

Assignment 4 - Modelling the spread of HIV

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Modelling the spread of HIV through sexual contact

To start with we were given equations (1), (2), (3) and (4). These equations describe the spread of HIV through sexual contact in four different groups:

- p_1 : Homosexual Males with x_1 infected persons
- p_2 : Bisexual Males with x_2 infected persons
- q : Heterosexual Females with y infected persons
- r : Heterosexual Males with z infected persons

Through the equations it is clear to see, that some groups are coupled to other groups for example bisexual males who are coupled to themselves, heterosexual females and homosexual males.

All equations are scaled with some constants a_1 , a_2 , b_1 etc. These all controls the rates of infection for a specific group through contact with some group (also themselves). The constants are mostly kept the same as specified in the assignment, but it is discussed in a later segment what effect changing some of them will have. Tables of the initial parameters used are shown below.

Parameter	Value
(a_1)	10
(a_2)	5
(b_1)	5
(b_2)	1
(b_3)	1
(c_1)	1
(c_2)	1
(d_1)	1

Symbol	Group	Total Population	Initially Infected
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Symbol	Group	Total Population	Initially Infected
$(p_1), (x_1)$	Homosexual males	10	$0.01 \times p_1 = 0.1$
$(p_2), (x_2)$	Bisexual males	5	0
$(q), (y)$	Heterosexual females	100	0
$(r), (z)$	Heterosexual males	100	0

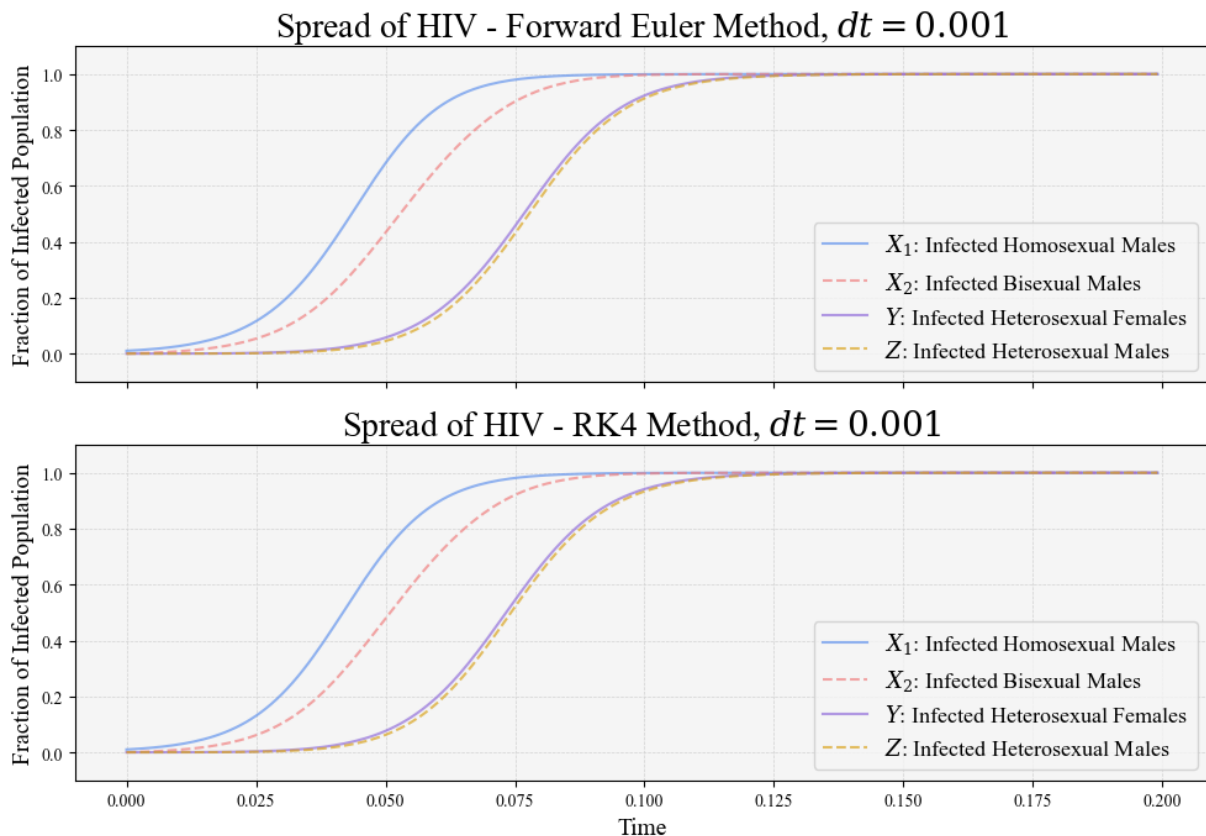
To make comparisons between the infected populations easier, the plots of the infected populations are scaled to their respective populations size $\frac{x_n}{p_n}$ where x_n is the infected population and p_n is the total population size. This means that the plots shown actually reflect the fraction of infected relative to the population size.

The model is simulated using two different methods:

1. Forward Euler stepping
2. Fourth Order Runge-Kutta stepping

and each plot will show results from both methods. The results for the simulations of the spread of HIV through sexual contact are shown below.

Modeling the Spread of HIV through Sexual Contact



Maximum residuals between Euler and RK4 methods:

X1: 0.048

X2: 0.046

Y: 0.089

Z: 0.090

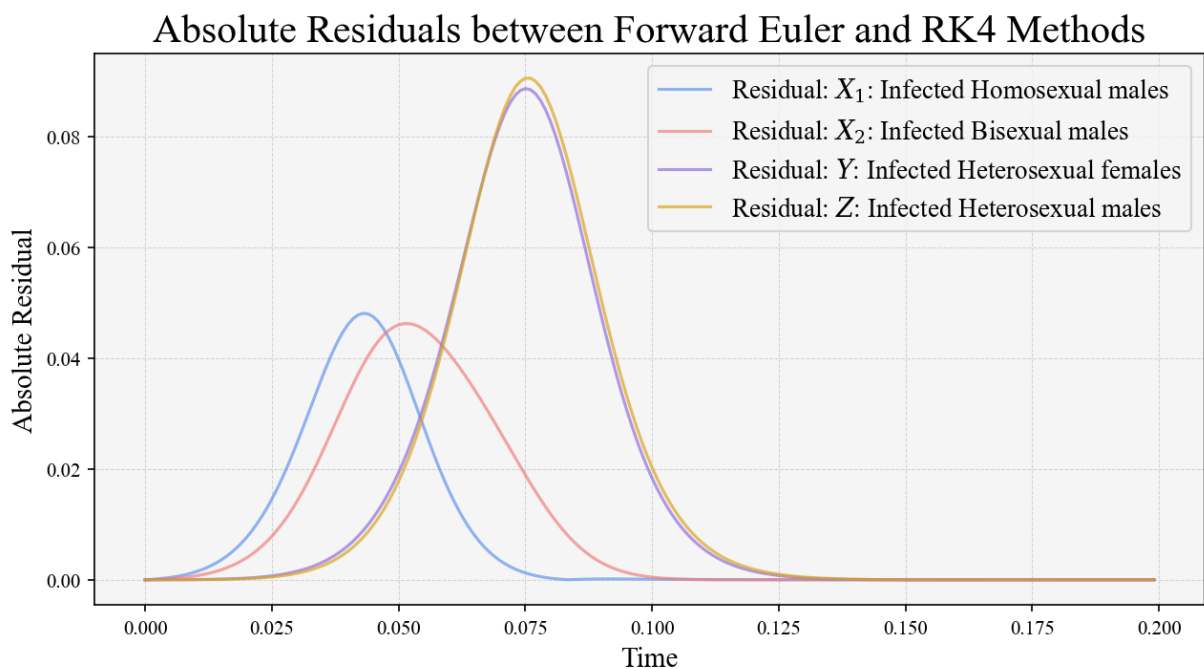
Above a simulation of the spread of HIV through sexual contact is seen.

The simulation is done with coefficients $a_1 = 10$, $a_2 = b_1 = 5$ and $b_2 = b_3 = c_1 = c_2 = d_1 = 1$.

After $t \approx 0.125$ all populations are completely infected, but it is clear that some populations get there before others fx. Homosexuals and Bisexuals. This is due to the relationship between the parameters where $a_1 > a_2 = b_1 > \dots$. Here a_1 and a_2 are the coefficients controlling the infection of Homosexual males. Decreasing these slightly would make the trajectories look more alike and reach full infection at about the same time.

The upper plot shows the simulation done with forward euler stepping and the lower shows the simulation done with fourth order Runge-Kutta stepping. The two plots doesn't look very different, but the maximum residuals between the two models are $[0.048, 0.046, 0.089, 0.090]$ for $[x_1, x_2, y, z]$ respectively, which is not negligible.

Below a plot is shown of the residuals between the two methods for all populations as a function of time.



Including blood transfusion

Blood transfusion is added to the equations by adding the terms

$$e(p_1 - x_1), \quad e(p_2 - x_2), \quad e(q - y), \quad e(r - z)$$

for $\frac{dx_1}{dt}$, $\frac{dx_2}{dt}$, $\frac{dy}{dt}$, $\frac{dz}{dt}$ respectively. Each of these terms adds a possibility of infecting a new person in a population through blood transfusion with a rate e . This parameter is defined in the following way:

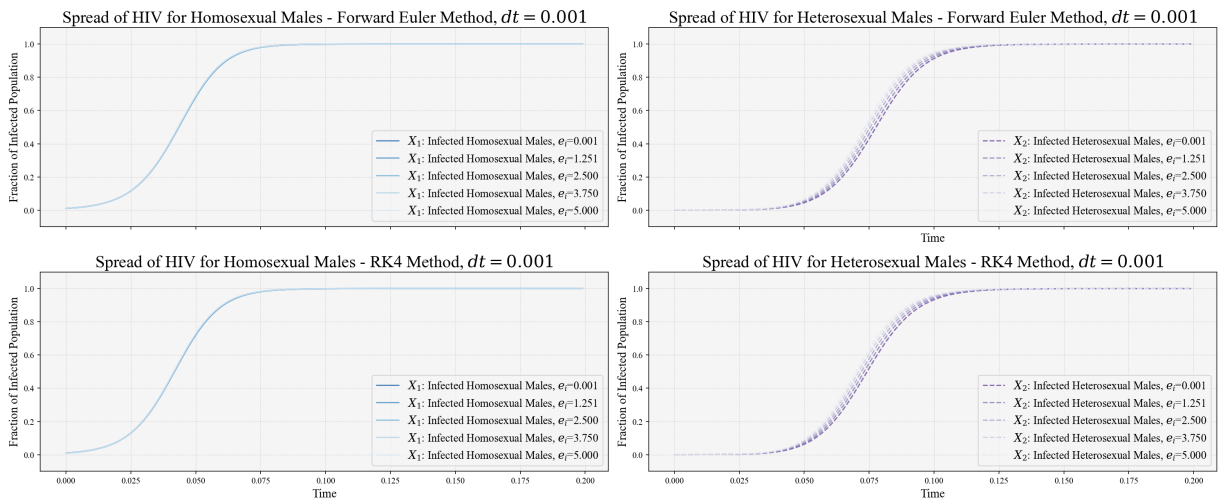
$$e = e_i \frac{x_1 + x_2 + y + z}{p_1 + p_2 + r + q}, \quad e_i \in [0.001, 5]$$

There are two things to note about the definition of the parameter. Firstly, e_i can be changed for different simulations yielding different effects from blood transfusion. Secondly, the fraction grows as more people are infected making it more likely that people get infected from blood transfusion as more people get sick.

The results of the simulations using both RK4 and euler stepping are shown below.

Modeling the Spread of HIV through Sexual Contact and Blood Transfusion

$$e = e_i \cdot \frac{\text{infected}}{\text{pop. size}}, \quad e_i \in [0.001, 5]$$



In the plots above the simulations including blood transfusion are shown. These were done with the same initial parameters as before (a_n, b_n etc), but with a varying e parameter: $e_i \in [0.001, 5]$

In the plots on the left hand side, the different simulations are very hard to tell apart, and this is due to the infection constants a_1 and a_2 dominating the equation for infection of homosexual Males. The effect of e is simply not large enough. In the equation for infection of heterosexual males $\frac{dz}{dt}$ where $d_1 = 1$ the effect of e is large enough, and the effect is visible in the plots on the right hand side. For larger e_i the infection rate increases which makes sense considering that e is sort of an added infection factor independent of sexual contact.

Even though the effect of e varies between populations, the end result is still the same:

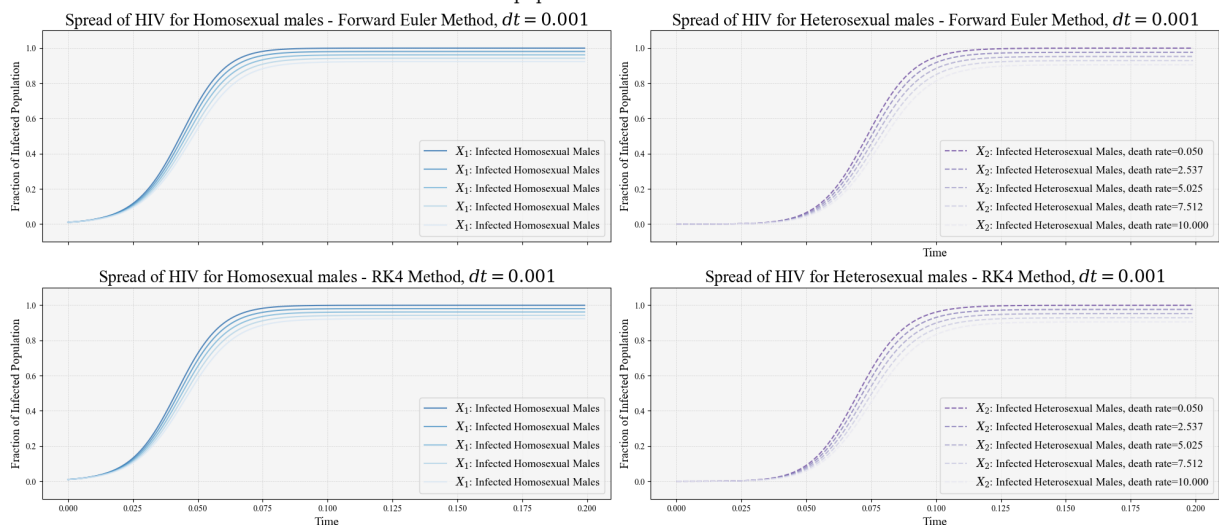
everyone gets infected, so the equilibrium seems to be where all populations are completely infected.

Inlcuding death of infected people

For the final part of the assignment we included the possibility of death in each infected group. This was done by adding a term $r_n x_n$ to each of the equations, where r_n is the rate of death for infected population n and x_n is the infected population n . Through all simulations $r_1 = r_2 = r_3 = r_4$ but they are changed to see the effect of a varying death rate. Death rates are tested in the space $r_n \in [0.05, 10]$.

Spread of HIV through Sexual Contact, Blood Transfusion and Death

$$e = 0.001 \cdot \frac{\text{infected}}{\text{pop. size}}, dr = dr_i \in [0.05, 10]$$



Above a plot is shown of the spread of HIV for Heterosexual (Greens) and Homosexual (Blues) men. Both groups show the same tendency for increasing death rates: As the death rate increases, the virus spreads slower and slower. This intuitively makes sense as less sick people are alive to infect more people. Each simulation also reaches a different equilibrium depending on the death rate, where the ratio between sick people and healthy people decreases for increasing death rates.

A weird but inherent effect of the model is that the the infected population doesn't diminish over time as would be expected in a real life scenario if the death ratio was high enough. This is due to the populations being kept constant: when a sick person dies, the total population number remains constant (p1 is still 5 for example) so it is kind of like adding a new healthy person. This is why the fraction of infected people never diminishes but instead reaches an equilibrium. The death rate and birth rate (of healthy people) are exatly the same so to speak.