Wahlund Effect

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Population subdivision

Genotype | A_1A_1 | A_1A_2 | A_2A_2
:——-: | : —— : | :——-: | :——-: |
sub-pop1 | 64 | 32 | 4 |
sub-pop2 | 4 | 32 | 64 |
Total | 68 | 64 | 68 |

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The frequencies of the A_1 allele in sub-pop1 and sub-pop2:

$$p_1 = \frac{2 \times 64 + 32}{2 \times 100} = 0.8$$

$$p_2 = \frac{2 \times 4 + 32}{2 \times 100} = 0.2$$

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The frequency of the A_1 allele in the combined population:

$$\bar{p} = \frac{2 \times 68 + 64}{2 \times 200} = 0.5$$

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The expected value of heterozygotes for the combined population is:

$$2\bar{p}\bar{q} \times n = 2 \times 0.5 \times 0.5 \times 200 = 100$$

Wahlund Effect

The *perceived deficiency* of heterozygotes due to treating two different populations as one — the **Wahlund effect**. > Wahlund, 1928

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```
geth <- function(p){return(2*p*(1-p))}
p <- seq(0, 1, by=0.01)
plot(p, geth(p), type="l", lwd=3, col="red", xlab="Allele freq (p)", ylab="Heterozygosity (H)")
lines(c(0.2, 0.2), c(0, geth(p=0.2)), lty=2, lwd=3) # add a line segment
lines(c(0, 0.2), c(geth(p=0.2), geth(p=0.2)), lty=2, lwd=3)
lines(c(0.4, 0.4), c(0, geth(p=0.4)), lty=2, lwd=3) # add a line segment
lines(c(0, 0.4), c(geth(p=0.4), geth(p=0.4)), lty=2, lwd=3)
lines(c(0.3, 0.3), c(0, geth(p=0.3)), lty=2, lwd=3)
lines(c(0, 0.3), c(geth(p=0.3), geth(p=0.3)), lty=2, lwd=3, col="blue")
lines(c(0.2, 0.4), c(geth(p=0.2), geth(p=0.4)), lty=1, lwd=3, col="blue")
lines(c(0, 0.3), c(mean(c(geth(p=0.2), geth(p=0.4))), mean(c(geth(p=0.2), geth(p=0.4)))), lty=2, lwd=3,
```
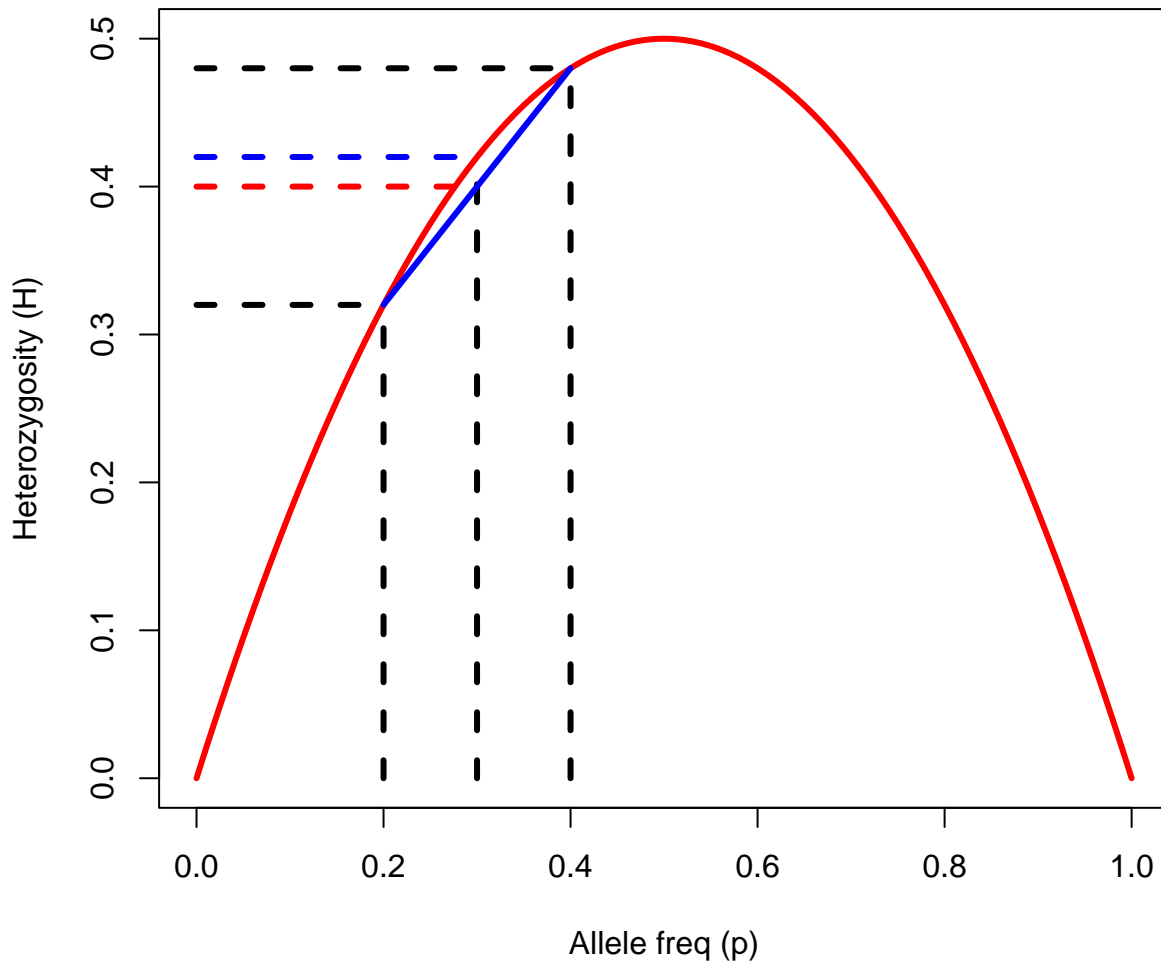

Wahlund Effect

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- The blue dashed horizontal segment is the $H_{exp} = 2\bar{p}\bar{q}$
- The red dashed horizontal segment is the H_{obs}

        – mean value of the H_1 and H_2

- Because the curve is concave downward, H_{obs} is always less than H_{exp}

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Even if subpopulations are **partially isolated**, the Wahlund effect is held true.