GGG-201D Problem Set 3

Ethan Holleman

5/10/2021

Problem 1

Part A

Generate a scatter plot that shows the properties of selection in large populations. The x-axis should be frequency of the advantageous allele and range from 0 to 1. The y-axis should be the change in frequency of the advantageous allele after one generation of selection. Perform calculations in steps of 0.01 for each of the following six (1a, 1b, 1c, 2a, 2b, 2c) scenarios: (1) the homozygous deleterious genotype has a selection coefficient of 0.1 and the advantageous allele is (a) recessive, (b) dominant or (c) additive; (2) the homozygous deleterious genotype has a selection coefficient of 0.25 and the advantageous allele is (a) recessive, (b) dominant or (c) additive.

```
# Function to calculate allele freq after selection given freq 2 alleles
# and selection coefficients of all genotypes
allele_freq_after_selection <- function(freq_a, freq_t, Saa, Sat, Stt){

  aa <- freq_a^2 * (1-Saa)
  at <- freq_a * freq_t * (1 - Sat)
  at2 <- 2 * freq_a * freq_t * (1 - Sat)
  tt <- freq_t^2 * (1 - Stt)

  (aa + at) / (aa + at2 + tt)

}
allele_freq_after_selection(0.4, 0.6, 0, 0.2, 0.4)  # check function is working
```

```
## [1] 0.4631579
```

```
# Infer selection coeffiencts if advantageous allele is recessive
sc_ressesive <- function(deleterious_sc){

  c(0, deleterious_sc, deleterious_sc)

}
# Infer selection coeffiencts if advantageous allele is dominant
sc_dominant <- function(deleterious_sc){

  c(0, 0, deleterious_sc)

}
# Infer selection coeffiencts if advantageous allele is additive
sc_additive <- function(deleterious_sc){
  c(0, 0.5 * deleterious_sc, deleterious_sc)

}
```

```
# New function that calculates allele freq in next generation given freq
# of two alleles but takes in the deleterious allele selection coefficient
# and a function to define other selection cofficient values

genotype_aware_afas <- function(freq_a, freq_t, sc_del_allele, sc_func){

  sc_vals <- sc_func(sc_del_allele)
  Saa <- sc_vals[1]
  Sat <- sc_vals[2]
  Stt <- sc_vals[3]

  allele_freq_after_selection(freq_a, freq_t, Saa, Sat, Stt)

}
```

```
scenerio_df <- function(del_sc, genotype_func, genotype_name){
  scenerio_name <- paste(genotype_name, as.character(del_sc))
  message(scenerio_name)
  df <- data.frame(advan_allele_freq=seq(0, 1, 0.01))
  post_1_gen <- list()
  for (i in 1:length(df$advan_allele_freq)){
    freq_a <- df[i, ]
    freq_t <- 1 - freq_a
    post_1_gen[[i]] <- genotype_aware_afas(freq_a, freq_t, del_sc, genotype_func) - freq_a

  }
  df$scenerio <- scenerio_name
  df$freq_gen_2 <- unlist(post_1_gen)
  df
}
```

```
# ugly
df.1 <- scenerio_df(0.1, sc_ressesive, "Ressesive")
```

```
## Ressesive 0.1
```

```
df.2 <- scenerio_df(0.1, sc_dominant, "Dominant")
```

```
## Dominant 0.1
```

```
df.3 <- scenerio_df(0.1, sc_additive, "Additive")
```

```
## Additive 0.1
```

```
df.4 <- scenerio_df(0.25, sc_ressesive, "Ressesive")
```

```
## Ressesive 0.25
```

```
df.5 <- scenerio_df(0.25, sc_dominant, "Dominant")
```

```
## Dominant 0.25
```

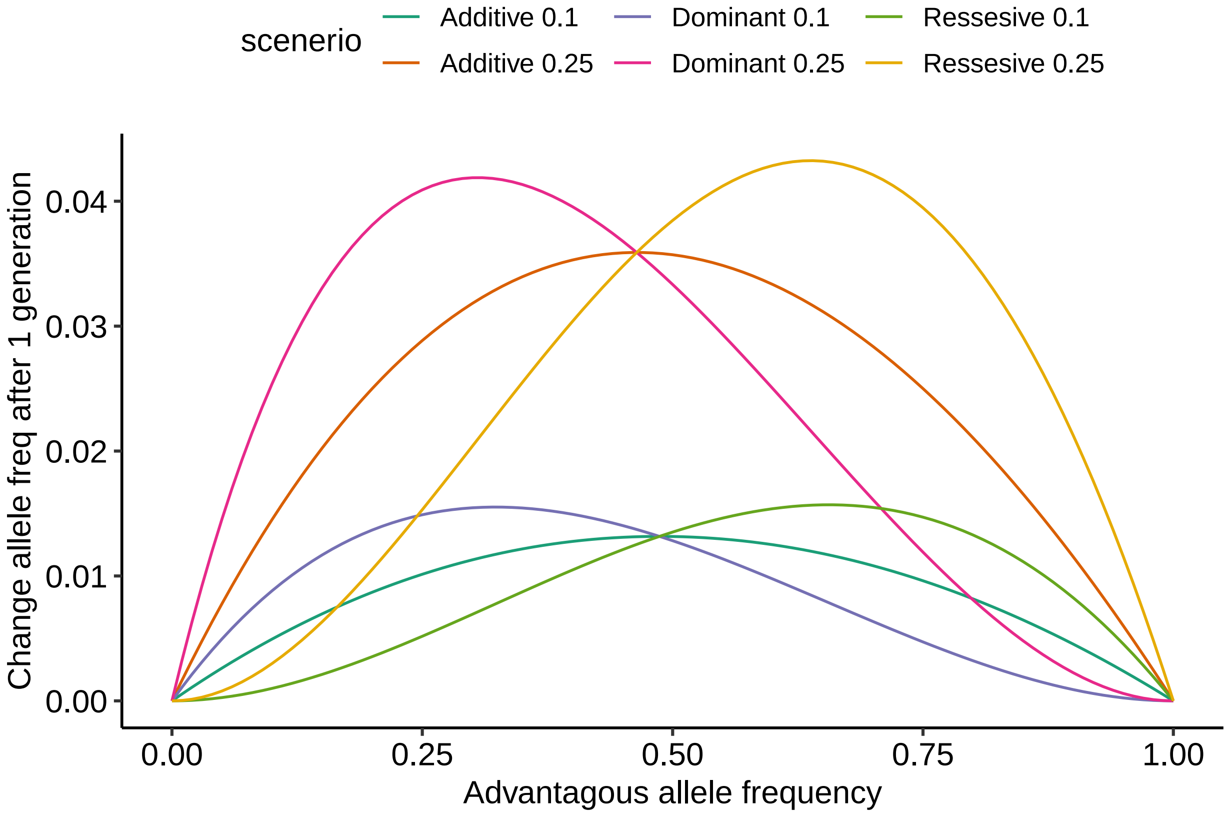
```
df.6 <- scenerio_df(0.25, sc_additive, "Additive")
```

```
## Additive 0.25
```

```
big.df <- rbind(df.1, df.2, df.3, df.4, df.5, df.6)
```

```
# Finally, plot everything
library(ggplot2)
library(ggpubr)
library(RColorBrewer)

ggplot(big.df, aes(x=advan_allele_freq, y=freq_gen_2, color=scenerio)) +
  geom_line() + theme_pubr() + scale_color_brewer(palette = "Dark2") +
  labs(x='Advantagous allele frequency', y='Change allele freq after 1 generation')
```



Part B

Four of the six plots from above are highly asymmetric. Explain the biological reason behind these asymmetric patterns.

Problem 2

You sequence a 5.6 kb locus in 5 diploid individuals and observe 11 segregating sites. What is your estimate of theta in this population? What property of the expected coalescent tree is this estimate based on? What is your estimate of coalescent Ne assuming a mutation rate of 10^-8 per bp per generation?

Problem 3

Explain the difference between coalescent effective population size (Ne) and instantaneous Ne. What isone way to estimate coalescent Ne? What is one way to estimate instantaneous Ne?

Problem 4

The expected time to the first coalescent event of four gene copies is 2N/6 generations before the present but the actual time could be much more or much less. If you sample 100 sets of four gene copies, each set has an actual time to the first coalescent event. Do you expect the number of sets that have an actual first coalescent before 2N/6 to be approximately equal to the number of sets to have an actual first coalescent after 2N/6? Explain your answer.