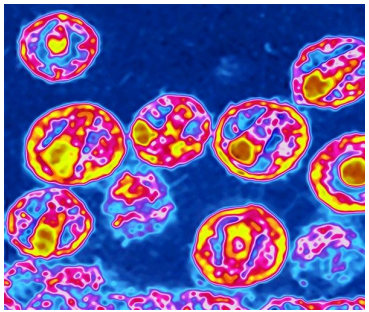

Software Requirements Specification for *Diagnosis_AIDs*:

Investigating the Viral Load of the Human Immunodeficiency Virus (HIV)

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BACKGROUND INFORMATION

Human immunodeficiency virus 1 (HIV -1)

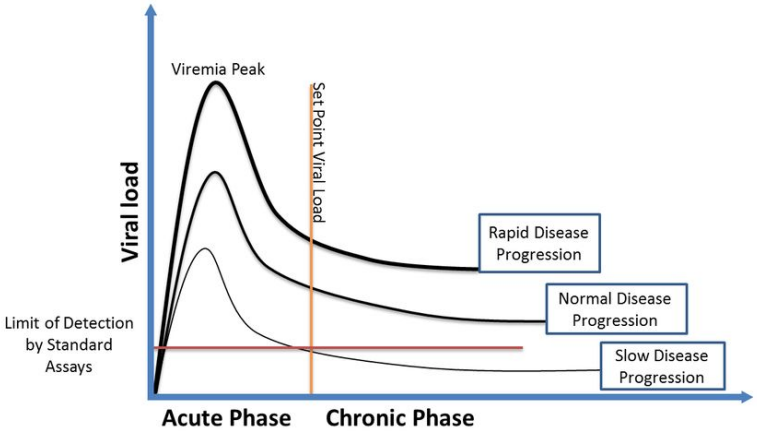
- HIV-1 is the most common type of HIV virus that attacks cells of the immune system needed to fight off diseases.
- When infected, the body's defences are weakened by the infection causing heightened susceptibility to other diseases.
- The HIV-1 virus causes Acquired immunodeficiency syndrome (AIDs), a disease which affects 38 million people worldwide.
- Currently, there is no cure but antiretroviral therapy.

VIRUS DYNAMICS

- Virus 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.

INTRODUCTION

Scope of Requirements	The scope of the requirements includes the analysis of human immunodeficiency virus (HIV) concentration over time with constant cell reproduction and clearance rates.
Problem Description	A system is needed to efficiently predict the set point of HIV viral load, possible progression and treatment.



viral load (HIV RNA): [virus].

Target cells: CD4+ T cells that fight against HIV..

Acute phase: Acute conditions are severe and sudden in onset.

Post-peak decay period: Time from Viremia Peak and set point

Set point: A relatively stable level of viral load after acute phase.

Disease Progression Speed: The quickness or slowness of an individual's experience through stages of a disease.

HIV-infected individuals who have a higher viral load set point have a faster progression to AIDS and death.

INPUT AND OUTPUT VARIABLES

ProgName Responsibilities: Detect what?

Figure 5: System Context - User Input and Output

THEORETICAL MODEL

Theoretical Models (basis of viral dynamics): -> s
- *P: Rate of virus production → based on average in clinical trials*

General Definitions that will be used to build the instance models:
- *c*: Clearance rate constant → based on concentration of [T cells]

INSTANCE MODEL

Name: Purpose	conc_v:The concentration of the virus over time.
Input	*P, c, V*
Output	*dV/dt*
Input Constraints	P, c, V > 0
Output Constraints	dV/dt < 0
Equation	$\frac{dV}{dt} = P - cV,$
Description	dV/dt is the rate of change in virus concentration over time. P is the rate of virus production. c is the clearance rate. V is the virus concentration at peak.

INSTANCE MODEL

Name: Purpose	setpoint: Determine set point.
Input	dV/dt, $t_{p\text{-}to\text{-}sp}$
Output	V_{sp}
Input Constraints	
Output Constraints	
Equation	$V_s = dV/dt\ t_{p\text{-}to\text{-}s}$
Description	dV/dt is the rate of change in virus concentration over time. $t_{p\text{-}to\text{-}sp}$ is the amount of time from peak to set point. V_{sp} is the viral load at set point.

INSTANCE MODEL

Name: Purpose	Progression: Determine progression of the disease (possibly treatment type/plan -> need to find correlation between disease progression and successful treatments).
Input	*Patient Profile (age etc.),* V_{sp}
Output	*Prog*
Input Constraints	
Output Constraints	
Equation	*Prog = piecewise function based on* V_{sp}
Description	*Prog is the progression of the disease.*

GOAL STATEMENTS

Given the rate of HIV-1 virus production, and the HIV-1 and CD4+ concentration at the Viremia Peak:

GS1: Predict the clearance rate of the virus with the CD4+ concentration.

GS2: Predict the rate of change of virus concentration.

GS3: **Determine Viral Load at the set point .**

$$\frac{dV}{dt} = P - cV,$$

dV/dt: The rate of change in virus concentration over time - specifically from peak to set point.

P: A function representing the rate of virus production - “early viral expansion is somewhat homogeneous across subjects”

c: A constant called the clearance rate for HIV-1 virus - from concentration of CD4+. “ viral growth depends on the availability of target cells”

V: The current virus concentration - specifically at peak.

GOAL STATEMENTS

Given the rate of change in virus load at set point, and patient profile:

GS1: Determine the progression of disease.

GS2: Determine the Initial HIV treatment plan based on patient profile.

ASSUMPTIONS

simplifies the original problem and helps in developing the theoretical models by filling in the missing information for the physical system. The assumptions refine the scope by providing more detail.

- Initial Diagnosis of an HIV patient
    - From initial infection
- Basic target-cell-limited viral dynamics: c([CD4+ t cells])
    - Meaning that the clearance rate will not be affected by other factors.
    - Essentially, an increase in the CD4+ T cells correlates with the human body's capability to clear the virus and clearance rate of virus.

USING DRASIL

- the Drasil framework will be used to document this investigation.

Questions?

References

[1]