

# Marine Ecological Genetics

## 02. Hardy-Weinberg equilibrium Computer practical

- Calculate allele and genotype frequencies
- Test for Hardy-Weinberg equilibrium
- Get familiar with microsatellite data
- Learn to interpret HW test results

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# Access files for practical

Download files from GitHub:

<https://github.com/mhelmkamp/meg24.git>

Alternatively, run git from terminal:

```
git clone https://github.com/mhelmkamp/meg24.git
```

Open R script called **02\_hwe.R** in RStudio

# Is this population in Hardy-Weinberg equilibrium?

## Exercise 1

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

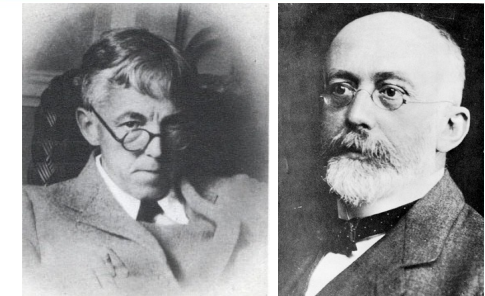
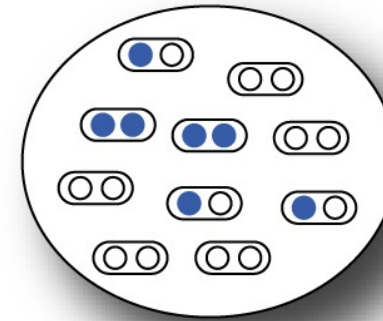




## HARDY-WEINBERG (1908)

Godfrey H. Hardy (1877-1947)

Wilhelm Weinberg (1862-1937)

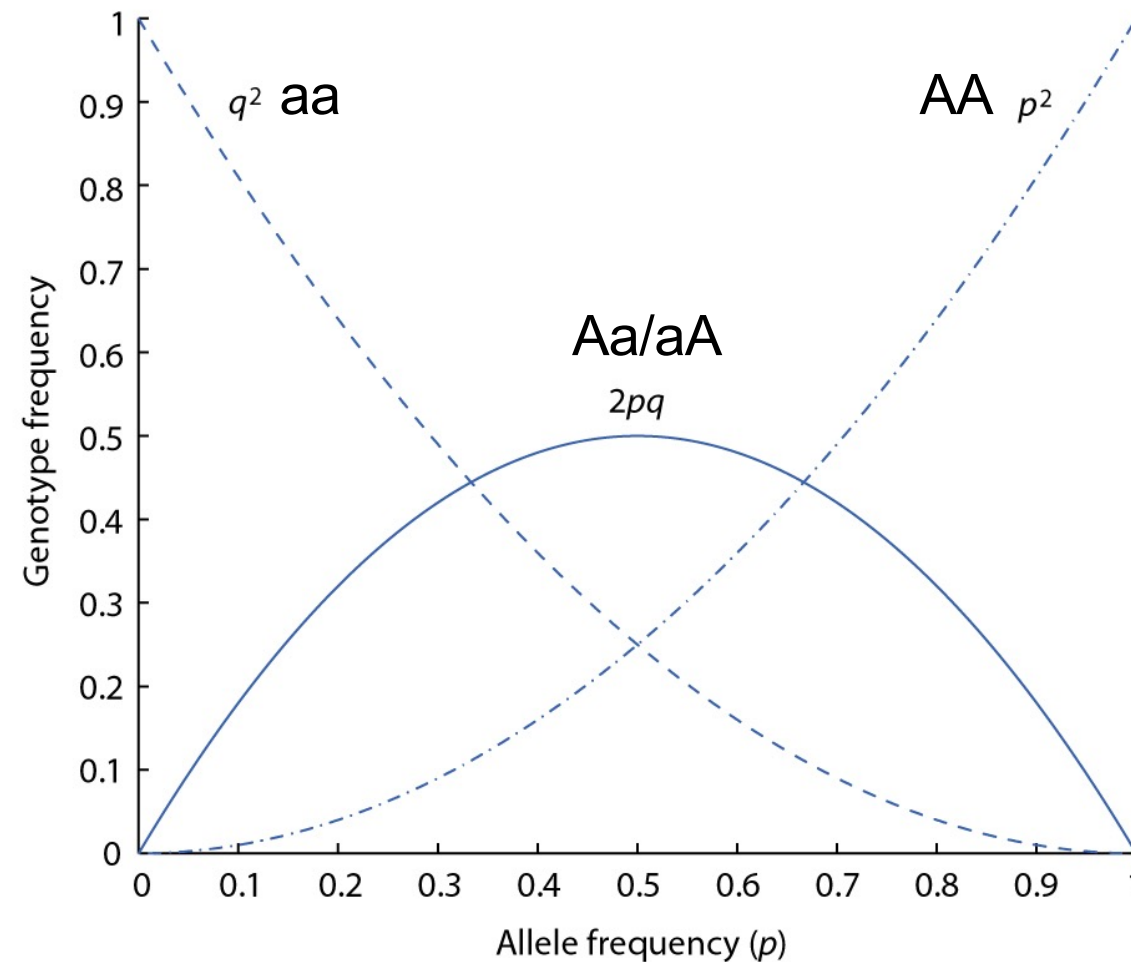


*Establish the relationship between allele frequencies and genotype frequencies in a population*

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

AA    Aa/aA    aa

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



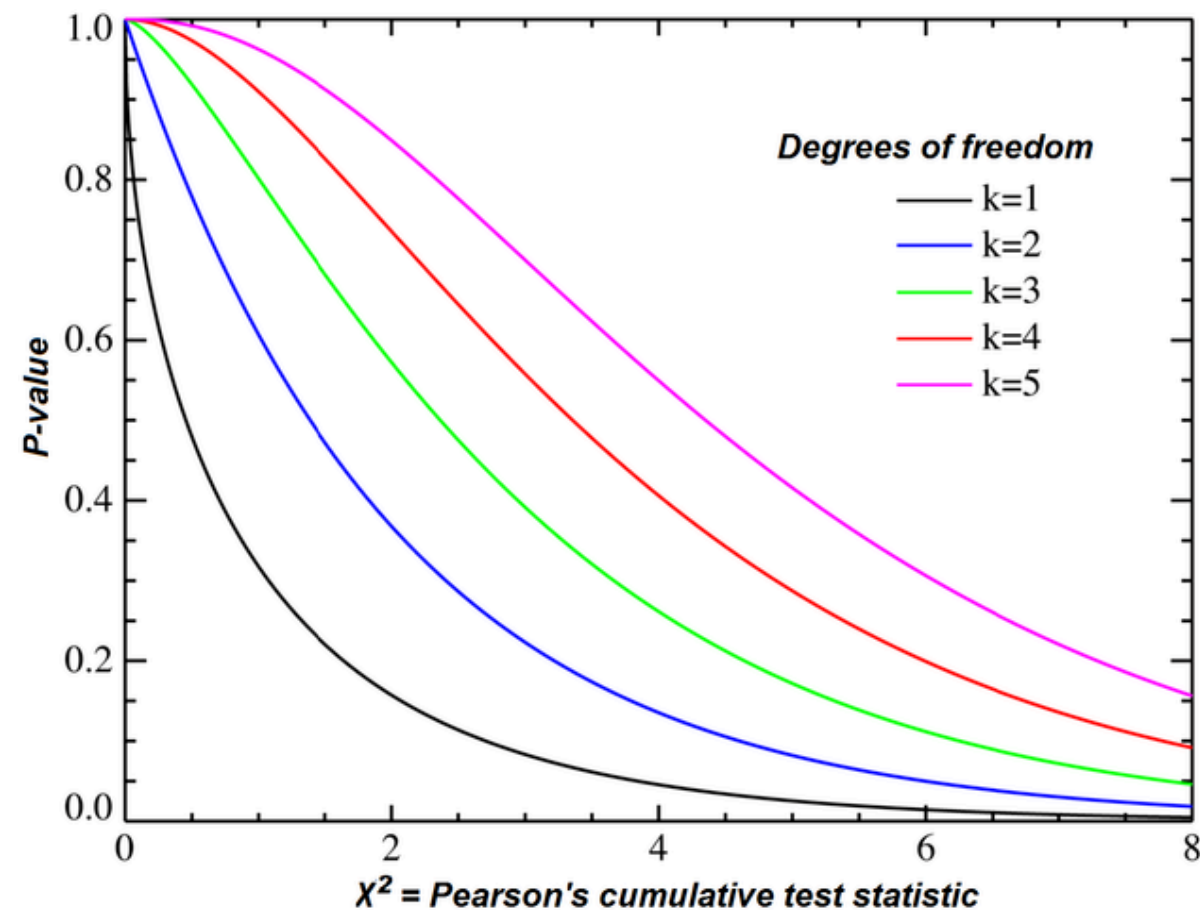
# Pearson's chi-squared test

## Exercise 1

Chi-square statistic:

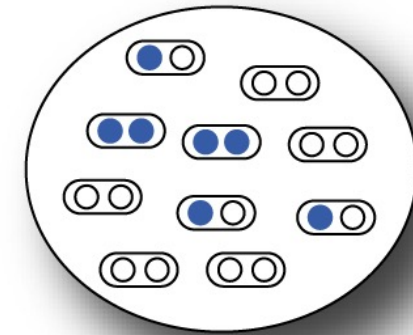
$$\chi^2 = \sum_{i=1}^n \frac{(O_i - E_i)^2}{E_i}$$

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)

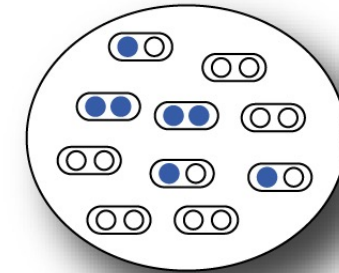
May be averaged over several loci  $\rightarrow$  reduces bias

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

yellowblue.txt

Example data

Color

POP

ind01, yy

ind02, yy

ind03, yy

ind04, yy

ind05, yy

ind06, yy

ind07, yb

ind08, bb

ind09, bb

ind10, bb

puella\_barbados.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

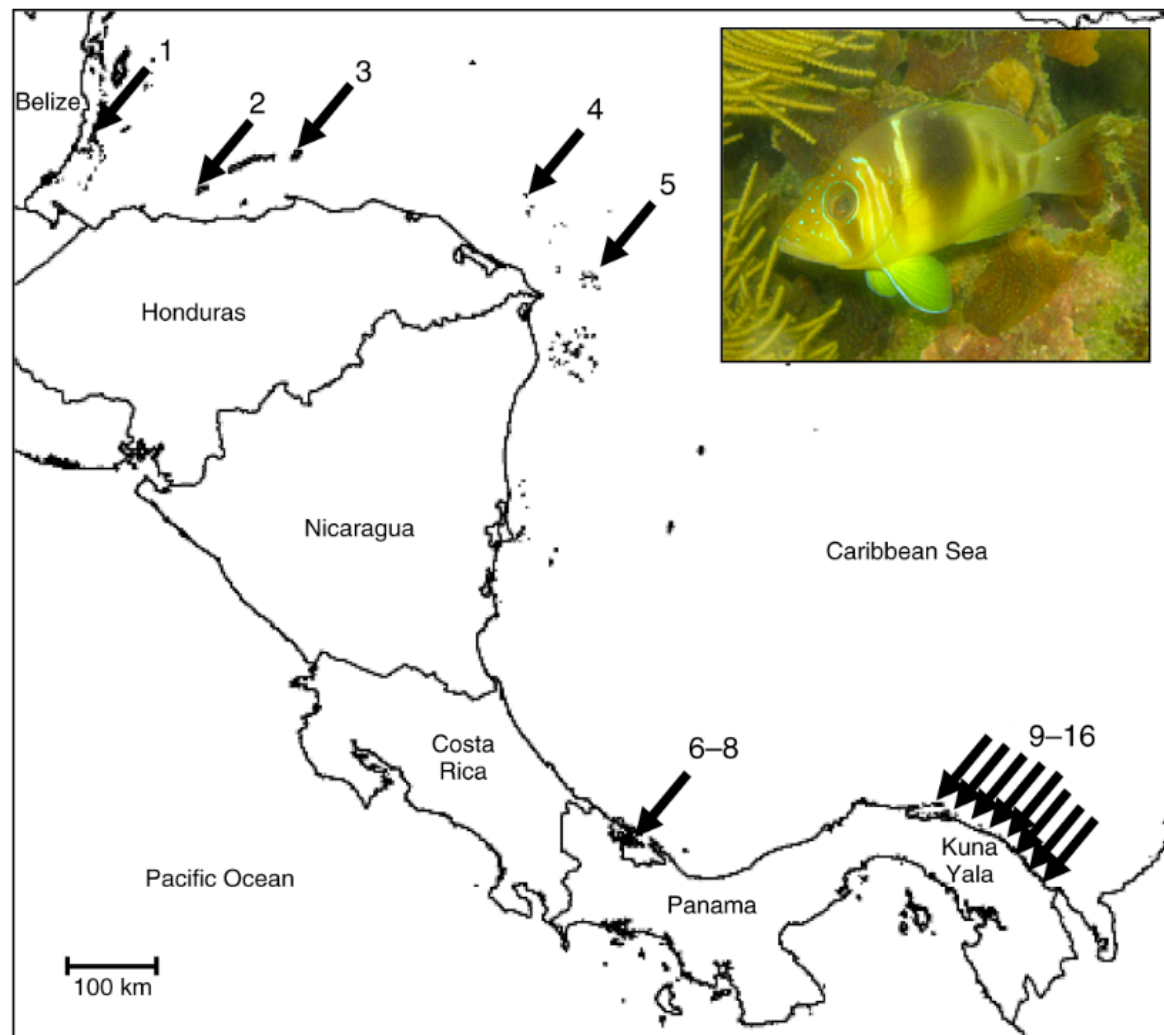
Sample / population

Alleles (000 = missing data)



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

## Exercise 3



*Ecology*, 90(11), 2009, pp. 3087–3098  
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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

# Take-home messages

- Testing for HWE can tell us whether a population is behaving like an ideal population or not
- Tests should be conducted over multiple loci, because not all loci may show the same pattern with respect to HWE
- Microsatellites are a widely used type of marker in population genetics