Project 2 - TMA4265 Stochastic Modelling

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Problem 1

a)

$\{X(t) : t \geq 0\}$ is a continuous-time Markov chain if it follows the Markov property. We recall that for continuous time, the Markov property is given as

$$Pr\{X(t+s) = j | X(s) = i, X(u) = 0 \leq u \leq s\} = Pr\{X(t+s) = j | X(s) = i\},$$

for $i, j = 0, 1, \ldots,$ and $\forall s \geq 0$ and $t \geq 0$. Because all sojourn times are exponentially distributed, and the exponential distribution is memoryless, we have that

$$Pr\{X(t+s) = i | X(s) = i, X(u) = 0 \leq u \leq s\} = Pr\{X(t+s) = i | X(s) = i\}$$

and so the Markov property holds for $j = i$. Furthermore, we know that when a sojourn time ends, the transition jump probabilities are all only dependent on what state you are in, and not how long you've been there, or what states you were in before. Thus, the Markov property holds for any pair of states.
Let us define S_i to be the sojourn time for state $i = \{S, I_L, I_H\} =: \{0, 1, 2\}$, where S is the susceptible state, I_L is the lightly infected state and I_H is the heavily infected state.
The **jump probabilities** are the probabilities of transitioning between a state i to a state j, when the sojourn times end. When S_S ends, we can jump to either state I_H with a probability $\alpha = 0.1$ or to I_L with a probability $1 - \alpha = 0.9$. When i state I_H or I_L, the only possible transition is back to S according to our model. Thus, the jump probabilities for I_H and I_L are both 1.

	0	1	2
0	-	1-α	α
1	1	-	0
2	1	0	-

Table 1: Jump probabilities for the states S, I_L and I_H.

The total transition rates of exiting each state are relatively immediate from the project description:

$$\begin{aligned} 1/\lambda = 100 &\iff q_0 = \lambda = 0.01 \\ 1/\mu_L = 7 &\iff q_1 = \mu_L = 1/7 \\ 1/\mu_H = 20 &\iff q_2 = \mu_H = 0.05 \end{aligned}$$

We also have the relation $q_{ij} = p_{ij}q_i$, which gives us the **transition rate matrix**

$$A = \begin{bmatrix} -q_0 & q_{01} & q_{02} \\ q_{10} & -q_1 & q_{12} \\ q_{20} & q_{21} & -q_2 \end{bmatrix} = \begin{bmatrix} -\lambda & (1-\alpha)\lambda & \alpha\lambda \\ \mu_L & -\mu_L & 0 \\ \mu_H & 0 & -\mu_H \end{bmatrix} = \begin{bmatrix} -0.01 & 0.009 & 0.001 \\ 1/7 & -1/7 & 0 \\ 0.05 & 0 & -0.05 \end{bmatrix}$$

The transition diagram of the Markov chain is given in Figure 1.

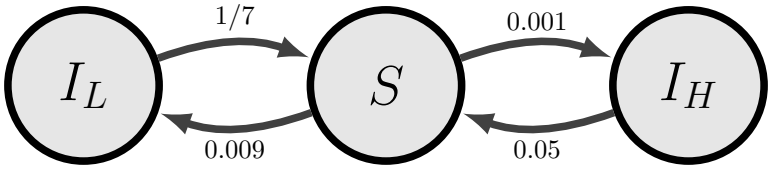

Figure 1: Transition diagram of the Markov chain.

b)

Since we have a continuous time Markov chain with no absorbing states, we have

$$\pi_S + \pi_{I_L} + \pi_{I_H} = 1.$$

This means that the total probability as $t \to \infty$ for all the three states combined is 1. Taking the forward Kolmogorov differential equations in the limit yields the equation

$$(\pi_S, \pi_{I_L}, \pi_{I_H})A = 0$$

which results in

$$\begin{aligned} \pi_{I_L}\mu_{I_L} &= \pi_S(1-\alpha)\lambda, \\ \pi_{I_H}\mu_H &= \pi_S\alpha\lambda, \\ \pi_S\lambda &= \pi_{I_L}\mu_L + \pi_{I_H}\mu_H. \end{aligned}$$

We now use this to find the long run mean fractions, i.e. π_I, π_{I_L} and π_{I_L}. We have

$$\pi_S = \frac{\pi_{I_L}\mu_L + \pi_{I_H}\mu_H}{\lambda},\ \pi_{I_L} = \frac{\pi_S(1-\alpha)\lambda}{\mu_{I_L}},\ \pi_{I_H} = \frac{\pi_S\alpha\lambda}{\mu_H},$$

which are three equations with three solutions. λ, μ_L, μ_H and α are given. Thus,

$$\pi_{I_L} = \frac{9}{143}\pi_S,\ \pi_{I_H} = \frac{\pi_S}{50}.$$

From the total sum of the fractions, we find $\pi_S \simeq 0.9234$, resulting in

$$\pi_{I_L} \simeq 0.058,\ \pi_{I_H} \simeq 0.0185.$$

Using these numerical values, a person will be infected on average 27.9 days each year, that is, either lightly infected or heavily infected.

c)

Figure 2 shows one realization of infection development over 5 years, that is, $0 \leq t \leq 5 \cdot 365$. The simulation of 1000 years is written in Python with the NumPy package, and an illustration of the 5 first years with the pyplot-module. We first simulate 1000 years by selection of exponentially distributed sojourn times until we have a simulation for $1000 \cdot 365$ days. The values are stored in a state-object, and all such objects are stored in an array. When plotting the results, we draw a horizontal line for each state between the state's start time and end time.

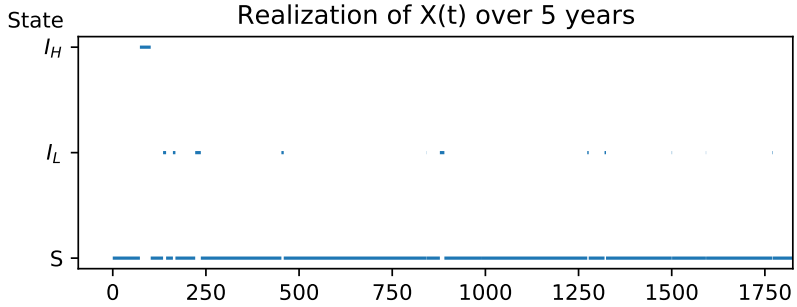

Figure 2: Plot of one realization over 5 years, where state 0 is susceptible, 1 is lightly infected and 2 is heavily infected.

d)

When calculating the long-run proportion of time in each state, we initialize a dictionary-container for each of the states (that is, with keys 0, 1, 2), and iteratively increment the item of the keys to be the time spent. We also store the total sojourn time, and thus the long-run proportion is simply the dictionary item, divided by total sojourn time.
We define $(\tilde{\pi}_S, \tilde{\pi}_{I_L}, \tilde{\pi}_{I_H})$ as the simulated long-run mean fractions of time for the states $S, I_L,$ andI_H, respectively. From the simulations we got the following long run proportions:

- $\tilde{\pi}_S = 0.9225$
- $\tilde{\pi}_{I_L} = 0.0571$
- $\tilde{\pi}_{I_H} = 0.0204$

The values seem to be in accordance with the analytical results, with marginal differences attributed to the stochastic nature of the simulation.

e)

Let T_{HH} be the time between heavy infections. When recovering from a heavy infection, one has to stay susceptible for a mean of 100 days. Then, one can either become heavily infected again, with a probability of $\alpha = 0.1$, or become lightly infected, and stay lightly infected for a mean of 7 days. This can continue indefinitely. This means

$$
\begin{aligned}
E[T] &= \frac{1}{\lambda} + \sum_{i=1}^{\infty} (1-\alpha)^i \left(\frac{1}{\mu_L} + \frac{1}{\lambda} \right) \\
&= \frac{1}{\lambda} + \left(\frac{1}{\mu_L} + \frac{1}{\lambda} \right) \left(\frac{1}{\alpha} - 1 \right) \\
&= 100 + (100 + 7) \left(\frac{1}{0.1} - 1 \right) = 1063
\end{aligned}
$$

According to a simulation of 1000 years, the distance should be about 1053 according to one realization. The average of 1000 realizations, all over 1000 years, resulted the average time should be about 1063.7 days, which is in good accordance with the analytical result.

f)

Because this is a continuous process, we have that the probability of two people transitioning at the same instant is zero. This means that for $\{Y(t) : t \geq 0\}$, no other transitions than from i to $i+1$ or $i-1$ are possible. Furthermore, all sojourn times are independent exponential distributions, and so $\{Y(t) : t \geq 0\}$ is a birth and death process.
The birth and death rates from state i are

$$
\lambda_i = (5.26 \cdot 10^6 - i)\lambda \quad \text{and} \quad \mu_i = i\mu,
$$

respectively.

g)

When the stationary distribution has been reached, the rate of people becoming infected is the same as the rate of people recovering.

$$
\begin{aligned}
i\mu &= (5.26 \cdot 10^6 - i)\lambda \\
i &= \frac{5.26 \cdot 10^6 \cdot \lambda}{\mu + \lambda} \\
&\simeq 344112
\end{aligned}
$$

Little's law can be expressed algebraically as $L = \lambda_H W$, where L is the number of customers, λ_H is the long-run customer rate and W is the average time the customer spends in the system. In this case, L is given to be 2000. The rate of infections that will require hospitalization is then

$$
\lambda_H = \lambda_i|_{i=344112} \cdot 1\% = (N-i)\lambda \cdot 1\% = (5.26 \cdot 10^6 - 344112)\frac{1}{100} \cdot 1\% \simeq 491.59
$$

thus reducing the problem to

$$
L = \lambda W \iff W = \frac{L}{\lambda} = \frac{2000}{491.59} \simeq 4.07.
$$

Since t is measured in days, Little's law indicates that the hospitals may only use about 4.1 days on each hospitalized patient when at maximum capacity.

Problem 2

a)

In order to construct the conditional mean vector $\boldsymbol{\mu}$ and conditional covariance matrix $\boldsymbol{\Sigma}$, we first define two stochastic variables: $\mathbf{X}_A \sim \mathcal{N}_{n_A}(\boldsymbol{\mu}_A, \boldsymbol{\Sigma}_A)$, where $\mathbf{X}_A$ is $Y(\theta)$ at the grid of $n_A = 51$ values for θ, and $\mathbf{X}_B \sim \mathcal{N}_{n_B}(\boldsymbol{\mu}_B, \boldsymbol{\Sigma}_B)$ is for the $n_B = 5$ known values. We then have

$$\mathbf{X} = (\mathbf{X}_A, \mathbf{X}_B) \sim \mathcal{N}_{n_A+n_b}\left(\begin{bmatrix} \boldsymbol{\mu}_A \\ \boldsymbol{\mu}_B \end{bmatrix}, \begin{bmatrix} \boldsymbol{\Sigma}_{AA} & \boldsymbol{\Sigma}_{AB} \\ \boldsymbol{\Sigma}_{BA} & \boldsymbol{\Sigma}_{BB} \end{bmatrix}\right)$$

The notation $\boldsymbol{\Sigma}_{ij}$ is short hand for $\text{Cov}[\mathbf{X}_i, \mathbf{X}_j]$, e.g. $\boldsymbol{\Sigma}_{AB} = \text{Cov}[\mathbf{X}_A, \mathbf{X}_B]$, $\boldsymbol{\Sigma}_{AA} = \text{Cov}[\mathbf{X}_A, \mathbf{X}_A]$ and so on.
The correlation between $Y(\theta_1)$ and $Y(\theta_2)$ is defined as

$$\text{Corr}[Y(\theta_1), Y(\theta_2)] = \frac{\text{Cov}[Y(\theta_1), Y(\theta_2)]}{\sqrt{\text{Var}[Y(\theta_1)]\text{Var}[Y(\theta_2)]}}$$

which gives

$$\text{Cov}[Y(\theta_1), Y(\theta_2)] = \sqrt{\text{Var}[Y(\theta_1)]\text{Var}[Y(\theta_2)]}\text{Corr}[Y(\theta_1), Y(\theta_2)] = 0.5^2(1 + 15|\theta_1 - \theta_2|)e^{-15|\theta_1-\theta_2|}$$

Then, the mean and the covariance matrix for the conditional stochastic variable $\mathbf{X}_C = (\mathbf{X}_A|\mathbf{X}_B = \mathbf{x}_B) \sim \mathcal{N}_{n_A+n_B}$ can be computed by

$$\boldsymbol{\mu}_C = \boldsymbol{\mu}_A + \boldsymbol{\Sigma}_{AB}\boldsymbol{\Sigma}_{BB}^{-1}(\mathbf{x}_B - \boldsymbol{\mu}_\mathbf{B}) \tag{1}$$

$$\boldsymbol{\Sigma}_C = \boldsymbol{\Sigma}_{AA} - \boldsymbol{\Sigma}_{AB}\boldsymbol{\Sigma}_{BB}^{-1}\boldsymbol{\Sigma}_{BA} \tag{2}$$

Using equations (1) and (2), we are able to calculate a prediction $y(\theta)$, and plot this prediction with 90% prediction intervals over $\theta_i \in [0.25, 0.5]$, resulting in Figure 3.

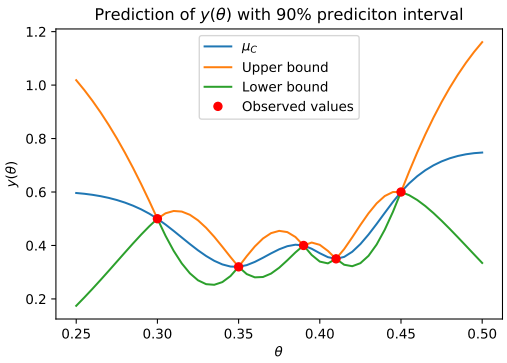

Figure 3: Prediction $y(\theta)$ conditioned on the 5 observed values. Plots show $\boldsymbol{\mu}_C$ and its upper and lower bound with a 90% prediction interval.

b)

Applying the cumulative distribution function of $\mathcal{N}(\boldsymbol{\mu}_C, \boldsymbol{\Sigma}_C)$ evaluated at $y(\theta) = 0.3 \quad \forall \quad \theta$, we can find the conditional probabilities that $Y(\theta) < 0.3$ given the 5 observed values. Figure 2 shows this probability as a function of θ. We may observe that there is a 0% probability of $Y(\theta) < 0.3$ for all observed θ, i.e. $\{0.3, 0.35, 0.39, 0.41, 0.45\}$, which is logical considering all observed values are above the threshold of 0.3.

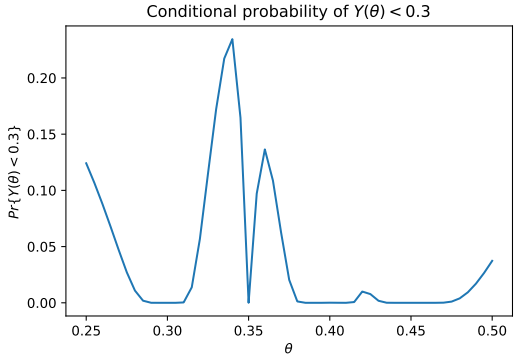

Figure 4: Plot illustrating the probabilities of $Y(\theta) < 0.3$ for each θ in the interval.

c)

Using the same methods as described in 2a) and 2b), we once again calculate the the predicted $y(\theta)$ conditioned on 6 observations, and plot the probability of $Y(\theta) < 0.3$ for all θ in Figure 5. We observe that $\theta = 0.36$ yields the highest probability, $Pr\{Y(\theta) < 0.3\} = 0.18$. Thus, the scientists should use $\theta = 0.36$ for the best chance of achieving $y(\theta) < 0.3$.

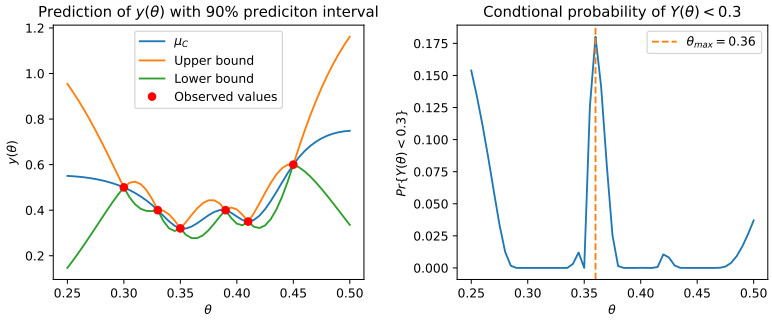

Figure 5: The plot to the left draws the predicted $y(\theta)$ conditioned on the 6 observations with a prediction interval, similarly to that of Figure 3. The plot to the right shows the probabilities of $Y(\theta) < 0.3$ including the 6th observation, similarly to that of Figure 4.