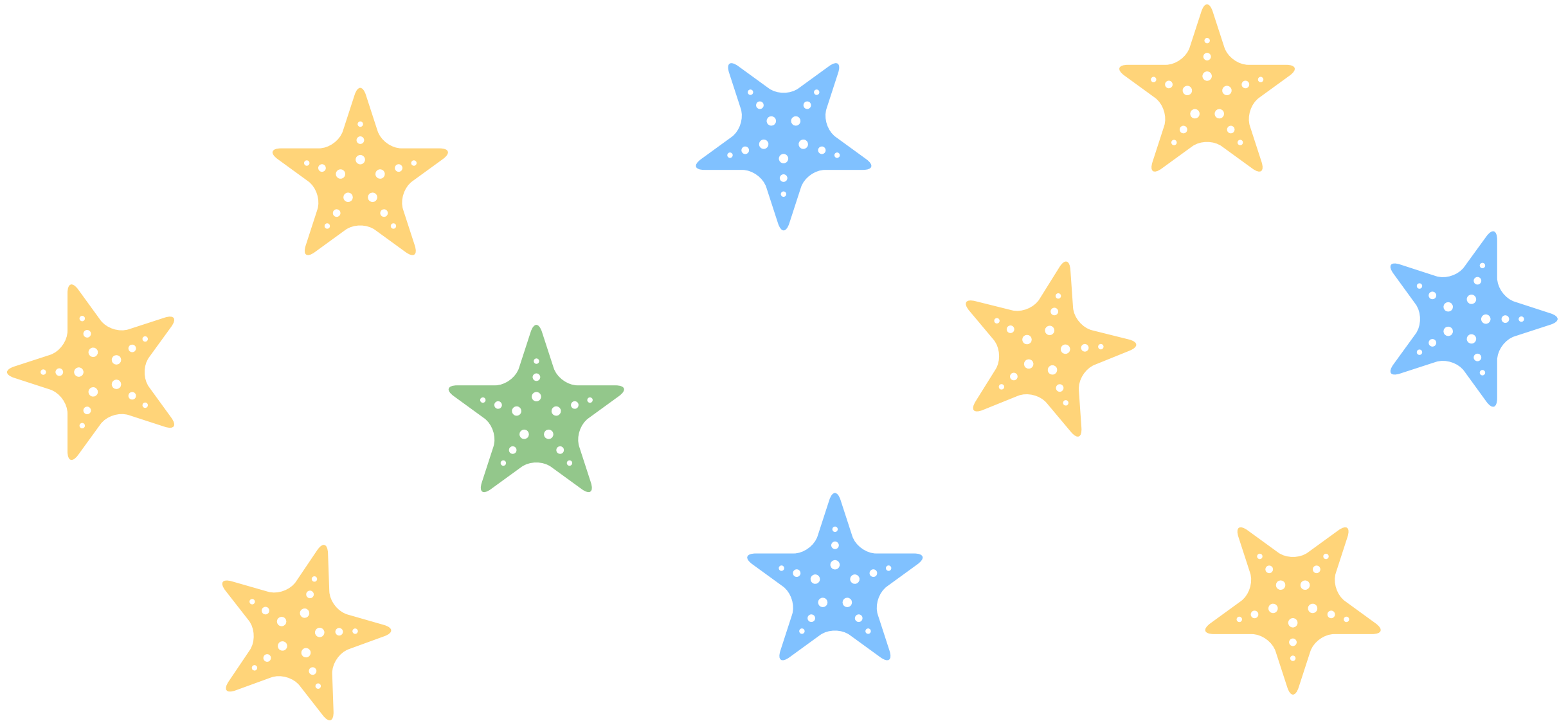
Delete old repository and re-download from GitHub

```
rm -rf meg23_repo  
git clone https://github.com/mhelmkampf/meg23\_repo.git
```

# Is this population in Hardy-Weinberg equilibrium?

## Exercise 1

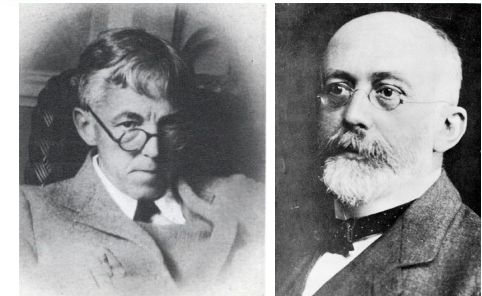
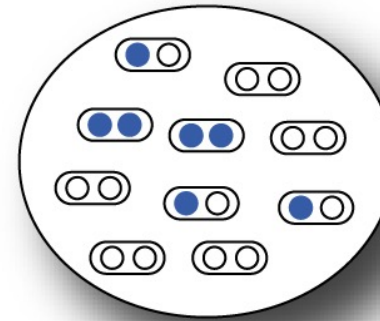
Diploid, sexual reproduction, 1 locus, 2 co-dominant alleles (yellow, blue)



## HARDY-WEINBERG (1908)

Godfrey H. Hardy (1877-1947)

Wilhelm Weinberg (1862-1937)

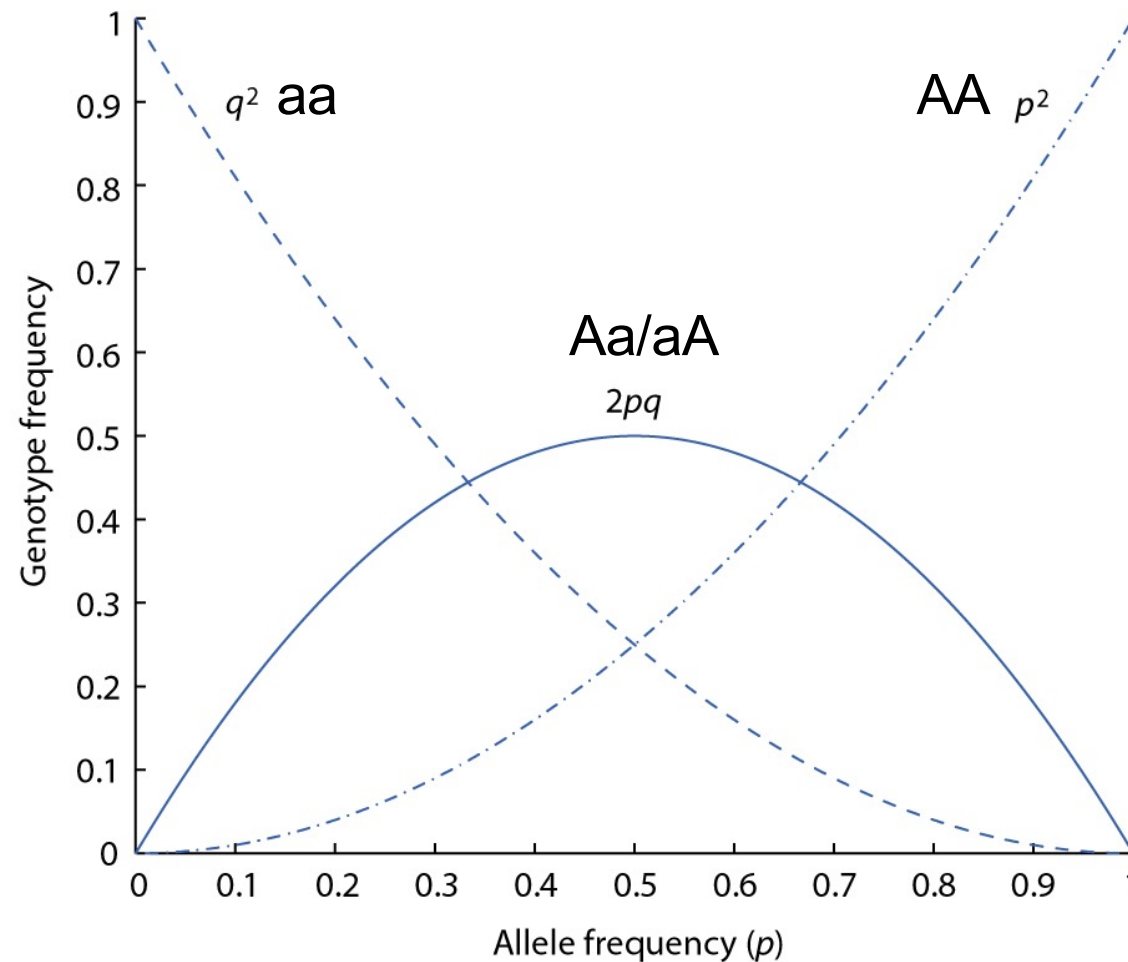


*Establish the relationship between allele frequencies and genotype frequencies in a population*

$$p^2 + 2pq + q^2 = 1$$

AA    Aa/aA    aa

$p$  and  $q$ : allele frequencies for a locus with two alleles (A and a)  
( $p + q = 1$ )





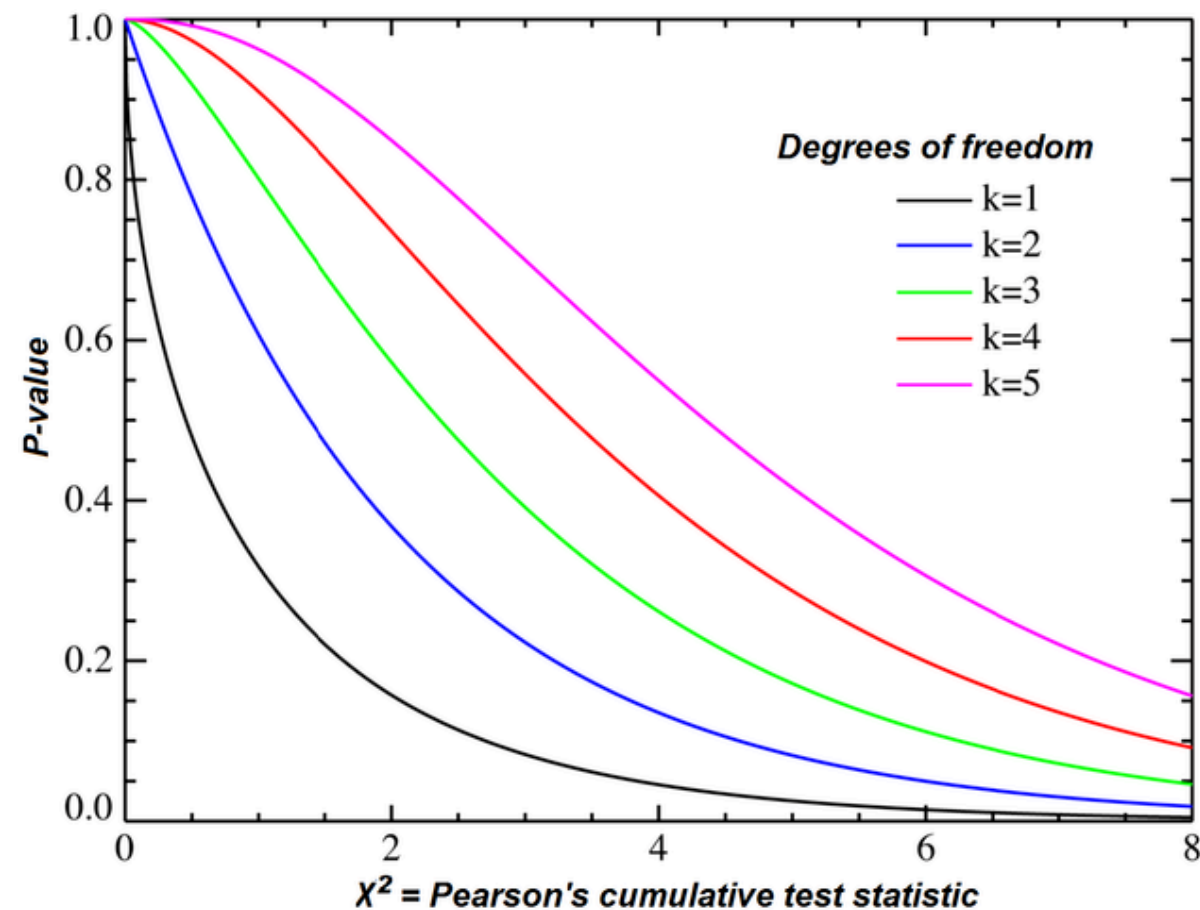
# Pearson's chi-squared test

## Exercise 1

Chi-square statistic:

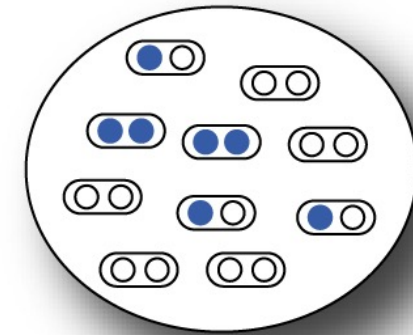
$$\chi^2 = \sum_{i=1}^n \frac{(O_i - E_i)^2}{E_i}$$

Chi-square distribution:



## HETEROZYGOSITY

In one population



$H_o$  = proportion of heterozygote individuals, observed heterozygosity

$H_e = 2pq = 1 - p^2 - q^2$ , expected heterozygosity (assuming HW equilibrium)

$$F = \frac{H_e - H_o}{H_e}$$

Fixation index: *proportion by which heterozygosity is reduced or increased relative to the heterozygosity of a population at HW equilibrium with the same allele frequencies.*

Divided by  $H_e \rightarrow$  *proportion* (of expected heterozygosity)

Varies between -1 and 1

$F < 0$ : heterozygote excess

$F > 0$  heterozygote deficit (homozygote excess)

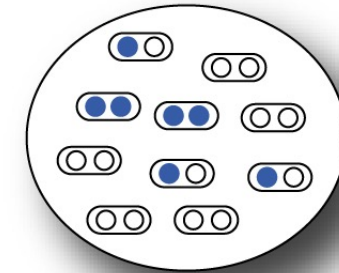
May be averaged over several loci  $\rightarrow$  reduces bias

May be extended to  $k$  alleles

*A single generation of reproduction will result in a population that meets the expected Hardy-Weinberg frequencies, i.e. is at Hardy-Weinberg (HW) equilibrium*

Assuming an “ideal” population, i.e. :

- Diploid organisms
- Sexual reproduction (as opposed to clonal)
- Random mating (as opposed to e.g. assortative) with respect to genotype
- Random union of gametes
- Discrete, non-overlapping generations
- Very large (infinite) population
- No migration
- No population structure
- No natural selection
- Two alleles
- Identical allele frequencies in both sexes



-> Departures from HW equilibrium may indicate:

- Inbreeding
- Assortative mating
- Self-fertilization
- Natural selection
- Population structure
- ...



# Genepop format

## Exercises 2/3

Example data

Color

POP

ind01, yy

ind02, yy

ind03, yy

ind04, yy

ind05, yy

ind06, yy

ind07, yb

ind08, bb

ind09, bb

ind10, bb

yellowblue.txt

Microsatellite genotypes of Hypoplectrus puella from Barbados

g2

gag010

h24

hyp001

hyp015

hyp018

e2

hyp008

hyp016

pam013

POP

barbados ind#735 , 203235 121127 210248 225231 126132 190192 157157 236244 194220 114128

barbados ind#736 , 205217 119119 204216 225229 126126 190192 157165 236236 216222 106144

barbados ind#737 , 203203 135147 224226 233235 126136 190198 157163 238250 202226 126160

barbados ind#738 , 211217 119121 228230 223231 126130 190190 157157 240244 220226 138160

barbados ind#739 , 205225 121125 208216 227231 132132 192192 158159 244256 192196 146146

barbados ind#740 , 217233 119121 216228 227233 126126 192198 157157 242256 194216 000000

barbados ind#741 , 203209 000000 216222 223229 126130 192198 157157 234236 188226 118130

barbados ind#742 , 203215 119119 222234 233233 130130 190190 157157 240246 182188 108126

barbados ind#743 , 203243 111121 216224 231231 126126 190192 157159 234249 188198 118126

barbados ind#744 , 203225 121135 206232 231231 126130 192198 157159 240249 182222 122156

barbados ind#745 , 203211 121123 224236 227231 126132 192192 157163 238238 182204 138148

barbados ind#746 , 227233 119123 216234 227233 126130 190190 157159 236245 186188 124142

barbados ind#747 , 203223 133141 236240 231231 126126 192198 157157 234236 194204 118126

barbados ind#748 , 203217 141145 222226 227235 126126 190192 145157 238240 182196 108108

barbados ind#749 , 205221 125147 210238 223231 126132 192198 157157 234234 188200 106148

barbados ind#750 , 203235 123123 230234 223231 126132 192198 157157 236256 188214 122136

barbados ind#751 , 203211 121143 212248 223229 126132 190196 157159 234242 214216 118128

barbados ind#752 , 213217 123169 204234 223231 126134 190198 157163 236248 193224 142148

Free text

Locus names

Sample / population

Alleles (000 = missing data)



# Genepop format

## Exercises 2/3

Example data

Color

POP

ind01, yy

ind02, yy

ind03, yy

ind04, yy

ind05, yy

ind06, yy

ind07, yb

ind08, bb

ind09, bb

ind10, bb

yellowblue.txt

puella\_barbados.txt

Microsatellite genotypes of Hypoplectrus puella from Barbados

g2

gag010

h24

hyp001

hyp015

hyp018

e2

hyp008

hyp016

pam013

POP

Sample / population	Locus names	Alleles (000 = missing data)
barbados ind#735	203235	121127 210248 225231 126132 190192 157157 236244 194220 114128
barbados ind#736	205217	119119 204216 225229 126126 190192 157165 236236 216222 106144
barbados ind#737	203203	135147 224226 233235 126136 190198 157163 238250 202226 126160
barbados ind#738	211217	119121 228230 223231 126130 190190 157157 240244 220226 138160
barbados ind#739	205225	121125 208216 227231 132132 192192 158159 244256 192196 146146
barbados ind#740	217233	119121 216228 227233 126126 192198 157157 242256 194216 000000
barbados ind#741	203209	000000 216222 223229 126130 192198 157157 234236 188226 118130
barbados ind#742	203215	119119 222234 233233 130130 190190 157157 240246 182188 108126
barbados ind#743	203243	111121 216224 231231 126126 190192 157159 234249 188198 118126
barbados ind#744	203225	121135 206232 231231 126130 192198 157159 240249 182222 122156
barbados ind#745	203211	121123 224236 227231 126132 192192 157163 238238 182204 138148
barbados ind#746	227233	119123 216234 227233 126130 190190 157159 236245 186188 124142
barbados ind#747	203223	133141 236240 231231 126126 192198 157157 234236 194204 118126
barbados ind#748	203217	141145 222226 227235 126126 190192 145157 238240 182196 108108
barbados ind#749	205221	125147 210238 223231 126132 192198 157157 234234 188200 106148
barbados ind#750	203235	123123 230234 223231 126132 192198 157157 236256 188214 122136
barbados ind#751	203211	121143 212248 223229 126132 190196 157159 234242 214216 118128
barbados ind#752	213217	123169 204234 223231 126134 190198 157163 236248 193224 142148

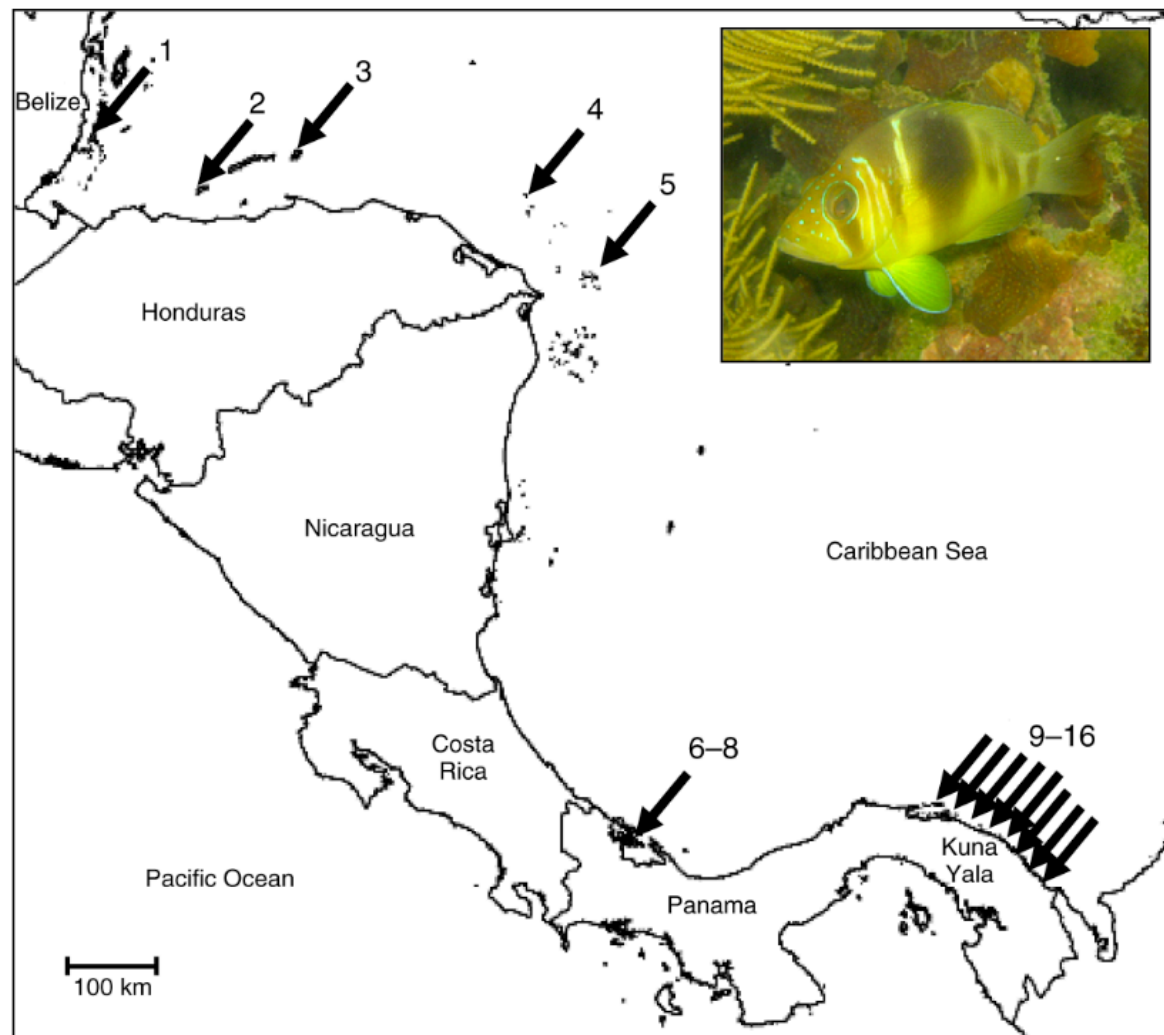
Summer 2023

Exercises in Marine Ecological Genetics  
02. Hardy-Weinberg equilibrium

Carl von Ossietzky  
Universität  
Oldenburg

# Barred hamlet (*H. puella*) microsatellite dataset

## Exercise 3



*Ecology*, 90(11), 2009, pp. 3087–3098  
© 2009 by the Ecological Society of America

Estimating dispersal from genetic isolation by distance  
in a coral reef fish (*Hypoplectrus puella*)

OSCAR PUEBLA,<sup>1,2,3</sup> ELDREDGE BERMINGHAM,<sup>1,2</sup> AND FRÉDÉRIC GUICHARD<sup>2</sup>

- 10 highly variable microsatellite loci
- 854 individuals
- 15 Caribbean locations



# Useful R functions for population genetics

Exercises 2/3

```
## Import Genepop file as genind object  
read.genepop(file, node = n)  
  
## Locus statistics  
locus_table(genind)  
  
## Quick test for HWE  
test.hw(genind)  
  
## Detailed test for HWE, can write output to file  
test_hw(file, outputFile = newfile)
```

# Course outline

May be subject to change

Class	Date	Topics	Script
01	Apr 14	Introduction, software installation	01_intro.R
02	Apr 21	Hardy-Weinberg equilibrium	02_hwe.R
03	Apr 28	Genetic drift and effective population size	03_Ne.R
04	May 05	Population structure and gene flow	04_structure.R
05	May 12	Isolation by distance (lecture online, exercises in person)	05_ibd.R
–	May 19	<a href="#">Himmelfahrt break</a>	–
06	May 26	Whole-genome sequencing and genome assembly	06_genseq.sh
07	Jun 02	Genotyping, SNPs and population genomics	07_snps.R
08	Jun 09	Recombination and linkage disequilibrium	08_linkage.R
–	Jun 16	<a href="#">Student presentations</a>	–
09	Jun 23	Selection and mutation	09_selection.R
10	Jun 30	DNA barcoding	10_barcode.sh
11	Jul 07	Metabarcoding	11_meta.sh
–	Jul 14	To be determined	–