This project deals with Epidemic Models in Discrete time, as presented in [EM-4] (Chapter 4 of, "Epidemic Modelling: an introduction" by Daryl Daley and Joe Gani). We only use parts of sections 4.1 and 4.2 from [EM-4]. It is also useful to read the short section 1.4 from the introduction chapter of the same book, as it describes how such discrete time epidemic models can be related to our continuous time world.

We deal with the Greenwood model and the Reed-Frost model. Both of these are aimed at a very small population in a household or similar. In both cases, X_t is the number of susceptible individuals and Y_t is the number of infected individuals from the previous time period, where at each time period, the infected individuals are removed after inflicting their (unintended) damage.

Before starting, you should spend some time to understand the modeling ideas that leads to the two basic equations used by both models. This amounts to two equations describing transition probabilities. Equation (4.1.2) presents the dynamics of the Greenwood model. Equation (4.1.3) presents the dynamics of the Reed-Frost model (this equation is the same as equation (1.4.1) in the introduction of that book).

The project involves a series questions and tasks, the last of which is slightly more open ended. Please hand in a single PDF file for your solutions to the questions. The file may involve a combination of scanned hand written results, typed text/formulas, and computer output (and code). In any case, it must have questions answered in order and cannot exceed 8MB in size. Make sure to have your name and student ID on the PDF file, even if you hand in via e-mail.

Questions/Tasks, with weighting out of 100 in "( )":

1. Equation (4.1.4) presents the expected numbers in the Greenwood model.
   (a) Derive these equations. (2)
   (b) Assume $x_0 = 6$ and $\alpha = 0.8$. Then plot these expected values for some sensible time horizon. (3)
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. (5)
   (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). (5)
3. Consider the Markov Chain $\{X_t,\ t = 0, 1, 2, \dots\}$ 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 $\{0, 1, 2, \dots, x_0\}$.
   (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. (4)
   (b) Determine the communicating classes of this Markov chain. How many are there? Which are recurrent? Which are transient? (4)
   (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 1a above. For this, take the the power P^t and compute $e_{x_0+1}^T P^t v$, where e_{x_0+1} is the $x_0 + 1$ long unit vector $[0\ \ 0\ \ \dots\ \ 1]^T$ and v is the vector $[0\ \ 1\ \ 2\ \ \dots\ \ x_0]^T$. Compute this numerically and see that the results numerically agree with those in the plot of 1b. Explain why this holds.(4)
   (d) Attempt to carry out a similar numerical computation for the expectation of Y_t in equation (4.1.4) and explain your method. (3)
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,
   $$\Gamma(k, n \mid x_0) = \mathbb{P}\Big((W, T) = (k, n) \mid X_0 = x_0, Y_0 > 0\Big),$$
   for $k = 0, 1, \dots, x_0$ and $n = 1, 2, \dots$. 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). (3)
   (b) Use the recursive relationship $\Gamma(k, n \mid x_0) = p_{x_0-k}^{n-1} \alpha^{x_0-k}$ to (numerically) compute $\mathbb{P}(W > 4)$. (5)
   (c) Compare your numerical result to an estimate obtained by a Monte-Carlo simulation creating 10^6 repeated trajectories and using those to estimate $\mathbb{P}(W > 4)$. (5)
   (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). (2)

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 $x_0 = 6$, some y_0 of your choice, 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? (3)

   (b) Try to describe the communicating classes in a compact manner? If not possible, constrain to a small fixed x_0. (4)

   (c) Plot a heat-map similarly to 3a (you may want to use block-matrices in your software). (4)

   (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. (4)

6. In this final task we consider slightly more involved modeling of a situation in steady state. Assume a small motel in a regional town, with capacity for up to x_0 people. As there is a pandemic with travel restrictions and security measures, all new arrivals to the town are supposed to quarantine. Assume there are dozens of arrivals to the town per day and hence there is always enough demand on the motel.

   Further, assume we are in a long period of time during the pandemic where the probability of new arrivals being infected by COVID-19, is $\eta = 0.05$. Also assume that there is not any immunity to COVID-19 (this is mostly wrong).

   The motel's policy (managed by local government) is to accept x_0 new individuals all at once and to test them for COVID-19 upon arrival with results announced the next day. If all x_0 are not infected, they are released and a new batch of x_0 arrives into the motel and each person from that batch is tested as the process repeats. However, if there is an infection to any of the x_0 then they all stay in the motel until there are no more infected in the motel. In every day of their stay, they are tested again and those that test positive are removed (taken to health centre elsewhere), while those that are not positive remain. Still, because of the day's delay in results, further infections may occur (because those that tested positive were there for a whole day). Assume the infections inside the motel follow the Reed-Frost Model with $p = 0.1$ and $\beta = 0.05$ (see page 106 of [EM-4]).

   Your goal is now to determine the long term expected rate of infections per day coming out of this motel. Do this as a function of x_0. That is, without this motel, the rate of infections per person into the regional town is at $\eta = 0.05$. However with this motel and $x_0 > 1$, the rate of resulting infections should be bigger. Carry out the (partially numerical) analysis for $x_0 = 1, \ldots, 10$. Feel free to use explicit computation, numerical computations, Monte-Carlo or some combination there-of.

   If you find using the Reed-Frost model too difficult, you can use the Greenwood model for partial marks. In any case, starting with Greenwood as a (personal) warmup and then going to Reed-Frost may be a good strategy.

   Present your analysis in the form of a stand alone report (not longer than 1 or 2 pages - at the end of the PDF document containing your other work). In this report, state the scenario, the model, the assumptions and the results. Also state what part of the analysis is unrealistic in your view (and perhaps requires further detailed analysis).
   (40)