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

Martin Bohner
Department of Mathematics and Statistics
Missouri S&T, Rolla, MO 65409, USA
bohner@mst.edu

# 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 di erential 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 rst 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

$$S^0 = B \quad SI \quad mS I$$

Figure 2: Solutions of (3) when $T = Z$

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 $T = Z$ and in Figure 3 for $T = q^{N_0}$.

## 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 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 $T = q^{N_0}$

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

$$X' = B(1 \quad r) \quad mX \quad \frac{{}_1C}{N} XY_1$$

29 0 l S Q BT 298.523 324.192 Td (N)Tj 14.696 8.201 Td Td (29 0 l S Q

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

$$\begin{aligned}
X &= B(1 - r) - mX - \frac{{}_1c}{N}X\,Y_1 - \frac{{}_2c}{N}X\,Y_2;\\
V &= Br - mV - \frac{(1 - {}_1)\,{}_1c}{N}V\,Y_1 - \frac{(1 - {}_2)\,{}_2c}{N}V\,Y_2;\\
Y_1 &= \frac{{}_1c}{N}X\,Y_1 + \frac{(1 - {}_1)\,{}_1c}{N}V\,Y_1 - (m + {}_1 + )Y_1;\\
Y_2 &= \frac{{}_2c}{N}X\,Y_2 + \frac{(1 - {}_2)\,{}_2c}{N}V\,Y_2 - (m + {}_2 + )Y_2:
\end{aligned} \tag{5}$$

For isolated time scales (e.g., when $T = Z$ or $T = q^{N_0}$), (5) can be, after some time scales calculations, rewritten as

$$\begin{aligned}
X &= \frac{X + B(1 - r)}{1 + m + \frac{{}_1c}{N}Y_1 + \frac{{}_2c}{N}Y_2};\\
V &= \frac{V + Br}{1 + m + \frac{(1 - {}_1)\,{}_1c}{N}Y_1 + \frac{(1 - {}_2)\,{}_2c}{N}Y_2};\\
Y_1 &= \frac{1 + \frac{{}_1c}{N}X + \frac{(1 - {}_1)\,{}_1c}{N}V}{1 + (m + {}_1 + )}Y_1;\\
Y_2 &= \frac{1 + \frac{{}_2c}{N}X + \frac{(1 - {}_2)\,{}_2c}{N}V}{1 + (m + {}_2 + )}Y_2:
\end{aligned} \tag{6}$$

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 nal 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

$$
\begin{aligned}
S_1^0 &= B \quad S_1 \quad \frac{k_1 I_1 + k_2 I_2}{N} \quad {}_1 S_1 \quad f(H) H S_1; \\
E_1^0 &= ((1 \quad p_1) S_1 \quad q_1 E_1) \quad \frac{k_1 I_1 + k_2 I_2}{N} \quad (a_1 + \quad {}_1) E_1 + b_1 I_1 \\
&\quad f(H) H E_1; \\
I_1^0 &= (p_1 S_1 + q_1 E_1) \quad \frac{k_1 I_1 + k_2 I_2}{N} \quad (b_1 + m_1) I_1 + a_1 E_1 \\
&\quad f(H) H I_1; \\
S_2^0 &= \quad S_2 \quad \frac{k_1 I_1 + k_2 I_2}{N} \quad {}_2 S_2 + f(H) H S_1; \\
E_2^0 &= ((1 \quad p_2) S_2 \quad q_2 E_2) \quad \frac{k_1 I_1 + k_2 I_2}{N} \quad (a_2 + \quad {}_2) E_2 + b_2 I_2 \\
&\quad + f(H) H E_1; \\
I_2^0 &= (p_2 S_2 + q_2 E_2) \quad \frac{k_1 I_1 + k_2 I_2}{N} \quad (b_2 + m_2) I_2 + a_2 E_2 \\
&\quad + f(H) H I_1;
\end{aligned}
\tag{7}
$$

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

$$
\begin{aligned}
S_1 &= B \quad S_1 \quad \frac{k_1 I_1 + k_2 I_2}{N} \qquad {}_1 S_1 \quad f(H) H S_1 ; \\
E_1 &= ((1 \quad p_1) S_1 \quad q_1 E_1) \quad \frac{k_1 I_1 + k_2 I_2}{N} \qquad (a_1 + \ {}_1) E_1 + b_1 I_1 \\
&\qquad f(H) H E_1 ; \\
I_1 &= (p_1 S_1 + q_1 E_1) \quad \frac{k_1 I_1 + k_2 I_2}{N} \qquad (b_1 + m_1) I_1 + a_1 E_1 \\
&\qquad f(H) H I_1 ; \\
S_2 &= \quad S_2 \quad \frac{k_1 I_1 + k_2 I_2}{N} \qquad {}_2 S_2 + f(H) H S_1 ; \\
E_2 &= ((1 \quad p_2) S_2 \quad q_2 E_2) \quad \frac{k_1 I_1 + k_2 I_2}{N} \qquad (a_2 + \ {}_2) E_2 + b_2 I_2 \\
&\qquad + f(H) H E_1 ; \\
I_2 &= (p_2 S_2 + q_2 E_2) \quad \frac{k_1 I_1 + k_2 I_2}{N} \qquad (b_2 + m_2) I_2 + a_2 E_2 \\
&\qquad + f(H) H I_1 :
\end{aligned}
\tag{8}
$$

[3] Martin Bohner and Allan Peterson.