A model of Partial Differential Equations for HIV propagation in lymph nodes

by: E.B.S. Marinho, F.S. Bacelar, R.F.S Andrade (2012)
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Introduction

- Modelling of the interaction between HIV and $CD4^+T$ cells, which are the main target of HIV.
- Infection seen inside the lymph nodes, which is the previous location of IS cells before going to the bloodstream.
- Addition of space dependence to previous models considering only time based solutions.

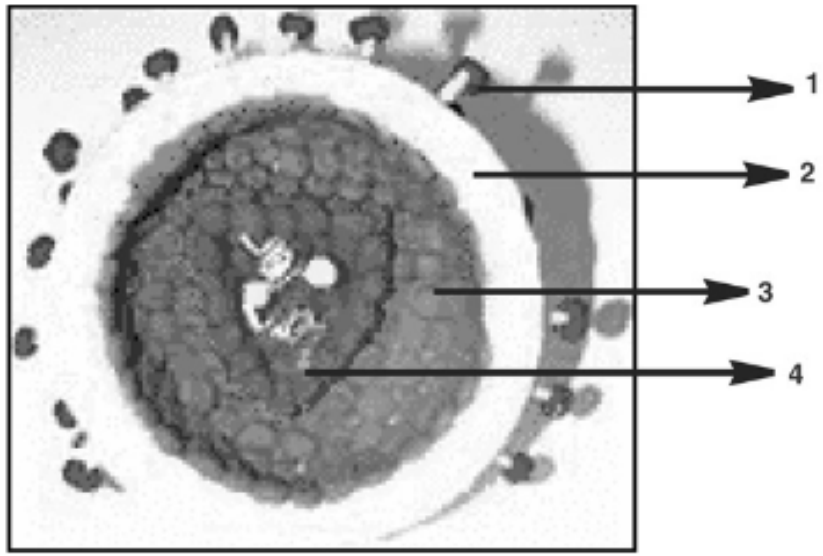

Figure: HIV Structure. 1. Envelope composed of proteins gp120 and gp41; 2. Internal capsule composed of protein p17; 3. Membrane composed of protein p24 and 4. Genetic material composed of RNA and proteins. [2]

Methods: Partial Differential Equation System

Model dependant on time t and space $\vec{r} = \langle x\hat{x}, y\hat{y} \rangle$; $\hat{x}, \hat{y} \in [0, L], [0, L]$

$$
\begin{aligned}
\frac{\partial H_1}{\partial t} &= -k_5 H_1 A^p - k_6 H_1 B^n + k_9 H_1 \nabla^2 A, \\
\frac{\partial H_2}{\partial t} &= k_3 D - k_5 H_2 A^q - k_6 H_2 B^n + k_9 H_2 \nabla^2 A, \\
\frac{\partial A}{\partial t} &= -k_1 A(t-\tau) + k_4 D + k_5 (H_1 A^p + H_2 A^q) + \\
&\quad k_6 (H_1 + H_2) B^n - k_9 (H_1 + H_2) \nabla^2 A, \\
\frac{\partial B}{\partial t} &= k_1 A(t-\tau) - k_2 B, \\
\frac{\partial D}{\partial t} &= -k_3 D - k_4 D + k_2 B
\end{aligned}
$$

Figure: Partial Differential Equation System describing the HIV infection in the lymph nodes. [3]

Model considering 4 variables:

- $H_1(t, \vec{r})$: Healthy cells already in the region
- $H_2(t, \vec{r})$: Healthy cells newly differentiated
- $A(t, \vec{r})$: Newly infected cells
- $B(t, \vec{r})$: Old infected cells
- $D(t, \vec{r})$: Dead cells

parameter	meaning	value
k_1	Transition rate from A to B	0.163
k_2	Transition rate from B to D	0.228
k_3	Replenishment rate from D to H_2	0.650
k_4	Replenishment rate from D to A	3.25×10^{-5}
k_5	Infection rate from H_1 and H_2 to A	0.650
K_6	Infection rate from H_1 and H_2 to B	0.169
K_9	Diffusion rate of A cells	$\in (0.2, 8) \times 10^{-3}$
p	Infection order from H_1 to A	1
q	Infection order from H_2 to A	1.15
n	Infection order from H_1 and H_2 to B	4
τ	Time delay from A to B	4 weeks

Table: The parameters taken after the *Dynamics of HIV infection* literature, presented with their functions and meanings along the model. [1]

Results: Temporal evolution

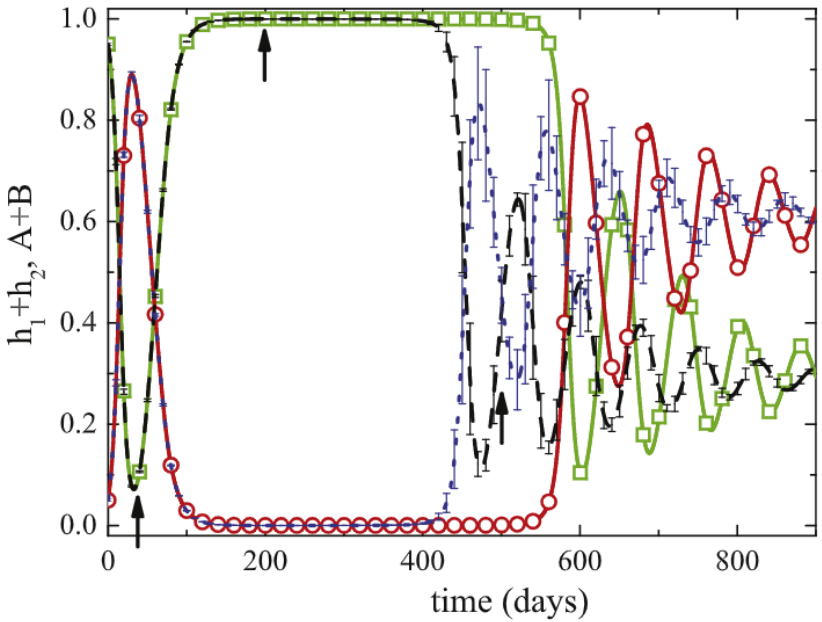

Figure: Time evolution of $(H_1 + H_2)$ and $(A + B)$ predicted by the system of **Figure 2** in a square lattice of tissue of area L^2. The squares $(H_1 + H_2)$ and circles $(A + B)$ are the solution for uniform initial conditions $(H_1, H_2, A, B, D) = (0.95, 0, 0.05, 0, 0); (\hat{H_1}, \hat{H_2}, \hat{A}, \hat{B}, \hat{D}) = (0, 1, 0, 0)$. The dashed $(H_1 + H_2)$ and dotted $(A + B)$ lines are the solution for non uniform initial conditions; $A_0 = 0.06$ in a small square of the lattice [3].

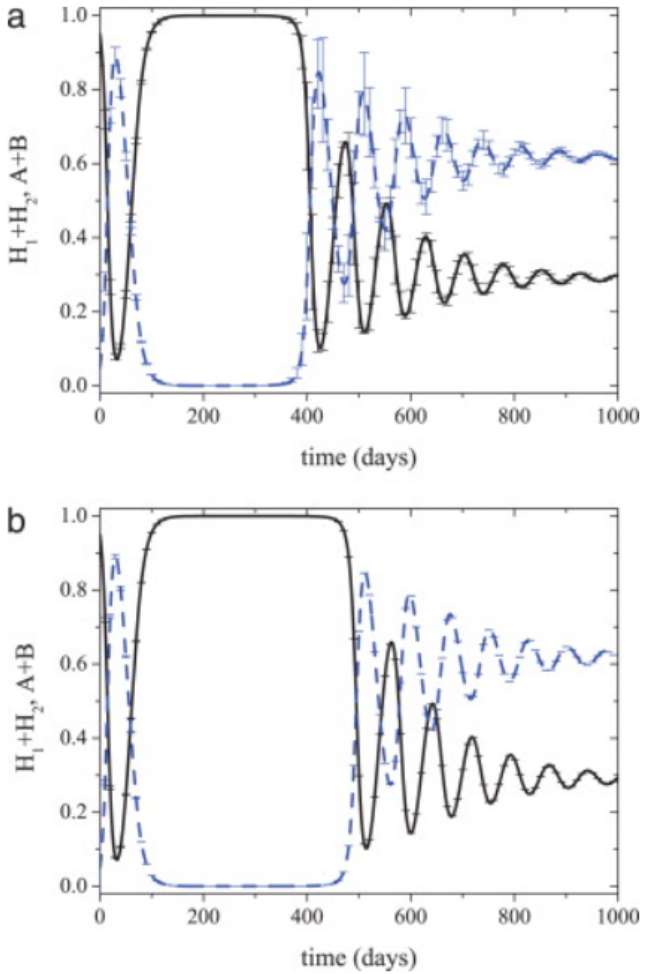

Figure: Time evolution for the fluctuation of the parameter K_9 with values of $K_9 = 2 \times 10^{-4}$ (a) and $k_9 = 2 \times 10^{-3}$ (b), with solid and dashed lines representing $(H_1 + H_2)$ and $A + B$ respectively [3].

Results: Spatial Evolution

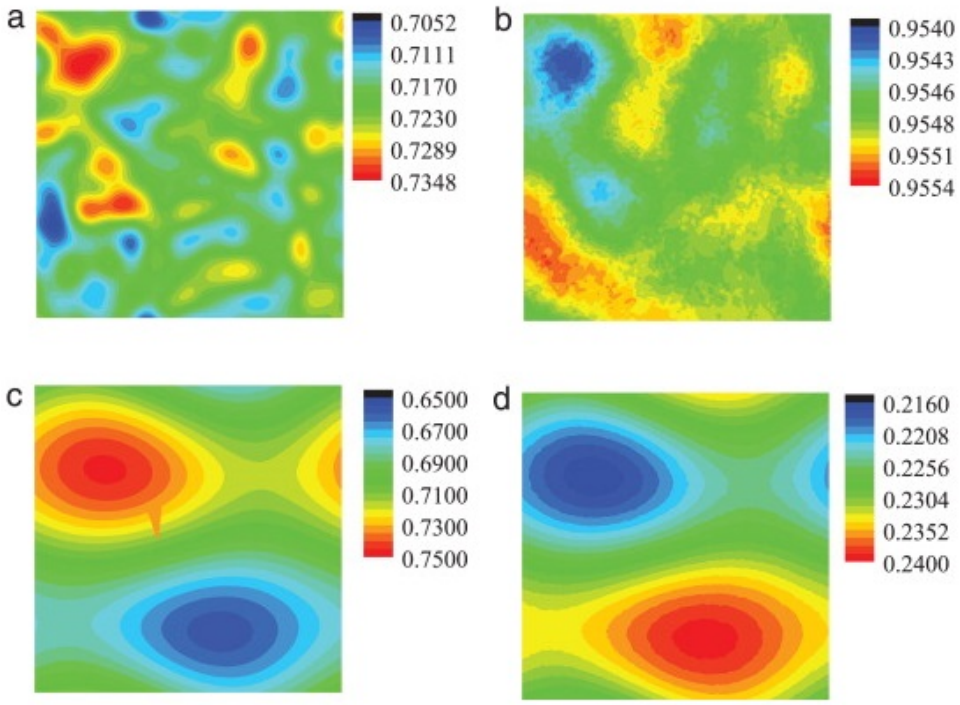

Figure: Four spatial patterns for the fraction of $H_1 + H_2$ at $t_1 = 10$ (a), $t_2 = 100$ (b), $t_3 = 400$ (c) and $t_4 = 600$ days (d) resulting from random non homogeneous initial conditions. The same parameters as the **Figure 3** are considered [3].

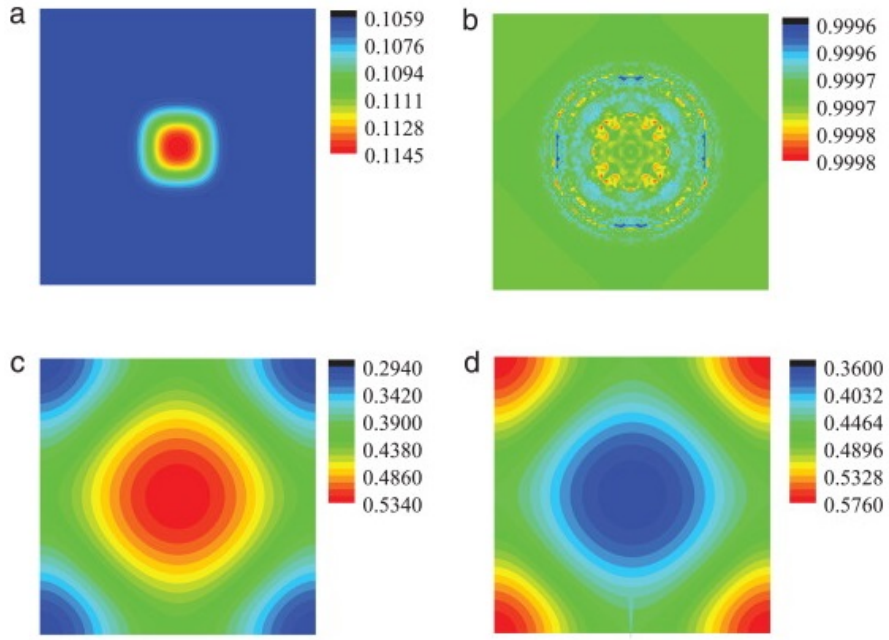

Figure: Representation of the dynamic concentration of healthy cells $(H_1 + H_2)$ in a square lattice presented with non-homogeneous initial concentrations at $t_1 = 40$days (a), $t_2 = 200$days (b), $t_3 = 500$days (c), using a diffusion coefficient $k_9 = 2 \times 10^{-4}$. Panel (d) shows concentration of infected cells $(A + B)$ at $t = t_3$. [3]

Conclusions

- The time and space evolution of the infection is widely influenced by the diffusion factors and initial distributions over the evaluation area.
- Identification of the influence of non linear diffusion terms to describe the movement of the infected cells across a given area of the lymph nodes.
- Identification of fluctuations and changes in behavior with given changes in diffusion parameters and the introduction of non uniform initial conditions over the evaluation area.


Rita Maria Zorzenon Dos Santos and Sérgio Coutinho.
Dynamics of hiv infection: A cellular automata approach.
Physical review letters, 87(16):168102, 2001.


R Motta Jafelice, BFZ Bechara, Laécio C Barros, Rodney Carlos Bassanezi, and F Gomide.
Cellular automata with fuzzy parameters in microscopic study of positive hiv individuals.
Mathematical and Computer Modelling, 50(1-2):32–44, 2009.


EBS Marinho, Flora S Bacelar, and Roberto F S Andrade.
A model of partial differential equations for hiv propagation in lymph nodes.
Physica A: Statistical Mechanics and its Applications, 391(1-2):132–141, 2012.