Example 4.6 Suppose a die has been loaded so the numbers 1, 2, 3, 4, 5, 6 come up 10%, 10%, 20%, 30%, 10%, 20% of the time, respectively. Suppose you play a game where you win $10 each time an odd number comes up, and lose $7 each time an even number comes up. How much should you expect to win/lose after 100 tosses?

Ω = \{1, 2, 3, 4, 5, 6\}

X = payoff in dollars

X(1) = X(3) = X(5) = 10, \quad X(2) = X(4) = X(6) = -7

Two possible values of X are 10, x_1 = 10, x_2 = -7

\sum_{i=1}^{n} x_i f_i:

\begin{align*}
10 & \quad \{1, 3, 5\} & 0.1 + 0.2 + 0.1 = 0.4 \\
-7 & \quad \{2, 4, 6\} & 0.1 + 0.3 + 0.2 = 0.6
\end{align*}

Mean \( \bar{x} = \sum_{i=1}^{n} x_i f_i = 10 \times 0.4 - 7 \times 0.6 = -0.2 \)

Expect to lose on average $0.20 per toss.

For 100 tosses, expect to lose $20.

Example 4.7 Genetics and the evolution (Fisher-Haldane-Wright)

Same assumptions as Example 4.5 (Hardy-Weinberg) except that survival to maturity depends on genotype.

Start with parent generation, with allele frequencies \( p_0, q_0 \) \( (q_0 = 1 - p_0) \)

Random mating as before, but now offspring with genotype frequencies at birth:

\( x = p_0^2, \quad y = 2p_0 q_0, \quad z = q_0^2 \)

Suppose survival of these 1st generation offspring until they mate depends on genotype called "fitness".

Let \( W \) be a random variable defined on the space of genotypes \{AA, AB, BB\}.

Possible values: \( W_{AA}, W_{AB}, W_{BB} \) \( (\text{all } \geq 0) \). Usually one of these values is 1 to reference \( (e.g. W_{AA} = 1) \) and all others measure fitness relative to reference genotype.

By mating time the relative frequencies of the different genotypes \( x, y, z \) are multiplied

\[ W_{AA} x, W_{AB} y, W_{BB} z \]
To get probabilities (or frequencies) which must add to 1, divide by mean fitness
\[
W = W_{A} \cdot P(\text{individual is } AA) + W_{AB} \cdot P(\text{individual is } AB) + W_{B} \cdot P(\text{individual is } BB)
\]
\[
= W_{A} p_{A} + W_{AB} p_{A} p_{B} + W_{B} p_{B}
\]

Compute
\[
\frac{W_{A}}{W} = P(\text{AA individual survives to breeding})
\]

et cetera.

At time of mating, freq. of set A allele in gene pool of 1st generation is
\[
p_{1} = \frac{W_{A} p_{A}^2 + \frac{1}{2} W_{AB} 2 p_{A} p_{B}}{W} = \frac{W_{A} p_{A}^2 + W_{AB} p_{A} p_{B}}{W_{A} p_{A}^2 + W_{AB} p_{A} p_{B} + W_{B} p_{B}}
\]

\[ (q_{0} = 1 - p_{0}) \]

Succeeding generations
\[
p_{n+1} = f(p_{n})
\]

Hence
\[
f(p) = \frac{W_{A} p_{A}^2 + W_{AB} p_{A} p_{B} + W_{B} p_{B}^2}{W_{A} p_{A}^2 + W_{AB} p_{A} p_{B} + W_{B} p_{B}^2}
\]

\[ 0 \leq p \leq 1 \]

Some algebra
\[
f(p) - p = \frac{(W_{A} p_{A}^2 + W_{AB} p_{A} p_{B} + W_{B} p_{B}^2) - W_{A} p_{A}^2 + W_{AB} p_{A} p_{B} + W_{B} p_{B}^2}{W_{A} p_{A}^2 + W_{AB} p_{A} p_{B} + W_{B} p_{B}^2}
\]

\[ (\text{Exercise}) = \frac{p_{n+1} - (W_{A} p_{A} - W_{AB} p_{A} + W_{B} p_{B})}{W} \]

so \( f \) has a fixed point
\[
f(p) - p = 0 \Rightarrow p = p_{0} \text{ or } q_{0} = 1 - p_{0} = 0 \text{ or } (W_{A} p_{A} - W_{AB} p_{A} + W_{B} p_{B}) = 0
\]
\[ p_{0} \text{ is always a fixed point, } p_{1} \text{ is always a fixed point} \]

There may be another fixed point between 0 and 1 depending on values of \( W_{A}, W_{AB}, W_{B} \)

\[ 0.15 p + 0.15 (1-p) = 0.25 W_{A} p_{A}^2 + 0.25 W_{AB} p_{A} p_{B} + 0.25 W_{B} p_{B}^2 \]

\[ 0.15 = 0.25 \]

\[ 0.25 (W_{A} p_{A} - W_{AB} p_{A} + W_{B} p_{B}) = 0 \]

\[ W_{A} = \frac{0.15}{0.25} = 0.6 \]

Use a computer/calculator to plot \( y = f(p) \)

There are only two fixed points \( p_{0} = 0, 1 \)

\( p_{0} = 0 \) is unstable, \( p_{1} = 1 \) is stable (from staircase diagram, could compute \( f'(0), f'(1) \) but messy)

Unless \( p_{0} = 0 \), we have \( p_{n+1} = 1 \)

When \( p_{0} \neq 0 \), use graph to verify \( p_{n+1} = 1 \)

After many generations, the freq. of the A allele will be nearly 1: \( p_{n} \approx 1 \)

\( AA \) is the fittest genotype, eventually the population will consist of nearly all \( AA \) individuals, hence almost all are \( A \) alleles.
\[
f := p \rightarrow \frac{(w[AA] \cdot p^2 + w[AB] \cdot p \cdot (1 - p))}{w[AA] \cdot p^2 + 2 \cdot w[AB] \cdot p \cdot (1 - p) + w[BB] \cdot (1 - p)^2};
\]

\[
p \rightarrow \frac{w_{AA} \cdot p^2 + w_{AB} \cdot p \cdot (1 - p)}{w_{AA} \cdot p^2 + 2 \cdot w_{AB} \cdot p \cdot (1 - p) + w_{BB} \cdot (1 - p)^2}
\]

\(w[AA] := 1;\) \hfill (1)

\(w[AB] := 0.75;\) \hfill (2)

\(w[BB] := 0.5;\) \hfill (3)

\(\text{plot}\{f(p), \ p = 0..1, \ \text{scaling} = \text{constrained}\};\)

\(\text{solve}(f(p) = p);\) \hfill (5)

\(0., 1.\) \hfill (4)
\[ w_A = 1, \quad w_A = 0.5, \quad w_B = 0.5 \]

\[(w_A - w_B)p + (w_B - w_A)q = 0, \quad 0.5p + (-1)q = 0 \]

\[ 0.5p - (1-p) = 0 \]

\[ p^2 = \frac{1}{15} = \frac{2}{3} \]

Thus we have 3 fixed points: \[ p^* = 0, \frac{2}{3}, 1 \]

From the phase diagram, \( p^* = 0 \) is stable, \( p^* = \frac{2}{3} \) is unstable, \( p^* = 1 \) is stable.

This example has bistability.

Unless \( p_0 = 0, \frac{1}{3}, 1 \), we have \( \lim_{n \to \infty} p_n = 0 \) or 1 depending on whether \( p_0 < \frac{2}{3} \) or \( p_0 > \frac{2}{3} \).

AB is a dead-fit genotype, eventually population will consist of AB and BB individuals.
\[ f := p \rightarrow \frac{(w[AA] \cdot p^2 + w[AB] \cdot p \cdot (1 - p))}{w[AA] \cdot p^2 + 2 \cdot w[AB] \cdot p \cdot (1 - p) + w[BB] \cdot (1 - p)^2}; \]

\[ p \rightarrow \frac{w_{AA} \cdot p^2 + w_{AB} \cdot p \cdot (1 - p)}{w_{AA} \cdot p^2 + 2 \cdot w_{AB} \cdot p \cdot (1 - p) + w_{BB} \cdot (1 - p)^2} \]

(1)

\[ w[AA] := 1; \]

1. (2)

\[ w[AB] := 0.5; \]

0.5 (3)

\[ w[BB] := 1.5; \]

1.5 (4)

plot( \{f(p), p \}, p = 0..1, scaling = constrained);