

GGG-201D-problem-set-2

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Problem 1

Part A

Use a program such as R or Excel to generate a scatter plot that shows how expected allele frequency change from genetic drift depends on initial allele frequency. The x-axis should be initial allele frequency and range from 0 to 1. The y-axis should be expected change in allele frequency after one generation. Perform calculations in steps of 0.1 for a population size of $2N=20$.

```
expected <- function(init_allele_freq, pop_size, delta_allele_freq){

  num_delta_alleles <- pop_size * delta_allele_freq
  num_init_alleles <- pop_size * init_allele_freq
  routes <- num_init_alleles + c(-1*num_delta_alleles, num_delta_alleles)
  routes <- unique(routes[routes >= 0]) # remove negative values since not possible
  sum(mapply(dbinom, routes, pop_size, init_allele_freq))

}

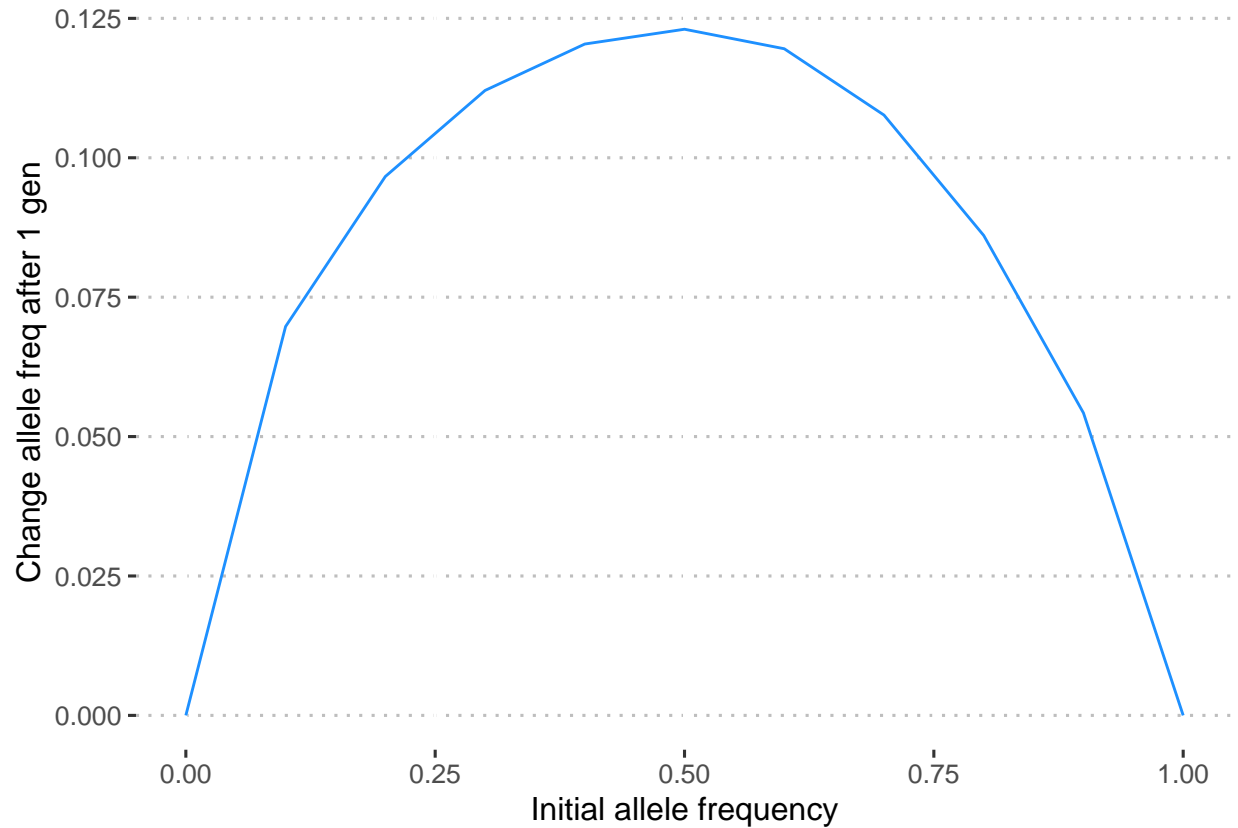
expected_change <- function(init_allele_freq, pop_size){

  magnitudes <- seq(0, 1-init_allele_freq, 0.1)
  sum(mapply(expected, init_allele_freq, pop_size, magnitudes) * magnitudes)

}

library(ggplot2)
library(ggpubr)

df.a <- data.frame(init_allele_freq=seq(0, 1, 0.1), pop_size=10)
df.a$delta_allele_freq <- mapply(expected_change, df.a$init_allele_freq, df.a$pop_size)
ggplot(df.a, aes(x=init_allele_freq, y=delta_allele_freq)) + geom_line(color='dodgerblue') +
  theme_pubclean() + labs(x='Initial allele frequency', y='Change allele freq after 1 gen')
```

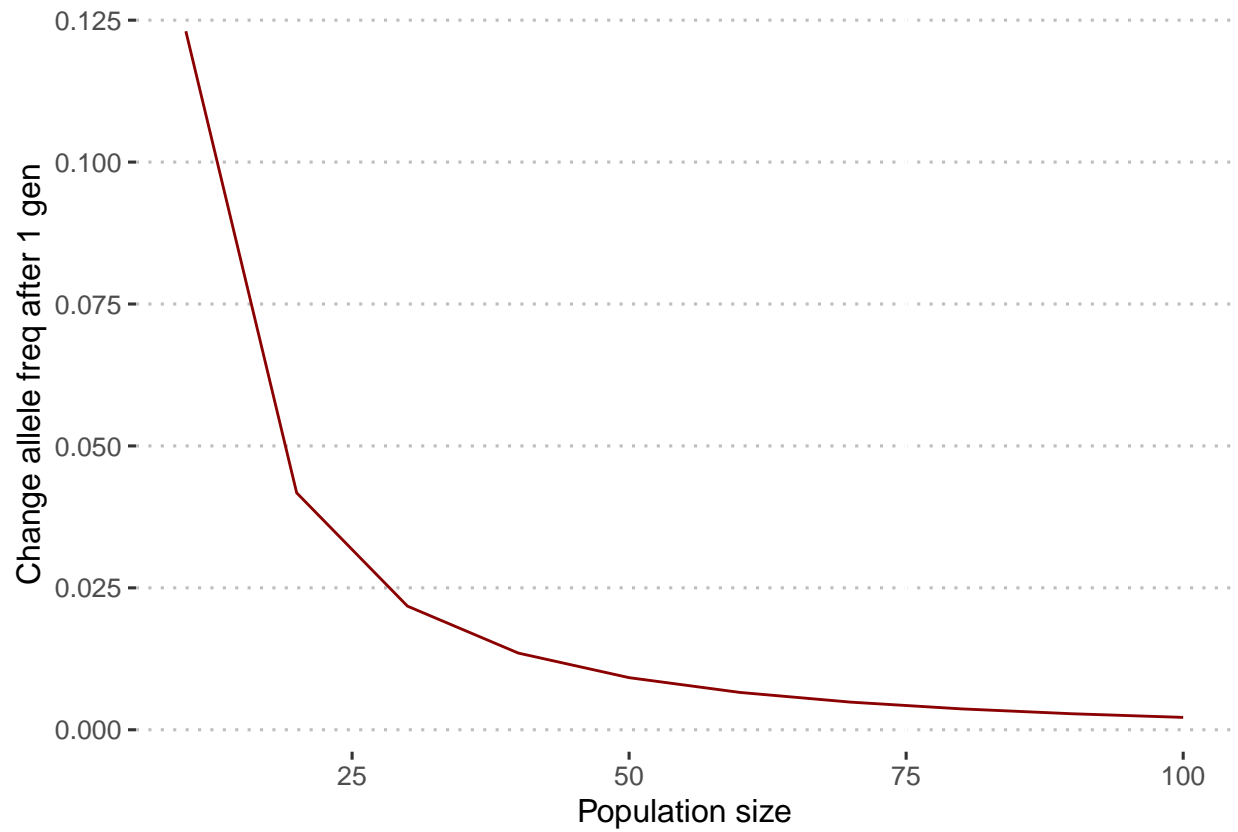


Initial allele frequency	Pop size	Delta allele freq 1 gen
0.0	10	0.0000000
0.1	10	0.0697357
0.2	10	0.0966368
0.3	10	0.1120677
0.4	10	0.1203949
0.5	10	0.1230469
0.6	10	0.1195455
0.7	10	0.1076569
0.8	10	0.0860671
0.9	10	0.0542389
1.0	10	0.0000000

Part B

Use the same program to generate a scatter plot that shows how expected allele frequency change from genetic drift depends on population size. The x-axis should be population size and range from $2N=10$ to $2N=100$. The y-axis should be expected change in allele frequency after one generation. Perform calculations in steps of 10 with an allele frequency of 0.5

```
df.b <- data.frame(init_allele_freq=0.5, pop_size=seq(10, 100, 10))
df.b$delta_allele_freq <- mapply(expected_change, df.b$init_allele_freq, df.b$pop_size)
ggplot(df.b, aes(x=pop_size, y=delta_allele_freq)) + geom_line(color='darkred') +
  theme_pubclean() + labs(x='Population size', y='Change allele freq after 1 gen')
```



Initial allele frequency	Pop size	Delta allele freq 1 gen
0.5	10	0.1230469
0.5	20	0.0417309
0.5	30	0.0217753
0.5	40	0.0135072
0.5	50	0.0091770
0.5	60	0.0065758
0.5	70	0.0048678
0.5	80	0.0036784
0.5	90	0.0028174
0.5	100	0.0021780