HANDOUT I.2: Sex linkage and Hardy-Weinberg

Let's consider a diploid population with X-Y sex determination (females are XX; males are XY). We want to study evolution of a locus with two alleles on the X-chromosome (with no counterpart on the Y-chromosome).

Some notation:

 $p_t(t)$ = frequency of the A allele among X gametes in females in generation t;

 $p_m(t)$ = frequency of the A allele among X gametes in males in generation t.

Under the H-W assumptions, the following offspring genotype frequencies are found:

 $\begin{array}{ll} \underline{\text{Daughters}} & \underline{\text{Sons}} \\ AA: \ P_{AA}(t+1) = p_f(t) \ p_m(t) & AA: \ P_{AA}(t+1) = p_f(t) [1-p_m(t)] + p_m(t) [1-p_f(t)] & AY: \ P_{AY}(t+1) = p_f(t) \\ aa: \ P_{aa}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{aY}(t+1) = 1-p_f(t) \\ aa: \ P_{aa}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{aa}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{aa}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{aa}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{aa}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = 1-p_f(t) \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] [1-p_m(t)] & AY: \ P_{AY}(t+1) = [1-p_f(t)] \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] & AY: \ P_{AY}(t+1) = [1-p_f(t)] \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] & AY: \ P_{AA}(t+1) = [1-p_f(t)] \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] & AY: \ P_{AA}(t+1) = [1-p_f(t)] \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] & AY: \ P_{AA}(t+1) = [1-p_f(t)] \\ AA: \ P_{AA}(t+1) = [1-p_f(t)] & AY: \ P_{AA}(t+1) = [1-p_f(t)] \\ AA: \ P_{$

<u>Allele</u> frequencies among the offspring (computed from these genotype frequencies) are:

• $p_f(t+1) = \frac{1}{2} [p_f(t) + p_m(t)]$ (average of allele frequencies in both parent sexes) • $p_m(t+1) = p_f(t)$ (the allele frequency among just the *female* parents)

Evolutionary Dynamics: Suppose we have the extreme case $p_m(0) = 1$, $p_f(0) = 0$:



Unlike cases we've seen up until now, the evolutionary paths <u>oscillate</u> towards an equilibrium. What equilibrium is eventually reached? It turns out that the frequency of the A allele becomes $p_{eq} = \frac{1}{2}p_m(0) + \frac{2}{3}p_f(0)$ in both sexes. In the above case, $p_{eq} = \frac{1}{3}(1) + \frac{2}{3}(0) = \frac{1}{3}$.