Exercises in Marine Ecological Genetics

02. Hardy-Weinberg equilibrium

- Calculate allele and genotype frequencies
- Test for Hardy-Weinberg equilibrium
- Work with microsatellite data / Genepop format

Martin Helmkampf

https://github.com/mhelmkampf/meg25



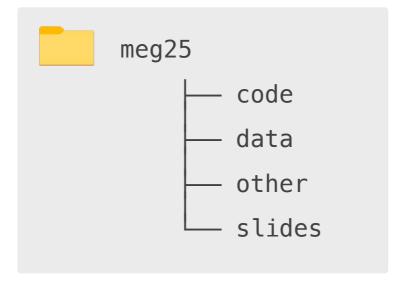
Preliminary, may be subject to change

Class	Date	Topics	Script
01	Apr 11	Introduction, setup	01_intro.R
_	Apr 18	Good Friday	
02	Apr 25	Hardy-Weinberg equilibrium / N _e	02_hwe.R
03	May 02	Population structure and gene flow	
04	May 09	Genome assembly and metrics	
05	May 16	SNPs and population genomics	
06	May 23	Recombination and linkage disequilibrium	
_	May 30	Himmelfahrt break	
07	Jun 06	Measures of genetic diversity	
_	Jun 13	Selection and Mutation	
08	Jun 20	Student presentations – no exercises	
09	Jun 27	DNA barcoding	
10	Jul 04	Metabarcoding / eDNA	
11	Jul 11	Metabarcoding / eDNA II	

Accessing the course materials

All code and data for the course will be provided through a Git repository:

https://github.com/mhelmkampf/meg25





Windows

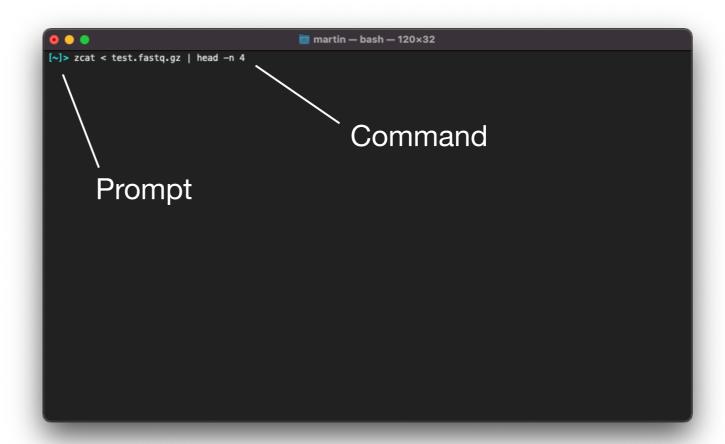
- Launch git bash from Start menu
- Alternatively, install Windows Subsystem for Linux (WSL) on Windows 10 or above (see https://learn.microsoft.com/en-us/windows/wsl/install)

macOS

Open Terminal app
 in /Applications/Utilities

Typical usage

command [-options] [file]



Basic bash commands

Recap

```
ls  # List directory contents
ls -l  # List directory contents in long format

cd  # Change into home directory
cd <directory_name>  # Change into directory
cd ..  # Change into directory above / back

pwd  # Print current (working) directory
```

Basic R commands

Recap

```
y \leftarrow ((6 * 2) + 1) / 20
                                         # Assign value to variable
                                         # Recall
У
[1] 0.65
c(...)
                                         # Combine elements into vector
data.frame(...)
                                         # Create data frame (table)
# Example
dat <- data.frame(row.names = c("yy", "yb", "bb"),</pre>
                   "observed" = c(6, 1, 3),
                   "expected" = c(yy_e, yb_e, bb_e)
help(function_name)
                                         # Show help page for function
```



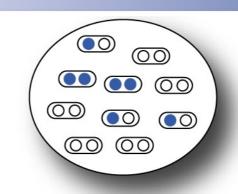
HARDY-WEINBERG (1908)

Godfrey H. Hardy (1877-1947) Wilhelm Weinberg (1862-1937)

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

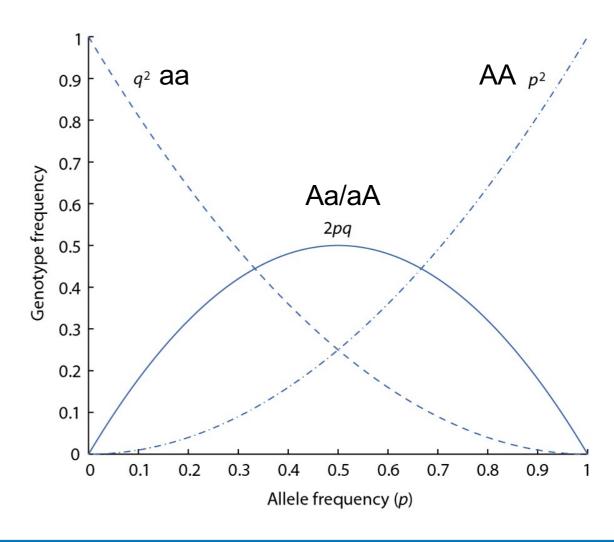
$$p^2 + 2pq + q^2 = 1$$
AA Aa/aA aa

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









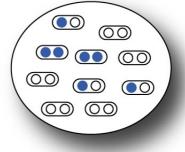


A single generation of reproduction will result in a population that meets the expected Hardy-Weinberg frequencies, i.e. is at Hardy-Weinberg (HW) equilibrium

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

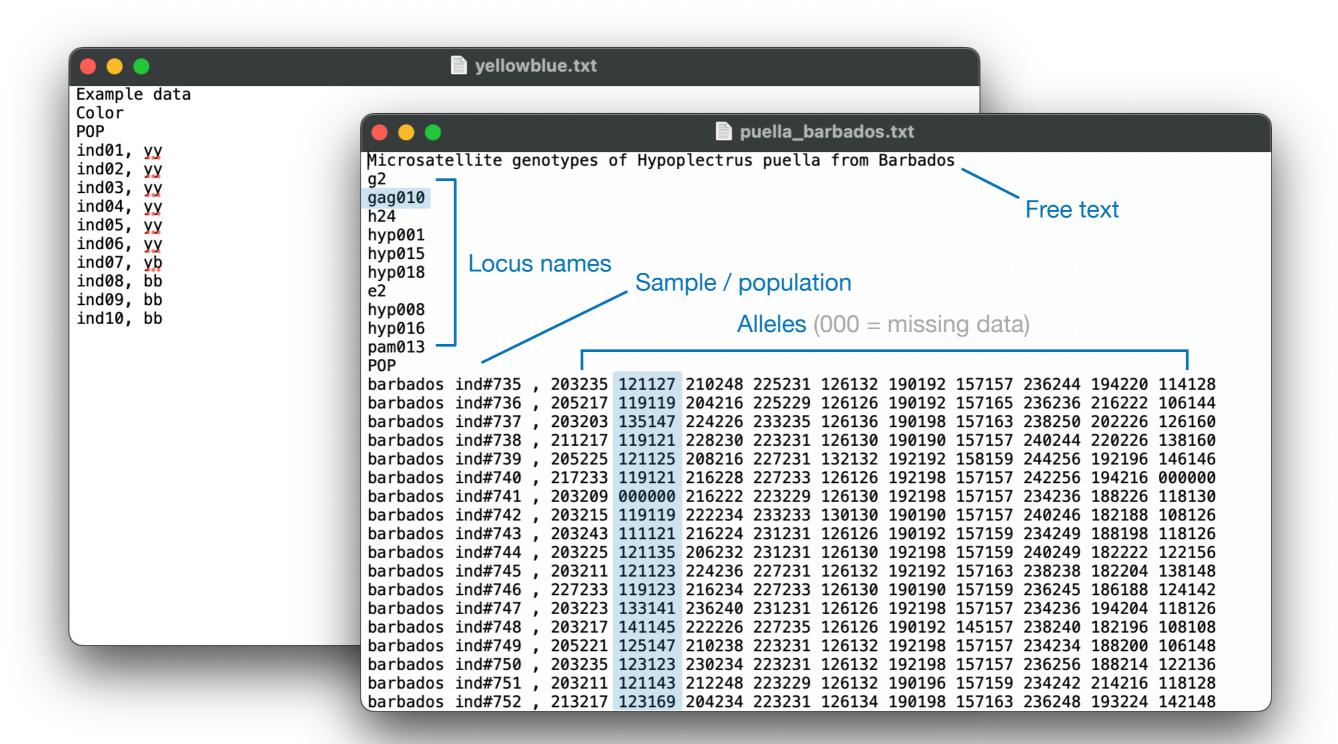
- -> Departures from HW equilibrium may indicate:
- Inbreeding
- Assortative mating
- Self-fertilization
- Natural selection
- Population structure
- ...



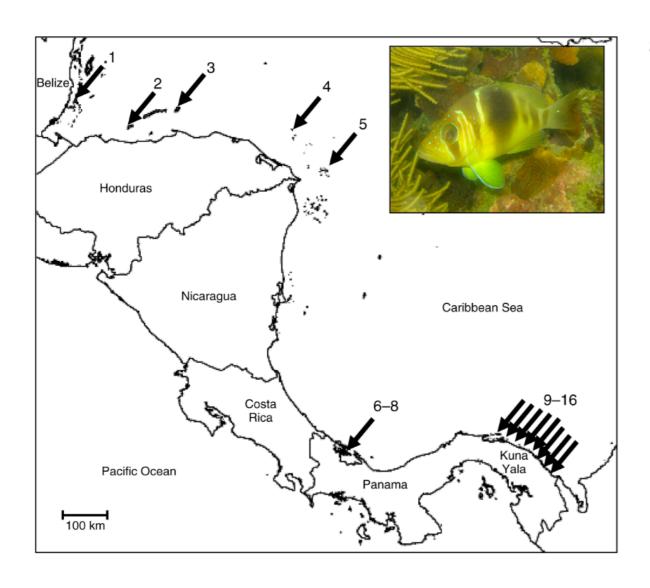
Diploid, sexual reproduction, 1 locus, 2 co-dominant alleles (yellow, blue)



Genepop format



Barred hamlet (H. puella) microsatellite dataset



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

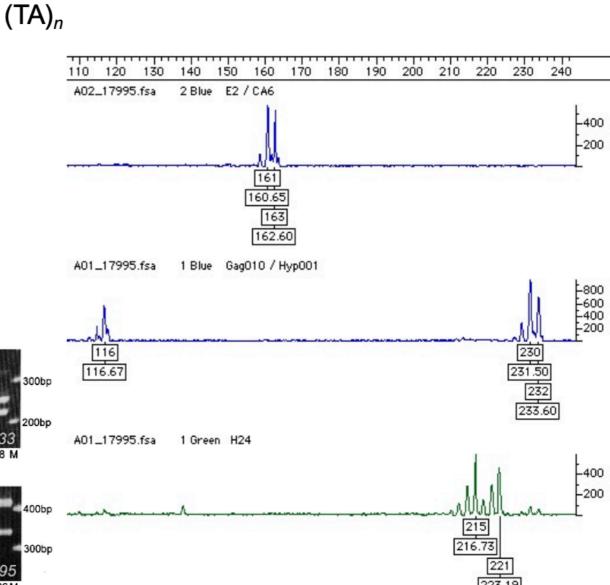
Estimating dispersal from genetic isolation by distance in a coral reef fish (*Hypoplectrus puella*)

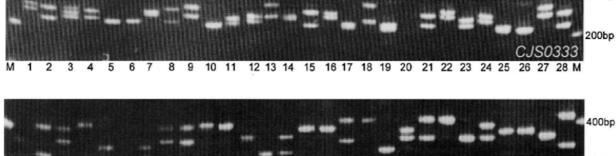
Oscar Puebla, 1,2,3 Eldredge Bermingham, 1,2 and Frédéric Guichard 2

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

ACAGTTACAGCAGGAAGTTC [...] TATATATATATATATATATA [...] CGCTAATG ACAGCACGCTAAC

Co-dominant
Many alleles
High mutation rates
High heterozygosities





Barred hamlet (H. puella) microsatellite dataset

Hamlets are simultaneous hermaphrodites with external fertilization.



Test whether self-fertilization occurs regularly using population genetic data