Pop Gen HW5

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1

 \mathbf{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 $t \geq 0.05$:

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

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

$$= s \Big|_{0}^{0.05} + \frac{s}{10} \Big|_{0.05}^{t}$$

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

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

while $t \leq 0.05$:

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

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:

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

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

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

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

$$= -e^{\frac{9k(k-1)}{400}} * \frac{20}{k(k-1)} * [e^{-\frac{20k(k-1)}{400}} t]_{0}^{\infty}$$

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

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

$$\begin{array}{lll}
\begin{pmatrix}
\lambda_{0,c} &=& \frac{12}{l_{0} l_{0} l_{0} l_{0} l_{0}} \\
l_{0} &=& \frac{12}{20} = 0.6
\end{pmatrix} & N_{0,c} &=& \frac{12}{12} = 0.25 \\
\begin{pmatrix}
\lambda_{0} &=& \frac{12}{20} = 0.5
\end{pmatrix} & N_{0,c} &=& \frac{12}{12} = 0.25
\end{pmatrix} & N_{0,c} &=& \frac{12}{20} = 0.25
\end{pmatrix} & N_{0,c} &=& \frac{12}{20} = 0.45
\end{pmatrix} & N_{0,c} &=& \frac{12}{20} = 0.25
\end{pmatrix} & N_{0,c} &=& \frac{12}{20} = 0.25$$

$$r_{ac}^{2} = \frac{0.0049}{0.0594} = 0.0925$$

$$r_{ac}^{2} = \frac{0}{0.06} = 0$$

$$r_{ac}^{2} = \frac{0.000625}{0.061375} = 0.01$$

Figure 1: Computing LD

Genealogical Ancestral Process Simulator

```
set.seed(420)
# for rexp()
genealogicalAncestralProcessSimulator <- function(L = 200, rho = 0.002, n = 10, trajectories = 1000, fa
  for(i in seq(trajectories)){ # for each i simulation in trajectories
    k \leftarrow n \# init
    genealogical.df <- data.frame(matrix(ncol = 1, nrow = 1e5))</pre>
    # 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$simLineages[1] <- k # init k in df</pre>
    genealogical.df$t[1] <- 0 # init time in df</pre>
    genealogical.df <- select(genealogical.df,t, simLineages)</pre>
    # 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))</pre>
      # make probability weight vector
      k <- genealogical.df$simLineages[j] <- k + move</pre>
      # update number of lineages at time i, use sample from distribution of probs of lineage increasin
      # this value is the new k as well as row value for this lineage column
      # prob of decreasing is typically higher
      rate = k * ((rho/2) * (L-1)) + choose(k,2)
      # rate updates each loop with new k at each t
      time <- rexp(1, rate)
      # rate of time, exponentially distributed
      # ATTN: this is how t increases (very slowly), so simulations typically do not reach t > 20 befor
      # This is based on my understanding of the problem,
        # I believe if t increased more rapidly then there would be fewer simulations that reach k == 1
      newTime <- time + oldTime</pre>
      genealogical.df$t[j] <- newTime</pre>
      # 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

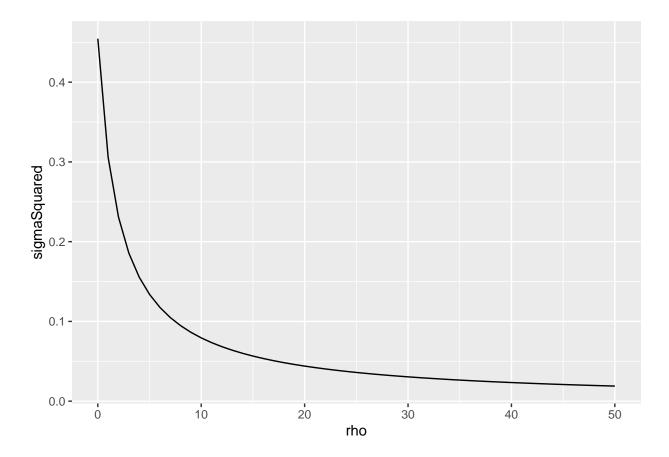
if(failedSimulation$t[1] < 20) { # critical to
    failedTrajectories <- failedTrajectories + 1
  }
} cat(failedTrajectories, 'trajectories reach k == 1 before t == 20')
}
genealogicalAncestralProcessSimulator()</pre>
```

```
## 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))</pre>
```



```
rho0 <- sigmaSquared[1]
cat('sigmaSquared for rho = 0 is:',rho0)</pre>
```

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:

```
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)</pre>
```

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

 \mathbf{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:

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

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

This rho corresponds to: 82312.78 bp.