

CAS 741: Investigation of Human immunodeficiency virus (HIV-1) viral load

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1 Revision History

Table 1: Revision History

Date	Developer(s)	Change
Sept 21	Andrea Clemeno	First Draft of Problem Statement
Sept 25	Andrea Clemeno	Second Draft of Problem Statement
Sept 30	Andrea Clemeno	Third Draft of Problem Statement
Dec 9	Andrea Clemeno	Final Document of Problem Statement

2 Problem Statement

The common cold, influenza, acquired immunodeficiency syndrome (AIDs) and the novel coronavirus (COVID-19) are infectious diseases transmitted among humans. The culprit behind these contagions are submicroscopic parasites that infect cells called viruses. Once a virus comes into contact with a host cell, the infected cell will begin to rapidly reproduce the genetic material of the virus rather than it's own products. This phenomena causes devastating damage to the body as it may kill or modify cells. The human body's immune system will work to counteract this attack by recognizing and implementing several methods of defense.

Different viruses cause different responses from the human body. The human immunodeficiency virus 1 (HIV-1) is the most common type of HIV virus that attacks a type of white blood cell through direct contact with infected bodily fluids. These white blood cells (Helper T cells) are instrumental in fighting off diseases. The body's defences are weakened by the infection causing heightened susceptibility to other diseases. The HIV-1 virus causes AIDs, a disease which affects 38 million people worldwide (who, 2020).

Currently, there is no formative cure for AIDs; patients are treated with antiretroviral therapy to minimize the transmission of AIDs and the contraction of other infections. Analyzing the interaction between HIV-1 and the human body is essential in understanding and treating AIDs.

$$N_t = N_o e^{-kt}$$

Equation 1: The closed-form equation representing the concentration of a virus over time.

- N_o is the initial amount that will undergo an exponential decrease. N_o is equivalent to $N(t = 0)$.
- N_t is the viral load at time t .
- k is the clearing constant.
- t is the time.

This project will investigate the immunological response of the human body to HIV-1 through the use of the closed-form equation representing the concentration of a virus over time seen in Equation 1. This simple dynamic

model is based on the exponential decline of the concentration of the virus. Exploring the changing viral concentration will help determine the stage of the condition. In addition, modelling the virus growth may lead to developments of a cure or better treatment options for AIDs. Moreover, the Drasil framework will be implemented to generate different project artifacts throughout the investigation. The Drasil method will be used to improve different aspects of software quality, including maintainability, verifiability, and traceability (Owojaiye, 2020).

References

Hiv/aids, 2020. URL <https://www.who.int/news-room/fact-sheets/detail/hiv-aids>.

Oluwaseun Owojaiye. Creating your project in drasil, 2020. URL <https://github.com/JacquesCarette/Drasil/wiki/Creating-Your-Project-in-Drasil>.