

Models

Models

- Intentional simplification of complex relationships
 - Eliminate extraneous detail, focus on key parameters
 - Appropriate and useful first approximations
- Evaluate fit of data to model
 - Poor fit may implicate violation of model assumptions
 - Refining of models tells us which parameters most important
- Population genetics relies heavily on mathematical models
 - Specify the mathematical relationships among parameters that characterize a population

Random Mating

- One of the most important models in population genetics
- Frequency of mating pairs determined by genotype frequencies

Male Genotype

Frequency

A_1A_1 (P_M)

A_1A_2 (H_M)

A_2A_2 (Q_M)

Female Genotype Frequency

A_1A_1 (P_F)

A_1A_2 (H_F)

A_2A_2 (Q_F)

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$P_M P_F$

$P_M H_F$

$P_M Q_F$

$H_M P_F$

$H_M H_F$

$H_M Q_F$

$Q_M P_F$

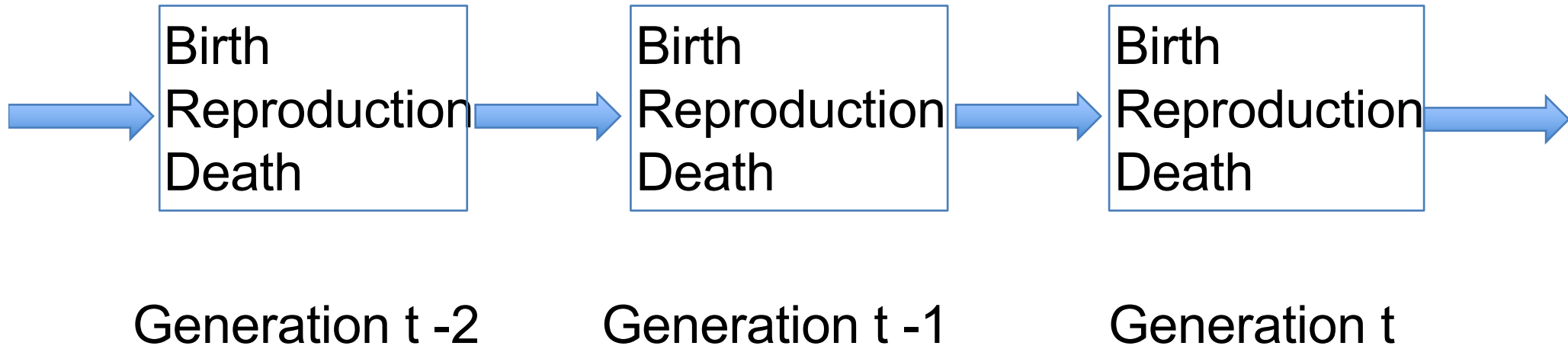
$Q_M H_F$

$Q_M Q_F$

Random Mating

- One of the most important models in population genetics
- Frequency of mating pairs determined by genotype frequencies
- Also called 'panmictic' model

Non-overlapping Generations



Hardy-Weinberg Model

- Both models convenient first approximations for complex populations
- What happens when we combine them?
- What are consequences of random mating in a non-overlapping generation model?



Godfrey Harold Hardy



Wilhelm Weinberg

HW Model Assumptions

- Discrete generations
- Random mating
- Sexual reproduction
- Diploid
- Bi-allelic locus
- Allele frequencies equal in males, females
- Large population size
- No migration
- No mutation
- No selection

Hardy-Weinberg Principle

- One of first major principles in population genetics
- Describes relationship between **genotype** frequency and **allele** frequency
 - Equilibrium state
- Autosomal locus with alleles A, a
 - Frequencies of A, a: p , q
- Genotypes AA, Aa, aa

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Hardy-Weinberg Principle

Frequency(A) = p

Frequency(a) = q

Frequency(AA) = P

Frequency(Aa) = H

Frequency(aa) = Q

Mating

AA x AA

AA x Aa

AA x aa

Aa x Aa

Aa x aa

aa x aa

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Frequency of Mating

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$$p' = P' + \frac{1}{2}H'$$

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$$p' = P' + \frac{1}{2}H' = p^2 + \frac{1}{2}2pq = p(p + q)$$

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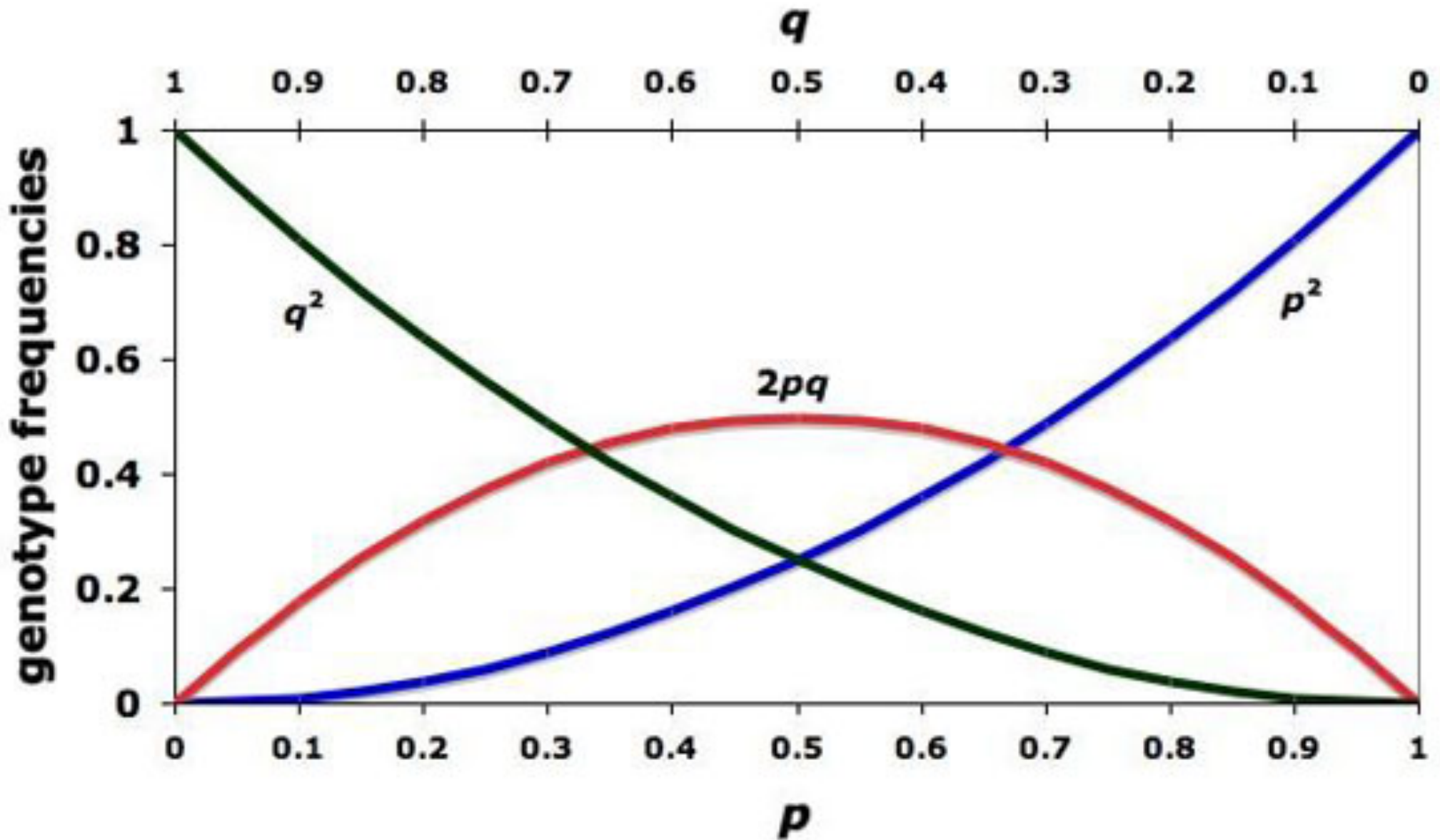
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$$p' = P' + \frac{1}{2}H' = p^2 + \frac{1}{2}2pq = p(p + q) = p$$

$$q' = Q' + \frac{1}{2}H' = q^2 + \frac{1}{2}2pq = q(q + p) = q$$

- Allele frequency unchanged across generations
 - Mendelian inheritance itself preserves variation
- HWE achieved in ONE generation
 - Equal allele frequencies in males & females, discrete generations

HWE Genotype Frequencies



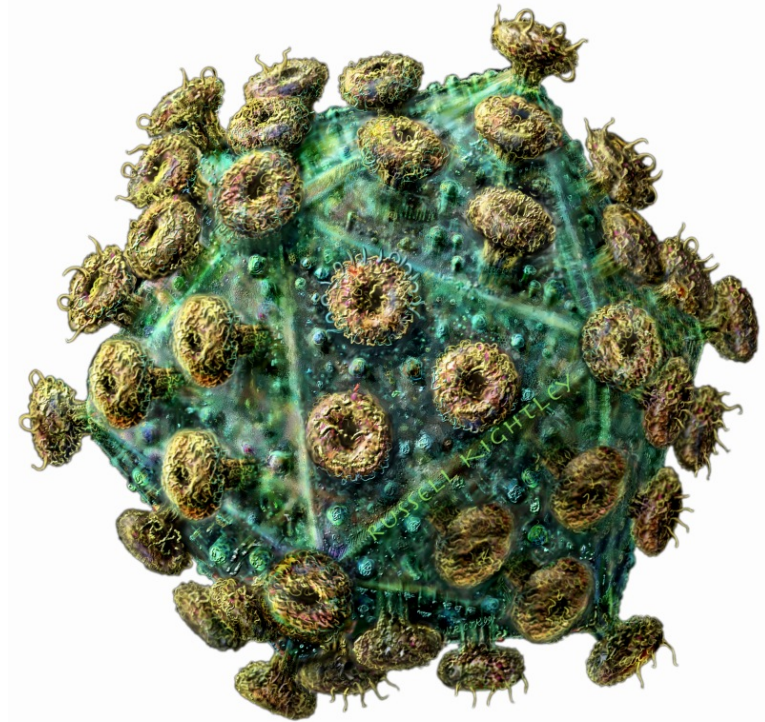
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 - HW frequencies: p^2 , $2pq$, q^2
- Once at HWE, allele & genotype freq constant

Example test of HWE

- $CCR5\Delta$
- 338 individuals sampled
 - Denmark, Germany

	Observed	Expected
CCR5/CCR5	265	
CCR5/CCR5 Δ	66	
CCR5 Δ /CCR5 Δ	7	



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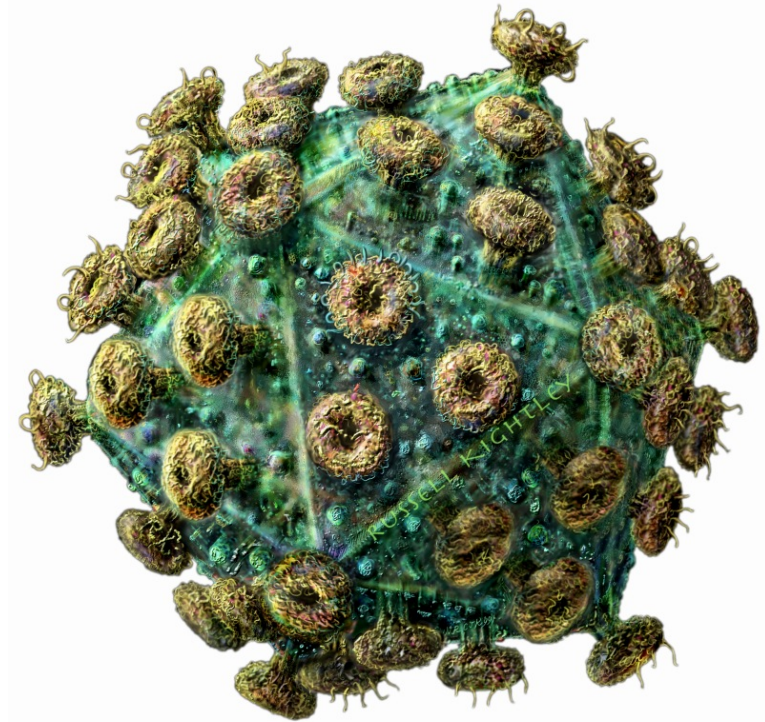
$$\hat{p} = \frac{265 + \frac{1}{2}(66)}{338} = 0.882$$

$$P = \hat{p}^2 = (0.882)^2 = 0.78$$

$$H = 2\hat{p}\hat{q} = 2(0.882)(0.118) = 0.21$$

$$\hat{q} = \frac{7 + \frac{1}{2}(66)}{338} = 0.118$$

$$Q = \hat{q}^2 = (0.118)^2 = 0.01$$



Example test of HWE

- $CCR5\Delta$
- 338 individuals sampled
 - Denmark, Germany

	Observed	Expected
CCR5/CCR5	265	262.9
CCR5/CCR5 Δ	66	70.4
CCR5 Δ /CCR5 Δ	7	4.7

$$\chi^2 = \sum \frac{(\text{observed} - \text{expected})^2}{\text{expected}}$$

$$\chi^2 = \frac{(265 - 262.9)^2}{262.9} + \frac{(66 - 70.4)^2}{70.4} + \frac{(7 - 4.7)^2}{4.7}$$

$$\chi^2 = 1.42$$

df = Number of data classes - number parameters estimated from data - 1

$$df = 3 - 1 - 1 = 1$$

$$P = 0.25$$

