- Gene pool
- Allele Frequencies
- Hardy-Weinberg Equilibrium
- HW assumptions
- Testing for HW
- Inbreeding



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Gene pools

- A gene pool is the collection of different *genes* within a population.
- Gene pool is the sum of all the *alleles* at all of the genes of a population.



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Allele Frequencies

• Consider a locus with two possible alleles (A and a)

A = p, a = q

• We can estimate the frequency of AA genotype by dividing the number of AA individuals by total number of individuals in the population.

$$AA + Aa + aa = 1$$

• Allele Frequencies:

 $p = f(AA) + \frac{1}{2}f(Aa) = frequency of A$

q= f(aa) + $\frac{1}{2}$ f(Aa) = 1 - p frequency of a

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Hardy-Weinberg Equilibrium

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

 p^2 = dominant homozygous frequency (AA) 2pq = heterozygous frequency (Aa) q^2 = recessive homozygous frequency (aa)

Expected genotype frequencies (random mating) $p(AA)=p^2$, pq(Aa)=2pq, $q(aa)=q^2$



p= f(AA) +
$$\frac{1}{2}$$
 f (Aa) = frequency of A
p = (3/14) + $\frac{1}{2}$ (8/14) = 0.5
q = 1-0.5 = 0.5

aa = 3

Aa = 8

$$AA = 3$$



Hardy-Weinberg Equilibrium

N = 14, AA = 3 , Aa = 8, aa = 3

p = 0.5 q = 0.5

Expected genotype frequencies :

 $p(AA)=p^2$, p(Aa)=2pq, $p(aa)=q^2$

$$p^2$$
 + 2pq + q²
0.5² + 2(0.5*0.5) + 0.5² = 0.25, 0.5, 0.25



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Hardy-Weinberg assumptions

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Hardy-Weinberg equilibrium

	Genoty	pe frequ	Gene frequencies		
Generation	A/A	A/a	a/a	A	a
t_0	0.64	0.32	0.04	0.8	0.2
t ₁	0.64	0.32	0.04	0.8	0.2
• Hardy-Wei	nberg Equ		N-1078		
t_n	0.64	0.32	0.04	0.8	0.2

Genetic variation is neither created nor destroyed

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• Genes out of expected proportions indicate that at least one of the HW assumptions is not true.

Banged South and Sta	enzedo mas			
aligners permit	A/A	A/G	G/G	Sum
Observed number	17	55	12	84
Observed frequency	0.202	0.655	0.143	1
Expected frequency	0.281	0.498	0.221	1
Expected number	23.574	41.851	18.574	84
(Observed - expected) ² /expected	1.833	4.131	2.327	8.29

$$X^2 = \sum \frac{(O-E)^2}{E}$$

Source: International HapMap Project (www.hapmap.org).

Observed frequency $p^2 = 17/84 = 0.202$ 2pq = 55/84 = 0.655 $q^2 = 12/84 = 0.143$ $p = f(AA) + \frac{1}{2}f(AG) = 0.202 + \frac{1}{2}0.655 = 0.53$ q = 1-p = 0.47

Expected	d freq	uency			
p ²	+	2pq	+	q ²	= 1
0.53 ²	+	2 (0.53*0.47)	+	0.47 ²	
0.281	+	0.498	+	0.221	= 1

Bang ad Source and the	and the man	Genotypes					
	A/A	A/G	G/G	Sum			
Observed number Observed frequency	17 0.202	55 0.655	12 0.143	84 1			
Expected frequency Expected number	0.281 23.574	0.498 41.851	0.221 18.574	1 84			
(Observed - expected) ² /expected	1.833	4.131	2.327	8.29			
Source: International HapMap Project (w	ww.hapmap.o	rg).	Not the second s				

$$X^{2} = \sum \frac{(O-E)^{2}}{E} = (17 - 23.574)^{2}/23.574 = 1.833$$

Edite of some or the	Service And			
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	Degree of	ree of Probability of Exceeding the Critical Value								
	Freedom	0.99	0.95	0.90	0.75	0.50	0.25	0.10	0.05	0.01
We use 1 df	1	0.000	0.004	0.016	0.102	0.455	1.32	2.71	3.84	6.63
	2	0.020	0.103	0.211	0.575	1.386	2.77	4.61	5.99	9.21
	3	0.115	0.352	0.584	1.212	2.366	4.11	6.25	7.81	11.34
	4	0.297	0.711	1.064	1.923	3.357	5.39	7.78	9.49	13.28
	5	0.554	1.145	1.610	2.675	4.351	6.63	9.24	11.07	15.09
	6	0.872	1.635	2.204	3.455	5.348	7.84	10.64	12.59	16.81
	7	1.239	2.167	2.833	4.255	6.346	9.04	12.02	14.07	18.48
	8	1.647	2.733	3.490	5.071	7.344	10.22	13.36	15.51	20.09
	9	2.088	3.325	4.168	5.899	8.343	11.39	14.68	16.92	21.67
	10	2.558	3.940	4.865	6.737	9.342	12.55	15.99	18.31	23.21

Sum
84
-Bt slder 1
1
84
8.29

We use 1 df



surver international maphiap mobile (in in intaphiap.org).

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Bias in mate choice: isolation by distance



http://academygenbioii.pbworks.com/

Bias in mate choice: assortative mating



en.ppt-online.org

Bias in mate choice: inbreeding





www.slideshare.net

Inbreeding or mating between relatives!

Review

Graphical Representation of the Hardy-Weinberg Principle

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