Lecture Handout 2

Announcements:

Please read chapters 1 & 2 ; read the other chapters before their date on the syllabus

Problems at the end of chapter 1: #1, 2, 5, 6 check answers at back of book

Bring a calculator to exams

Hedrick Table 2.1

TABLE 2.1 A list of some of the more commonly used software packages used in population genetics and related topics, their websites (subject to change), and the analyses and tests that they carry out. All of these packages are free except PAUP.

Software Package	Address	Analyses and Tests
Arlequin	http://lgb.unige.ch/arlequin/	AMOVA, MSN, nucleotide diversity, mismatch distribution, linkage disequilibrium, Hardy–Weinberg, neutrality tests, Mantel test, pairwise population genetic distances
DnaSP (DNA sequence polymorphisms)	http://www.ub.es/dnasp/	Sequence variation within and between populations, linkage disequilibrium, recombination, gene flow, gene conversion, tests of neutrality
GDA (genetic data analysis)	http://lewis.eeb.uconn.edu/lewishome/software.html	Linkage disequilibrium, Hardy–Weinberg, genetic distances, and hierarchical F-statistics
Genepop	http://wbiomed.curtin.edu.au/genepop/	Linkage disequilibrium, Hardy–Weinberg, gene flow, F-statistics
LAMARC (likelihood analysis with metropolis algorithm using random coalescence)	http://evolution.genetics.washington.edu/lamarc.html	Maximum likelihood estimates of effective population size, gene flow, growth parameters, and recombination
MEGA (molecular evolutionary genetics analysis)	http://evolgen.biol.metro-u.ac.jp/MEGA	Pairwise distance matrices, nonsynonymous/synonymous ratios, neutrality tests, phylogenetic analyses
PAUP (phylogenetic analysis using parsimony)	http://paup.csit.fsu.edu/	Phylogenetic analysis using maximum likelihood, parsimony, and distance methods
PHYLIP (phylogeny inference package)	http://evolution.genetics.washington.edu/phylip.html	Phylogenetic analysis using maximum likelihood, parsimony, and distance methods
PowerMarker	http://152.14.14.48/	Linkage disequilibrium, Hardy–Weinberg, F-statistics, coancestry matrices, phylogenetic analysis, designed especially for SSR/SNP data analysis

If Mendelian laws of genetics apply to people, then why doesn't 3/4 of the population display the dominant trait bracydactyly?

Reginald Crundall Punnett

Punnett Square

		Maternal	
		B	b
Paternal	B	BB	Bb
	b	Bb	bb

Hardy-Weinberg Principle (p63)

Assumes a random mating population: 'group in which the probability of a mating between individuals of particular genotypes or phenotypes is equal to the product of their individual frequencies in the population.'
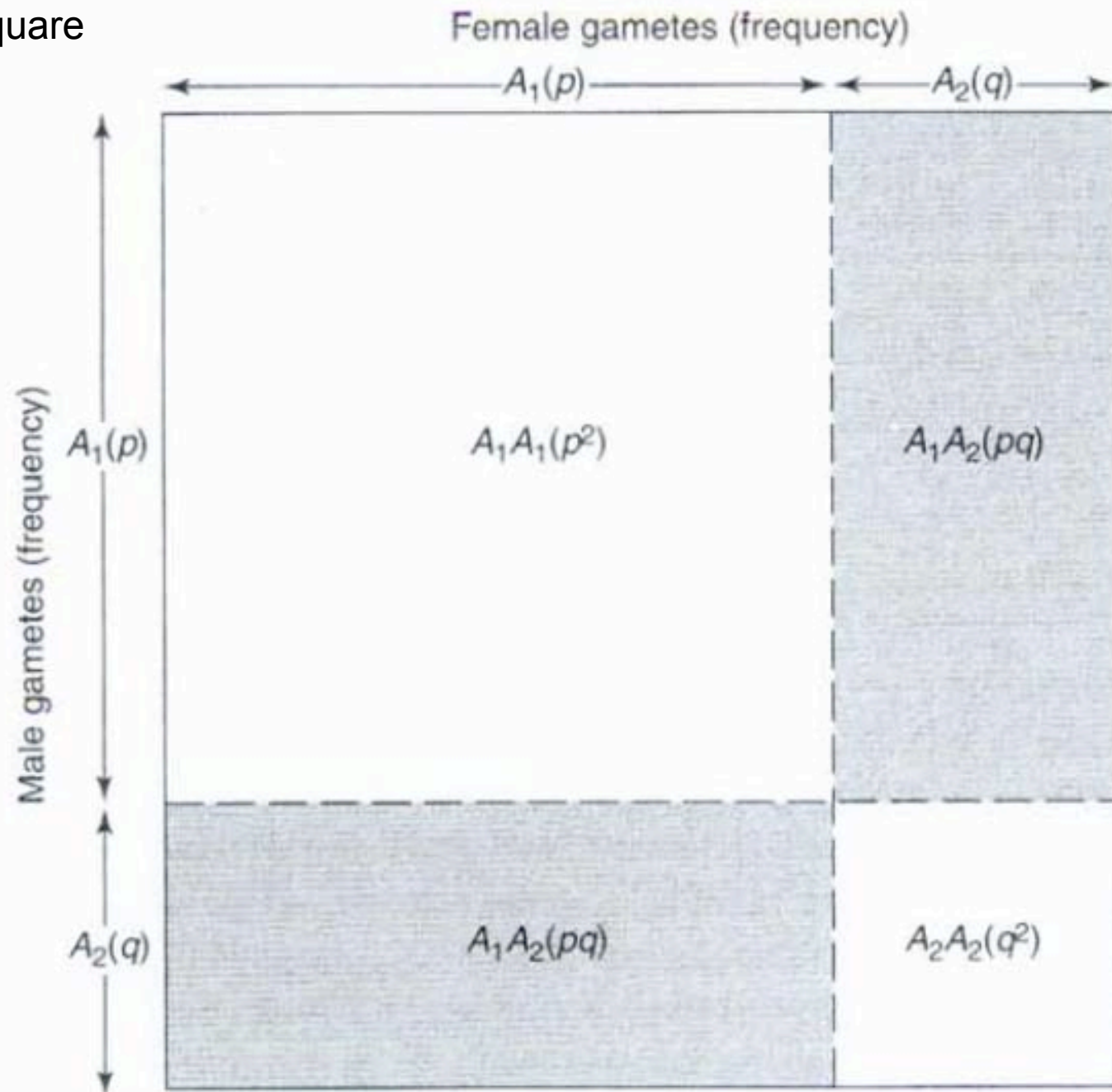
Hardy-Weinberg Principle (p64)

- 'after one generation of random mating, single-locus genotype frequencies can be represented by a binomial (with two alleles) or multinomial (with multiple alleles) function of the allele frequencies.'

Godfrey Harold Hardy

Wilhelm Weinberg

Unit Square

Female gametes (frequency)

$A_1(p)$ $\longrightarrow$ $\longleftarrow$ $A_2(q)$ $\longrightarrow$

Male gametes (frequency)

$A_1(p)$

$A_2(q)$

$A_1A_1(p^2)$

$A_1A_2(pq)$

$A_1A_2(pq)$

$A_2A_2(q^2)$

H-W, two alleles (p64)

- Autosomal locus
- Two alleles, A_1 and A_2, with frequencies of p and q, respectively.
- p + q = 1
- Three genotypes
  - A_1A_1, A_1A_2, A_2A_2 with frequencies of
  - p^2, 2pq, q^2
- **$p^2 + 2pq + q^2 = 1$**

- Three genotypes
  - A_1A_1, A_1A_2, A_2A_2 with frequencies of
  - P, H, and Q

$p = P + ½ H$

$q = Q + ½ H$

Important:

allele frequencies are lower case letters

genotype frequencies upper case letters

Mating types
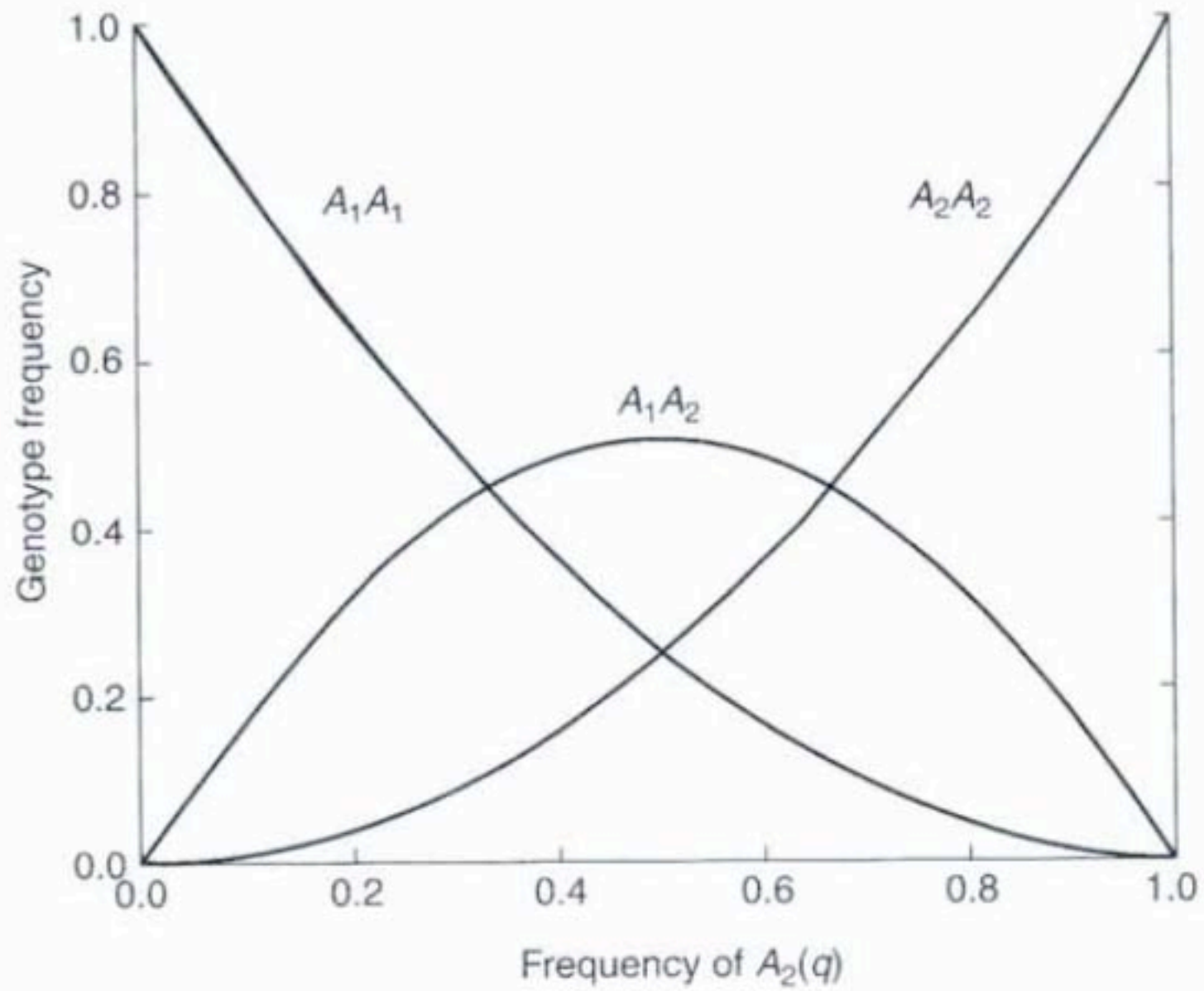
Mating type	Freq	Progeny		
		A_1A_1	A_1A_2	A_2A_2
$A_1A_1 \times A_1A_1$	P^2	1		
$A_1A_1 \times A_1A_2$	$2PH$	1/2	½	
$A_1A_1 \times A_2A_2$	$2PQ$		1	
$A_1A_2 \times A_1A_2$	H^2	1/4	1/2	¼
$A_1A_2 \times A_2A_2$	$2HQ$		1/2	½
$A_2A_2 \times A_2A_2$	Q^2			1
Total	1	$(P+1/2H)^2=p^2$	$2pq$	q^2

- Show that $(P + 1/2H)^2 = p^2$
- Show that $2(P + 1/2H)(Q + 1/2H) = 2pq$
- Show that $(Q + 1/2H)^2 = q^2$

What is the most frequent genotype?(p67)

- If $q < 1/3$ then A_1A_1.
- If $q > 2/3$ then A_2A_2.
- If $q > 1/3$ and $< 2/3$ then A_1A_2.
- See Figure 2.2

What is maximum heterozygote frequency? (p68)

- Define function.

  $2pq = 2q(1-q)$

- Equate derivative to zero.

  $d[2q(1-q)]/dq = 2- 4q = 0$

- Solve for q.

- Maximum at q = .5

Genotypic frequencies

- N_{11} of A_1A_1 individuals
- N_{12} of A_1A_2 individuals
- N_{22} of A_2A_2 individuals
- $N = N_{11} + N_{12} + N_{22}$

- $P = N_{11}/N$
- $H = N_{12}/N$
- $Q = N_{22}/N$

Gene-counting method (p69)

- $\hat{p} = (N_{11} + 1/2N_{12})/N$

- $\hat{q} = (N_{22} + 1/2N_{12})/N$

- See example 2.1 and table 2.4

Multiple alleles (p70)

- Genotype A_iA_i with frequency p_{ii}
- Genotype A_iA_j with frequency p_{ij}
- Allele A_i with frequency p_i
- $p_i = P_{ii} + \frac{1}{2} \Sigma P_{ij}$ where $j \neq i$

Expected heterozygosity (p70)

- $H_E = 1 - \Sigma p_i^2$ = expected heterozygosity
- Maximum at equal allele frequency
- $p_i = 1/n$
- Maximum $H_E = n-1 / n$
- $H_O = \Sigma N_{ij} / N$ where $i \neq j$
- H_O = Observed heterozygosity

Hardy-Weinberg Principle (p64)

- 'after one generation of random mating, single-locus genotype frequencies can be represented by a binomial (with two alleles) or multinomial (with multiple alleles) function of the allele frequencies.'

Deviations from HW proportions (p 96): Nonrandom mating; Positive assortative mating; Negative assortative mating; Inbreeding; Small population size; Selection; Subdivided populations; Others?