GENE613 - Homework 4

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Decay of disequilibrium is a function of r and generations t

$$D^t_{AB} = (1-r)^t \, D^0_{AB}$$

1. As $t \to \infty$ what happens to D^t_{AB}?
   As D^t_{AB} changes in function of t and $(1-r)^t$ will be always a smaller number as t increases, the $(1-r)^t \, D^0_{AB}$ will tend to 0.

2. Derive a general solution for the number of generations t required to move from initial disequilibrium D^0_{AB} to a target, or eventual disequilibrium D^t_{AB}

$$\begin{aligned} D^t_{AB} &= (1-r)^t \times D^0_{AB} \\ log\left(D^t_{AB}\right) &= t \times log\,(1-r) + log\left(D^0_{AB}\right) \\ log\left(D^t_{AB}\right) - log\left(D^0_{AB}\right) &= t \times log\,(1-r) \\ log\left(D^t_{AB}\right) - log\left(D^0_{AB}\right) &= t \times log\,(1-r) \\ \frac{log\,(D^t_{AB}) - log\,(D^0_{AB})}{log\,(1-r)} &= t \end{aligned} \tag{1}$$

```
> requiredGenerations <- function(start, end, r) {
+   return (ceiling((log(end) - log(start)) / log(1 - r)))
+ }
```

3. If initial disequilibrium is 0.2 and recombination rate between a pair of loci is 0.2

   a) Evaluate the magnitude of this disequilibrium
   As the disequilibrium coefficient D_{AB} varies in magnitude between a minimum of -0.25 and a maximum of +0.25 when there are only repulsion gametes or they are not present, a $D_{AB} = 0.2$ is a high value that represents the 80 % of the maximum disequilibrium possible.

   b) Interpret and evaluate the magnitude of this recombination rate
   As the recombination rate (r) ranges in value between 0 and 0.5 the maximum is at 0.5 because, with an independent assortment of the two loci, one-half of the gametes produced will still be the parental type. A r value of 0.2 is the 40 % of the maximum recombination rate possible.

   c) How many generations would be required to reach a disequilibrium value of

   1) 0.1?

   ```
   > requiredGenerations(start = 0.2, r = 0.2, end = 0.1)
   [1] 4
   ```

   2) 0.05?

```
> requiredGenerations(start = 0.2, r = 0.2, end = 0.05)
[1] 7
```

3) 0?

```
> requiredGenerations(start = 0.2, r = 0.2, end = 0)
[1] Inf
```

4. Given $P_{AB} = 0{,}6$, $P_{Ab} = 0{,}1$, $P_{aB} = 0{,}2$ and $P_{ab} = 0{,}1$ calculate:

a) Allele frquencies

```
> alleleFrequencies <- function(AB, Ab, aB, ab) {
+   return(c(
+     A = AB + Ab,
+     B = AB + aB,
+     a = aB + ab,
+     b = Ab + ab
+   ))
+ }
> alleleFrequencies(AB = 0.6, Ab = 0.1, aB = 0.2, ab = 0.1)

  A   B   a   b
0.7 0.8 0.3 0.2
```

b) D_{AB}

```
> D <- function(a = NULL, A=NULL, b=NULL, B=NULL, observedF) {
+   if(length(c(A,B)) > 1 | length(c(a,b)) > 1){
+     return(observedF - c((A*B),(a*b)))
+   } else{
+     return(c((A*b),(a*B)) - observedF)
+   }
+ }
> D(A = 0.7, B = 0.8, observedF = 0.6)

[1] 0.04
```

c) D_{Ab}

```
> D(A = 0.7, b = 0.2, observedF = 0.1)

[1] 0.04
```

d) D_{aB}

```
> D(a = 0.3, B = 0.8, observedF = 0.2)

[1] 0.04
```

e) D_{ab}

```
> D(a = 0.3, b = 0.2, observedF = 0.1)

[1] 0.04
```

f) D'

```
> lewontinD <- function (DAB, PA, PB, Pa, Pb) {
+   ifelse(test = DAB > 0,
+          yes = (DAB / min(c(PA * Pb, Pa * PB))),
+          no = (DAB / min(c(PA * PB, Pa * Pb))))
+ }
> lewontinD(DAB = 0.04, PA = 0.7, PB = 0.8, Pa = 0.3, Pb = 0.2)
```

```
[1] 0.2857143
```

g) r^2

```
> rSquared <- function(DAB, PA, PB, Pa, Pb) {
+   (DAB ^ 2) / (PA * Pa * PB * Pb)
+ }
> rSquared(DAB = 0.04, PA = 0.7, PB = 0.8, Pa = 0.3, Pb = 0.2)
```

```
[1] 0.04761905
```

5. Show thar $D_{ab} = D_{AB}$

$$
\begin{aligned}
D_{ab} &= D_{AB} \\
P(ab) - P(a) \times P(b) &= P(AB) - (P(A) \times P(B)) \\
P(ab) - [(1 - P(A)) \times (1 - P(B))] &= P(AB) - (P(A) \times P(B)) \\
P(ab) - [1 - P(A) - P(B) + (P(A) \times P(B))] &= P(AB) - (P(A) \times P(B)) \\
P(ab) - 1 + P(A) + P(B) \cancel{- (P(A) \times P(B))} &= P(AB) \cancel{- (P(A) \times P(B))} \\
P(ab) - 1 + P(A) + P(B) &= P(AB) \\
\cancel{P(ab)} - P(AB) - P(Ab) - P(aB) \cancel{- P(ab)} + P(A) + P(B) &= P(AB) \\
-P(AB) - P(Ab) - P(aB) + P(A) + P(B) &= P(AB) \\
-P(AB) - P(Ab) - P(aB) + P(AB) + P(Ab) + P(B) &= P(AB) \\
\cancel{-P(AB)} - P(Ab) - P(aB) \cancel{+ P(AB)} + P(Ab) + P(B) &= P(AB) \\
\cancel{-P(Ab)} - P(aB) \cancel{+ P(Ab)} + P(B) &= P(AB) \\
-P(aB) + P(B) &= P(AB) \\
\cancel{-P(aB)} + P(AB) \cancel{+ P(aB)} &= P(AB) \\
P(AB) &= P(AB)
\end{aligned} \tag{2}
$$