

Networks and Random Processes Assignment 1

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October 2018

1 Question 1

This section considers a Simple Random Walk on $1, \dots, L$ with probabilities $p \in [0, 1]$ and $q = 1 - p$ to jump right and left respectively.

Different boundary conditions are considered.

1.1 Part A

1.1.1 Case 1 - Periodic

Periodic boundary conditions, $p(0, L) = q$ and $p(L, 0) = p$

The transition matrix is:

$$P = \begin{bmatrix} 0 & p & 0 & \dots & 0 & q \\ q & 0 & p & \dots & 0 & 0 \\ 0 & q & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \\ 0 & 0 & 0 & \dots & 0 & p \\ p & 0 & 0 & \dots & q & 0 \end{bmatrix}$$

The process is irreducible i.e. every state can, eventually, reach every other state. And there is a finite state space so there is 1 unique stationary distribution.

The process can "loop" around from state L to 1 and vice versa. The state path can be visualised as a circular loop. Considering the symmetry, the stationary distribution must be uniform.

$\pi = (1/L, 1/L, \dots, 1/L)$ for all $p \in (0, 1)$

The stationary distribution is reversible only for the case $p = q = \frac{1}{2}$.

1.1.2 Case 2 - Closed

Transition matrix:

$$P = \begin{bmatrix} q & p & 0 & \dots & 0 & 0 \\ q & 0 & p & \dots & 0 & 0 \\ 0 & q & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \\ 0 & 0 & 0 & \dots & 0 & p \\ 0 & 0 & 0 & \dots & q & p \end{bmatrix}$$

If $p = 1$ there is an absorbing state at L and the stationary distribution is $\pi = (0, 0, \dots, 0, 1)$. This stationary distribution is reversible because all terms in the detailed balance equations are zero. This is not irreducible because the walk can only move from s_x to s_{x+1} , and not in the opposite direction.

If $q = 1$ there is an absorbing state at 1 and the stationary distribution is $\pi = (1, 0, \dots, 0, 0)$. This stationary distribution is reversible because all terms in the detailed balance equations are zero. This is not irreducible, as the walk can only move from s_x to s_{x-1} and not in the opposite direction.

If $p = q = \frac{1}{2}$ the process is irreducible because every state can, eventually, be reached from every other state. There is also a finite state space and so there is only 1 stationary distribution. All of the columns in the transition matrix sum to 1 and so there is a constant left eigenvector. Therefore the unique stationary distribution is uniform and given by $\pi = (1/L, 1/L, \dots, 1/L)$. This stationary distribution is reversible.

If $p, q \neq [0, 1/2, 1]$ then the process is irreducible and it has a finite state space. So the process is ergodic and there is only 1 stationary distribution. Looking at the detailed balance equations, we can find a recurrence relation of the form:

$$\pi_{x-1}p = \pi_x q \text{ over } x = \{2, 3, \dots, L\}$$

$$\pi_x = \pi_{x-1} \frac{p}{q}$$

By induction, the solution is

$$\pi_x = \pi_1 \left(\frac{p}{q}\right)^{x-1}$$

This is a reversible distribution, and so must also be stationary. As the process is ergodic, this is the unique stationary distribution.

We can check this distribution is stationary for a closed simple random walk with 4 states

$$\begin{bmatrix} \pi_1 \\ \pi_1 \frac{p}{q} \\ \pi_1 \left(\frac{p}{q}\right)^2 \\ \pi_1 \left(\frac{p}{q}\right)^3 \end{bmatrix} \begin{bmatrix} q & p & 0 & 0 \\ q & 0 & p & 0 \\ 0 & q & 0 & p \\ 0 & 0 & q & p \end{bmatrix} = \begin{bmatrix} \pi_1 \\ \pi_1 \frac{p}{q} \\ \pi_1 \left(\frac{p}{q}\right)^2 \\ \pi_1 \left(\frac{p}{q}\right)^3 \end{bmatrix}$$

The normalised stationary distribution is

$$\pi_x = \frac{\pi_1 \left(\frac{p}{q}\right)^{x-1}}{\sum_i^L \pi_i}$$

1.2 Part B - Absorbing

The transition matrix for a simple random walk with absorbing boundary conditions is

$$P = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 & 0 \\ q & 0 & p & \dots & 0 & 0 \\ 0 & q & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \\ 0 & 0 & 0 & \dots & 0 & p \\ 0 & 0 & 0 & \dots & 0 & 1 \end{bmatrix}$$

The process is not irreducible, as no other states can be reached from state 1 or state L.

The two stationary distributions suggested by the absorbing states are

$$\pi_1 = [1, 0, 0, \dots, 0]$$

$$\pi_2 = [0, 0, 0, \dots, 1]$$

These can be combined linearly to give stationary distributions of the form

$$\pi_0 = [a, 0, 0, \dots, 0, 1 - a] \text{ where } a \in [0, 1]$$

These distributions are reversible. Looking at the detailed balance conditions:

$$\pi(x)p(x, y) = \pi(y)p(y, x)$$

All terms for all equations are zero and therefore it is reversible.

The absorption probability in site L is

$$h_k^L = P(X_n = L \text{ for some } n \geq 0 | X_0 = k)$$

or

$$h_k^L = P(X_n = L | X_0 = k)$$

Considering k+1, k-1, and by law of total probability:

$$h_k^L = P(X_n = L | X_1 = k+1, X_0 = k) * p + P(X_n = L | X_1 = k-1, X_0 = k) * q$$

Using the Markov property:

$$h_k^L = P(X_n = L | X_1 = k+1) \times p + P(X_n = L | X_1 = k-1) \times q$$

or

$$h_k^L = h_{k+1}^L \times p + h_{k-1}^L \times q$$

The boundary conditions are:

$$h_1^L = 0 \text{ and } h_L^L = 1$$

If $p = q$ then this recursion relation becomes

$$h_k^L = \frac{h_{k+1}^L + h_{k-1}^L}{2}$$

This is linear interpolation between the two surrounding states and therefore the absorption probability is linear in k. Considering the boundary conditions the solution is:

$$h_k^L = \frac{k-1}{L-1}$$

If $p \neq q$, consider the ansatz:

$$h_k^L = \lambda^k$$

Using this ansatz the recursion relation becomes

$$\lambda = p\lambda^2 + q$$

This has roots:

$$\lambda_1 = 1 \text{ and } \lambda_2 = q/p$$

The general solution is of the form:

$$h_k^L = a\lambda_1 + b\lambda_2$$

$$h_k^L = a + b\left(\frac{q}{p}\right)^k$$

Looking at the boundary conditions:

$$h_1^L = 0 = a + b\left(\frac{q}{p}\right)$$

$$h_L^L = 1 = a + b\left(\frac{q}{p}\right)^L$$

Subtracting the first equation from the second equation, and solving for b:

$$b = \frac{1}{\left(\frac{q}{p}\right)^L - \frac{q}{p}}$$

$$a = \frac{-1}{\left(\frac{q}{p}\right)^{L-1} - 1}$$

1.3 Part C - simulations

A simple random walk with $L=10$ and closed boundary conditions was simulated 500 times, with $p = 0.6$ and starting at $x=1$ at $t=0$.

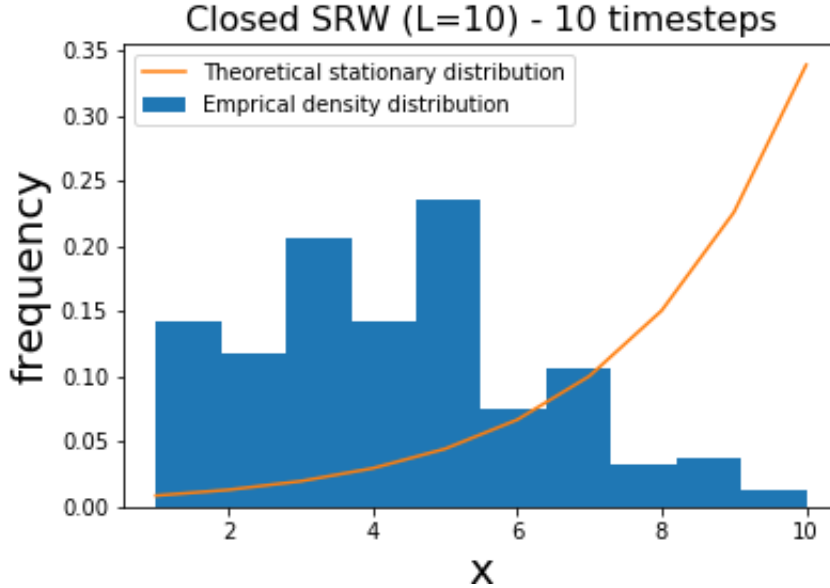


Figure 1. The frequency distribution over 500 different realisations after 10 timesteps.

Ergodic processes tend towards the stationary distribution after a large number of time steps. After 10 time steps (Figure 1), the empirical distribution is

still heavily influenced by the starting condition of $x(0) = 1$.

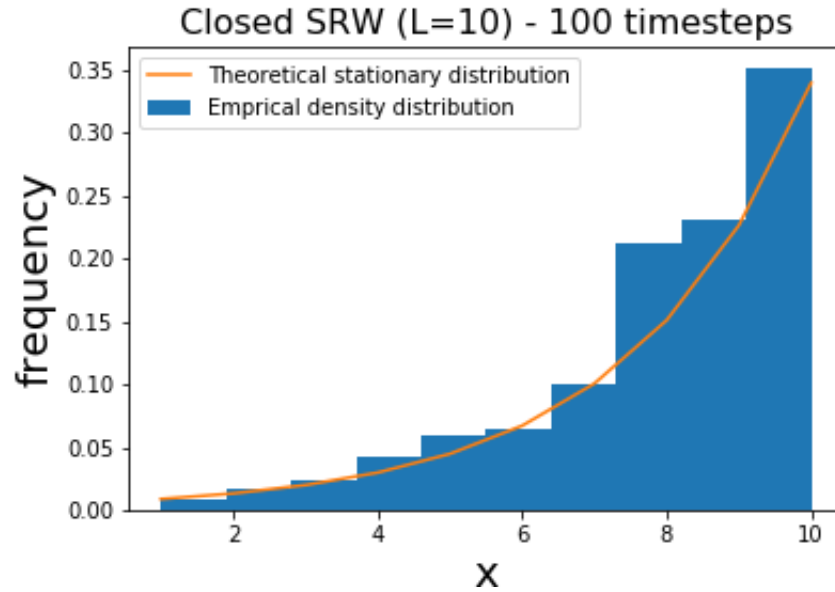


Figure 2. The frequency distribution over 500 different realisations after 100 timesteps.

After 100 time steps (Figure 2), enough time has passed so that the empirical distribution is similar to the theoretical stationary distribution.

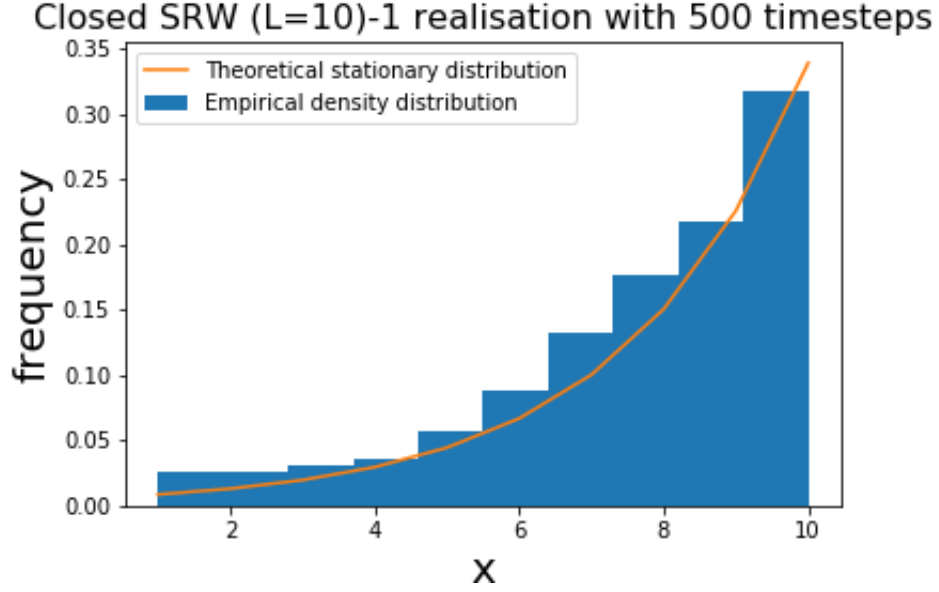


Figure 3. The frequency distribution of states over 500 timesteps of 1 single realisations.

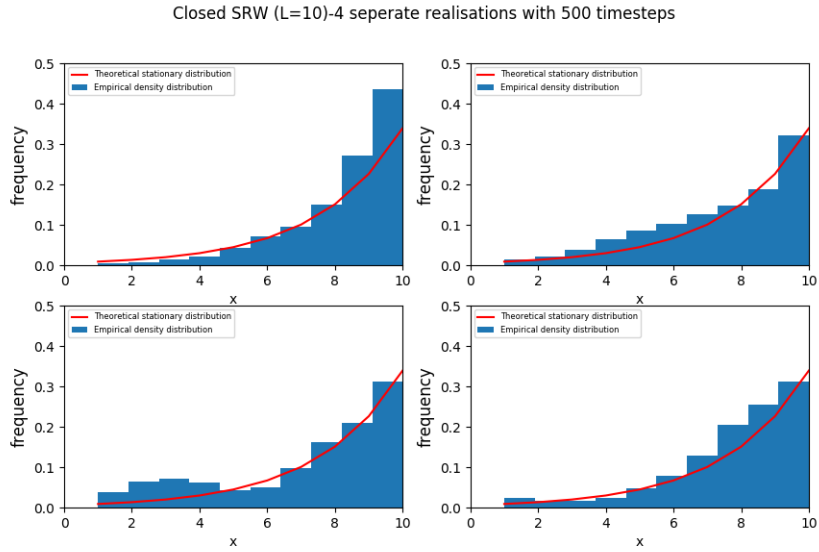


Figure 4. The frequency distribution of states over 500 timesteps of 4 seperate single realisations.

After 500 time steps of 1 realisation (Figure 3), the empirical distribution is similar to the theoretical stationary distribution. Over just 1 realisation

there is a lot of stochasticity in the specific distribution generated. To give a representative sample 4 further separate realisations are shown in Figure 4.

2 Question 2

X_1, X_2, \dots is a sequence of independent, identically distributed random variables (iirdvs) with

$$X_i \sim N(\mu, \sigma^2)$$

$$\mu \in R \text{ and } \sigma^2 > 0$$

Discrete time random walk on state space R

$$(Y_n : n \geq 0) \text{ with } Y_{n+1} = Y_n + X_{n+1} \text{ and } Y_0 = 0$$

2.1 Part A

The weak law of large numbers for Y_n :

$$\frac{1}{n}Y_n = \frac{1}{n} \sum_{k=1}^n X_k \rightarrow \mu \text{ as } n \rightarrow \infty$$

The value of $\frac{Y_n}{n}$ will converge to μ with large n .

The central limit theorem for Y_n :

$$\frac{Y_n - n\mu}{\sigma n^{\frac{1}{2}}} = \frac{1}{\sigma n^{\frac{1}{2}}} \sum_{k=1}^n (X_k - \mu) \rightarrow \xi \text{ as } n \rightarrow \infty$$

where $\xi \sim N(0, 1)$

2.2 Part B - distribution of Y_n

$$Y_n \sim N(n\mu, n\sigma^2) \text{ for } n \geq 0$$

Y_n is normally distributed with mean equal to $n\mu$, where μ is the mean of the random variable X , and with variance $n\sigma^2$, where σ^2 is the variance of the random variable X .

2.3 Part C

Z_n has a recursive relationship given by

$$Z_{n+1} = \exp(Y_n + X_{n+1})$$

$$Z_{n+1} = Z_n \exp(X_{n+1})$$

2.3.1 Derivation of pdf

Y is distributed normally, and

$$Y = \ln(Z)$$

Consider the cumulative distribution function:

$$F_z(z) = P(Z \leq z) = P(Y \leq \ln(z)) = F_y(\ln(z)) = \Phi\left(\frac{\ln(z) - n\mu}{\sigma\sqrt{n}}\right)$$

$$f_z(z) = \frac{d}{dz}F_z(z)$$

by the chain rule, this gives

$$f_z(z) = \frac{1}{z} \frac{1}{\sigma_y \sqrt{2\pi}} \exp\left(\frac{-(\ln(z) - \mu_y)^2}{2\sigma_y^2}\right)$$

Or, in terms of the standard deviation and mean of x

$$f_z(z) = \frac{1}{z\sigma_x \sqrt{2n\pi}} \exp\left(\frac{-(\ln(z) - n\mu_x)^2}{2n\sigma_x^2}\right)$$

Z_0 is fixed by the initial conditions as $Z_0 = 1$. So the log-normal distribution given above applies for $n \geq 1$.

From wikipedia:

$$E(Z_n) = \exp(n\mu + \frac{n\sigma^2}{2})$$

$$Var(Z_n) = \exp(2n\mu + n\sigma^2)(\exp(n\sigma^2) - 1)$$

$$Med(Z_n) = \exp(n\mu)$$

Where μ and σ^2 are the mean and variance of X .

2.4 Part D

Z_n was simulated 500 times over 100 timesteps with $\mu_x = 0$ and $\sigma_x = 0.2$.

2.4.1 Empirical Average

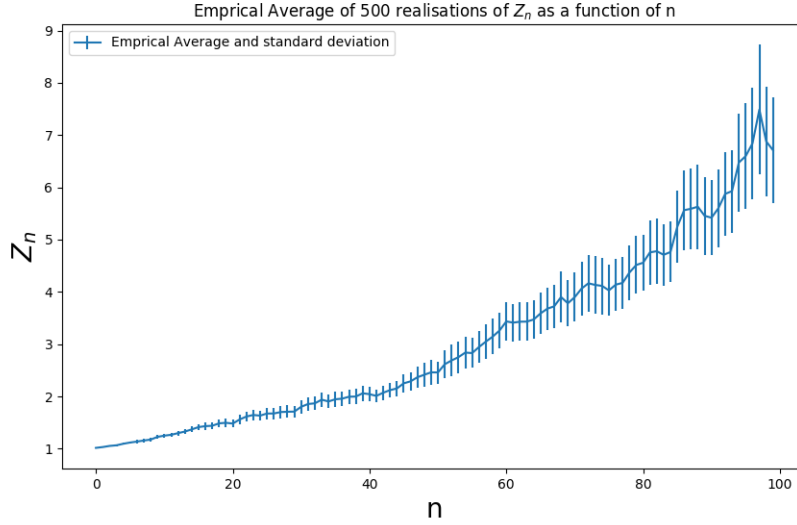


Figure 5. The empirical average of 500 simulations of Z_n as a function of n over 100 timesteps.

Figure shows the empirical average of Z_n as a function of time, n . The error bars show the empirical standard deviation at each point.

2.4.2 Boxplots

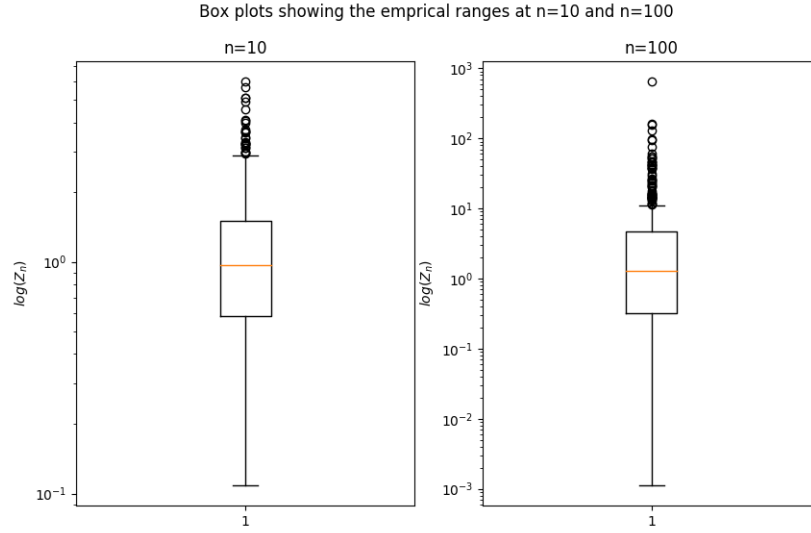


Figure 6. The empirical ranges of Z_n over 500 realisations at $n=10$ and $n=100$. The whiskers are set at $1.5 \times IQR$ where IQR is the interquartile range.

Figure 6 shows the ranges of empirical data at 10 and 100 timesteps. The distribution at 100 timesteps has a much larger range than at 10 timesteps.

2.4.3 Empirical PDF and theoretical PDF

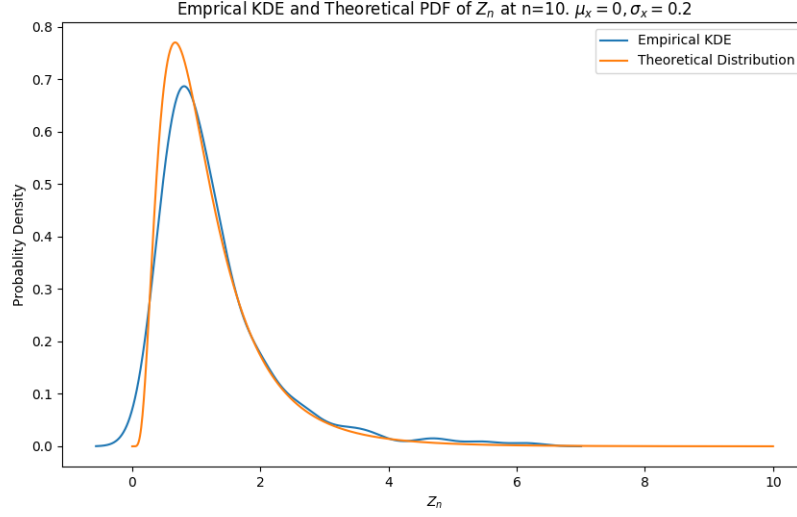


Figure 7. Empirical kernel density estimation and theoretical probability density function for Z_n with $\mu_x = 0$ and $\sigma = 0.2$ at $n = 10$ timesteps over 500 realisations.

Figure 7 shows a reasonably close fit between the empirical kernel density estimate and the theoretical probability density function for Z_n at $n = 10$ timesteps for 500 realisations. The closeness of the fit improves with more realisations.

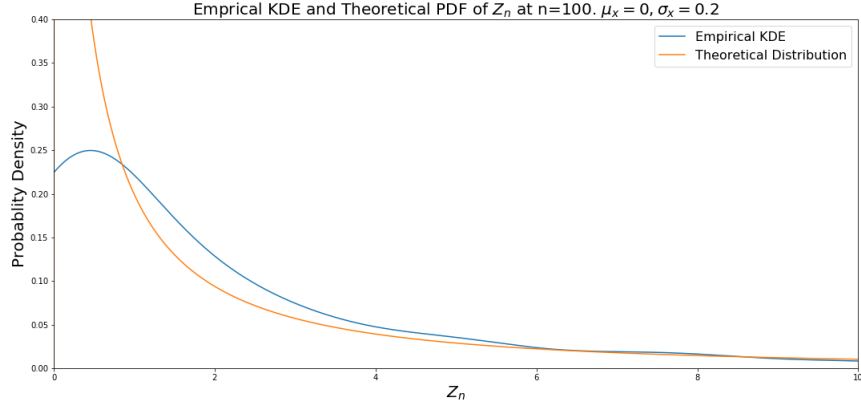


Figure 8. Empirical kernel density estimation and theoretical probability density function for Z_n with $\mu_x = 0$ and $\sigma = 0.2$ at $n = 100$ timesteps over 500 realisations.

Figure shows the empirical kernel density estimate and the theoretical prob-

ability density function for Z_n at $n = 100$ timesteps for 500 realisations. The fit is reasonable close for $Z_n > 1$. Below $Z_n = 1$, the theoretical distribution is much higher than the KDE. This is most likely due to the KDE smoothing function avoiding large fluctuations.

2.4.4 Ergodic Average

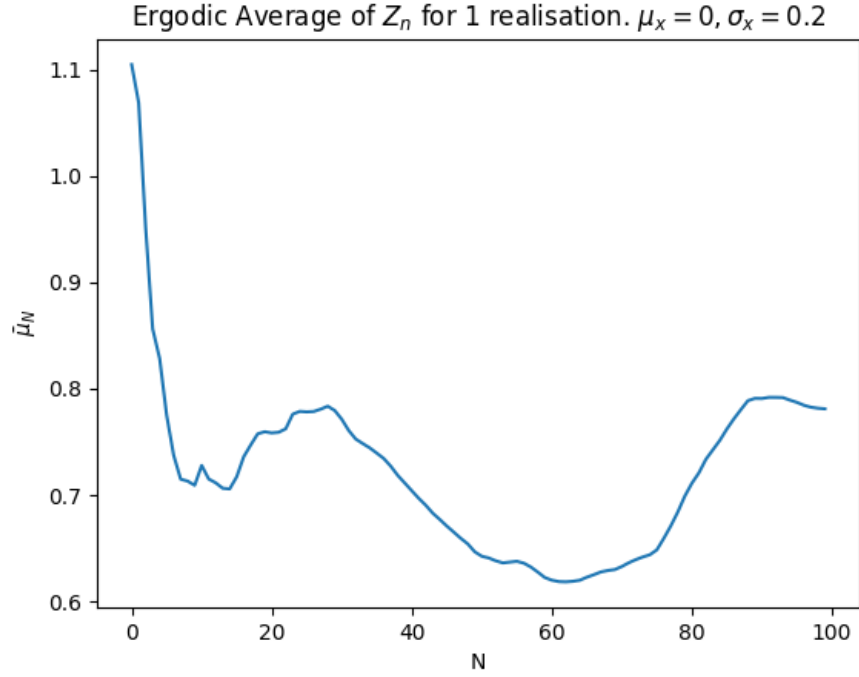


Figure 9. Ergodic average of Z_n for a single realisation as a function of total timesteps, N . $\mu_x = 0$ and $\sigma_x = 0.2$.

Figure shows the ergodic average for a single realisation plotted over 100 timesteps.

2.5 Part E - Empirical Tail

$E(Z_n) = 1$ for all $n \geq 0$

$$E(Z_n) = \exp(n\mu + \frac{n\sigma^2}{2}) = 1$$

$$\mu + \frac{\sigma^2}{2} = 0$$

$$\mu = -\frac{\sigma^2}{2}$$

$$\mu = -\frac{1}{50}$$

A value of μ_x of -0.02 will give $E(Z_n) = 1$ for all $n \geq 0$.

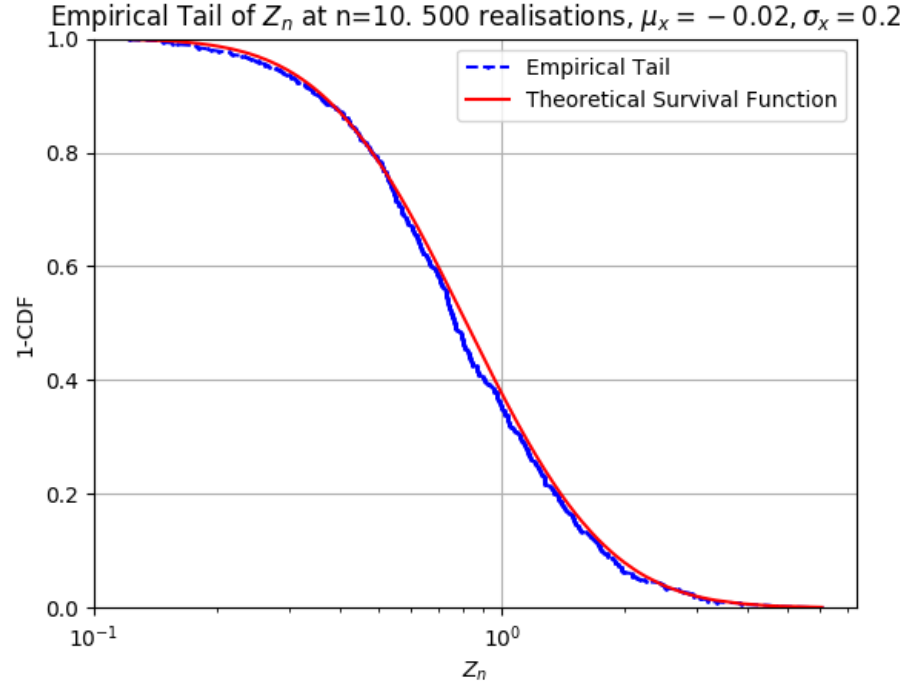


Figure 10. Empirical tail of Z_n compared to the theoretical prediction of the survival function, 1-Cumulative Density Function. At timestep 10. 500 realisations, $\mu_x = -0.02$, $\sigma_x = 0.02$.

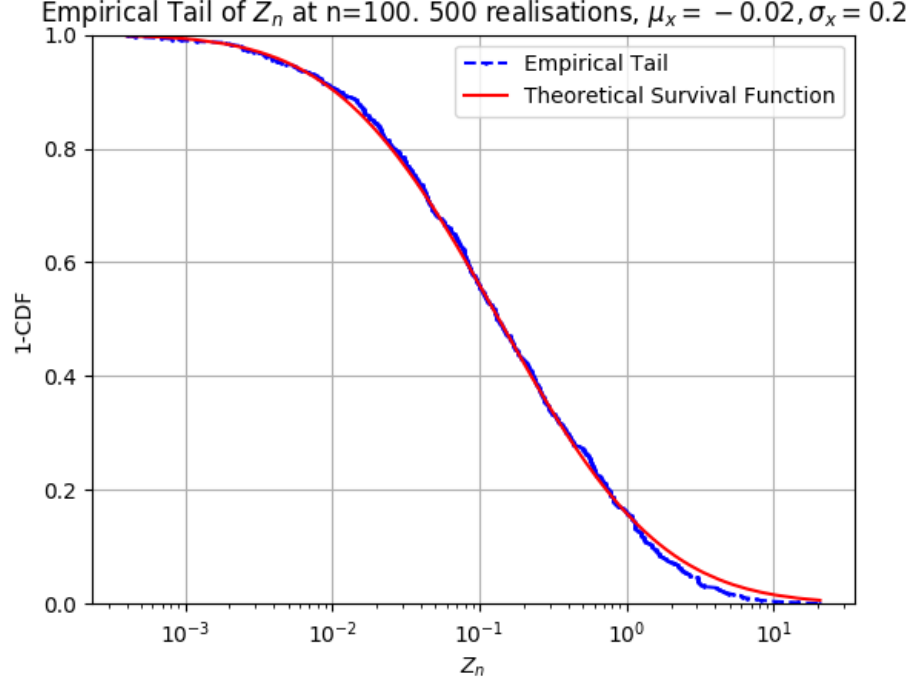


Figure 11. Empirical tail of Z_n compared to the theoretical prediction of the survival function, 1-Cumulative Density Function. At timestep 100. 500 realisations, $\mu_x = -0.02$, $\sigma_x = 0.02$.

Figures 10 and 11 show the empirical tail of Z_n at timesteps $n = 10$ and $n = 100$ respectively, with a close fit to the theoretical prediction.

Figure shows the empirical tail of the data compared to the theoretical survival function, defined as 1 minus the cumulative distribution function.

2.6 Part f

2.6.1 Ergodicity of Z_n

$X_n \sim N(-0.02, 0.2^2)$ and $Y_n = \sum_i^n X_n$ and $Z_n = \exp(Y_n)$
 $\mu_x < 0$, therefore as $n \rightarrow \infty$, $Y_n \rightarrow -\infty$, $Z_n \rightarrow 0$

With a non-zero starting distribution, the distribution will flatten with time as the variance scales with timesteps. And so there can be no stationary non-zero distribution.

The only stationary distribution is the delta function at zero, $\delta(0)$ this will remain zero as the recurrence relation is

$$Z_{n+1} = Z_n \exp(X_{n+1})$$

The process is ergodic.

By the law of large numbers, the empirical average

$$\hat{\mu}^M = \frac{1}{M} \sum_{i=1}^M Z_n^i \rightarrow E(Z_n) \text{ as } M \rightarrow \infty$$

$$E(Z_n) = 1$$

Therefore, as $M \rightarrow \infty$, the empirical average should converge to 1 for fixed

n.

At very large n, the expected value of Z_n is still 1, so for fixed finite M

$$\hat{\mu}_n^M \rightarrow 0 \text{ as } n \rightarrow \infty$$

Assuming that the limits do commute:

$$\lim_{n \rightarrow \infty} \lim_{M \rightarrow \infty} \hat{\mu}_n^M = \lim_{M \rightarrow \infty} \lim_{n \rightarrow \infty} \hat{\mu}_n^M$$

$$\lim_{n \rightarrow \infty} 1 = \lim_{M \rightarrow \infty} 0$$

$$1 = 0$$

we reach a contradiction and so the limits do not commute.

The limit of $\bar{\mu}_N$ as $N \rightarrow \infty$ is equivalent to the right hand side of the previous limit equation, which converges to 0. This does not contradict the ergodic theorem because the empirical average converges to the stationary distribution at zero. The ergodic theorem applies even though the function is not bounded.

3 Question 3

3.1 Part a

Each individual can have the starting type of any other individual. Let T equal the set of all unique starting states, so

$$T = \{X_0(1), X_0(2), \dots, X_0(L)\}$$

Each individual can have a type of any element in that set. This gives a total state space of size L^2 . In mathematical notation:

$$X(i) \in T \quad \forall i \in \{1, 2, \dots, L\}$$

$$X(i) \in \{X_0(1), X_0(2), \dots, X_0(L)\} \quad \forall i \in \{1, 2, \dots, L\}$$

$$X(i) \in X_0(j) \text{ where } j \in \{1, 2, \dots, L\} \quad \forall i \in \{1, 2, \dots, L\}$$

The process is not irreducible, as once a type goes extinct it stays extinct, and so not every state can be reached from every other state.

The stationary distributions are where all individuals are of one type i.e. all $X(i)$ are equal to the same one of the initial types $X_0(j)$. In mathematical notation:

$$X(i) = X_0(j) \text{ where } j \in \{1, 2, \dots, L\}$$

3.2 Part b

3.2.1 State space

The future state of the process depends only on the current state at each time step, so yes it is Markov.

The state space is

$$N \in \{0, 1, \dots, L\}$$

For each type, there can be an integer number of individuals of that type between 0 and L.

3.2.2 Transition Probabilities

Let $N_t(j)$ be the number of individuals of a particular species, j in a generation, and L individuals in total. For individual of the next generation, the probability of being of this particular species is equal to the proportion of individuals of that type in the parent generation.

$$p(X_{t+1}(i) = j) = N_t(j)/L$$

So the transition probabilities for $N_t + 1$ are given by a binomial distribution:

$$p(N_{t+1}(j) = k) = \binom{L}{k} \left(\frac{N_t(j)}{L}\right)^k \left(1 - \frac{N_t(j)}{L}\right)^{L-k}, \quad k = 0, 1, \dots, L$$

The process is not irreducible, if the number of individuals of the given species reaches zero, then it is extinct and can never grow again above zero. If the number of individuals reaches L , then this species is the only species left and will always remain so.

3.2.3 Stationary Distributions

If we define a distribution vector as

$$\pi = [N_t(0), N_t(1), \dots, N_t(L)]$$

Then there are stationary distributions on the absorbing states

$$\pi_1 = [1, 0, \dots, 0, 0]$$

$$\pi_2 = [0, 0, \dots, 0, 1]$$

and any normalised linear combination of these states, so

$$\pi_0 = [a, 0, \dots, 0, 1 - a] \text{ where } a \in [0, 1]$$

With the initial condition $N_0 = 1$, there is one individual of this type in the population. By symmetry, the probability of this species taking over has to be equal to $1/L$. So the limiting distribution as $t \rightarrow \infty$ is

$$\pi_\infty = [1 - \frac{1}{L}, 0, \dots, 0, \frac{1}{L}]$$

The process is not irreducible, as once a state has $N_i = 0$ for any i , i.e. a type goes extinct, the state space where $N_i > 0$ is no longer accessible.

3.3 Part C - Simulations

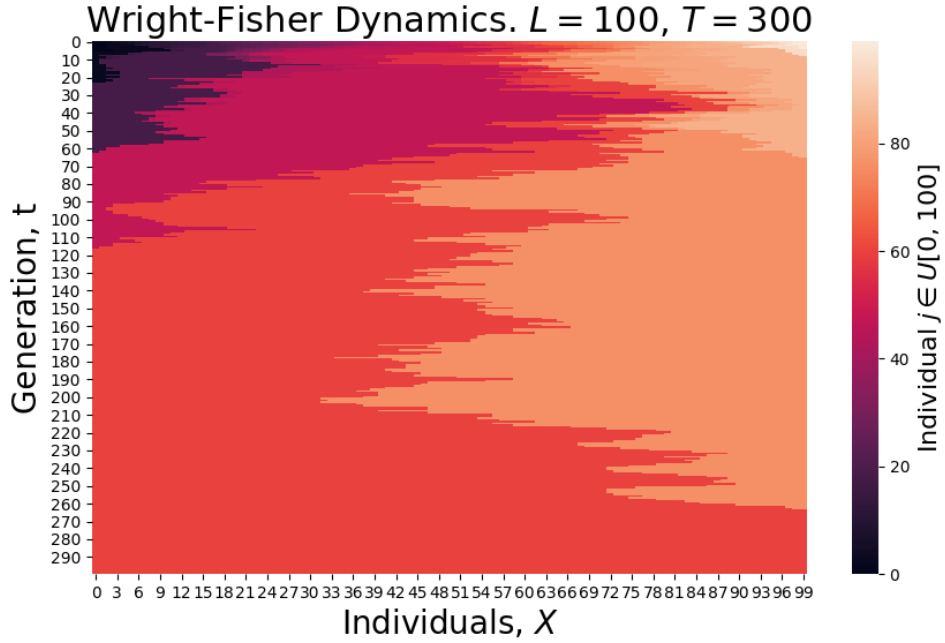


Figure 12. Dynamics of Wright-Fisher model of population dynamics with $L = 100$ individuals of unique type at generation $t = 0$.

Figure shows a heatmap of a simulation of Wright-Fisher dynamics with 100 individuals. The process reaches fixation, with only one unique type left, after about 260 generations. There are 2 unique types left after about 120 generations and 3 unique types after about 70 generations.

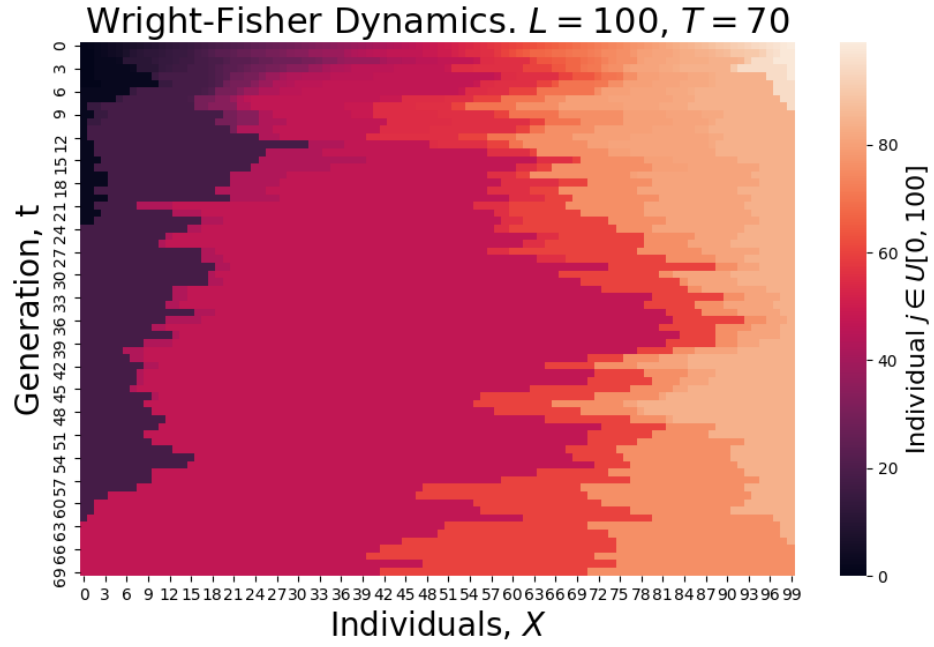


Figure 12. Dynamics of Wright-Fisher model of population dynamics with $L = 100$ individuals of unique type at generation $t = 0$, up to timestep $t = 70$.

Figure shows the same simulation up to generation 70 only. In the earlier generations, the number of types is quickly reduced as types go extinct.

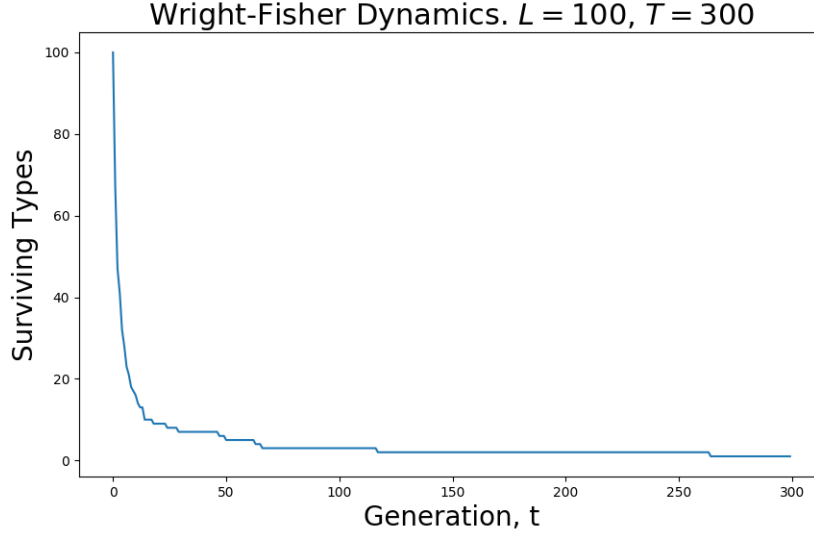


Figure 13. Number of surviving unique types for Wright-Fisher model as a function of generation, t , for one simulation.

Figure shows the number of surviving unique types as a function of generation for the same simulation. The number of

The probability of any particular type going extinct in the next generation is

$$p(N_{t+1}(j) = 0) = (1 - \frac{N_t(j)}{L})^L$$

If there is only one individual of a type, as in generation 0, then this is approximately 0.37. In later generations, there are often many individuals of a surviving type, and so the chance of that type going extinct is lower, but non-zero.

While there is more than one type, there is always a probability that one or more of the types will go extinct in the following generation. So over time the number of unique generations reduces. Given enough time, the number of types will always go to 1.

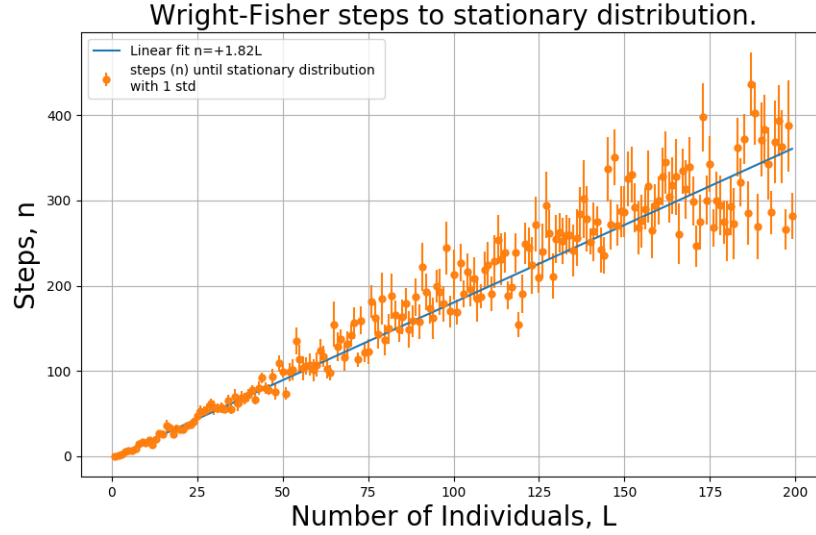


Figure 13. Average time to fixation for Wright-Fisher model as a function of number of individuals. Each L was simulated 20 times, with the empirical average and 1 standard deviation shown.

Figure shows an empirical simulation of the time to absorption, n_{abs} as a function of the number of individuals. There appears to be a linear relationship, approximately of the form:

$$n_{abs} = 1.82L$$

This is an approximate relationship and further work should be done to determine the confidence interval.