Question 1

Equation (4.1.4) presents the expected numbers in the Greenwood model.

(a). *Derive these equations, namely*

$$\begin{aligned}\mathbb{E}[X_t \mid X_0 = x_0] &= \alpha^t x_0, \\ \mathbb{E}[Y_t \mid X_0 = x_0] &= \alpha^{t-1}(1-\alpha)x_0.\end{aligned} \tag{4.1.4}$$

(b). *Assume $x_0 = 6$ and $\alpha = 0.8$. Then plot these expected values for some sensible time*

(a). We recall that

$$\begin{aligned}p_{(x,y)_t,(x,y)_{t+1}} &\equiv \mathbb{P}\{(X,Y)_{t+1} = (x,y)_{t+1} \mid (X,Y)_t = (x,y)_t\} \\ &= \binom{x_t}{x_{t+1}} \alpha^{x_{t+1}}(1-\alpha)^{y_{t+1}} = \binom{x_t}{x_{t+1}} \alpha^{x_{t+1}}(1-\alpha)^{x_t - x_{t+1}}\end{aligned} \tag{4.1.2}$$

We note that given this pmf for $p_{(x,y)t,(x,y)t+1}$, we can say $X_{t+1} \sim \mathsf{Bin}(X_t, \alpha)$. Thus it follows from the fact $\mathbb{E}X = np$ for $X \sim \mathsf{Bin}(n,p)$ that

$$\mathbb{E}[X_{t+1} \mid X_t] = \alpha X_t. \tag{$\star$}$$

We use this to show $\mathbb{E}[X_t | X_0 = x_0] = \alpha^t x_0$. Now, using the tower property,

$$\begin{aligned}\mathbb{E}[X_t \mid X_0 = x_0] &= \mathbb{E}_{(X_{t-1})}\left[\mathbb{E}[X_t | X_{t-1}] \mid X_0 = 0\right] \\ &= \mathbb{E}[\alpha X_{t-1} \mid X_0 = x_0] \text{ by } (\star). \\ &= \alpha\mathbb{E}[X_{t-1} \mid X_0 = x_0] \text{ by linearity of } \mathbb{E}. \\ &= \alpha\mathbb{E}_{(X_{t-2})}\left[\mathbb{E}[X_{t-1} \mid X_{t-2}] \mid X_0 = x_0\right] \\ &= \alpha\mathbb{E}\left[\alpha X_{t-2} \mid X_0 = x_0\right] \\ &= \alpha^2\mathbb{E}\left[X_{t-2} \mid X_0 = x_0\right]. \text{ Repeating recursively,} \\ \implies \mathbb{E}[X_t \mid X_0 = x_0] &= \alpha^t\mathbb{E}\left[X_{t-t} \mid X_0 = x_0\right] = \alpha^t\mathbb{E}[X_0 | X_0 = x_0] \\ \implies \mathbb{E}[X_t \mid X_0 = x_0] &= \alpha^t x_0.\end{aligned}$$

Now to compute the expectation of Y_t we make use of the fact that $X_t + Y_t = X_{t-1}$ by definition, and again the linearity of the expectation:

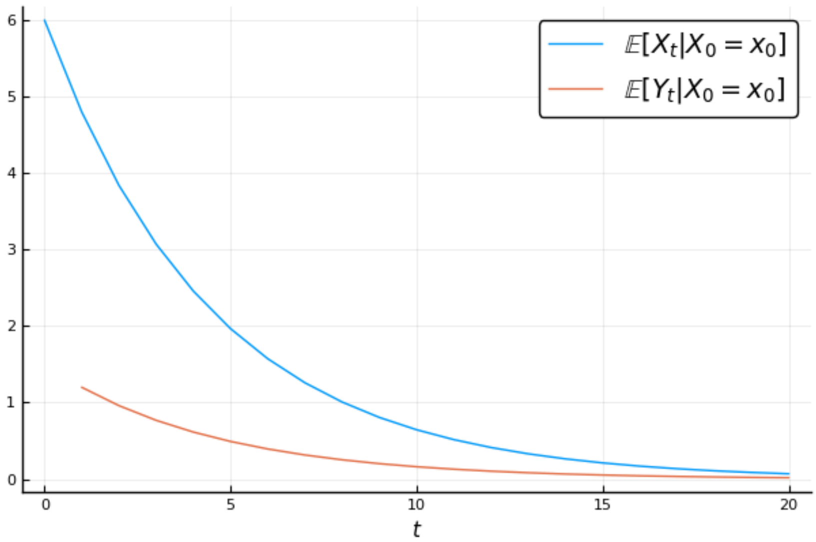
$$\begin{aligned}Y_t &= X_{t-1} - X_t \\ \implies \mathbb{E}Y_t &= \mathbb{E}[X_{t-1} - X_t] = \mathbb{E}X_{t-1} - \mathbb{E}X_t \\ \implies \mathbb{E}[Y_t \mid X_0 = x_0] &= \alpha^{t-1}x_0 - \alpha^t x_0 \\ &= \alpha^{t-1}x_0(1-\alpha).\end{aligned}$$

These are exactly the expressions in 4.1.4

(b). Note that all the code in this assignment is written in Julia 1.3.1 using Jupyter Lab. For brevity, imports with `using` are often omitted, that is some later cells rely on the fact that `Plots, LaTeXStrings, Distributions, LinearAlgebra` have already been imported.

[6]:
```
using LaTeXStrings; pyplot()
ExpectationX(t,x0)  = α.^t * x0
ExpectationY(t,x0)  = α.^(t.-1) .*(1-α) *x0
T2 = 1:20
plot([0, T2...], [x0, ExpectationX...](T2, x0), label=L"\mathbb{E}[X_t |X_0 = x_0]",␣
↪legendfontsize=14)
plot!(T2, ExpectationY(T2, x0), label=L"\mathbb{E}[Y_t |X_0 = x_0]")
```

[6]:



Question 2

Equation (4.2.1) presents a recursion for the expected number of susceptibles and infected in the Reed-Frost model.

(a). *Derive these equations, namely*

$$\mathbb{E}[(X,Y)_{t+1} \mid (X,Y)_t = (x,y)+t] = (x_t\alpha^{y_t}, x_t(1-\alpha^{y_t})). \tag{4.2.1}$$

(b). *Reproduce Figure 4.2 and also plot the trajectory of expected values, jointly on the (X, Y) plane in a similar manner to Figure 10.1 of [SWJ-10] (there, the plot is for a predator pray model).*

(a). First we begin by recalling (4.1.3), the transition probability matrix;

$$p_{(x,y)t,(x,y)t+1} = \binom{x_t}{x_{t+1}} \alpha^{y_t x_{t+1}}(1-\alpha^{y_t})^{y_{t+1}}. \tag{4.1.3}$$

It is easy to see that here $X_{t+1} \sim \mathsf{Bin}(X_t, \alpha^{Y_t})$. This makes the conditional expectation straightforward (again noting $\mathbb{E}X = np \mid X \sim \mathsf{Bin}(n,p)$);

$$\begin{aligned} &\mathbb{E}(X_{t+1} \mid X_t = x_t, Y_t = y_t) = X_t\alpha^{Y_t} \mid X_t = x_t, Y_y = y_t \\ \implies &\mathbb{E}(X_{t+1} \mid X_t = x_t, Y_t = y_t) = x_t\alpha^{y_t} \end{aligned}$$

To compute $\mathbb{E}(Y_{t+1} \mid X_t = x_t, Y_t = y_t)$ we again note by definition $X_{t-1} = X_t + Y_t$ and the linearity of the expectation;

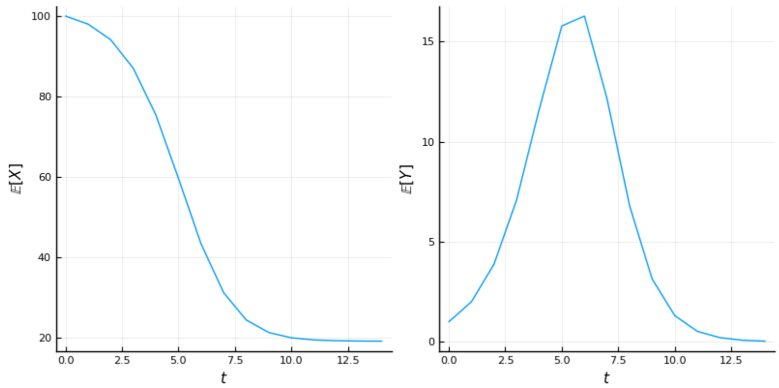
$$\begin{aligned} \mathbb{E}(Y_{t+1} \mid X_t = x_t, Y_t = y_t) &= \mathbb{E}(X_t - X_{t+1} \mid X_t = x_t, Y_t = y_t) \\ &= \mathbb{E}(X_t \mid X_t = x_t, Y_t = y_t) - \mathbb{E}(X_{t+1} \mid X_t = x_t, Y_t = y_t) \\ &= x_t - x_t\alpha^{y_t} = x_t(1-\alpha^{y_t}) \end{aligned}$$

(b). Note that a scatter plot would probably be more appropriate given the discrete data points, a line plot has been used to be consistent with the figure in [EM]

[4]:
```
using Plots, LaTeXStrings; pyplot()
(x0, y0, α) = (100, 1.0, 0.98)
tmax2 = 15
EX = zeros(Float64, tmax2)
EY = zeros(Float64, tmax2)
EX[1] = x0
EY[1] = y0
```

```
        for i =1:(tmax2-1)
        EX[i+1] = EX[i] * α^EY[i]
        EY[i+1] = EX[i] * (1- α^EY[i])
end
fig1 = plot(0:tmax2-1, EX, xlabel=L"t", ylabel=L"\mathbb{E}[X]", label=L"x_0= $x0")
fig2 =plot(0:tmax2-1, EY, xlabel=L"t", ylabel=L"\mathbb{E}[Y]", label=L"x_0= $x0")
plot(fig1, fig2, size=(800, 400), legend=:none)
```

[4]:



[5]:

```
tmax2 = 30
EX = zeros(Float64, tmax2)
EY = zeros(Float64, tmax2)
fig = plot();
for x = [100,105,95] # plot a few trajectories
        EY[1] = y0
        EX[1] = x
        for i =1:(tmax2-1)
                EX[i+1] = EX[i] * α^EY[i]
                EY[i+1] = EX[i] *(1- α^EY[i])
        end
        plot!(EX, EY, xlabel=L"\mathbb{E}X", ylabel=L"\mathbb{E}Y",
        title="\"Phase Portrait\" trajectory of RF Model Expectations",
        label=L"x_0= " * "$x")
end
fig
```

[5]:

Question 3

3. *Consider the Markov Chain* $\{X_t, t = 0, 1, 2, \ldots\}$ *defined by* $X_0 = x_0$ *and the transition probability matrix as in equation (4.1.5) for the Greenwood model. The state space is* $I := \{0, 1, 2, ..., x_0\}$.

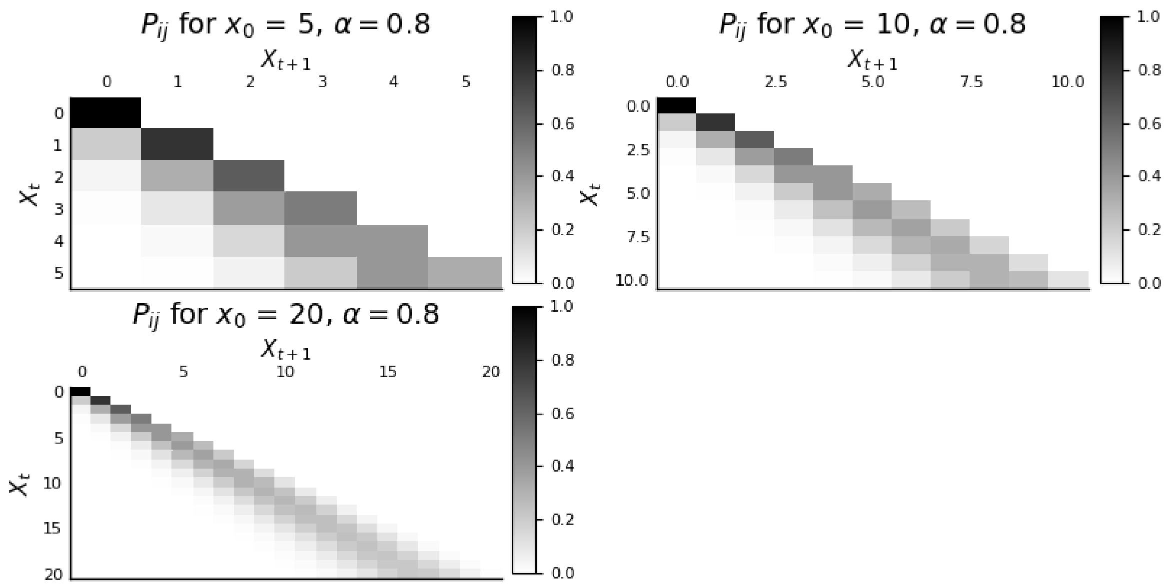
(a). *Plot a heat-map of this transition probability matrix for $x_0 = 5, x_0 = 10$, and $x_0 = 20$ and some $\alpha \in (0.5, 0.9)$ of your choice.*

[6]:
```
α = 0.8
function constructTransitionMatrix(α, N)
        # N = 10 # N = x0
        P = zeros(N+1,N+1)
        probsBin(n,k,p) = binomial(n,k)*p^k*(1-p)^(n-k)
        for i = 0:N
                for j = 0:N
                        P[i+1,j+1] = probsBin(i,j,α)
                end
        end
        return P
end

out_plots = []
for x0 in [5, 10, 20]
        f = f=heatmap(0:x0, 0:x0, constructTransitionMatrix(α, x0), title= L"P_{ij}" * "␣
 ↪for " *L"x_0" * " = $x0, " * L"\alpha = " * "$α",
        ylabel=L"X_t", xlabel=L"X_{t+1}", yflip=true,
        c=cgrad([:white, :black]),
        xmirror=true
        );
        push!(out_plots, f)

end
f =plot(out_plots..., size=(800, 400), legend=:none)
```

[6]:



(b). *Determine the communicating classes of this Markov chain. How many are there? Which are recurrent? Which are transient?*

The communicating classes of the chain are $\{0\}, \{1\}, \dots \{x_0\}$. By definition $i \to i \forall i \in I$. Additionally the lower diagonal nature of the chain dictates that for $j \neq i$, $i \to j \implies j < i$ and $j \not\to i$. Thus none of these classes can be merged. First we note that 0 is a recurrent class, we can see this directly from the transition probability matrix as the only possible future state is returning to zero. More formally note this implies $\rho_{00} = 1 \implies \rho_{00}^k = 1$ meaning the state is returned to infinitely many times, and is by definition recurrent. The other communicating classes are transient as they all have positive transition probabilities to the class $\{0\}$ which is recurrent.

We can see this by considering $T_x := \inf\{n \in N : S_n = x\}$ and $\mathbb{P}_x(T_x < \infty) = 1 - \mathbb{P}_x(T_x = \infty)$ using the subscript to denote that $X_0 = x$.
Now $\mathbb{P}_1(T_1 = \infty) \geq \mathbb{P}_1(\text{any single path which never returns to 1})$. So $\mathbb{P}_1(T_1 = \infty) \geq \mathbb{P}_1(\{1\} \to \{0\}) = P_{10} = 1 - \alpha > 0$. So

$$\begin{aligned} \mathbb{P}(T_1 = \infty) &> 0 \\ \implies 1 - \mathbb{P}(T_1 = \infty) &\in [0, 1) < 1 \\ \implies \mathbb{P}(T_1 < \infty) = 1 - \mathbb{P}(T_1 = \infty) &< 1 \end{aligned}$$

Since $\mathbb{P}_1(T_1 < \infty) = \rho_{11} < 1$ we must have that $\{1\}$ is transient. Since this analysis only was conditional on the fact that there existed a path with positive probability which could never return to the start state (in this case P_{10}), it applies equally well for any other state j as $P_{j0} > 0$ for each element in the state space. As a side note, this is not clearly apparent in the above graphics, as these probabilities are tiny (but nonzero) and are not visible on colour map scale from 0 to 1.

Alternatively, we could invoke Theorem 1.5 from [SP1] Which states if $\rho_{xy} > 0$ but $\rho_{yx} < 1$, then x is transient, since for any $j \in I \setminus \{0\}, \rho_{j0} > 0$ and $\rho_{0j} = 0$.

(c). *The part of equation equation (4.1.4) for X_t , presenting the expected value, can be obtained in a much more cumbersome way to what you did in* 1*a above. For this, take the the power P^t and compute $e_{x_0+1}^T P^t v$ where $e_{x_0+1} = [0, 0, \ldots 1]^T$ which is of length x_0+1 and $v = [0, 1, 2, \ldots x_0]^T$. Compute this numerically and see that the results numerically agree with those in the plot of* 1*b. Explain why this holds.*

In the lectures we considered the matrix vector product $P\boldsymbol{v}$ where P is a stochastic matrix with elements given as p_{ij} with dimension $n \times n$. We note that these n dimensions correspond to the state space $I = [0, 1, 2, \ldots n-1 \equiv x_0]$. Considering the ith row, we note by definition of matrix multiplication:

$$(P\boldsymbol{v})_i = \sum_{k=1}^{n} p_{ik} v_k$$

Now, if we have that $v_k = k-1$ (as it is defined above), this is analogous to the formula for expectation. Taking $m = k - 1$ we have

$$(P\boldsymbol{v})_i = \sum_{m=0}^{n-1} m p_{im}$$

Here however we are interested in considering this expression with the tth power of P rather than P itself. Denoting the elements of P^t as $(P^t)_{ij}$ we recognise this describes the transition probabilities over a t period gap and have

$$(P^t\boldsymbol{v})_i = \sum_{m=0}^{n-1} m(P^t)_{im}.$$

At this point we recognise that if the expression were $\sum mf(m)$ it would be equivalent to $\mathbb{E}X_t$, however we instead have transition probabilities dependent on i. As such, we have a conditional expectation:

$$(P^t\boldsymbol{v})_i = \mathbb{E}[X_t|X_0 = i].$$

Now if we consider the vector $P^t\boldsymbol{v}$, and left multiply by $e_{x_0+1}^T = [0, 0, \ldots 1]$, the result will only contain one nonzero term; that corresponding to the final row:

$$\begin{aligned} [0, 0, \ldots 1]P^t\boldsymbol{v} = (P\boldsymbol{v})_n &= \mathbb{E}[X_t|X_0 = n-1]. \\ e_{x_0+1}P^t\boldsymbol{v} &= \mathbb{E}[X_t|X_0 = x_0] \end{aligned}$$

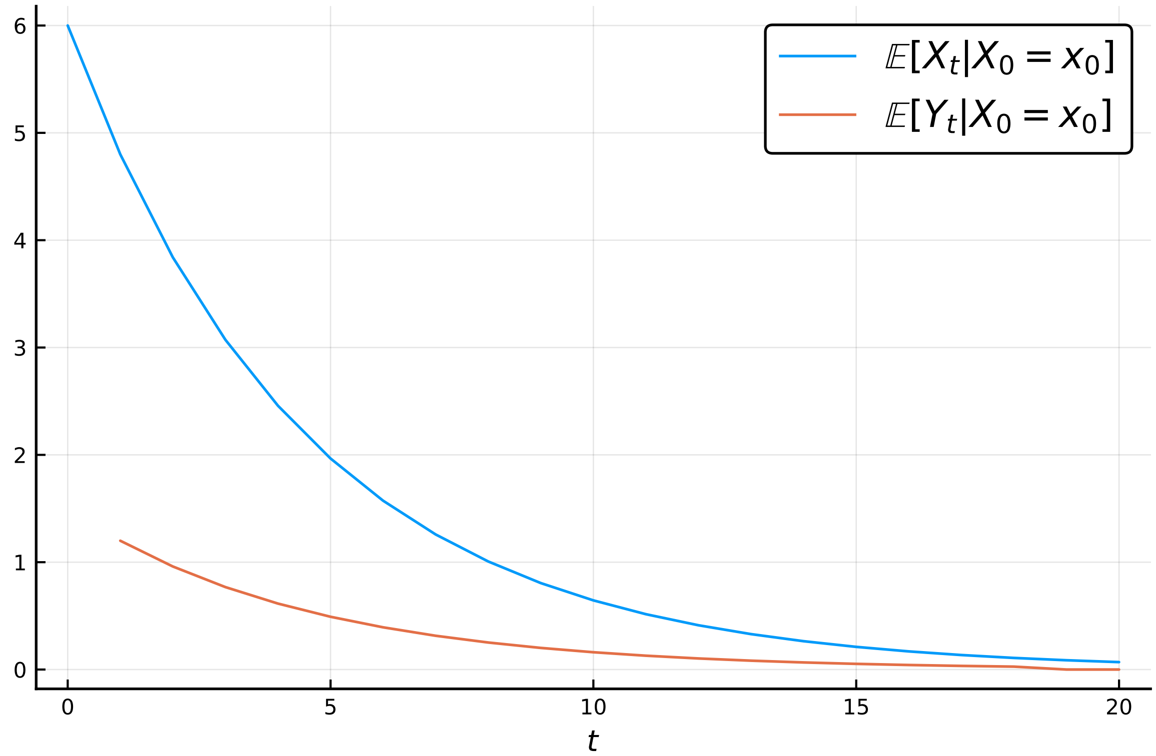
We note the state space has n sequential integer elements, including zero, so $n-1$ is the final maximum element which is equal to x_0.

[30]:
```
(x0, α) =(6, 0.8) # fixed from 1b
evec = zeros(1,x0+1)
evec[end] =1
vvec = 0:x0
P = constructTransitionMatrix(α, x0); # from Q3a

T2 = 0:20
T2y = 1:T2[end]; # y isn't defined at t =0
```

[31]:
```
EXnew = [(evec * P^i *vvec)[1] for i in T2] # note [1] is to kill second dimension
EYnew = zeros(length(T2y)) # Ey starts at t=1
EYnew[1] = 1
for i =2:T2[end]-1
        # note different from defn since EY starts at 1
        EYnew[i-1] = EXnew[i-1] - EXnew[i]
end
plot(T2, EXnew, label=L"\mathbb{E}[X_t |X_0 = x_0]", legendfontsize=14)
plot!(T2y, EYnew, label=L"\mathbb{E}[Y_t |X_0 = x_0]", legendfontsize=14)
```

[31]:



We see that this is identical to that in (1b), however the point at $(0, x_0)$ has actually been included here, there it was omitted for convenience.

(d). *Attempt to carry out a similar numerical computation for the expectation of Y_t in equation (4.1.4) and explain your method.*
Although it is likely not the intended method, we can consider a modification of the above calculation in the same vein as is done in Question 1. There we used the fact that $Y_{t+1} = X_t - X_{t+1}$ and so $\mathbb{E}Y = \mathbb{E}(X_t - X_{t+1}) = \mathbb{E}X_t - \mathbb{E}X_{t+1}$. So,

$$\begin{aligned}\mathbb{E}[Y_{t+1} \mid X_0 = x_0] &= \mathbb{E}[X_t|X_0 = x_0] - \mathbb{E}[X_{t+1}|X_0 = x_0] \\ &= e_{x_0+1}P^t\boldsymbol{v} - e_{x_0+1}P^{t+1}\boldsymbol{v} \\ &= e_{x_0+1}\left(P^t - P^{t+1}\right)\boldsymbol{v} \\ &= e_{x_0+1}P^t\left(I - P\right)\boldsymbol{v}\end{aligned}$$

Unsurprisingly, this yields the same results as performing the calculation directly using the computed values for $\mathbb{E}X_t$.

Question 4

Consider now the joint distribution of (W, T) as described in subsection 4.1.1 (dealing with the Greenwood model). Here T is the first time in which there are no infectives and W is the number of susceptibles that have been infected by that time. That is the random variables T and W describe the "end of the infection". The main aim is to know the probabilities,

$$\Gamma(k, n|x_0) = \mathbb{P}\left((W, T) = (k, n)|X_0 = x_0, Y_0 > 0\right),$$

for $k = 0, 1, \ldots, x0$ and $n = 1, 2, \ldots$. These assume that at onset x_0 family members are sick and there is an infection in the household. For all the numerical computations in this question, use $x_0 = 6$ and some fixed $\alpha \in (0.7, 0.9)$ of your choice.

(a). Explain equation (4.1.6).

(b). Use the recursive relationship $\Gamma(k, n|x_0) = p^{n-1}_{x_0-k}\alpha^{x_0-k}$ to (numerically) compute $\mathbb{P}(W > 4)$.

(c). Compare your numerical result to an estimate obtained by a Monte-Carlo simulation creating 10^6 repeated trajectories and using those to estimate $\mathbb{P}(W > 4)$.

(d). Attempt to reproduce the PGF computations in subsection 4.1.1 to then obtain the same numerical result (this item is longer and slightly more challenging).

(a).

$$p^t_j \equiv \mathbb{P}(X_t = j, Y_t > 0) = \sum_{i=j+1}^{x_0-(t-1)} p^{t-1}_i p_{ij} \tag{4.1.6}$$

In order to derive this expression, we first consider computing the simpler quantity, $\mathbb{P}(X_t = j)$, irrespective of Y_t. Additionally, we make use of the fact that $p^0_i = \mathbb{P}(X_0 = i) = \delta_{x_0 i}$, and denote I as the state space. Now,

$$\mathbb{P}(X_t = j) = \sum_{k\in I} \mathbb{P}(X_t = j, X_{t-1} = k).$$

By definition of conditional probability, we have

$$\mathbb{P}(X_t = j, X_{t-1} = k) = \mathbb{P}(X_t = j|X_{t-1} = k)\mathbb{P}(x_{t-1} = k),$$

We can write this in compact notation, analoguous to (4.1.6). Let p_{ij} denote the one step transition probability matrix, and we let the $q^t_j := \mathbb{P}(X_t = j)$, to differentiate from p^t_j:

$$\implies \mathbb{P}(X_t = j, X_{t-1} = k) = p_{kj} q^{t-1}_k$$
$$\implies q^t_j = \mathbb{P}(X_t = j) = \sum_{k\in I} q^{t-1}_k p_{kj}$$

The modification to yield (4.1.6) follows from the condition that the outbreak must be ongoing, or $Y_t > 0$. Recall that $X_t = X_{t-1} - Y_t$. Since $Y_t > 0$ we must have $X_t < X_{t-1}$, which restricts the transitions in p_{kj}. We require that $j < k$ for all k and as such, the lower bound of k must be $j + 1$. Secondly, having $Y_t > 0$ means that there must have been at least one infected person at each time $\bar{t} < t$. As such, we cannot have been in state x_0 at time $t - 1$, or there would have been days with zero infections. This restricts the upper bound for valid indices in the transition p_{kj}. To have reached the t-th day with the outbreak still ongoing, there must have been at minimum, one infection on all prior days, so the maximum possible susceptible people at time $t - 1$ is $x_0 - (t - 1)$. Thus with these restrictions on the transitions when $Y_t > 0$ we conclude that

$$p^t_j = \mathbb{P}(X_t = j, Y_t > 0) = \sum_{k=j+1}^{x_0-(t-1)} p^{t-1}_k p_{kj}$$

(b). First we simply construct the functions outlined above, p^t_j, Γ and p_{ij}

[3]:
```julia
α = 0.74
x0 = 6

"Transition matrix in index notation consistent with (4.1.6)"
function transition_probs(i,j)
 return binomial(i,j)*α^j*(1-α)^(i-j)
end

"Multistep transition function (4.1.6)"
function cumulative_time_prob(t, j)
 if t ==0 # recursion base case
     return j == x0 ? 1 : 0
 end
 # handle if sum is empty
 if j+1 > x0 - (t-1)
     return 0
 end

 return sum(cumulative_time_prob(t-1, i) * transition_probs(i,j)
             for i in j+1:x0-(t-1))
end

"Pr(W=k, T=n) where W is # infected total, T is time of eradication"
function gamma(k,n, i=x0) #x0 =i is assignment case, keep i
     # for notation consistent with [EM 4]
     return cumulative_time_prob(n-1, i-k) * α^(i-k)
end
```

[4]:
```julia
#Compute Pr(W>4) by summing joint cdf to recover marginal
tfinal = x0 +1 # maximum time before eradication
marginalprob = 0.0
for w in 4+1:x0 # valid range of W>4 (max infect all x0 people)
 # sum over the all possible end times n
 # with current w
 marginalprob+=sum(gamma(w,n) for n in 1:tfinal)
end
println("Pr(W>4) = $marginalprob")
```

```
Pr(W>4) = 0.265253435130611
```

(c). The code for the Greenwood simulation is relatively straightforward, we take in vectors to store the realisations of X_t and Y_t and simulate X_{t+1} from the binomial distribution $\mathsf{Bin}(X_t, \alpha)$. The function returns the number of people infected, and the time taken. We then repeatedly re-run the simulation to determine an estimate for $\mathbb{P}(W > 4)$:

[5]:
```julia
N = 1e6 # number of simulations
α = 0.74
"Function which simulates greenwood model,
stores simulated values in input vectors X and Y.
returns realisations of (W, N)"
function greenwoodSimulation!(X, Y)
 X = fill!(X, 0) # Reset to zero
 Y = fill!(Y, 0)
 X[1] = x0 # initial condition, leave y0 undefined

 for i=1:tfinal-1
     X[i+1] = rand(Binomial(X[i], α) )
     Y[i+1] = X[i] - X[i+1]
     # if infection died out stop early
     if Y[i+1] == 0
         # return (W, T) realisations
         return (sum(Y), i )
```

```
        end
    end
    # return (W, T) realisations
    return (sum(Y), tfinal )
end

# Repeat simulation N times:
X = zeros(Int, tfinal)
Y = zeros(Int, tfinal);
count = 0
gamma_test = 0
for sim in 1:N
    w, n = greenwoodSimulation!(X, Y)
    if w > 4
        count +=1
    end
end
println("Proportion of simulated trajectories where" *"\nW > 4 = ", count/N)
```

```
Proportion of simulated trajectories where
W > 4 = 0.26485
```

(d). Given that this question is only 2 marks, we skim over some of the details in explaining section 4.1.1. We start with the computation of $\mathbb{P}(T = t)$, that the infection ends at time and note that for this to occur, we must finish in a recurrent state for X_t, that is $Y_t = 0$ and the infection has died out. This corresponds to any of the diagonal element of the transition probability matrix P, and so we can decompose $P = \bar{P} + Q$ to correspond to this. To end at time t, the only transition through the states in Q must be the final one, we write $P^{t-1}Q$ as the probabilities for such a transition. Next we impose the initial state of x_0 by left multiplying by $e_{x_0+1} \equiv \boldsymbol{A}$. $\boldsymbol{A}\bar{P}^{(t-1)}Q$ is still a $1 \times x_0$ vector of possible paths to end in state t, we sum over these by right multiplying by a vector of 1's to get

$$\mathbb{P}(T = t) = \boldsymbol{A}\bar{P}^{(t-1)}Q\mathbf{1}$$

Now to compute the pgf, by definition we have that

$$\begin{aligned}
G(z) = \mathbb{E}z^X &= \sum_{n=0}^{\infty} z^n \mathbb{P}(X = n) \\
\implies \Phi_T(\theta) &= \sum_{t=1}^{\infty} \theta^t \boldsymbol{A}\bar{P}^{(t-1)}Q\mathbf{1} \\
&= \boldsymbol{A}(\sum_{t=1}^{\infty} \bar{P}^{(t-1)}\theta^{(t-1)})\theta Q\mathbf{1} \\
&= \boldsymbol{A}(I - \theta\bar{P})^{-1}\theta Q\mathbf{1}, |\theta| < 1
\end{aligned}$$

By the properties of the geometric series. In fact, we will use the line above, since $\bar{P}$ is lower diagonal, and the $x_0 + 1$th power of the matrix will be zero. To determine the number of people infected, we consider the joint pgf, where each entry in $\bar{P}$ is multiplied by φ^{i-j}, the number of new people infected by such a transition in the matrix. Analogously, we have

$$\mathbb{P}(W = w, T = t) = \boldsymbol{A}\bar{P}^{(t-1)}(\varphi)Q\mathbf{1}$$

and

$$\begin{aligned}
\Phi_{W,T}(\theta, \varphi) &= \mathbb{E}[\theta^T \phi^W] = \boldsymbol{A}(I - \theta\bar{P}(\varphi))^{-1}\theta Q\mathbf{1}, |\theta|, |\varphi| < 1 \\
\implies \Phi_{W,T}(1, \varphi) &= \mathbb{E}[1^T \phi^W] = \Phi_W(\varphi) \text{ by definition.} \\
\text{So, } \Phi_W(\varphi) &= \boldsymbol{A}(I - \bar{P}(\varphi))^{-1}Q\mathbf{1} \\
\text{or } \Phi_W(\varphi) &= \boldsymbol{A}(\sum_{t=1}^{\infty} \bar{P}^{(t-1)}(\varphi)\theta^{(t-1)})Q\mathbf{1}
\end{aligned}$$

As was already noted, for a lower triangular matrix $\bar{P}^{n>x0} = 0$ so this is a finite sum, with only 7 terms for $x_0 = 1$. To save manual computation, we use the SymPy julia wrapper of the sympy python package. The final step to compute $\mathbb{P}(W > 4)$ is to note that this is simply $\mathbb{P}(W = 5) + \mathbb{P}(W = 6)$ since at most $x_0 = 6$ people can be infected. Finally we can compute these probabilities from the pgf by taking derivatives and evaluating them at zero, this was shown in early lectures and is straightforward to see regardless:

$$\mathbb{P}(X = n) = \left.\frac{G^{(n)}(z)}{n!}\right|_{z=0}$$

In these computations, I've left α as a symbolic variable until the end, to make the structure of P easier to see, and thereby $\bar{P}$ and Q.

[12]:
```
using LinearAlgebra
import SymPy
(x0, fixed_alpha) = (6, 0.74)
ϕ = SymPy.symbols("ϕ")
α = SymPy.symbols("α")
N = x0+1
P = zeros(SymPy.Sym, N,N)
probsBin(n,k,p) = binomial(n,k)*p^k*(1-p)^(Float64(n-k))

#Construct duration transition matrix
for i = 0:N-1
        for j = 0:N-1
                P[i+1,j+1] = SymPy.simplify(probsBin(i,j,α))
        end
end
display(P)
Q = Diagonal(P)
Pbar = P .-Q

"Create corresponding power of duration, infection matrix.
Note this is less efficient than including ϕ in Pbar and taking those powers
but this is more explicitly the textbook notation, even though they are equivalent."
function Pphi(;power=1)
        Ppower = zeros(SymPy.Sym, N,N)
        for i = 0:N-1
                for j = 0:N-1
                   Ppower[i+1,j+1] = SymPy.simplify((Pbar^power)[i+1, j+1] *ϕ^float(i-j))
                end
        end
        return Ppower
end

A = zeros(1,x0+1)
A[end] = 1
E = ones(x0+1)
eyeNN = Matrix{Float64}(I, N,N) #identity

# Compute PGF
Gw = A * (eyeNN + sum(Pphi(power=i) for i in 1:x0))* Q * E
Gw = Gw[1] # julia returns a singleton array, want a scalar
display(Gw)
```

$$\begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ (1-\alpha)^{1.0} & \alpha & 0 & 0 & 0 & 0 & 0 \\ (1-\alpha)^{2.0} & 2\alpha(1-\alpha)^{1.0} & \alpha^2 & 0 & 0 & 0 & 0 \\ (1-\alpha)^{3.0} & 3\alpha(1-\alpha)^{2.0} & 3\alpha^2(1-\alpha)^{1.0} & \alpha^3 & 0 & 0 & 0 \\ (1-\alpha)^{4.0} & 4\alpha(1-\alpha)^{3.0} & 6\alpha^2(1-\alpha)^{2.0} & 4\alpha^3(1-\alpha)^{1.0} & \alpha^4 & 0 & 0 \\ (1-\alpha)^{5.0} & 5\alpha(1-\alpha)^{4.0} & 10\alpha^2(1-\alpha)^{3.0} & 10\alpha^3(1-\alpha)^{2.0} & 5\alpha^4(1-\alpha)^{1.0} & \alpha^5 & 0 \\ (1-\alpha)^{6.0} & 6\alpha(1-\alpha)^{5.0} & 15\alpha^2(1-\alpha)^{4.0} & 20\alpha^3(1-\alpha)^{3.0} & 15\alpha^4(1-\alpha)^{2.0} & 6\alpha^5(1-\alpha)^{1.0} & \alpha^6 \end{bmatrix}$$

$$720.0\alpha^{15}\phi^{6.0}(1-\alpha)^{6.0}+6.0\alpha^{10}\phi^{1.0}(1-\alpha)^{1.0}+360.0\alpha^{10}\phi^{6.0}(1-\alpha)^{6.0}\left(\alpha(\alpha+1)\left(\alpha^2+1\right)+1\right)\ldots+\text{ many terms}$$

[28]:
```
sumtot = 0 # Sum probabilities for 5 & 6 (also check sum 0:6) = 1
for j = 5:6
        tmp = SymPy.simplify(SymPy.diff(Gw, ϕ, j)(ϕ=>0)/factorial(j))
        sumtot +=tmp
        println("P(x==$j) = ", tmp)
end
prob = sumtot(α=>fixed_alpha)
println("P(W>4) = $prob") # we evaluate at \alpha = 0.74
```

```
P(x==5) = α^2*(1 - α)^5.0*(720.0*α^14 + 360.0*α^12 + 360.0*α^11 + 360.0*α^10
          + 480.0*α^9 + 180.0*α^8 + 300.0*α^7 + 180.0*α^6 + 150.0*α^5
          + 60.0*α^4 + 60.0*α^3 + 30.0*α^2 + 6.0)
P(x==6) = (1 - α)^6.0*(720.0*α^15 + 360.0*α^14 + 360.0*α^13 + 480.0*α^12
          + 540.0*α^11 + 660.0*α^10 + 390.0*α^9 + 360.0*α^8 + 300.0*α^7
          + 240.0*α^6 + 126.0*α^5 + 75.0*α^4 + 50.0*α^3 + 15.0*α^2 + 6.0*α
          + 1.0)
P(W>4) = 0.265253435130611
```

This is correspondent with the other two methods of calculation.

Question 5

Consider the Markov chain for the Reed-Frost model with transition probability matrix as in (4.2.2). For all the numerical computations in this question, use $x_0 = 6$ and some fixed $\alpha \in (0.7, 0.9)$ of your choice (use the same α which you used for the previous question).

(a). What is the state space?

(b). Try to describe the communicating classes in a compact manner? If not possible, constrain to a small fixed x_0.

(c). Plot a heat-map similarly to 3a (you may want to use block-matrices in your software).

(d). Run a Monte-Carlo simulation to obtain an estimate for $\mathbb{P}(W > 4)$ similarly to 4c. How does the result compare to 4c? Explain why.

For this question, we choose $y_0 = 1$.

(a). The state space is

$$\{(x, y) | x, y \in \{0, 1, 2, \ldots, x_0\}\}$$

We note that this description considers a fixed x_0 susceptibles and a variable number of $y_0 \leq x_0$ infectives. From the perspective of Question 6 however, for a fixed number of arrivals (as opposed to susceptibles), we would instead have a state space of $\{(x, y) \mid x + y \leq \hat{x}_0\}$

(b). Before noting the communicating classes, it is beneficial to first consider the states which lead to one another. The key insight for the transition of $(X_t, Y_t) \to (X_{t+1}, Y_{t+1})$ is the relationship $X_t = X_{t+1} + Y_{t+1}$. This means that the transition $X_t \to X_{t+1}$ is sufficient to determine Y_{t+1}. Additionally, the occurrence of this transition is independent of Y_t, so long as it is not zero. Indeed, considering the heatmap in 5*c*, one can see that the same entries are nonzero for any nonzero Y_t, only the magnitude of the probabilities is affected.

The transitions which "lead to" one another are thus

$$(x, y) \to i \mid i \in \{(x, 0), (x-1, 1), \dots, (1, x-1), (0, x)\}$$

for any initial (x, y). Hence we can see the sum of the state components is strictly decreasing unless one of x or y are zero. Therefore the communicating classes must again be the singleton state space elements $\{(0,0)\}, \dots \{(0, x_0)\}, \{(1,0)\}, \dots \{(x_0, 0)\}, \dots \{(x_0, x_0)\}$. The case when $y = 0$ requires that $X_t = X_{t+1} + 0$ and so $(x, 0) \to (x, 0)$ for all future states. Therefore, $\{(x, 0) \mid x \in \{0, \dots, x_0\}\}$ are recurrent states. If $X_t = 0$, $X_{t+1} = 0$ and $Y_{t+1} = 0$ regardless of Y_t so any such states will transitions to $(0, 0)$, which is a recurrent closed class.

The remaining states are transient since they all have positive probability of transitioning to a recurrent state. Furthermore, since $X_t = X_{t+1} + Y_{t+1}$ we have that $X_t + Y_t < X_{t+1} + Y_{t+1}$ if $Y_t \neq 0$. Since this is a strictly decreasing recurrence, we conclude that these states which are not already outlined as recurrent are transient.

(c). This is the code used to produce the heatmap, first the transition matrix P_{ij} is constructed using a block array, and then it is plotted.

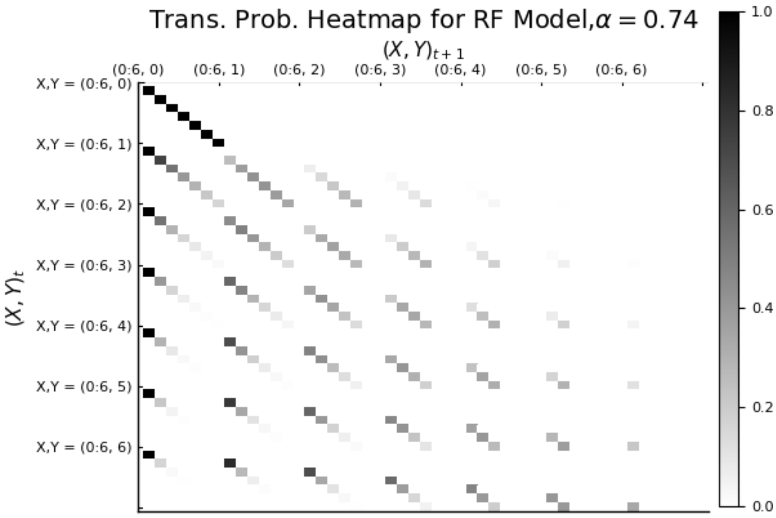
[29]:
```
x0 = 6
α = 0.74
N = x0+1
shape_vec = [N for i in 1:N] # n*n blocks , each on n*n grid
block_array =BlockArray{Float64}(undef_blocks, shape_vec, shape_vec)

probFunc(k,i,l,j) = binomial(k, l) * (1-α^i)^j*α^(i*l)
for i = 0:x0
    for j = 0:x0
        # Build block array for fixed (i,j)
        Pij = zeros(N, N)
            for l = 0:x0
                k = l+j # condition of X[t] = X[t+1] + Y[t+1]
                    if k >= N # k meeting condition is invalid
                        continue
                    end
                Pij[k+1, l+1] = probFunc(k,i,l,j)
            end
        block_array[Block(i+1, j+1)] = Pij # fill local Pij into Block Array
    end
end

b = Array(block_array);
```

[30]:
```
f=heatmap(1:N^2, 1:N^2, b, title = "Trans. Prob. Heatmap for RF Model," * L"\alpha="␣
↪*"$α",
    ylabel=L"(X,Y)_t", xlabel=L"(X,Y)_{t+1}", yflip=true,
    c=cgrad([:white, :black]),
    xmirror=true,
    xticks = (0:x0+1:50, ["(0:$x0, $i)" for i in 0:x0]) ,
    yticks = (0:x0+1:50, ["X,Y = (0:$x0, $i)" for i in 0:x0])
)
```

[30]:



Here, the coordinates listing $X = (0:6)$ indicate that X increments $[0, 1, 2, \ldots, 6]$ and is reset to zero in a cyclic fashion when Y increments. This was deemed the best way to indicate this notationally.

(d). The Monte Carlo simulation for the Reed Frost model is near identical to that for the Greenwood model. The `reedFrostSimulation` function now defines $y_0 = 1$ as x_{t+1} is drawn from $\mathsf{Bin}(X_t, \alpha^{Y_t})$, which needs a definition for $t = 0$. This is in contrast to the greenwood model, where $X_{t+1} \sim \mathsf{Bin}(X_t, \alpha)$.

[31]:
```
N = 1e6 # number of simulations
tfinal = x0 +1
"Function which simulates Reed-Frost model,
stores simulated values in input vectors X and Y.
returns realisations of (W, N) along with c,
the number of times Y[i] != 1"
function reedFrostSimulation!(X, Y)
    step_diff_from_greenwood = 0
    X = fill!(X, 0) # Reset to zero
    Y = fill!(Y, 0)
    X[1] = x0
    #Reed Frost needs a y0,
    Y[1] = 1

    for i=1:tfinal-1
        X[i+1] = rand(Binomial(X[i], α^Y[i]) )
        Y[i+1] = X[i] - X[i+1]

        # if infection died out stop early
        if Y[i+1] == 0
            # return (W, T) realisations
            return (sum(Y), i , step_diff_from_greenwood)
        elseif Y[i+1] != 1
            step_diff_from_greenwood +=1
        end
    end
    # return (W, T) realisations
    return (sum(Y), tfinal , step_diff_from_greenwood)
end

# Repeat simulation N times:
X = zeros(Int, tfinal)
Y = zeros(Int, tfinal);
count = 0
count_c = 0
```

```
for sim in 1:N
    w, n, cout = reedFrostSimulation!(X, Y)
    count_c += cout
    if w > 4
        count +=1
    end
end
println("Proportion of simulated trajectories where" *"\nW > 4 = ", count/N)
println("Average number of steps per simulation where probabilities are different to␣
↪greenwood: ", count_c/N)
```

```
Proportion of simulated trajectories where
W > 4 = 0.606355
Average number of steps per simulation where probabilities are different to
greenwood: 1.073278
```

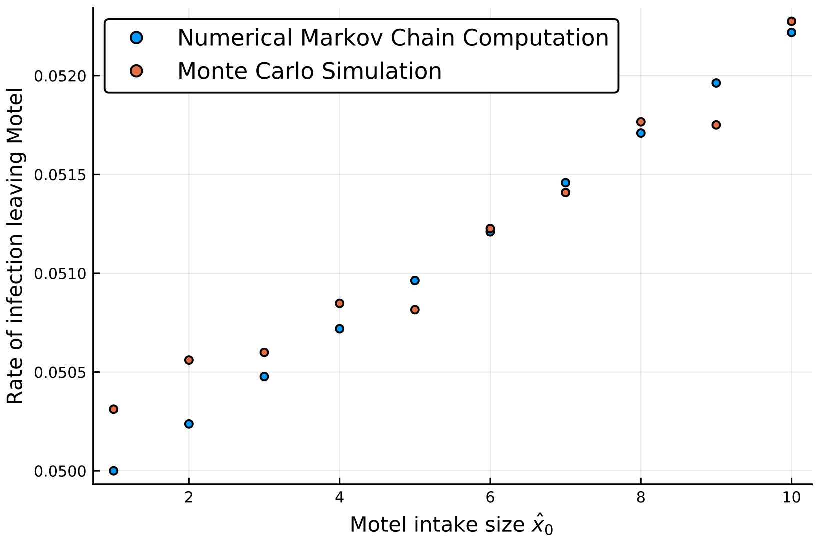
We see a significantly larger proportion of simulated trajectories where the total number of infectives is greater than 4. This should not be surprising since the probability of each of the susceptibles to avoid infection is α^{y_t} rather than α in the Greenwood Model. These are only equivalent in the case that $y_t \in \{0, 1\} \forall t$ which is not necessarily true. The second numerical figure produced from the simulation is the average number of times where $y_t \notin \{0, 1\}$, which means that X_{t+1} is drawn from a different distribution to a Greenwood model in the same state. This happens an average of once per simulation so it seems reasonable that the outcome proportion is significantly higher.

Question 6 on next page

Group Quarantine Policies in Regional Towns

This reports models the infection control policy of quarantining arrivals into a regional town in groups, and considers the subsequent implications. It is assumed there are $\hat{x}_0$ arrivals into the town on a given day, who are all quarantined in the same motel, whereupon they are tested for the presence of the infection. The test results are obtained after a day delay, during which new infections may occur among the $\hat{x}_0$. Those testing positive are removed from the hotel for treatment, and the testing regime repeats on subsequent days until all remaining occupants test negative, or are all infected. The assumption is made that is a cyclic process, once the motel is emptied, it is re-inhabited by $\hat{x}_0$ new arrivals on the same day. Furthermore, there are parameter estimates that the population rate of infection is $\eta = 0.05$, and that in the motel, there is a $p = 0.1$ probability of occupants coming in contact with one another, and probability $\beta = 0.05$ that this contact results in infection.

The analysis conducted uses the Reed-Frost model to explain the spread of the infection within the motel. It was found that this infection control policy is detrimental towards containing the infection; quarantining new arrivals together results in a larger rate of infected people entering the town, than if arrival was unrestricted. Figure 1 shows the relationship that increasing the size of quarantine groups resulting in a linearly increasing proportion of incumbent infectives. Despite this, the increased margin at $\hat{x}_0 = 10$ is still quite small relative to the population rate of $\eta = 0.05$. As such, the increase in incident case numbers may be warranted as the quarantine process ensures infected individuals cannot continue to spread the infection unmitigated after arriving in the town.



These simulated results were obtained using a conjunction of Monte Carlo simulation and direction computation using a Markov chain representing the number of susceptible and infectives in the motel at any given time. The details of these approaches are outlined the follow sections and we conclude with some analysis of the underlying assumptions in the model.

Monte Carlo Approach

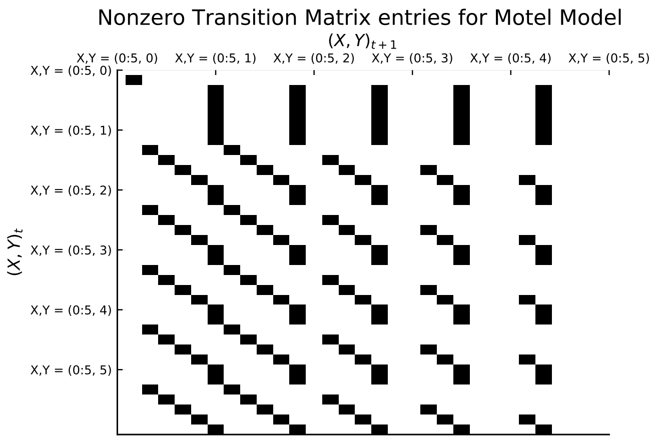
Throughout, we assume that the reader is somewhat familiar with the Reed-Frost model. The approach considers the long term averages after N simulations of the Reed-Frost model, correspondent to N motel arrival groups. The main modification is that y_0, the initial number of infectives is $\mathsf{Bin}(\hat{x}_0, \eta)$ distributed, and the initial number of susceptibles, x_0 is correspondingly defined as $\hat{x}_0 - y_0$. Given that $\eta = 0.05$, this leads to the degenerate case where there are no initial infectives (and thus no spreading) in the vast majority of cases. We keep track of the total number of infectives and days past over all N simulations. It is then straight forward to compute the number of rate of infection per day, and also the proportion of people who become infected:

$$R_{\text{p/day}} = \frac{y_{tot}}{t_{tot}}, \quad R_{\text{p/person}} = \frac{R_{\text{p/day}}}{\hat{x}_0 \cdot N}$$

.

Markov Chain Approach

Similarly to the Monte Carlo approach, we consider a modification of the Reed-Frost model by altering the $\{(X_t, Y_t)\}$ susceptible, infective chain. In particular, certain entries of the probability transition matrix $P_{(k,i)\to(l,j)}$ are modified to capture the recurrent nature of the motel scenario. To aid discussion we present a "colourmap" of the nonzero transition matrix entries for $\hat{x}_0 = 5$. Nonzero entries have been plotted rather than a colourmap as probabilities become vanishingly small where the number of infectives is large; the right half of the matrix, which are very difficult to distinguish on a graduated colourmap.



The entries modified are of the form $(x, 0)$ and $(0, y)$ as these are recurrent terminating states in the Reed-Frost model. The motel model, they are the end of a particular intake, and additionally serve as proxy starting states, before the $\hat{x}_0$ arrivals are partitioned into the x_0 susceptible and y_0 infectives. Correspondingly, these states now lead to $\{(x, y) \mid x + y = \hat{x}_0\}$, where y is determined according to the pmf of $\mathsf{Bin}(\hat{x}_0, \eta)$. This results in the vertical bands in the first 6 rows, along with the first row in each block of y. The state $(0, 0)$ is a closed recurrent class as it is not possible to start in this state, nor is possible to transition to. Additionally, there are a number of highly transient states; $\{(x, y) \mid x + y > \hat{x}_0\}$. These state typically can only be started in, however this is prevented by the fixing of $\hat{x}_0$ arrivals. The also cannot be transitioned to, as $Y_t < \hat{x}_0 \forall t$ and $X_t = X_{t+1} + Y_{t+1} \implies X_{t+1} \le X_t$. This is reflected by the empty columns in the matrix. Whilst these states could be removed outright, they are kept for comparability with the Reed-Frost model. The determined stationary distribution is the same regardless of whether they are present, as the correspondent entries will be zero. The remaining transitions are unmodified from the Reed-Frost model.

Next, we outline the procedure for computing the rate of infection. Initially we compute the stationary distribution of the matrix $P_{(k,i)\to(l,j)}$. Since this matrix has zero determinant, we determine the stationary distribution through the crude method of raising P^k for large k and take π equal to the transpose of any row, excluding the first (which has single entry 1 corresponding to the $(0, 0)$ recurrent state). We ensure this is the stationary distribution by checking $\pi P = \pi$. In order to compute the rate of infection amongst those leaving the motel, we first compute the rate at which infectives leave. This is given by the following expression (where (a, b) represents the 1D row/ column index corresponding to the pair of states (a, b)):

$$R_{\text{infect.}} = \sum_{(k,i)} \sum_{(l,j)} \pi_{(k,i)} P_{(k,i)\to(l,j)} \cdot j.$$

This computes the proportion of any particular transition occurring, weighted with the number of infectives that transition yields. Note that the cases where the motel is refilled lead to genuine infection and so do not need to be handled specially. In order to compute the proportion of people leaving who are infected, we also need to know the rate at which healthy people leave the motel (or equivalently, the total rate at which people leave). This is computed in a similar manner; $R_{\text{healthy}} = \sum_{(k,i)} \sum_{(l,0)} \pi_{(k,i)} P_{(k,i)\to(l,0)} \cdot l$, where people only leave if the number of infectives is zero, and that number of people leaving is l by definition. Finally, the rate of infection among the people leaving the hotel is

$$R_{\text{p/person}} = \frac{R_{\text{infect.}}}{R_{\text{infect.}} + R_{\text{healthy}}}.$$

Analysis of Assumptions

We briefly make comment on some of the more unrealistic assumptions associated with the model. Foremost is the perfect sensitivity and specificity of the described test. The repeated daily testing procedure is prone to spurious comparisons in the case that the tests are fallible. The assumption that the motel can always be filled is not necessarily accurate, unless perhaps there are several such motels admitting people into the town. In this respect we can regard the described model as a worst case, if the number of arrivals are less than x_0, than the probability of infection through the motel will also be reduced. Additionally, we make comment on the fact that the population rate of infection η is unlikely to be constant in practice, it will vary as the infection spreads and is controlled. Any such estimate will also have an associated confidence interval, it perhaps should not necessarily be treated as a point estimate. It may however be an appropriate estimate on a shorter timescale where imperfect control measures (such as physical distancing, closure of borders) are in place such that number of cases is no longer rapidly evolving.