Exercises in Marine Ecological Genetics

01. Introduction

- General info and course outline
- Connecting to the HPC cluster
- Working with course materials
- Test for HWE using R

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General course info

- Suggestion: we start at 14:00 and finish at 15:30
- Course language will be English, but questions can always be asked in German
- There will be no tests or grades
- Slides will be provided, but please do not post them online
- Contact: martin.helmkampf (at) uni-oldenburg.de

Objectives

- Apply theory and concepts of population genetics, genomics and DNA barcoding in practice
- Learn to analyze, visualize and interpret real world data
- Learn how to work on a high performance computing cluster (using bash) / a scripting environment (using R)
- Become familiar with the most common data types and file formats

Course outline

Preliminary, may be subject to change

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

Required software

- Browser
- Text editor (e.g. Notepad, TextEdit, VSCodium)
- Terminal / ssh client (e.g. git bash, Terminal)

To connect to the high performance computing cluster ROSA, a shh client is required

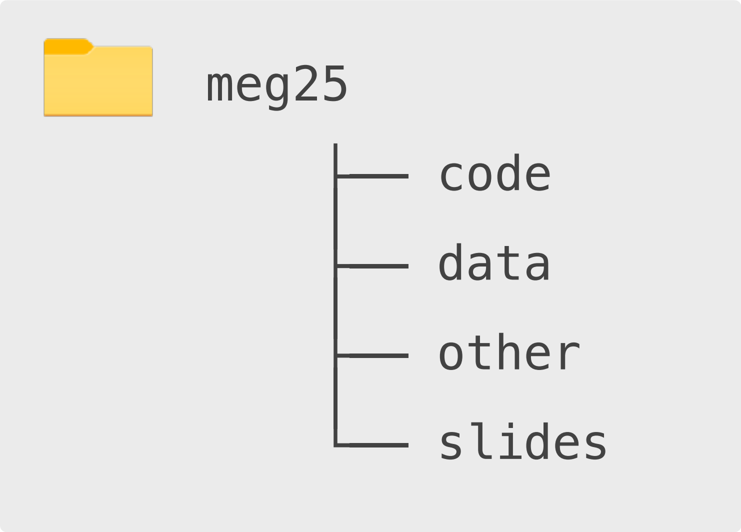
On Windows, a good option is git bash, which is part of Git for Windows. Install from https://gitforwindows.org with default settings (alternative: WSL)

On macOS or Linux, a terminal (and git) come preinstalled

Accessing the course materials

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

https://github.com/mhelmkampf/meg25



meg25

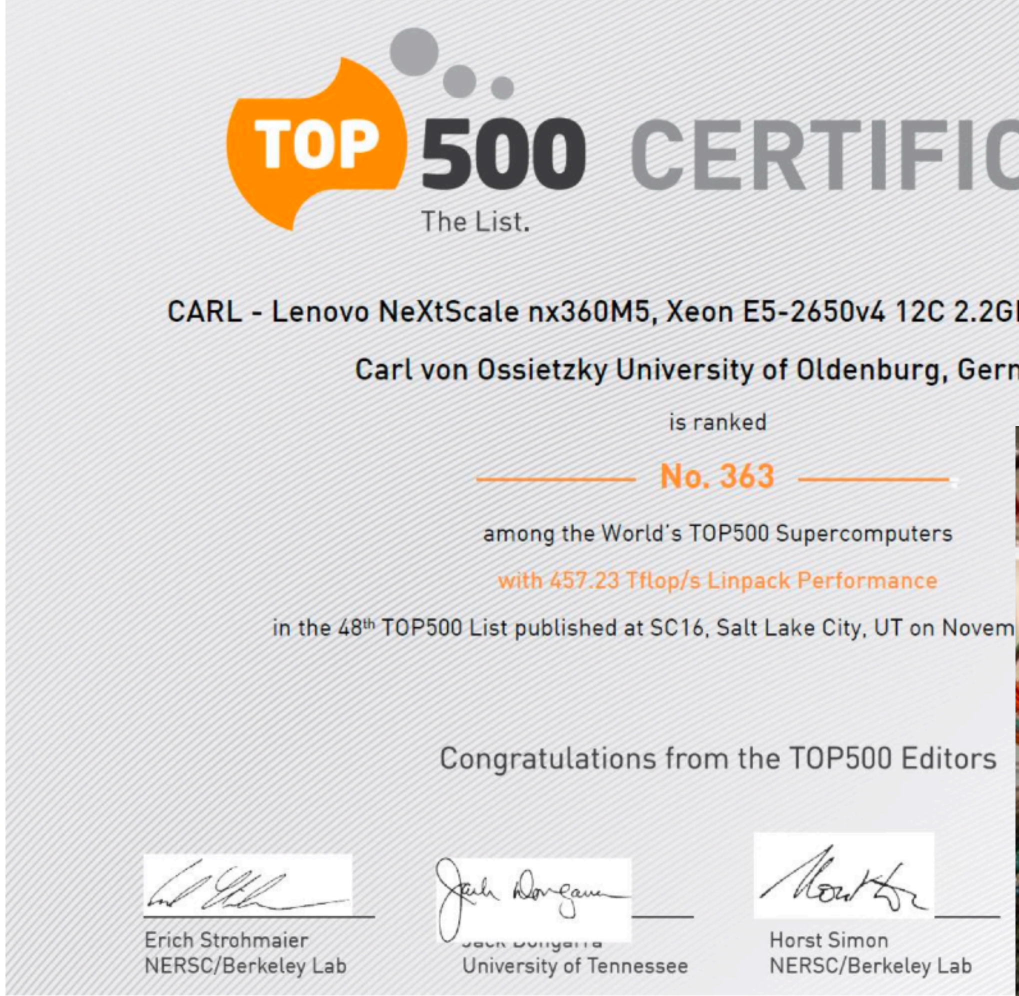
code

data

other

slides

High performance computing (HPC) at UOL



TOP 500 CERTIFICATE
The List.

CARL - Lenovo NeXtScale nx360M5, Xeon E5-2650v4 12C 2.2GHz, Infiniband FDR

Carl von Ossietzky University of Oldenburg, Germany

is ranked

No. 363

among the World's TOP500 Supercomputers

with 457.23 Tflop/s Linpack Performance

in the 48th TOP500 List published at SC16, Salt Lake City, UT on Novem

Congratulations from the TOP500 Editors

Erich Strohmaier
NERSC/Berkeley Lab

Jack Dongarra
University of Tennessee

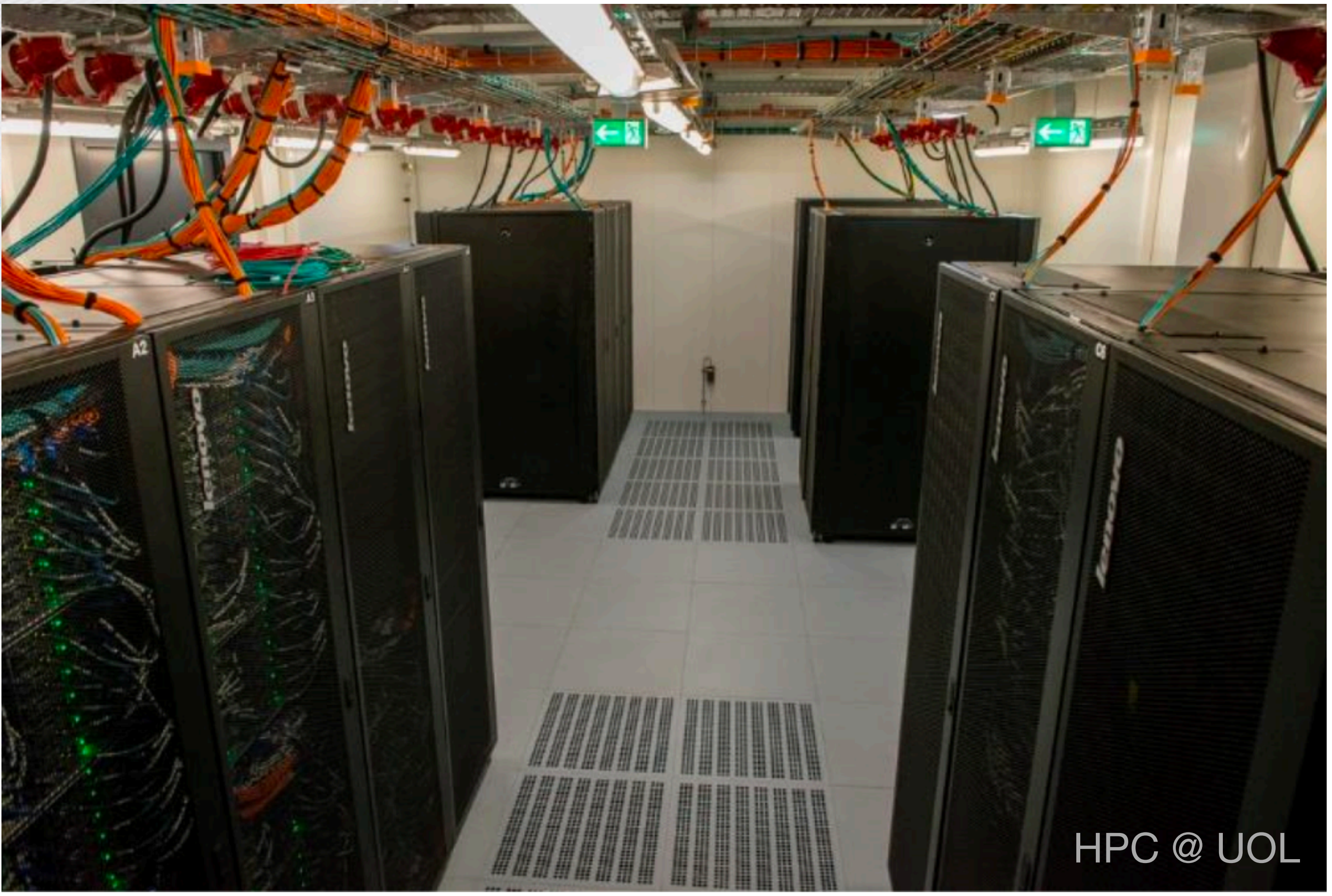
Horst Simon
NERSC/Berkeley Lab

327 compute nodes

7640 cores (CPUs)

77 TB RAM total

271 TFlop/s



HPC @ UOL

Advantages of command line / scripting tools

- Highly flexible
- Can be automated and combined into complex workflows
- Reproducible, easy to document
- Can run on high performance computers

Accessing the cluster from the command line (ssh)

Windows

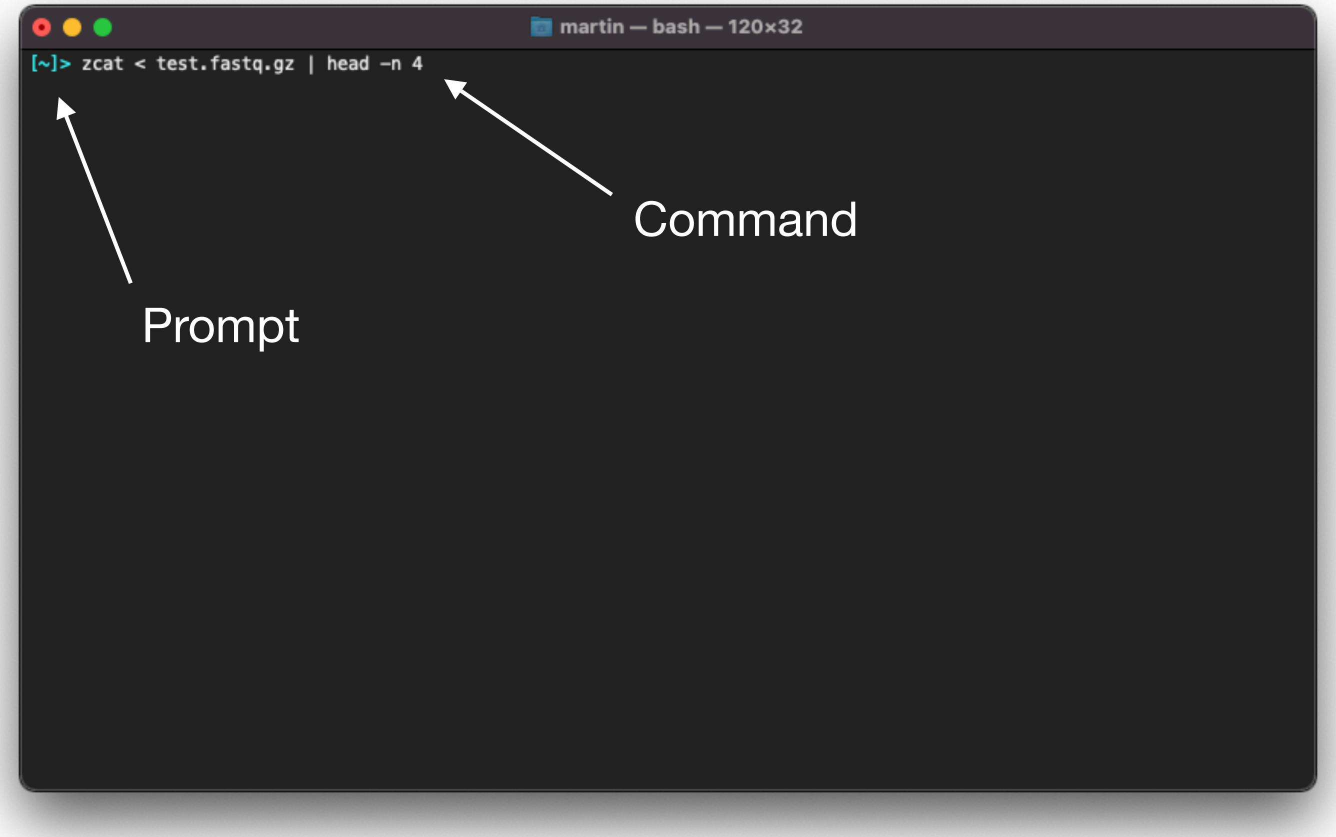
- launch git bash from Start menu
- alternatively, install Windows Subsystem for Linux (WSL) on Windows 10 or above (see https://learn.microsoft.com/en-us/windows/wsl/install)

macOS

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

Typical usage

```
command [-options] [file]
```



```
[~]> zcat < test.fastq.gz | head -n 4
```

Get set up on the HPC cluster

Connect to login node

```
# Pick and write down a course account id and password (passed around)
ssh -X user1234@rosa.hpc.uni-oldenburg.de
```

Download course materials to cluster account using git

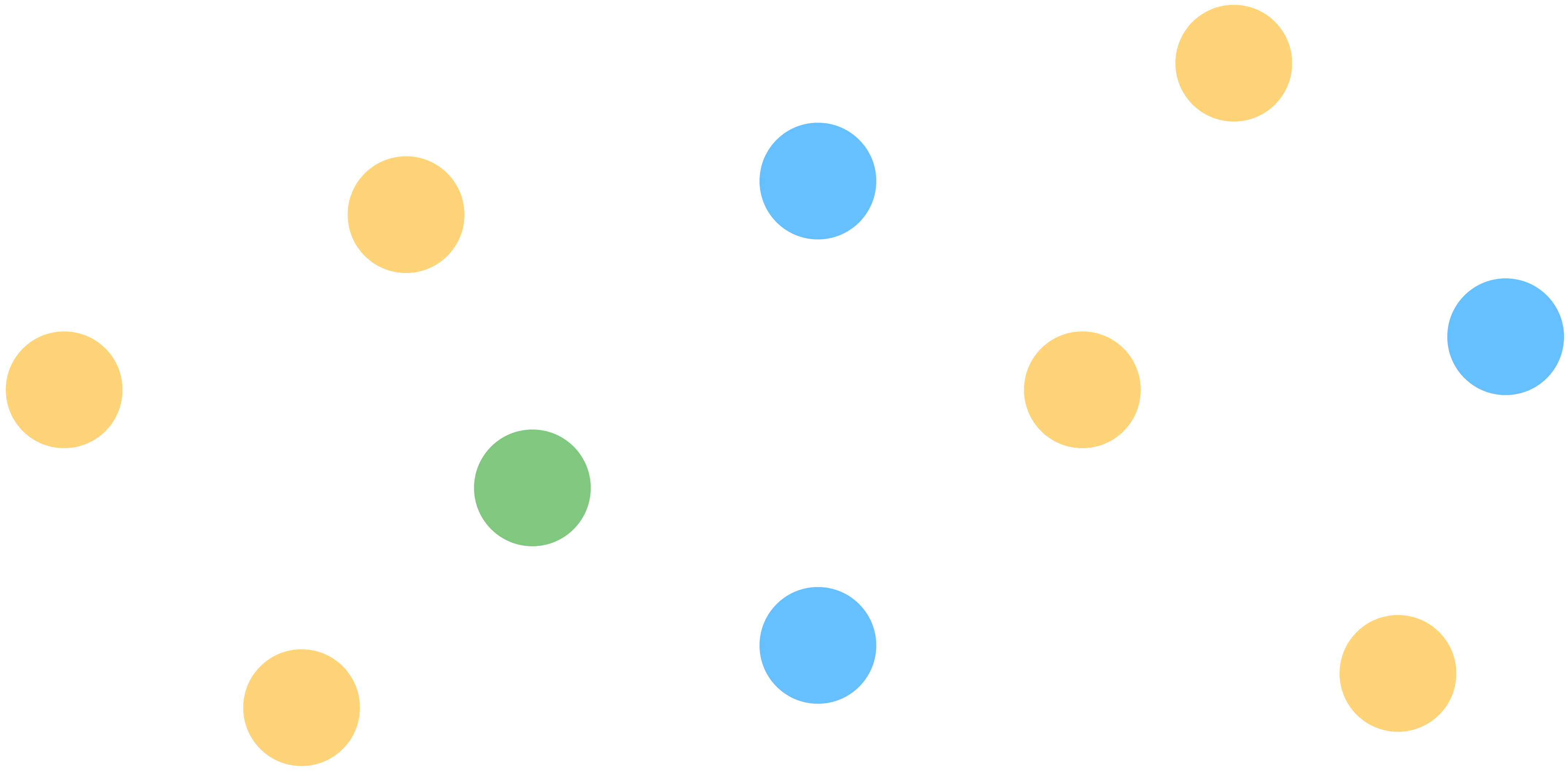
```
git clone https://github.com/mhelmkampf/meg25.git
```

Hardy-Weinberg Equilibrium

Exercise 1

Is this population in HWE?

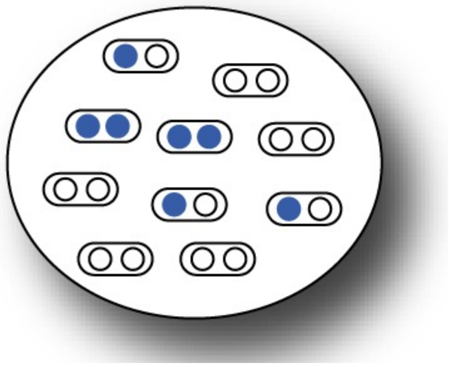
Diploid, 1 locus, 2 co-dominant alleles (yellow, blue)

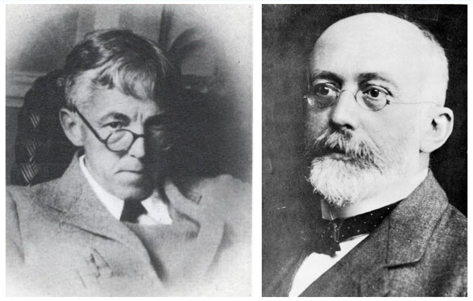


HARDY-WEINBERG (1908)

Godfrey H. Hardy (1877-1947)

Wilhelm Weinberg (1862-1937)



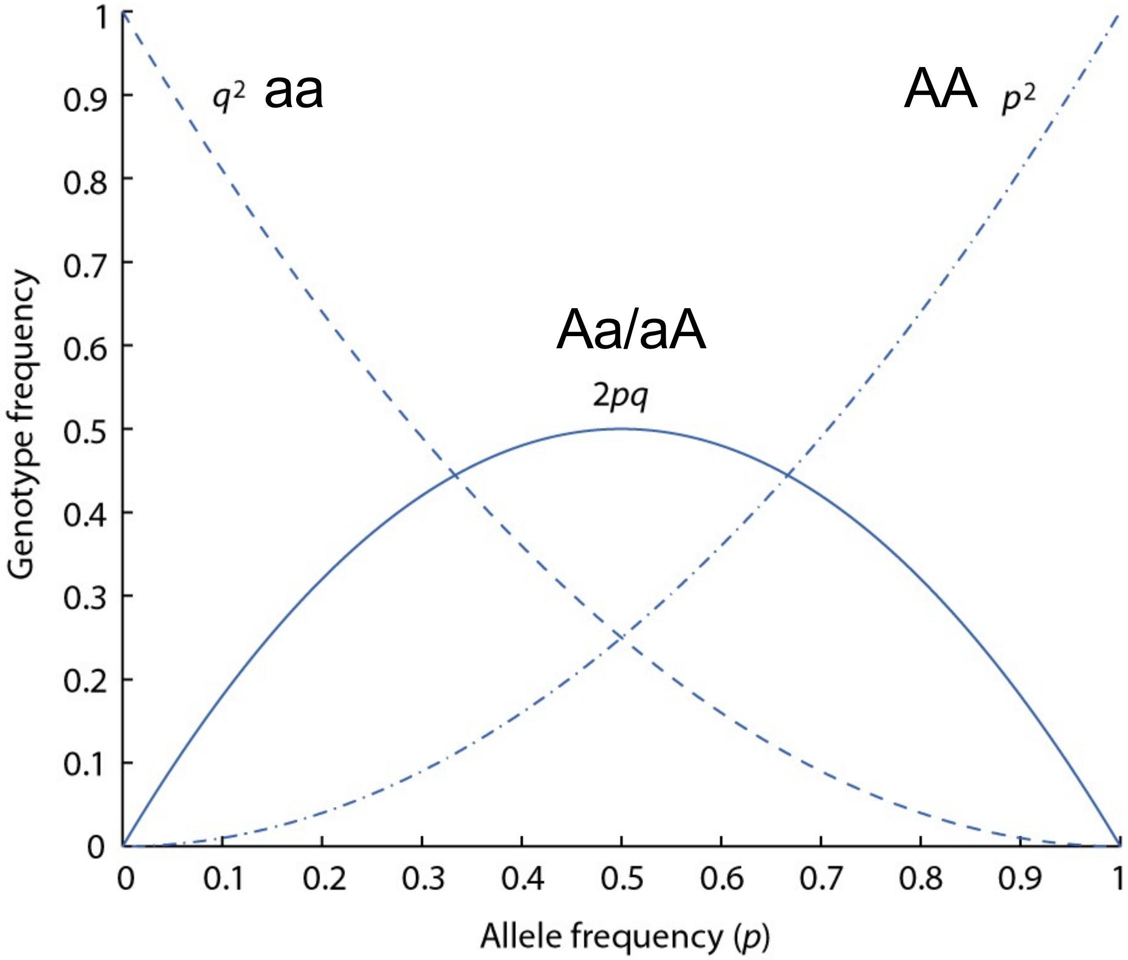


Establish the relationship between allele frequencies and genotype frequencies in a population

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

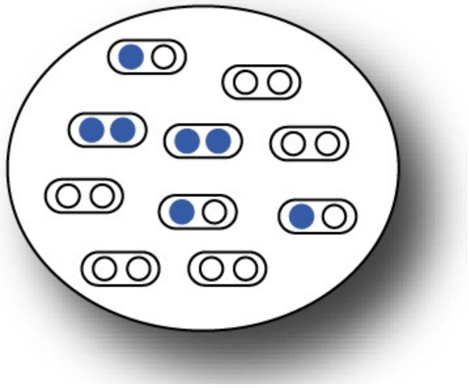
AA Aa/aA aa

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



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 −> *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 −> reduces bias

May be extended to *k* alleles

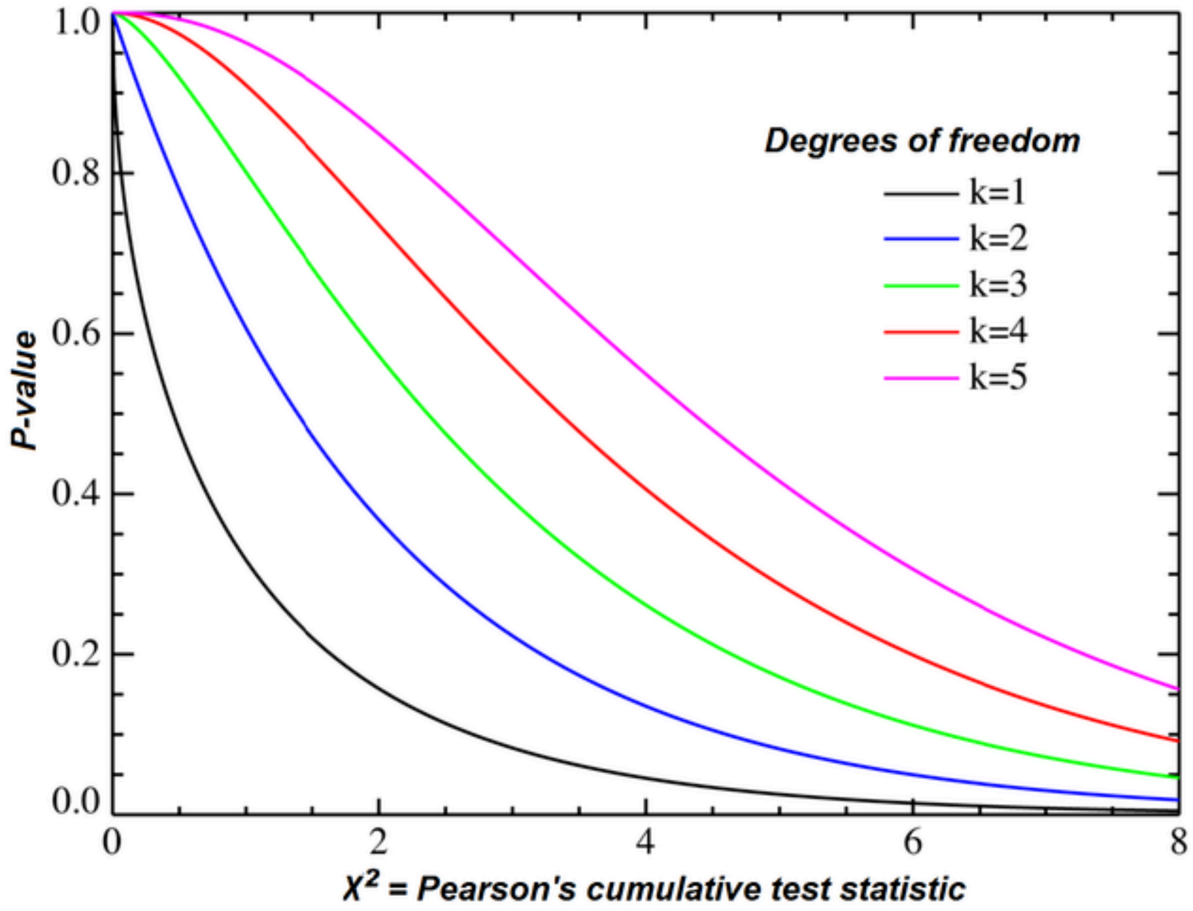
Pearson’s chi-squared test

Exercise 1

Chi-square statistic:

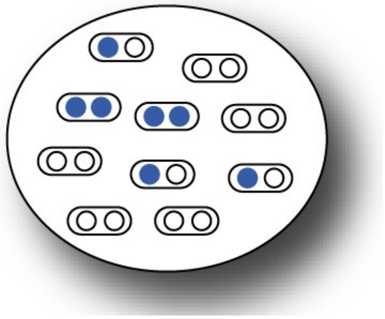
$$\chi^2 = \sum_{i=1}^{n} \frac{(O_i - E_i)^2}{E_i}$$

Chi-square distribution:



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
- ...