TMA4265 - Stochastic Modeling
Project 2

Group 39
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Problem 1: Modelling the common cold

a)

Using the definition from the lecture notes, a stochastic process $X(t)$ is a continuous-time Markov chain if

1. The state space Ω is discrete and finite, $\Omega = \{0, 1, 2, ...\}$
2. The Markov property holds,
   $\Pr\{X(t+s) = j \mid X(s) = i, X(u) = x(u), 0 \leq u < s\} = \Pr\{X(t+s) = j \mid X(s) = i\}$
3. The transition probability functions $P_{ij}(t) = \Pr\{X(t+u) = j \mid X(u) = i\}$ are independent of u

The model for the common cold has two states: susceptible (S) and infected (I), such that the state space Ω is discrete and finite. Additionally, the holding times $\mathcal{S}_S$ and $\mathcal{S}_I$ for each state are independently exponentially distributed, with $\mathcal{S}_S \sim \text{Exp}(\lambda)$ and $\mathcal{S}_I \sim \text{Exp}(\mu)$, where λ and μ are constant for all t. Due to the memorylessness property of the exponential distribution, $\Pr\{T > t + s \mid T > s\} = \Pr\{T > t\}$, the Markov property must hold for $X(t)$, as knowledge about a state at a previous time will not alter the duration before the next transition. Finally, this memorylessness property also ensures that the transition probability functions are independent of where the process is in time.

The transition rates between the states are $\lambda = 0.01$ and $\mu = 0.143$, and a transition diagram for the process is depicted in Figure 1.

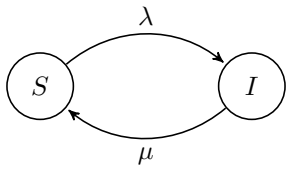


Figure 1: *Transition diagram for $X(t)$*

b)

Defining a limiting distribution as $\pi_j = \lim_{t\to\infty} P_{ij}(t)$, the rate in to each state should be equal to the rate out, giving,

$$\begin{aligned} \pi_I \lambda &= \pi_S \mu, \quad \pi_S + \pi_I = 1 \\ \pi_I &= \frac{\lambda}{\mu + \lambda} \\ &= 0.0654 \end{aligned}$$

as the fraction of time an individual spends while infected in the long-run.

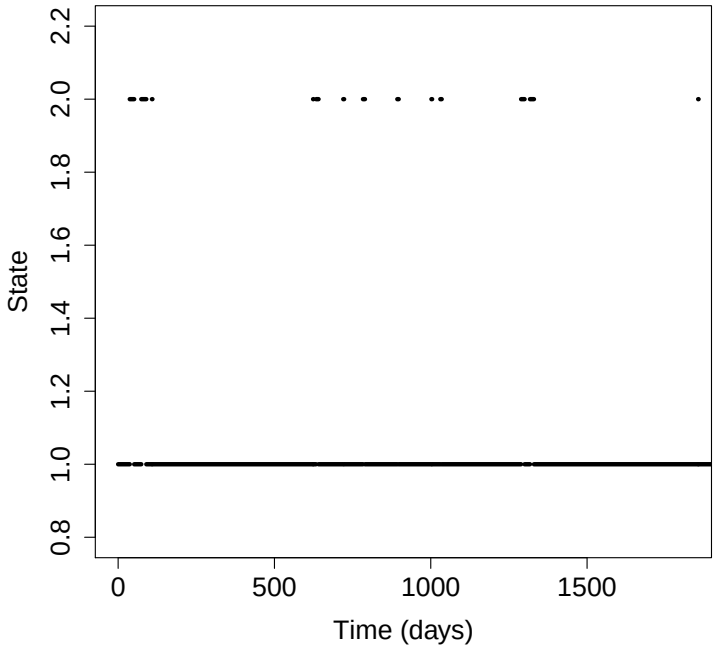


Figure 2: *One realization of $X(t)$ for $0 \leq t \leq 5 \cdot 365$, with Susceptible coded as 1 and Infected coded as 2*

c)

In Figure 2 the realization of $X(t)$ is simulated for a period of 5 years. The individual can be seen as susceptible for greater parts of the period.

To confirm the result of the previous task, one may estimate the long-run mean fraction of time that an individual is infected by simulation. This is done by iteratively sampling the sojourn time at the infected state for each other day, adding the sojourn times together and dividing by the total sojourn time for both susceptible and infected states. This should give an estimate for the fraction of time in the infected state, and gave a result of $\hat{\pi}_I = 0.0656$. Comparing with the theoretical value from the previous task, this seems like a good estimate for the fraction of time in infected state.

d)

Denoting $Y(t)$ as the number of infected individuals in a population of $N = 5.26$ million people, where each individual follows $X(t)$, the process may be modeled as a birth and death process as it is a continuous-time Markov chain where transitions only occur between neighbouring states or the state itself, where a state corresponds to the number of individuals that are infected at some time t. The transition rates are given as α_i and β_i for birth and death respectively, where the subscript i denotes the rate for a specific state $\Omega_i \in \{0, 1, ..., N\}$.

For this process, it is assumed that transitions only occur between neighbouring states and that the rates are constant over all states. The latter assumption may be a gross simplification, as the rate of infections are intuitively expected to increase with the number of infected individuals, but this is ignored here for simplicity.

Using the rates found for $X(t)$, the rates for $Y(t)$ are $\alpha = \lambda = 0.01$ and $\beta = \mu = 0.143$, and a transition diagram for the process is depicted in Figure 3.

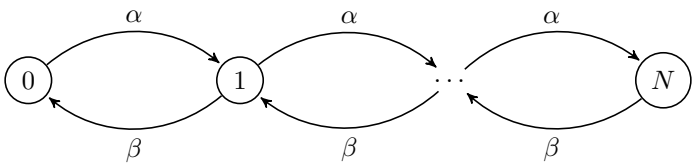


Figure 3: *Transition diagram for $Y(t)$*

e)

Denoting the probability that an infection results in a serious complication by $p = 0.01$, the capacity of patients in the hospital by $L = 2000$, the hospital's required treatment time per patient by W and the rate of arrivals to the hospital by γ, we can use Little's law to calculate the required treatment time per patient by,

$$\begin{aligned} W &= \frac{L}{\gamma} \\ &= \frac{L}{(1-\pi_I)\cdot N \cdot \alpha \cdot p} \\ &= 4.068 \text{ days} \end{aligned}$$

The main clue is determining γ, which is the rate at the stationary distribution. The number of susceptible individuals in the population at this time is on average $(1-\pi_I)N$, and it is this number of individuals that determine the rate into the hospital, given by the rate of infections scaled by the probability of an infection resulting in a hospitalization.

Problem 2: Calibrating climate models

a)

The Matérn correlation function is given as

$$\text{Corr}[Y(\theta_1,\theta_2)] = (1+\phi_M|\theta_1-\theta_2|\exp(-15|\theta_1-\theta_2|)), \quad \theta_1,\ \theta_2 \in [0,1]. \tag{1}$$

Based on Equation (1), the covariance matrix $\boldsymbol{\Sigma}$ of size $n \times n$ is constructed according to

$$\Sigma_{i,j} = (1+\phi_M|\theta_j-\theta_i|\exp(-15|\theta_j-\theta_i|)). \tag{2}$$

The θ values used to make $\boldsymbol{\Sigma}$ are taken from $\boldsymbol{\theta} = \begin{bmatrix}\boldsymbol{\theta}_{\text{grid}}^T & \boldsymbol{\theta}_{\text{cond}}^T\end{bmatrix}^T$, where $\boldsymbol{\theta}_{\text{grid}}$ is a vector containing all θ values in the given grid (0.25 to 0.50 with step size 0.005), and $\boldsymbol{\theta}_{\text{cond}} = [0.30 \quad 0.35 \quad 0.39 \quad 0.41 \quad 0.45]^T$. Thus, $\boldsymbol{\Sigma}$ can be partitioned as follows:

$$\boldsymbol{\Sigma} = \begin{bmatrix}\boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{grid}}\boldsymbol{\theta}_{\text{grid}}} & \boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{grid}}\boldsymbol{\theta}_{\text{cond}}} \\ \boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{cond}}\boldsymbol{\theta}_{\text{grid}}} & \boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{cond}}\boldsymbol{\theta}_{\text{cond}}}\end{bmatrix} \tag{3}$$

$\boldsymbol{\mu}$ can be constructed from $E[\boldsymbol{Y}(\boldsymbol{\theta})]$, resulting in $\begin{bmatrix}\boldsymbol{\mu}_{\text{grid}}^T & \boldsymbol{\mu}_{\text{cond}}^T\end{bmatrix} = [\mathbf{0.5}_{1\times 51} \quad \mathbf{0.5}_{1\times 5}]^T$. We are now able to derive the expected value vector $\bar{\boldsymbol{\mu}}$ and covariance matrix $\bar{\boldsymbol{\Sigma}}$ for the conditioned probability distribution $p(\boldsymbol{Y}(\boldsymbol{\theta}_{\text{grid}}) \mid \boldsymbol{y}(\boldsymbol{\theta}_{\text{cond}}))$ according to Equation (4) and Equation (5):

$$\bar{\boldsymbol{\mu}} = \boldsymbol{\mu}_{\text{grid}} + \boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{grid}}\boldsymbol{\theta}_{\text{cond}}}\boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{cond}}\boldsymbol{\theta}_{\text{cond}}}^{-1}(\boldsymbol{y}(\boldsymbol{\theta}_{\text{cond}}) - \boldsymbol{\mu}_{\text{cond}}) \tag{4}$$

$$\bar{\boldsymbol{\Sigma}} = \boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{grid}}\boldsymbol{\theta}_{\text{grid}}} - \boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{grid}}\boldsymbol{\theta}_{\text{cond}}}\boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{cond}}\boldsymbol{\theta}_{\text{cond}}}^{-1}\boldsymbol{\Sigma}_{\boldsymbol{\theta}_{\text{cond}}\boldsymbol{\theta}_{\text{grid}}} \tag{5}$$

The diagonal elements of $\bar{\boldsymbol{\Sigma}}$ give the variance of each $Y(\theta)$, and can be used to compute a 90% prediction interval according to Equation (6) and Equation (7):

$$y_{\text{lower}} = \mathrm{E}\left[Y(\theta_i \mid \boldsymbol{y}(\boldsymbol{\theta}_{\text{cond}})\right] - z_{0.05}\sqrt{\mathrm{Var}\left(Y(\theta_i \mid \boldsymbol{y}(\boldsymbol{\theta}_{\text{cond}})\right)} \tag{6}$$

$$y_{\text{upper}} = \mathrm{E}\left[Y(\theta_i \mid \boldsymbol{y}(\boldsymbol{\theta}_{\text{cond}})\right] + z_{0.05}\sqrt{\mathrm{Var}\left(Y(\theta_i \mid \boldsymbol{y}(\boldsymbol{\theta}_{\text{cond}})\right)} \tag{7}$$

where $z_{0.05} \approx 1.644854$ is the 95 percentile from the standard Gaussian distribution.
A plot of the conditioned expected values, together with the 90% prediction interval, is shown in Figure 4.

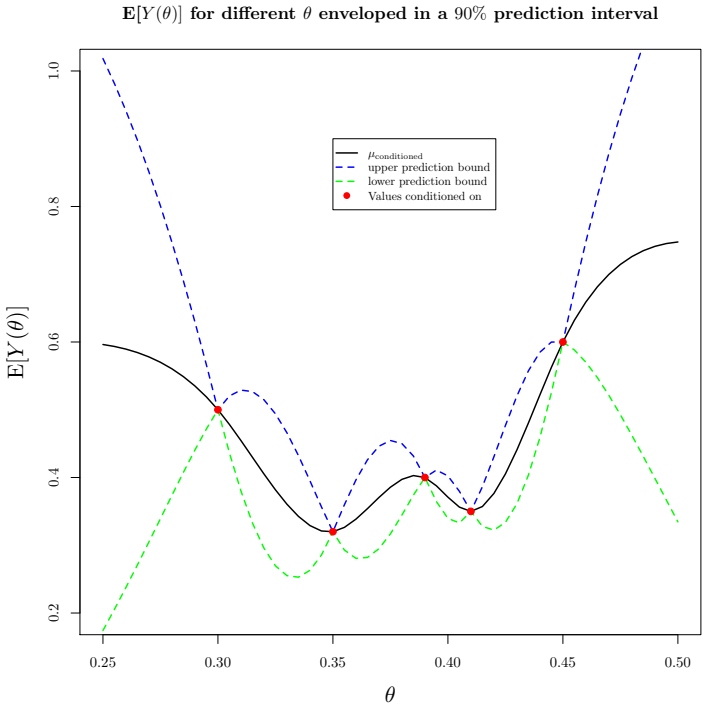


Figure 4: *Plot of conditioned expected value together with* 90% *prediction interval.*

b)

As marginalization of a Gaussian distribution is simply a matter of extracting the corresponding expected value and variance from the expected value vector and covariance matrix, each probability can be calculated from the scalar Gaussian distribution. A plot over all the probabilities for different $y(\theta)$ is shown in Figure 5.

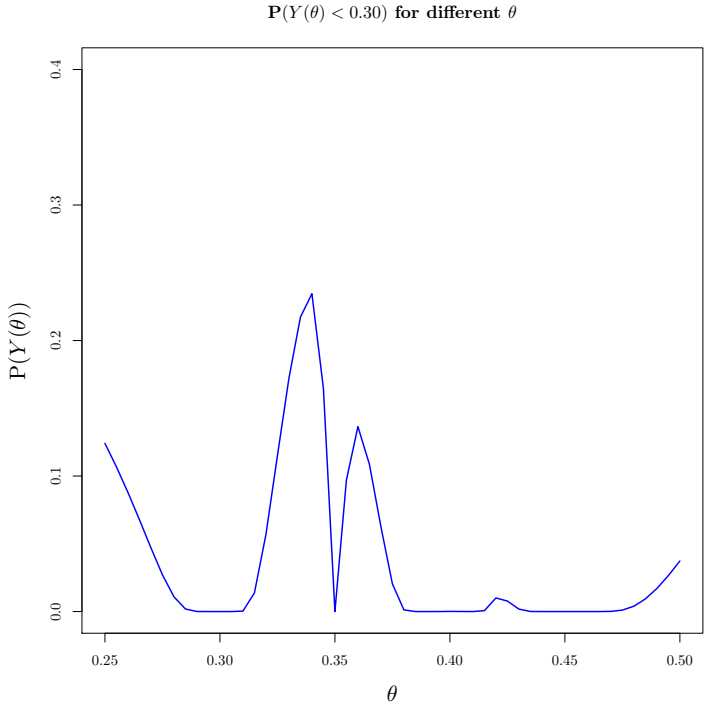
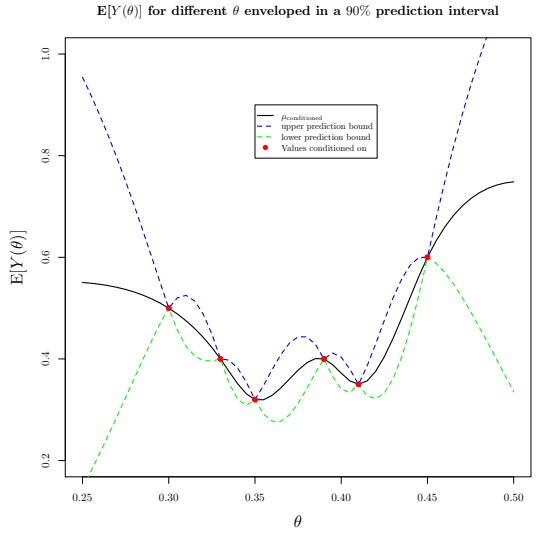


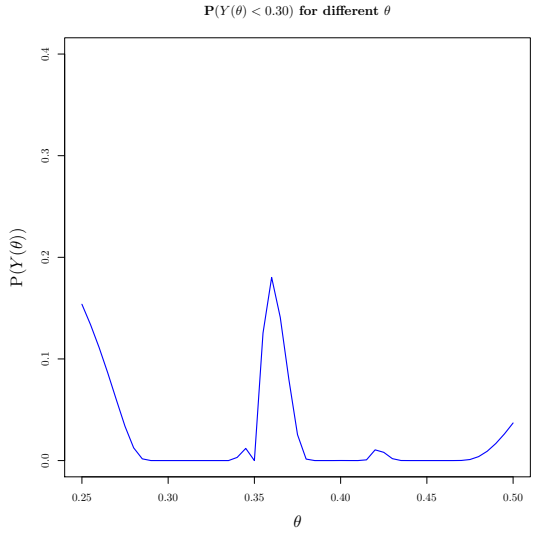
Figure 5: *Plot of* $P(Y(\theta) < 0.30)$ *for different* θ*.*

c)

Using the same procedure as in a), but adding the point $(y(\theta),\ \theta) = (0.40,\ 0.33)$ to the vector to condition on, we get the plots shown in Figure 6. The θ that is most probable to give $Y(\theta) < 0.30$ is 0.36, and is what the scientists should choose. This is evident from Figure 6b.



(a) *Plot of conditioned expected value together with* 90% *prediction interval.*



(b) *Plot of* $P(Y(\theta) < 0.30)$ *for different* θ*.*

Figure 6: *Updated plots with additional point* $(y(\theta),\ \theta) = (0.40,\ 0.33)$ *conditioned on.*