Stochastic Processes TMA4265 - Project 2

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1 Problem 1: Modelling the common cold

1.1 1 a)

For a process to be a CTMC(continuous-time Markov chain) requires that the transition probabilities depend only on the current state. This holds for the problem since for a single transition the process can only go from S to I_L or I_H with probabilities $1-\alpha$ and α respectively, and from I_L or I_H the process can only go back to S with probability 1. We can observe the following properties for the process.

- The sojourn times between transitions(jumps), are exponentially distributed.
- The state space is finite and equal to $\{S, I_L, I_H\}$.
- The transition probabilities are stationary.

Hence, all requirements for a CTMC are met.

The jump probabilities are as follows:

$$P_{SI_L} = 1-\alpha, \quad P_{SI_H} = \alpha, \quad P_{I_L S} = P_{I_H S} = 1 \tag{1}$$

Let r_i denote the rate at which the system leaves state i. Then let a_{ij} denote the transition rate from state i to state j. We define a_{ij} as

$$a_{ij} = r_i \cdot P_{ij} \tag{2}$$

Therefore, by inserting the transition probabilities and the parameters(λ, μ_L, μ_H) for the pdf of sojourn times given by the problem at hand, we get

$$\begin{aligned} a_{SI_L} &= \lambda \cdot (1-\alpha), \\ a_{SI_H} &= \lambda \cdot \alpha, \\ a_{I_L S} &= 1 \cdot \mu_L, \\ a_{I_H S} &= 1 \cdot \mu_H \end{aligned} \tag{3}$$

We represent the transition rates in the following transition diagram:

$$Q = \begin{bmatrix} -\lambda & \lambda(1-\alpha) & \lambda\alpha \\ \mu_L & -\mu_L & 0 \\ \mu_H & 0 & -\mu_H \end{bmatrix} \tag{4}$$

1.2 1 b)

To obtain the long-run mean fractions of time in each state we shall first find the limiting distribution of the states. We begin by deriving forward differential equations for the system. The Chapman-Kolmogorov equation for a CTMC states that

$$P_{ij}(t+s) = \sum_{k=0}^{N} P_{ik}(t) P_{kj}(s) \tag{5}$$

where N is the number of states in the state space. For the problem at hand we let the subscripts 0, 1 and 2 refer to the states S, I_L and I_H respectively. The Chapman-Kolmogorov equation gives:

$$P_{01}(t+h) = P_{00}(t)P_{01}(h) + P_{01}(t)P_{11}(h) + P_{02}(t)P_{21}(h) \tag{6}$$

From the postulates of a CTMC we have the following relations as $h \downarrow 0$:

$$\begin{aligned} P_{01}(h) &= h\lambda(1-\alpha) + o(h) \\ P_{02}(h) &= h\lambda\alpha + o(h) \\ P_{11}(h) &= 1 - h\mu_L + o(h) \\ P_{22}(h) &= 1 - h\mu_H + o(h) \end{aligned} \tag{7}$$

Now let $h \downarrow 0$ in 6 and apply the postulates 7. Then

$$\begin{aligned} P_{01}(t+h) &= h\lambda(1-\alpha)P_{00}(t) + (1-h\mu_L)P_{01}(t) + o(h) \\ \frac{P_{01}(t+h) - P_{01}(t)}{h} &= \lambda(1-\alpha)P_{00}(t) - \mu_L P_{01}(t) + \frac{o(h)}{h} \\ P'_{01}(t) &= \lambda(1-\alpha)P_{00}(t) - \mu_L P_{01}(t) \end{aligned} \tag{8}$$

Similarly for P_{02} we get

$$P'_{02}(t) = \lambda\alpha P_{00}(t) - \mu_H P_{02}(t) \tag{9}$$

Let the limiting distribution be characterized by

$$\pi_j = \lim_{t\to\infty} P_{ij} \tag{10}$$

Letting $t \to \infty$ we insert the notation 10 into the two differential equations in 8 and 9 to obtain following result:

$$\begin{aligned} 0 &= \lambda(1-\alpha)\cdot\pi_0 - \mu_L\cdot\pi_1 \\ 0 &= \lambda\alpha\cdot\pi_0 - \mu_H\cdot\pi_2 \end{aligned} \tag{11}$$

where for the left-hand sides we have used that $\pi'_1(t) = \pi'_2(t) = 0$ since π_j is constant. Rearranging 11 yields

$$\pi_1 = \frac{\lambda(1-\alpha)}{\mu_L}\pi_0, \quad \pi_2 = \frac{\lambda\alpha}{\mu_H}\pi_0 \tag{12}$$

Using the law of total probability and inserting the expressions from 12 we get

$$\sum_{j=0}^{2}\pi_j = 1 = \pi_0\left(1 + \frac{\lambda(1-\alpha)}{\mu_L} + \frac{\lambda\alpha}{\mu_H}\right) \tag{13}$$

Solving for π_0 and inserting the result into 12 we arrive at the limiting distribution

$$\pi = \left[\frac{1000}{1083}, \frac{21}{361}, \frac{20}{1083}\right] \approx [0.9234, 0.0582, 0.0185] \tag{14}$$

Let the long-run mean fraction of time that an individual has an infection be denoted by f_I. Then

$$f_I = 1 - \pi_0 = 1 - \frac{1000}{1083} \approx 0.0766 \tag{15}$$

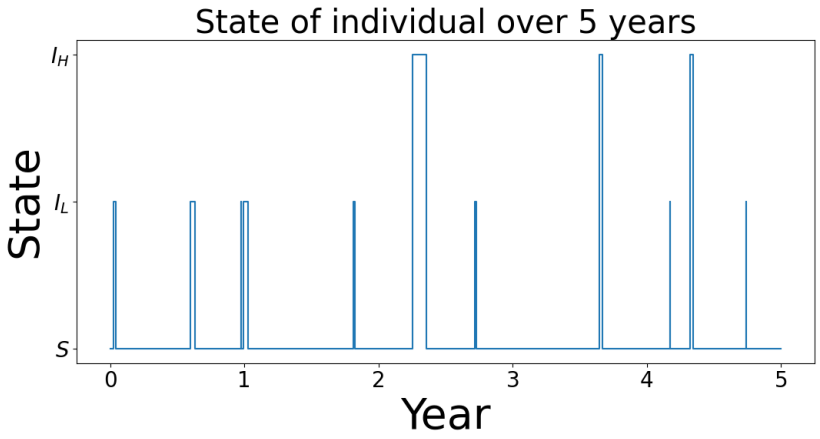
The expected number of days d_I of infection(either light or heavy) during a year is

$$E[d_I] = f_I \cdot 365 \text{ days} \approx 28 \text{ days} \tag{16}$$

1.3 1 c)

Python code is used to simulate the process. The figure below shows one realization for the process for 5 years.

Figure 1: A realization of the CTMC that models disease in a single individual over 5 years.
S: Susceptible, I_L: Lightly infected, I_H: Heavily infected



1.4 1 d)

In order to estimate f_I from computer code simulation we proceed as follows:
For all three states record the sum of the sojourn times that the process has spent in the given state. This results in a vector of 3 components $S = [S_0, S_1, S_2]$. The estimated limiting distribution then becomes

$$\tilde{\pi} = \frac{S}{\|S\|_1} \tag{17}$$

the long-run mean fraction of time that an individual has an infection is then equal to $1 - \tilde{\pi_0}$. Using this method for a simulation of 1000 years we obtain the estimate $\tilde{\pi} = [0.9211, 0.0592, 0.0197]$ and $\tilde{f_I} = 0.0789$, while from 15 the analytical result is $f_I = 0.0766$.

1.5 1 e)

Let the subscripts $0, 1$ and 2 denote the index of state S, I_L and I_H respectively. Let w_0 denote the expected time until the process first reaches state I_H starting in S. We define J_i as the sojourn time in state i. Then by the law of total expectation we have

$$\begin{aligned} w_0 &= E[J_0] + (1-\alpha)w_1 + \alpha w_2 \\ w_0 &= \frac{1}{\lambda} + (1-\alpha)w_1 \end{aligned} \tag{18}$$

where we used that $w_2 = 0$. For w_1 we get

$$w_1 = \frac{1}{\mu_L} + w_0 \tag{19}$$

Solving the system arising from 18 and 19 yields

$$w_0 = \frac{1}{\alpha}\left(\frac{1}{\lambda} + \frac{1-\alpha}{\mu_L}\right) = 1063 \tag{20}$$

A simulation of the process for $1000 \cdot 365$ days yields $\tilde{w_0} = 1087$.

1.6 1 f)

The process $Y(t)$ has a state space of size $N = 5.26 \cdot 10^6$. Since each individual in the population becomes infected or susceptible independently of other individuals, it must be the case that the state of any single individual follows a CTMC with transition rate matrix

$$Q = \begin{bmatrix} -\lambda & \lambda \\ \mu & -\mu \end{bmatrix} \tag{21}$$

Assuming that multiple individuals cannot change states simultaneously, it holds that if $Y(t)$ is in state I, then for a single transition it can only transition into $I+1$ or $I-1$. Hence $Y(t)$ is a birth and death process.
We shall now derive the transition rates for the process $Y(t)$. First, we shall introduce some notation. Let I be the state of $Y(t)$, i.e the number of infected individuals in the population. Then λ_I is the transition rate into state $I+1$ and μ_I is the transition rate into state $I-1$ given that the current state at time t is $Y(t) = I$. We will use S_i and I_i as shorthand for the i-th susceptible and the i-th infected individual respectively. At any time t We define $D_0(S_i)$ as the time that the i-th susceptible individual has already spent in the current susceptible state and $D(S_i)$ as the time until the susceptible individual leaves the susceptible state. The sojourn time of the individual in the current state S is then $J(S_i) = D_0(S_i) + D(S_i)$. We define $D_0(I_i)$, $D(I_i)$ and $J(I_i)$ equivalently.
To begin we will show that $D(S_i)$ is independent of $D_0(S_i)$ and that $D(I_i)$ is independent of $D_0(I_i)$.

Proof:
Pick any susceptible individual S_i. We assert that

$$\Pr\{D(S_i) = d \mid D_0(S_i) = d_0\} = \Pr\{J(S_i) = d_0 + d \mid J(S_i) \geq d_0\} \tag{22}$$

Since $J(S_i)$ is exponentially distributed with rate parameter λ, we get

$$\Pr\{J(S_i) = d_0 + d \mid J(S_i) \geq d_0\} = \frac{\lambda e^{-\lambda(d_0+d)}}{e^{-\lambda d_0}} = \lambda e^{-\lambda d} \tag{23}$$

Similarly, one can show that $\Pr\{D(I_i) = d \mid D_0(I_i) = d_0\} = \mu e^{-\mu d}$. $\square$

Let J be the sojourn time of $Y(t)$ in the current state $I = N - S$. Given any fixed time t we let D be the time between t and the next transition of Y. Clearly we have

$$D = \min\{\min\{D(S_i)\}, \min\{D(I_j)\}\} \tag{24}$$

where i is the index of the i-th susceptible individual and j is the index of the j-th infected individual. Then the cdf of D is

$$\Pr\{D \leq d\} = 1 - \left(\prod_{i=1}^{S} \Pr\{D(S_i) > d\}\right)\left(\prod_{j=1}^{I} \Pr\{D(I_j) > d\}\right) \tag{25}$$

From 23 we have the pdfs

$$\begin{aligned} \Pr\{D(S_i) = d \mid D_0(S_i) = d_0\} &= \lambda e^{-\lambda d} \\ \Pr\{D(I_j) = d \mid D_0(I_j) = d_0\} &= \mu e^{-\mu d} \end{aligned} \tag{26}$$

Inserting the cdfs related to the pdfs in 26 into 25 we get

$$\Pr\{D \leq d\} = 1 - e^{-S\lambda d} e^{-I\mu d} = 1 - e^{-(S\lambda + I\mu)d}, \tag{27}$$

Taking the derivative we get

$$\Pr\{D = d\} = (S\lambda + I\mu) e^{-(S\lambda + I\mu)d} \tag{28}$$

Hence D follows an exponential distribution with rate parameter $(S\lambda + I\mu)$. Using the proof in 23 one can show that J has the same pdf as 28. Denote by $\Delta Y \in \{-1, 1\}$ the next jump of the process. Then

$$\begin{aligned} \Pr\{J \leq j \mid \Delta Y = 1\} &= 1 - \prod_{i=1}^{S} \Pr\{J(S_i) > j\} = 1 - e^{-S\lambda j} \\ \Pr\{J = j \mid \Delta Y = 1\} &= S\lambda e^{-S\lambda j} = (N - I)\lambda e^{-(N-I)\lambda j} \end{aligned} \tag{29}$$

Hence the transition rate is $\lambda_I = (N - I)\lambda$. Equivalently we have $\mu_I = I\mu$. We represent the transition diagram by the transition rate matrix:

$$Q = \begin{bmatrix} -\lambda_0 & \lambda_0 & 0 & 0 & \dots \\ \mu_1 & -(\lambda_1 + \mu_1) & \lambda_1 & 0 & \dots \\ 0 & \mu_2 & -(\lambda_2 + \mu_2) & \lambda_2 & \dots \\ \vdots & \vdots & \vdots & \vdots & \ddots \end{bmatrix} \tag{30}$$

where the subscripts refer to the number of infected individuals.

1.7 1 g)

Let L be the long-run expected number of patients at the hospital, β be the expected number of patients arriving at the hospital per day, and W be the expected treatment time for each patient at the hospital. Then Little's Law gives that

$$L = \beta W \tag{31}$$

We impose the restriction $L = 2000$, such that

$$W = \frac{2000}{\beta} \tag{32}$$

The expected arrival rate β is

$$\beta = 0.01 \cdot \sum_{i=0}^{N} \Pr\{I = i\} \cdot ((N - i)\lambda) = 0.01 \cdot (N - E[I]) \cdot \lambda \tag{33}$$

Considering again the case of a single individual, we find using the forward differential equation for $P'_{01}(t)$ that the expected fraction of time spent infected is $\pi_1 = \frac{\lambda}{\mu+\lambda} = \frac{7}{107}$. Hence $E[I] = N\frac{\lambda}{\mu+\lambda}$, so that

$$W = \frac{2000}{0.01 \cdot N\lambda\left(1 - \frac{\lambda}{\mu+\lambda}\right)} \text{ days} = \frac{1070}{263} \text{ days} \approx 4.07 \text{ days} \tag{34}$$

2 Problem 2:

2.1 2 a, b)

Let the subscripts B and A denote the set of evaluation points(known points) and the set of unknown points respectively. We introduce the following notation:

$$\begin{aligned} \mu_A &= \mathrm{E}\left[\mathbf{y}_A\right] \\ \mu_{A|B} &= \mathrm{E}\left[\mathbf{y}_A \mid \mathbf{y}_B\right] \\ \mathbf{\Sigma}_A &= \mathrm{Cov}(\mathbf{y}_A) \\ \mathbf{\Sigma}_{A|B} &= \mathrm{Cov}(\mathbf{y}_A \mid \mathbf{y}_B) \\ \mathbf{\Sigma}_B &= \mathrm{Cov}(\mathbf{y}_B) \\ \mathbf{\Sigma}_{A,B} &= \mathbf{\Sigma}_{B,A} = \mathrm{Cov}(\mathbf{y}_A, \mathbf{y}_B) \end{aligned} \tag{35}$$

We may compute $\mu_{A|B}$ and $\mathbf{\Sigma}_{A|B}$ accordingly

$$\begin{aligned} \mu_{A|B} &= \mu_A + \mathbf{\Sigma}_{A,B}\mathbf{\Sigma}_B^{-1}(\mathbf{y}_B - \mu_A) \\ \mathbf{\Sigma}_{A,B} &= \mathbf{\Sigma}_A - \mathbf{\Sigma}_{A,B}{\mathbf{\Sigma}_B}^{-1}\mathbf{\Sigma}_{B,A} \end{aligned} \tag{36}$$

Let $d_\theta = |\theta_1 - \theta_2|$ for some parameter values θ_1 and θ_2, and $f = \mathrm{Corr}(d_\theta)$ be the correlation function of the gaussian process. We construct the covariance matrices in 36 as follows

$$\begin{aligned} \Sigma_B = f(\mathbf{H}_B), \quad \mathbf{H}_B = |\theta_B \cdot \mathbf{1}^T - \mathbf{1} \cdot \theta_B| \\ \Sigma_A = f(\mathbf{H}_A), \quad \mathbf{H}_A = |\theta_A \cdot \mathbf{1}^T - \mathbf{1} \cdot \theta_A| \\ \Sigma_{A,B} = f(\mathbf{H}_{A,B}), \quad \mathbf{H}_{A,B} = |\theta_A \cdot \mathbf{1}^T - \mathbf{1} \cdot \theta_B| \end{aligned} \tag{37}$$

where

$$f(\mathbf{H})_{ij} = f(\mathbf{H}_{ij}) \tag{38}$$

For the problem at hand we shall use the Matern type correlation function

$$f(d_\theta) = (1 + \phi d_\theta)\exp(-\phi d_\theta) \tag{39}$$

with $\phi = 15$.
Using the evaluation points $\{(\theta, y(\theta))\}_B$ and parameter value grid θ_A we compute $\mu_{A|B}$ and $\mathbf{\Sigma}_{A|B}$. Results are presented in the figures below

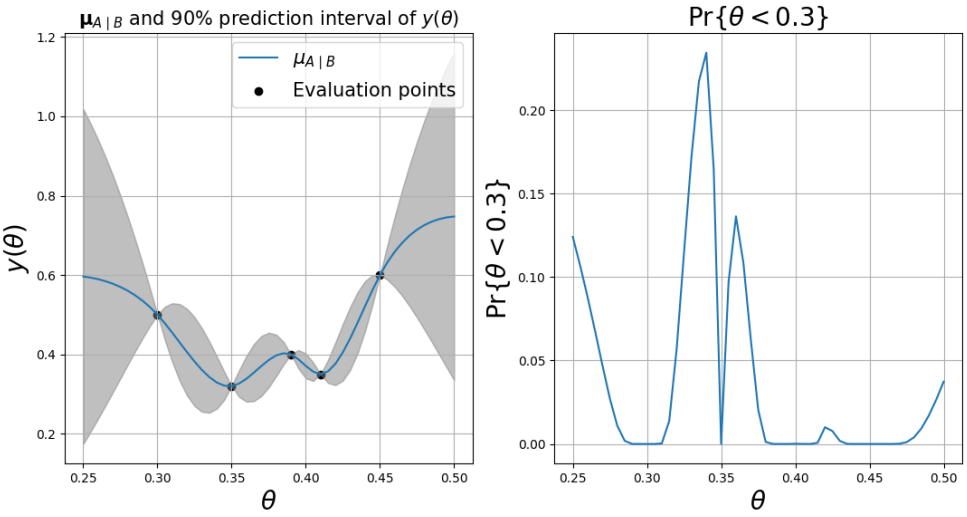


Figure 2:
Left: Blue line: $\mu_{A|B}$, gray area: 90% prediction interval of $\mathbf{y}_A$.
Right: $\Pr\{y(\theta) < 0.3\}$ for $\theta \in \{\theta_A \cup \theta_B\}$.

2.2 2 b, c)

We repeat the procedure in 2.1 with the added sixth evaluation point $(\theta_6, y(\theta_6)) = (0.33, 0.40)$ and present the results below

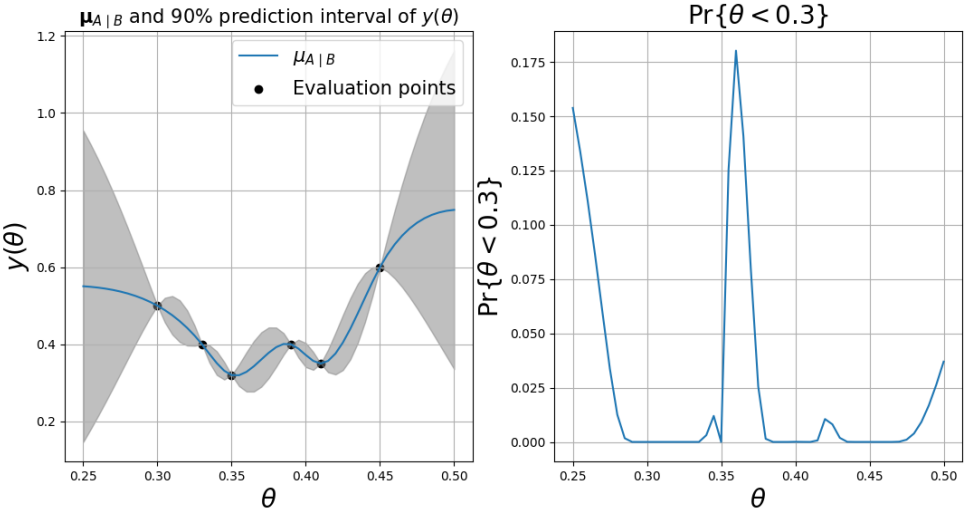


Figure 3:
Left: Blue line: $\mu_{A|B}$, gray area: 90% prediction interval of $\mathbf{y}_A$.
Right: $\Pr\{y(\theta) < 0.3\}$ for $\theta \in \{\theta_A \cup \theta_B\}$.

Using the information from previous task can we easily compute the probability that $Y(\theta) < 0.3$ given the current measured points. As shown in figure 3.

2.3 2 c)

We shall now introduce a 7-th evaluation point. We wish to select θ_7 in a way that maximizes $\Pr\{y(\theta_7) < 0.3\}$ given the 6 evaluation points already established. Restricting ourselves to $\theta_7 \in \theta_B$ it's clear from the righthand-plot in 3 that selecting $\theta_7 = 0.36$ maximizes $\Pr\{y(\theta_7) < 0.3\}$.