

UMSAEP Project Report: Time Scales Analysis of Mathematical Models in Population Biology

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Abstract

In this report, I am giving a summary of my visit at UWC in Cape Town, and I am describing the results we have achieved during this visit.

1 Summary of Visit

I arrived in CPT on Friday, May 19, 2023, and I left 21 days later, on Thursday, June 8, 2023. During my visit, I was accommodated in the Bell Rosen Guest House in Bellville. A rental car was arranged for me, which I used to travel to the campus of UWC and back. I had an office there. Together with my host, Professor Kailash Patidar, who is the Chair of the Department of Mathematics and Applied Mathematics at UWC, we held daily meetings, either in my office or in his office, sometimes at my hotel and at his house.



Figure 1: At Table Mountain

During the first week, we discussed the theory of time scales, as presented in my books [2, 3]. In the second week, we discussed discretization schemes, as constructed by Professor Patidar in [7, 8]. In the third week, we put these two ingredients together to develop a systematic approach how to translate these (continuous-time) models into dynamic equations on time scales. The details of our investigations are presented in Section 2 of this report. We are still in the process of preparing a research paper summarizing our results and submitting it for publication in a high-level international journal. During my visit, we also had a nice social program, visiting Franschhoek, Stellenbosch, and the sights of Cape Town, see Figure 1. We also visited together several restaurants and wineries. It was raining a lot during my visit, but on the last Sunday, the weather was nice, and I hiked up along the Table Mountain through the Platteklip Gorge.

2 Results of Visit

During my stay at UWC, Professor Patidar and I have developed a method how to “translate” any continuous-time model (consisting of differential equations) into a time-scales (see [2,3]) model in a “correct” way, namely preserving nonnegativity of solutions that start with nonnegative initial conditions, and preserving other important properties of solutions. Some related results are given in [4–6]. This has direct applications to discrete-time models and quantum-time models. In order to illustrate our method, we took three important systems from epidemiology literature and performed our analysis. The first pertinent system has two equations, the second one has four equations, and the third one has six equations. In the rest of this section, we now present our results for each of these models.

2.1 Two Equations

This system originates in [7, Equation (1)] and models the spread of a disease in a population that is subdivided into compartments of susceptible ($S(t)$) and infected ($I(t)$) subpopulations given by

$$\begin{aligned} S' &= B - \beta SI - mS + \gamma I, \\ I' &= \beta SI - (m + d + \gamma)I, \end{aligned} \tag{1}$$

where B is the recruitment rate of individuals into the population, β is the effective contact rate, m is the natural death rate, γ is the recovery rate, and d is the disease-induced death rate. Our time scales analogue of (1) appears as

$$\begin{aligned} S^\Delta &= B - \beta S^\sigma I - mS^\sigma + \gamma I^\sigma, \\ I^\Delta &= \beta S^\sigma I - (m + d + \gamma)I^\sigma. \end{aligned} \tag{2}$$

For isolated time scales (e.g., when $\mathbb{T} = \mathbb{Z}$ or $\mathbb{T} = q^{\mathbb{N}_0}$), (2) can be, after some time scales calculations, rewritten as

$$\begin{aligned} S^\sigma &= \frac{S + \mu B + \frac{\mu \gamma I}{1 + \mu(m + d + \gamma)}}{1 + \mu m + \frac{\mu \beta [1 + \mu(m + d)]}{1 + \mu(m + d + \gamma)}} I, \\ I^\sigma &= \frac{I(1 + \mu \beta S^\sigma)}{1 + \mu(m + d + \gamma)}. \end{aligned} \tag{3}$$

It is now clear, given all parameters are nonnegative and the initial conditions are nonnegative, that the solutions to (3) remain nonnegative. Furthermore,

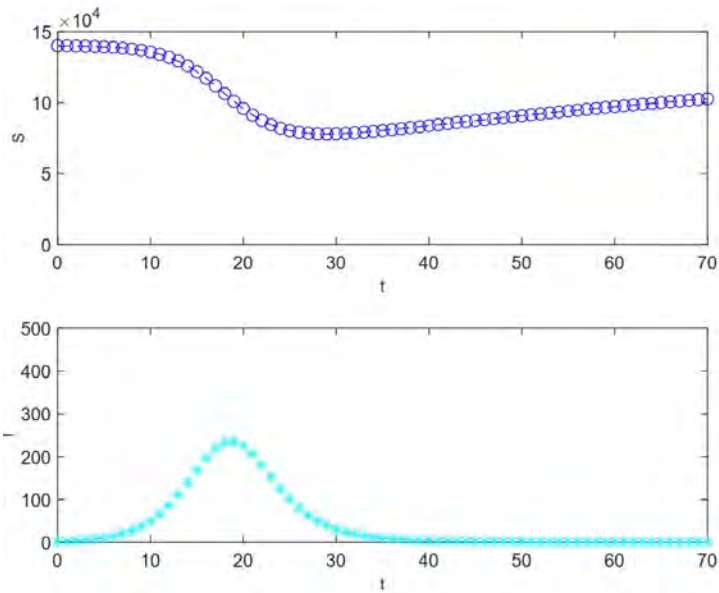


Figure 2: Solutions of (3) when $\mathbb{T} = \mathbb{Z}$

we calculated the endemic equilibrium and the disease-free equilibrium for (2) and performed other calculations. Some exemplary plots of solutions are pictured in Figure 2 for $\mathbb{T} = \mathbb{Z}$ and in Figure 3 for $\mathbb{T} = q^{\mathbb{N}_0}$.

2.2 Four Equations

This system stems from [7, Equation (16)] and appears as a vaccination model for the transmission dynamics of two HIV subtypes in a given community. The total population ($N(t)$) is subdivided into the sub-populations of wholly susceptible individuals ($X(t)$), vaccinated susceptible individuals ($V(t)$), individuals infected with an endemic HIV subtype 1 ($Y_1(t)$), and

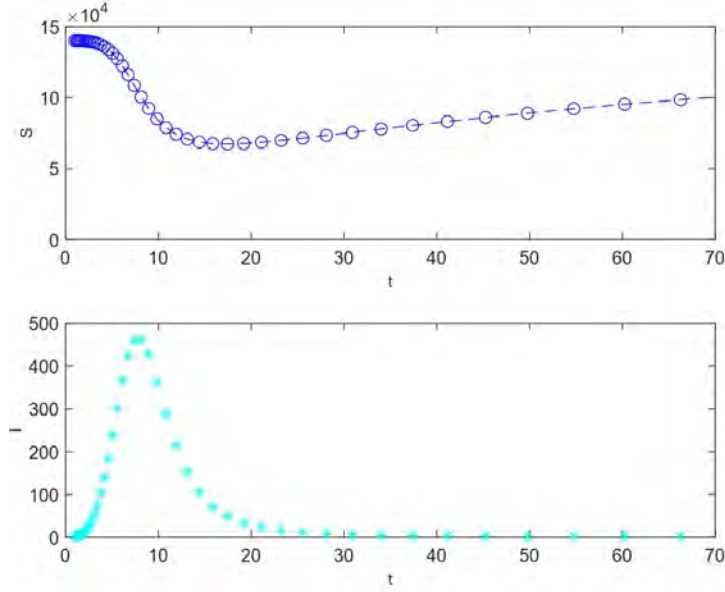


Figure 3: Solutions of (3) when $\mathbb{T} = q^{N_0}$

individuals infected with an invading HIV subtype 2 ($Y_2(t)$), given by

$$\begin{aligned}
 X' &= B(1-r) - mX - \frac{\beta_1 c}{N} XY_1 - \frac{\beta_2 c}{N} XY_2, \\
 V' &= Br - mV - \frac{(1-\xi_1)\beta_1 c}{N} VY_1 - \frac{(1-\xi_2)\beta_2 c}{N} VY_2, \\
 Y_1' &= \frac{\beta_1 c}{N} XY_1 + \frac{(1-\xi_1)\beta_1 c}{N} VY_1 - (m + \gamma_1 + \tau)Y_1, \\
 Y_2' &= \frac{\beta_2 c}{N} XY_2 + \frac{(1-\xi_2)\beta_2 c}{N} VY_2 - (m + \gamma_2 + \tau)Y_2,
 \end{aligned} \tag{4}$$

where the parameters are described in [7, Table 6]. Our time scales analogue of (4) appears as

$$\begin{aligned}
X^\Delta &= B(1-r) - mX^\sigma - \frac{\beta_1 c}{N} X^\sigma Y_1 - \frac{\beta_2 c}{N} X^\sigma Y_2, \\
V^\Delta &= Br - mV^\sigma - \frac{(1-\xi_1)\beta_1 c}{N} V^\sigma Y_1 - \frac{(1-\xi_2)\beta_2 c}{N} V^\sigma Y_2, \\
Y_1^\Delta &= \frac{\beta_1 c}{N} X^\sigma Y_1 + \frac{(1-\xi_1)\beta_1 c}{N} V^\sigma Y_1 - (m + \gamma_1 + \tau)Y_1^\sigma, \\
Y_2^\Delta &= \frac{\beta_2 c}{N} X^\sigma Y_2 + \frac{(1-\xi_2)\beta_2 c}{N} V^\sigma Y_2 - (m + \gamma_2 + \tau)Y_2^\sigma.
\end{aligned} \tag{5}$$

For isolated time scales (e.g., when $\mathbb{T} = \mathbb{Z}$ or $\mathbb{T} = q^{\mathbb{N}_0}$), (5) can be, after some time scales calculations, rewritten as

$$\begin{aligned}
X^\sigma &= \frac{X + \mu B(1-r)}{1 + \mu \left(m + \frac{\beta_1 c}{N} Y_1 + \frac{\beta_2 c}{N} Y_2 \right)}, \\
V^\sigma &= \frac{V + \mu Br}{1 + \mu \left(m + \frac{(1-\xi_1)\beta_1 c}{N} Y_1 + \frac{(1-\xi_2)\beta_2 c}{N} Y_2 \right)}, \\
Y_1^\sigma &= \frac{1 + \frac{\mu\beta_1 c}{N} X^\sigma + \frac{\mu(1-\xi_1)\beta_1 c}{N} V^\sigma}{1 + \mu(m + \gamma_1 + \tau)} Y_1, \\
Y_2^\sigma &= \frac{1 + \frac{\mu\beta_2 c}{N} X^\sigma + \frac{\mu(1-\xi_2)\beta_2 c}{N} V^\sigma}{1 + \mu(m + \gamma_2 + \tau)} Y_2.
\end{aligned} \tag{6}$$

It is now clear, given all parameters are nonnegative and the initial conditions are nonnegative, that the solutions to (6) remain nonnegative. Furthermore, we discussed the disease-free equilibrium, the subtype 1 only equilibrium, the subtype 2 only equilibrium, the co-existence equilibrium, and performed other calculations. equilibrium and the disease-free equilibrium for (2) and performed other calculations. We did some initial plots of solutions which reassured the ‘‘correctness’’ of our system (5), but we still have to prepare some exemplary plots of solutions, and these are therefore not pictured here. They will be pictured in the final version of the paper that will be submitted for publication.

2.3 Six Equations

This system comes from [8, Equation (2.1)] (see also [1]) and describes the transmission dynamics of an HIV-TB co-infection, combining two states for

HIV (HIV₋ and HIV₊) with three states for TB (susceptible (S_i), latent (E_i), and infectious (I_i) individuals). It is given by

$$\begin{aligned}
S'_1 &= B - S_1 \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - \nu_1 S_1 - f(H) H S_1, \\
E'_1 &= ((1 - p_1) S_1 - q_1 E_1) \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - (a_1 + \nu_1) E_1 + b_1 I_1 \\
&\quad - f(H) H E_1, \\
I'_1 &= (p_1 S_1 + q_1 E_1) \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - (b_1 + m_1) I_1 + a_1 E_1 \\
&\quad - f(H) H I_1, \\
S'_2 &= - S_2 \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - \nu_2 S_2 + f(H) H S_1, \\
E'_2 &= ((1 - p_2) S_2 - q_2 E_2) \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - (a_2 + \nu_2) E_2 + b_2 I_2 \\
&\quad + f(H) H E_1, \\
I'_2 &= (p_2 S_2 + q_2 E_2) \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - (b_2 + m_2) I_2 + a_2 E_2 \\
&\quad + f(H) H I_1,
\end{aligned} \tag{7}$$

where the parameters are described in [8, Table 1]. Our time scales analogue of (7) appears as

$$\begin{aligned}
S_1^\Delta &= B - S_1^\sigma \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - \nu_1 S_1^\sigma - f(H) H S_1^\sigma, \\
E_1^\Delta &= ((1 - p_1) S_1^\sigma - q_1 E_1^\sigma) \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - (a_1 + \nu_1) E_1^\sigma + b_1 I_1^\sigma \\
&\quad - f(H) H E_1^\sigma, \\
I_1^\Delta &= (p_1 S_1^\sigma + q_1 E_1^\sigma) \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - (b_1 + m_1) I_1^\sigma + a_1 E_1^\sigma \\
&\quad - f(H) H I_1^\sigma, \\
S_2^\Delta &= - S_2^\sigma \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - \nu_2 S_2^\sigma + f(H) H S_1^\sigma, \\
E_2^\Delta &= ((1 - p_2) S_2^\sigma - q_2 E_2^\sigma) \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - (a_2 + \nu_2) E_2^\sigma + b_2 I_2^\sigma \\
&\quad + f(H) H E_1^\sigma, \\
I_2^\Delta &= (p_2 S_2^\sigma + q_2 E_2^\sigma) \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) - (b_2 + m_2) I_2^\sigma + a_2 E_2^\sigma \\
&\quad + f(H) H I_1^\sigma.
\end{aligned} \tag{8}$$

For isolated time scales (e.g., when $\mathbb{T} = \mathbb{Z}$ or $\mathbb{T} = q^{\mathbb{N}_0}$), (8) can be, after some time scales calculations, rewritten as

$$\begin{aligned}
S_1^\sigma &= \frac{S_1 + \mu B}{1 + \mu \left(\left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + \nu_1 + f(H)H \right)}, \\
E_1^\sigma &= \frac{E_1 + \mu(1 - p_1)S_1^\sigma \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + \frac{\mu b_1 (I_1 + \mu p_1 S_1^\sigma \left(\frac{k_1 I_1 + k_2 I_2}{N} \right))}{1 + \mu(b_1 + m_1 + f(H)H)}}{1 + \mu(\nu_1 + f(H)H) + \frac{\mu(q_1 \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + a_1)[1 + \mu(m_1 + f(H)H)]}{1 + \mu(b_1 + m_1 + f(H)H)}}, \\
I_1^\sigma &= \frac{I_1 + \mu \left(p_1 S_1^\sigma \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + (q_1 \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + a_1) E_1^\sigma \right)}{1 + \mu(b_1 + m_1 + f(H)H)}, \\
S_2^\sigma &= \frac{S_2}{1 + \mu \left(\left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + \nu_2 - f(H)H \right)}, \\
E_2^\sigma &= \frac{E_2 + \mu(1 - p_2)S_2^\sigma \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + \frac{\mu b_2 (I_2 + \mu p_2 S_2^\sigma \left(\frac{k_1 I_1 + k_2 I_2}{N} \right))}{1 + \mu(b_2 + m_2 - f(H)H)}}{1 + \mu(\nu_2 - f(H)H) + \frac{\mu(q_2 \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + a_2)[1 + \mu(m_2 - f(H)H)]}{1 + \mu(b_2 + m_2 - f(H)H)}}, \\
I_2^\sigma &= \frac{I_2 + \mu \left(p_2 S_2^\sigma \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + (q_2 \left(\frac{k_1 I_1 + k_2 I_2}{N} \right) + a_2) E_2^\sigma \right)}{1 + \mu(b_2 + m_2 - f(H)H)}.
\end{aligned} \tag{9}$$

It is now clear, given all parameters are nonnegative and the initial conditions are nonnegative and f satisfies an appropriate assumption, that the solutions to (9) remain nonnegative. Furthermore, we discussed the HIV only model and the TB only model and performed other calculations. We still have to prepare some exemplary plots of solutions, and these are therefore not pictured here. They will be pictured in the final version of the paper that will be submitted for publication.

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