Pop Gen HW5

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1

a

With $N_0 = 10,000$
The size of the present population is: 10,000
Size of population before bottlneck: $N_0 * 10 = 100,000$
Bottleneck occured $0.05 * 2N$ generations ago

b

Compute the cumulative coalescent rate function:

$$\Lambda(t) := \int_{s=0}^{t} \frac{1}{f(s)} ds$$

while $t \geq 0.05$:

$$\Lambda(t) := \int_{s=0}^{t} \frac{1}{f(s)} ds$$

$$= \int_{s=0}^{t=0.05} ds + \int_{s=0.05}^{t} \frac{1}{10} ds$$

$$= s|_0^{0.05} + \frac{s}{10}|_{0.05}^{t}$$

$$0.05 + \frac{t}{10} - 0.005$$

$$= \frac{t}{10} + 0.045$$

while $t \leq 0.05$:

$$\Lambda(t) := \int_{s=0}^{t} \frac{1}{f(s)} ds$$

$$= \int_{s=0}^{t} ds$$

$$= t$$

c
Compute the expected value:

$$\mathbb{E}[T_k^{(k)}] = \int_{t=0}^{\infty} \mathbb{P}\{T_k^{(k)} > t\} dt$$

Substitue $e^{-\binom{k}{t}\Lambda(t)}$ for $\mathbb{P}\{T_k^{(k)} > t\}$

Which gives:

$$= \int_{t=0}^{\infty} e^{-\binom{k}{t}\Lambda(t)} dt$$

$$= \int_{t=0}^{\infty} e^{-\frac{k(k-1)}{2} * \frac{1}{200} * (20t+9)} dt$$

$$= \int_{t=0}^{\infty} e^{-\frac{k(k-1)}{400} * (20t+9)} dt$$

$$= e^{\frac{9k(k-1)}{400}} \int_{t=0}^{\infty} e^{\frac{9k(k-1)}{20} t} dt$$

$$= -e^{\frac{9k(k-1)}{400}} * \frac{20}{k(k-1)} * [e^{-\frac{20k(k-1)}{400}} t]_0^{\infty}$$

$$= \frac{20}{k(k-1)} * e^{-\frac{9k(k-1)}{400}}$$

$$= \mathbb{E}[T_k^{(k)}]$$

$\square$

2)

$$r^2_{a,c} = \frac{D^2_{a,c}}{p_a p_A p_c p_C}$$

$$p_a = \frac{n_a}{n}$$

$$D^2_{a,c} = (p_{a,c} - p_a p_c)^2$$

$$p_{a,c} = \frac{n_{a,c}}{n}$$

$$p_a = \frac{12}{20} = 0.6$$

$$p_b = \frac{10}{20} = 0.5$$

$$p_c = \frac{9}{20} = 0.45$$

$$p_A = 8/20 = 0.4$$

$$p_B = \frac{10}{20} = 0.5$$

$$p_C = 11/20 = 0.55$$

$$p_a p_A p_b p_B = 0.06$$

$$p_a p_A p_c p_C = 0.0594$$

$$p_b p_B p_c p_C = 0.061875$$

$$n_{ac} = 4/20 = 0.2$$

$$n_{ab} = 6/20 = 0.3$$

$$n_{bc} = 5/20 = 0.25$$

$$D^2_{ac} = (0.2 - (0.6(0.45))^2 = 0.0049$$

$$D^2_{ab} = (0.3 - (0.6(.5))^2 = 0$$

$$D^2_{bc} = 0.25 - (.5(.45))^2 = 0.000625$$

$$r^2_{ac} = \frac{0.0049}{0.0594} = 0.0825$$

$$r^2_{ab} = \frac{0}{0.06} = 0$$

$$r^2_{bc} = \frac{0.000625}{0.061875} \approx 0.01$$

Figure 1: Computing LD

3

Genealogical Ancestral Process Simulator

```
failedTrajectories <- 0
# Based on problem: init trajecotries that reach k == 1 before t == 20
trajectories <- 1000
L <- 200
rho <- 0.002
n = 10

set.seed(420)
# for rexp()

for(i in seq(trajectories)){ # for each i simulation in trajectories
  k <- n # init
  genealogical.df <- data.frame(matrix(ncol = 1, nrow = 1e5))
  # each simulation is a column, value is lineages of that simulation at time t
  # x is row, y is column
  # k is # lineages

  genealogical.df$simLineages[1] <- k # init k in df
  genealogical.df$t[1] <- 0 # init time in df
  genealogical.df <- select(genealogical.df,t, simLineages)
  j <- 2
  # init where we start filling rows == row 2 bc row 1 has init values for the simulation

  oldTime <- 0
  # print(i) testing

  while( k != 1 ){
    # print('in while') testing
    increaseLineageProb <- k * (rho/2) * (L-1) / ((k * (rho/2) * (L-1) + choose(k,2)))
    decreaseLineageProb <- choose(k,2) / ((k * (rho/2) * (L-1) + choose(k,2)))

    move <- sample( c(-1,1), 1, prob =  c(decreaseLineageProb, increaseLineageProb))
    # make probability weight vector

    k <- genealogical.df$simLineages[j] <- k + move
    # update number of lineages at time i, use sample from distribution of probs of lineage increasing/
    # this value is the new k as well as row value for this lineage column
    # prob of decreasing is typically higher

    rate = k * ((rho/2) * (L-1)) + choose(k,2)
    # rate updates each loop with new k at each t

    time <- rexp(1, rate)
    # rate of time, exponentially distributed
    # ATTN: this is how t increases (very slowly), so simulations typically do not reach t > 20 before 
    # This is based on my understanding of the problem,
      # I believe if t increased more rapidly then there would be fewer simulations that reach k == 1 w

    newTime <- time + oldTime
```

```
    genealogical.df$t[j] <- newTime
    # update which row we are on, update time value with current time

    oldTime <- newTime
    j <- j+1 # j is simply the row containing our time t, is not the t == 20 we need to check for
  }
  failedSimulation <- filter(genealogical.df, simLineages, simLineages == 1)
  # once k == 1, check what time the simulated pop went to 1 at

  if(failedSimulation$t[1] < 20) { # critical to
    failedTrajectories <- failedTrajectories + 1
  }
}
cat(failedTrajectories,'trajectories reach k == 1 before t == 20')
```

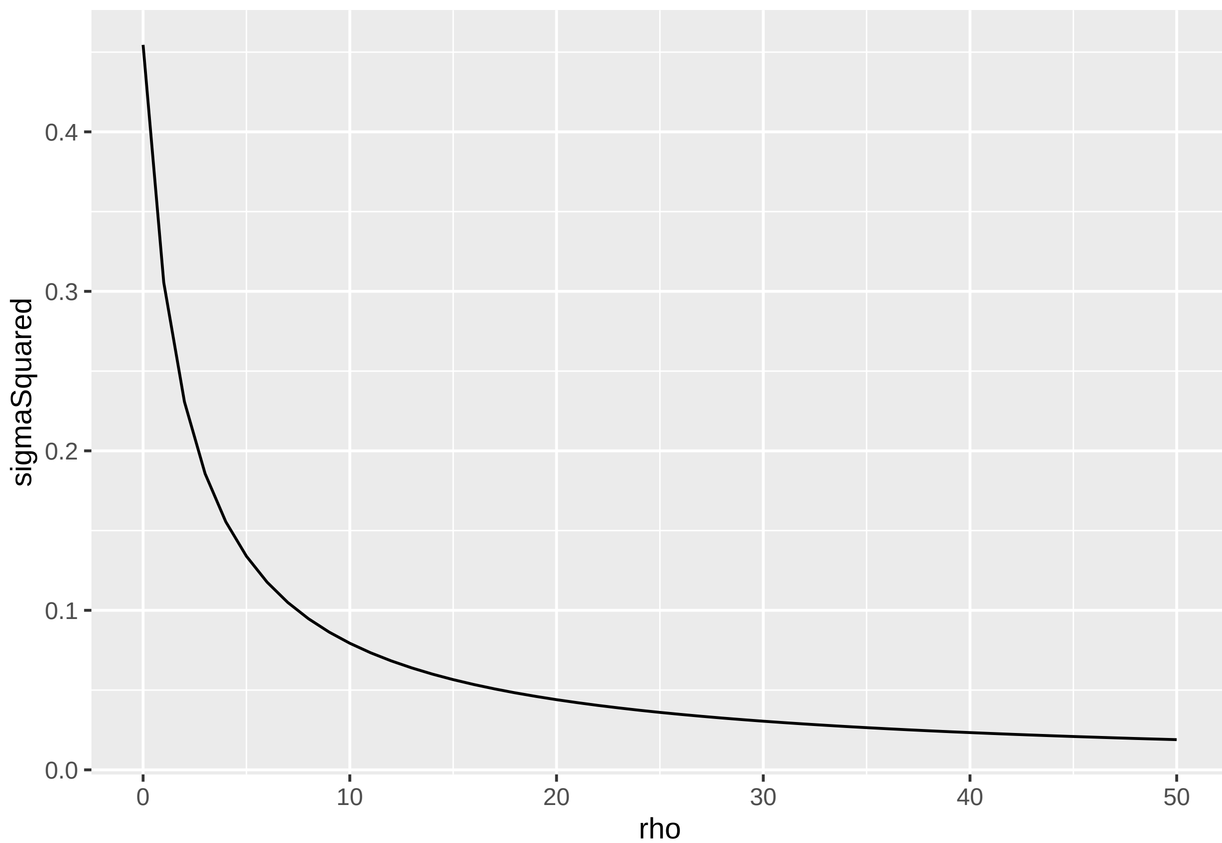
```
## 966 trajectories reach k == 1 before t == 20
```

4

a

```
rho <- seq(0,50)
sigmaSquared <- (rho + 10)/(rho**2 + 13*rho + 22)

ggplot() +
  geom_line(aes(rho, sigmaSquared))
```




```
rho0 <- sigmaSquared[1]

cat('sigmaSquared for rho = 0 is:',rho0)
```

```
## sigmaSquared for rho = 0 is: 0.4545455
```

```
cat('\n5% of rho at 0 is:',rho0*0.05)
```

```
##
## 5% of rho at 0 is: 0.02272727
```

b

Calculate the (positive) rho for which sigmaSquared == 5% of its value at rho == 0

Setting $\sigma_d^2 == rho0$, solving for ρ

$$0.02272727 = \frac{\rho + 10}{\rho^2 + 13\rho + 22}$$

$$0.02272727\rho^2 + 0.29545451\rho + 0.49999994 = \rho + 10$$

Solve for ρ, obtain quadratic equation

$$0.02272727\rho^2 - 0.7045455\rho - 9.50000006 = \rho$$

Solve quadratic equation:

```r
a <- 0.02272727
b <- -0.7045455
c <- -9.50000006

root <- ((-b) + sqrt(b**2 - (4*(a*c))))/(2*a)

cat('Positive rho value for which sigma**2 == 5% of its value at rho == 0:', root)
```

```
## Positive rho value for which sigma**2 == 5% of its value at rho == 0: 41.15639
```

c

$$\rho = 4N_e r$$

$$N_e = 10,000$$

$$r = 1.25 * 10^{-8}$$

Base-pairs that correspond to the ρ obtained from solving the quadratic equation:

$$bp = \frac{\rho}{4N_e r}$$

```r
bp = root/(4*1e4*1.25*(10**-8))
cat('This rho corresponds to:',bp,'bp.')
```

```
## This rho corresponds to: 82312.78 bp.
```