

22 HIV Treatment Using Optimal Control

Introduction

Viruses are the cause of many common illnesses in society today, such as ebola, influenza, the common cold, and Human Immunodeficiency Virus (HIV). Viruses are not considered to be living organisms as they cannot reproduce on their own. Instead they inject their genes in the form of DNA or RNA into a host's genome. They then use the cell's ribosomes and proteins to make the protein coat and replicate their genes. At the end they lyse the cell (tear it apart) and release many virus particles to infect other cells.

The body has an adaptive immune system which learns to recognize viruses and bacteria and their hosts, and how to destroy them. A major component of this system are T cells. These cells perform many necessary functions such as recognizing invaders, destroying infected cells, and remembering previous infections long after recovery. Of particular interest is the helper T cell, also known as the CD4+T cell, due to a protein found on its surface which regulates the immune responses. HIV is unique in that it specifically targets this particular type of T cell. This means that the system responsible for fighting infections is specifically targeted.

This loss of CD4+T cells is what causes Acquired Immune Deficiency Syndrome (AIDS). Note that AIDS itself is not an infection, which is a common misconception among the population. Due to the lack of T cells to recognize viruses and bacteria, the body becomes susceptible to other forms of infection. Whereas most people are easily able to shake off a common cold, someone suffering from the advanced stages of AIDS will be at serious risk of dying. Since AIDS comes from a loss of T cells, it may be several years before the host notices the effects of the infection. This enables the HIV virus to spread more easily since the host might not realize they are infected and continue in whatever behavior made them susceptible to the infection initially.

Currently there is no cure or vaccine for HIV. However, there are treatments that reduce the virus and bolster the immune system by increasing the CD4+T cell count. Since these treatments can be expensive and often have negative side effects, it is important to optimize the amount of drugs used. Sometimes combinations of these drugs are used to provide a better effect. In this lab we will use optimal control to find the optimal dosage of a two-drug combination¹.

¹SHORT COURSES ON THE MATHEMATICS OF BIOLOGICAL COMPLEXITY, Web. 15 Apr. 2015
<http://www.math.utk.edu/~lenhart/smb2003.v2.html>.

Derivation of Control

We begin by defining some variables. Let T represents the concentration of $CD4^+T$ cells and V the concentration of HIV particles. s_1 and s_2 represent the production of T cells by various processes. B_1 and B_2 are half saturation constants (sort of like crowd control in the blood stream and plasma). Let μ be the death rate of uninfected T cells, k the rate of infection of T cells, and c the death rate of the virus. Let g be the input rate of some external viral source. The control variables u_1 and u_2 represent the amount of drugs that introduce new T cells or kill the virus, respectively.²

Next we write the state system, the equations that describe the changes in T cells and viruses:

$$\begin{aligned}\frac{dT(t)}{dt} &= s_1 - \frac{s_2 V(t)}{B_1 + V(t)} - \mu T(t) - kV(t)T(t) + u_1(t)T(t), \\ \frac{dV(t)}{dt} &= \frac{gV(t)}{B_2 + V(t)}(1 - u_2(t)) - cV(t)T(t).\end{aligned}\tag{22.1}$$

The term $s_1 - \frac{s_2 V(t)}{B_1 + V(t)}$ is the source/proliferation of unaffected T cells, $\mu T(t)$ the natural loss of T cells, $kV(t)T(t)$ the loss of T cells by infection. $\frac{gV(t)}{B_2 + V(t)}$ represents the viral contribution to plasma, and $cV(t)T(t)$ the viral loss. To these equations we add initial conditions $T(0) = T_0$ and $V(0) = V_0$.³

We now seek to maximize the functional

$$J(u_1, u_2) = \int_0^{t_f} [T - (A_1 u_1^2 + A_2 u_2^2)] dt.$$

This functional considers i) the benefit of T cells, and ii) the systematic costs of drug treatments. The constants A_1 and A_2 represent scalars to adjust the size of terms coming from u_1^2 and u_2^2 respectively. We seek an optimal control u_1^*, u_2^* satisfying

$$J(u_1^*, u_2^*) = \max\{J(u_1, u_2) | (u_1, u_2) \in U\},$$

where $U = \{(u_1, u_2) | u_i \text{ is measurable, } a_i \leq u_i \leq b_i, t \in [0, t_f] \text{ for } i = 1, 2\}$.

Optimality System

The Hamiltonian is defined as:

$$\begin{aligned}H &= \vec{\lambda} \cdot \vec{f} - L \\ H &= \lambda_1 \left[s_1 - \frac{s_2 V}{B_1 + V} - \mu T - kVT + u_1 T \right] + \lambda_2 \left[\frac{g(1 - u_2)V}{B_2 + V} - cVT \right] \\ &\quad - [T - (A_1 u_1^2 + A_2 u_2^2)].\end{aligned}$$

Note that the costate is represented with λ instead of p . The costate evolution equations are:

$$\begin{aligned}\lambda_1' &= -\frac{\partial H}{\partial T} = 1 + \lambda_1[\mu + kV^* - u_1^*] + \lambda_2 cV^*, \\ \lambda_2' &= -\frac{\partial H}{\partial V} = \lambda_1 \left[\frac{B_1 s_2}{(B_1 + V^*)^2} + kT^* \right] - \lambda_2 \left[\frac{B_2 g(1 - u_2^*)}{(B_2 + V^*)^2} - cT^* \right].\end{aligned}$$

²'Immunotherapy of HIV-1 Infection', Kirschner, D. and Webb, G. F., Journal of Biological Systems, 6(1), 71-83 (1998)

³'Optimal Control of an HIV Immunology Model', H.R. Joshi

The transversality (or endpoint) conditions are $\lambda_1(t_f) = \lambda_2(t_f) = 0$, with $T(0) = T_0$ and $V(0) = V_0$. The optimality equations are:

$$\begin{aligned}\frac{\partial H}{\partial u_1} &= 2A_1 u_1^*(t) + \lambda_1 T^*(t) = 0 \\ \frac{\partial H}{\partial u_2} &= 2A_2 u_2^*(t) + \lambda_2 \left[\frac{-gV^*(t)}{B_2 + V^*(t)} \right] = 0\end{aligned}$$

From these conditions we obtain

$$\begin{aligned}u_1^*(t) &= \frac{-1}{2A_1} [\lambda_1 T^*(t)], \\ u_2^*(t) &= \frac{1}{2A_2} \left[\lambda_2 \frac{gV^*(t)}{B_2 + V^*(t)} \right].\end{aligned}$$

From the bounds on the controls we have

$$\begin{aligned}u_1^*(t) &= \min \left\{ \max \left\{ a_1, \frac{-1}{2A_1} (\lambda_1 T^*(t)) \right\}, b_1 \right\}, \\ u_2^*(t) &= \min \left\{ \max \left\{ a_2, \frac{\lambda_2}{2A_2} \frac{gV^*(t)}{B_2 + V^*(t)} \right\}, b_2 \right\}.\end{aligned}$$

This gives us the optimal system

$$\begin{aligned}T' &= s_1 - \frac{s_2 V}{B_1 + V} - \mu T - kVT + \min \left\{ \max \left\{ a_1, \frac{-1}{2A_1} (\lambda_1 T) \right\}, b_1 \right\} T, \\ V' &= \frac{g(1 - \min \left\{ \max \left\{ a_2, \frac{\lambda_2}{2A_2} \frac{gV}{B_2 + V} \right\}, b_2 \right\}) V}{B_2 + V} - cVT\end{aligned}\tag{22.2}$$

$$\begin{aligned}\lambda_1' &= 1 + \lambda_1 \left[\mu + kV - \min \left\{ \max \left\{ a_1, \frac{-1}{2A_1} (\lambda_1 T) \right\}, b_1 \right\} \right] + \lambda_2 cV, \\ \lambda_2' &= \lambda_1 \left[\frac{B_1 s_2}{(B_1 + V)^2} + kT \right] - \lambda_2 \left[\frac{B_2 g(1 - \min \left\{ \max \left\{ a_2, \frac{\lambda_2}{2A_2} \frac{V}{B_2 + V} \right\}, b_2 \right\})}{(B_2 + V)^2} - cT \right],\end{aligned}\tag{22.3}$$

with end conditions $\lambda_1(t_f) = \lambda_2(t_f) = 0$, and $T(0) = T_0, V(0) = V_0$.

Creating a Numerical Solver

We iteratively solve for our control u . In each iteration we solve our state equations and our costate equations numerically, then use those to find our new control. Lastly, we check to see if our control has converged. To solve each set of differential equations, we will use the RK4 solver from a previous lab with one minor adjustment. Our state equations depend on u , and our costate equations depend on our state equations. Therefore, we will pass another parameter into the function that RK4 takes in that will index the arrays our equations depend on.

```
# Dependencies for this lab's code:
import numpy as np
from matplotlib import pyplot as plt

#Code from RK4 Lab with minor edits
def initialize_all(y0, t0, t, n):
    """ An initialization routine for the different ODE solving
```

```

methods in the lab. This initializes Y, T, and h. """
if isinstance(y0, np.ndarray):
    Y = np.empty((n, y0.size)).squeeze()
else:
    Y = np.empty(n)
Y[0] = y0
T = np.linspace(t0, t, n)
h = float(t - t0) / (n - 1)
return Y, T, h

def RK4(f, y0, t0, t, n):
    """ Use the RK4 method to compute an approximate solution
    to the ODE  $y' = f(t, y)$  at  $n$  equispaced parameter values from  $t_0$  to  $t$ 
    with initial conditions  $y(t_0) = y_0$ .

     $y_0$  is assumed to be either a constant or a one-dimensional numpy array.
     $t$  and  $t_0$  are assumed to be constants.
     $f$  is assumed to accept three arguments.
    The first is a constant giving the value of  $t$ .
    The second is a one-dimensional numpy array of the same size as  $y$ .
    The third is an index to the other arrays.

    This function returns an array  $Y$  of shape  $(n,)$  if
     $y$  is a constant or an array of size 1.
    It returns an array of shape  $(n, y.size)$  otherwise.
    In either case,  $Y[i]$  is the approximate value of  $y$  at
    the  $i$ 'th value of  $\text{np.linspace}(t_0, t, n)$ .
    """
    Y, T, h = initialize_all(y0, t0, t, n)
    for i in xrange(n-1):
        K1 = f(T[i], Y[i], i)
        K2 = f(T[i]+h/2., Y[i]+h/2.*K1, i)
        K3 = f(T[i]+h/2., Y[i]+h/2.*K2, i)
        K4 = f(T[i+1], Y[i]+h*K3, i)
        Y[i+1] = Y[i] + h/6.*(K1+2*K2 +2*K3+K4)
    return Y

```

Problem 1. Create a function that defines the state equations and returns both equations in a single array. The function should be able to be passed into the RK4 solver. This function can depend on the global variables defined below.

ACHTUNG!

When solving the state equations, because of the nature of T' and V' , solve the original equations (22.1) from the beginning of the lab and not the equations (22.2) with $u_i^*(t)$ replaced by the minmax function.

```
a_1, a_2 = 0, 0
b_1, b_2 = 0.02, 0.9
s_1, s_2 = 2., 1.5
mu = 0.002
k = 0.000025
g = 30.
c = 0.007
B_1, B_2 = 14, 1
A_1, A_2 = 250000, 75
T0, V0 = 400, 3
t_f = 50
n = 1000
```

These constants come from both references cited at the end of this lab.

```
# initialize global variables, state, costate, and u.
state = np.zeros((n,2))
state0 = np.array([T0, V0])

costate = np.zeros((n,2))
costate0 = np.zeros(2)

u=np.zeros((n,2))
u[:,0] += .02
u[:,1] += .9

# define state equations
def state_equations(t,y,i):
    """
    Parameters
    -----
    t : float
        the time
    y : ndarray (2,)
        the T cell concentration and the Virus concentration at time t
    i : int
        index for the global variable u.
    Returns
    -----
    y_dot : ndarray (2,)
```

```

        the derivative of the T cell concentration and the virus ←
        concentration at time t
    ...
    pass

```

The state equations work great in the RK4 solver; however, the costate equations have end conditions rather than initial conditions. Thus we want our RK4 solver to iterate backwards from the end to the beginning. An easy way to accomplish this is to define a function $\hat{\lambda}_i(t) = \lambda_i(t_f - t)$. Then $\hat{\lambda}_i$ has the initial conditions $\hat{\lambda}_i(0) = \lambda_i(t_f)$. We get the new equations

$$\begin{aligned}\dot{\hat{\lambda}}_1(t) &= \lambda_1(t_f - t) (-\mu - kV(t_f - t) + u_1(t_f - t)) - c\lambda_2(t_f - t)V(t_f - t) - 1, \\ \dot{\hat{\lambda}}_2(t) &= -\lambda_1(t_f - t) \left(\frac{s_2 B_1}{(B_1 + V(t_f - t))^2} + kT(t_f - t) \right) \\ &\quad + \lambda_2(t_f - t) \left(\frac{gB_2(1 - u_2(t_f - t))}{(B_2 + V(t_f - t))^2} - cT(t_f - t) \right).\end{aligned}$$

These we can solve with our RK4 solver and recover the original costate equations by simply indexing the array backwards.

Problem 2. Create a function that defines the costate equations and returns both equations in a single array. The function should be able to be passed into the RK4 solver. Use the global variables as defined in Problem 1.

```

def lambda_hat(t,y,i):
    ...

    Parameters
    -----
    t : float
        the time
    y : ndarray (2,)
        the lambda_hat values at time t
    i : int
        index for global variables, u and state.

    Returns
    -----
    y_dot : ndarray (2,)
        the derivative of the lambda_hats at time t.
    ...
    pass

```

Finally, we can put these together to create our solver.

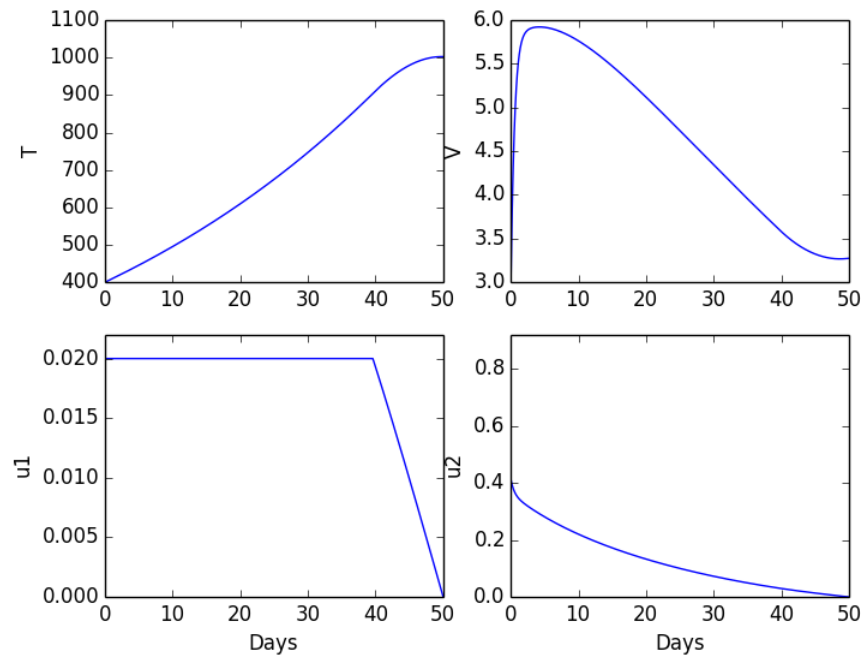


Figure 22.1: The solution to Problem 3.

Problem 3. Create and run a numerical solver for the HIV two drug model using the code below.

```
epsilon = 0.001
test = epsilon + 1

while(test > epsilon):
    oldu = u.copy();

    #solve the state equations with forward iteration
    #state = RK4(...)

    #solve the costate equations with backwards iteration
    #costate = RK4(...)[::-1]

    #solve for u1 and u2

    #update control
    u[:,0] = 0.5*(u1 + oldu[:,0])
    u[:,1] = 0.5*(u2 + oldu[:,1])

    #test for convergence
```

```
test = abs(oldu - u).sum()
```

Your solutions should match Figure 22.1.

In modern medicine, patients generally take combinations of five or more medications with different functions. These include Nucleotide Reverse Transcriptase Inhibitors, which prevent HIV inserting its genes into host DNA, Non-Nucleoside Reverse Transcriptase Inhibitors, which do the same job as NRTIs in a different fashion, Protease Inhibitors, which cut up replicated HIV strands, Fusion Inhibitors, which block the virus from entering the cells to begin with, and Integrase Inhibitors, which prevents the virus' replicated DNA from being inserted into a cell's DNA. These drugs often can interact with each other and have different side effects on the body. Also, doctors rotate medications as the body and virus develop immunity.