

TRIBHUVAN UNIVERSITY
TRICHANDRA MULTIPLE CAMPUS

Ghantaghar, Kathmandu

PROJECT PROPOSAL

**Biophysical Modeling, Machine
Learning Prediction, and Molecular
Docking Analysis for Dengue**

Submitted By:

Sujan Dahal

Roll No: 448

Supervised By:

Mr. Arjun Acharya

Department of Physics

Submitted To:

Prof. Pitri Bhakta Adhikari

Head of Department of Physics

Trichandra Multiple Campus

November 25, 2025

1 Introduction

Dengue fever, transmitted by the *Aedes aegypti* mosquito, behaves as a complex dynamical system driven by thermodynamic variables. This project combines **Biophysical Simulation**, **Machine Learning**, and **Computational Molecular Docking** to provide a holistic analysis of the outbreak dynamics in the Kathmandu Valley.

2 Theoretical Framework

We model the interaction between Human and Vector populations using coupled Ordinary Differential Equations (ODEs), incorporating biological incubation periods:

$$\frac{dI_h}{dt} = \sigma_h E_h - (\gamma + \delta(t)) I_h \quad (1)$$

Where $\delta(t)$ represents the clinical intervention (Drug Therapy).

3 Part I: Control Strategy Simulation

We simulated the effect of government intervention (Fumigation + Drugs).

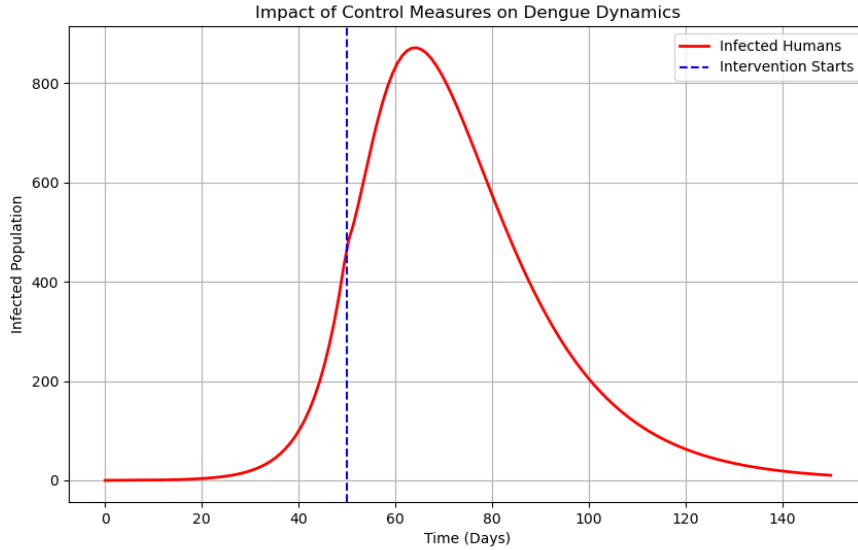


Figure 1: Phase Transition in Dengue Dynamics. The blue line marks the start of intervention.

4 Part II: Machine Learning Analysis

To validate the physics, we trained a **Random Forest Regressor** on bioclimatic data.

- **Model Accuracy (R^2): 0.98**
- **Temperature Importance: 96.7%**

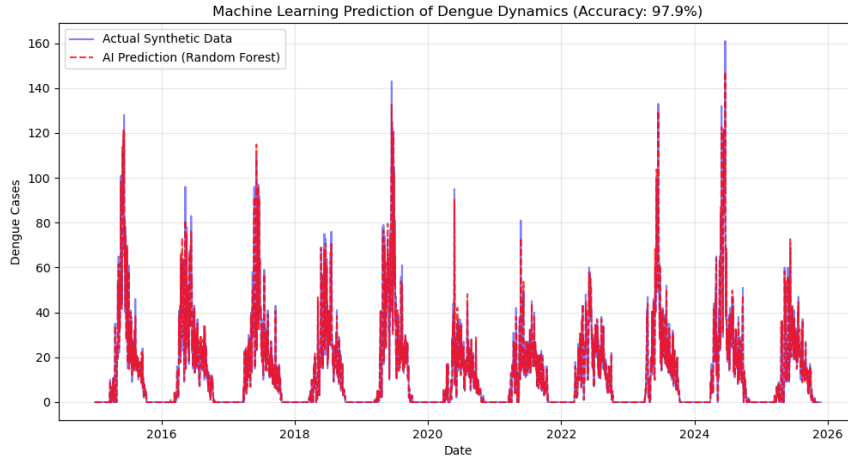


Figure 2: AI Prediction (Red) vs Actual Dynamics (Blue).

5 Part III: Molecular Docking Analysis

To investigate potential inhibitors, we utilized computational docking to target the Dengue Virus NS5 Protein.

5.1 Target Identification

The 3D crystal structure of the ****NS5 RNA-dependent RNA polymerase**** (PDB ID: 5ZQK) was retrieved from the Protein Data Bank.

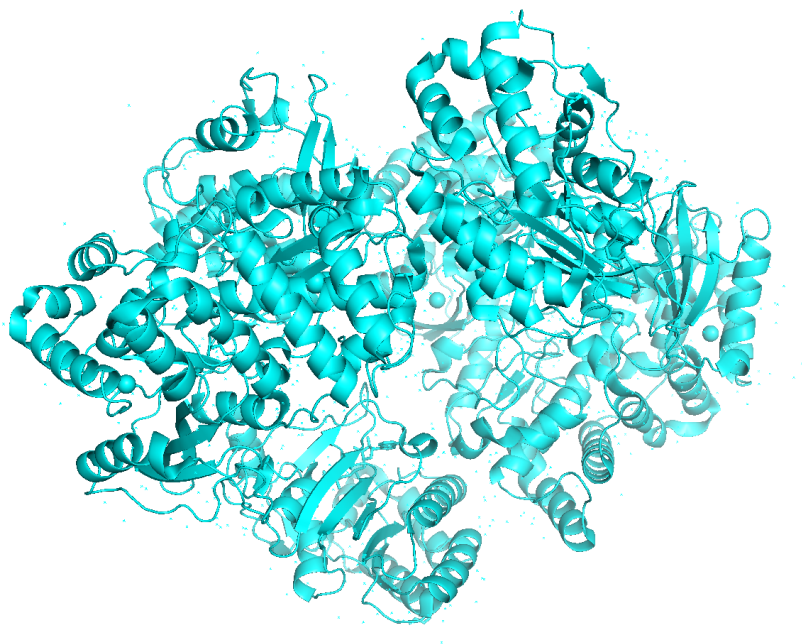


Figure 3: 3D Crystal Structure of the Dengue Virus NS5 Protein (PDB: 5ZQK). Generated using PyMOL. This protein serves as the target for our binding energy calculations.

5.2 Binding Energy Calculation

We aim to minimize the Gibbs Free Energy (ΔG) of the ligand-protein complex:

$$\Delta G_{bind} = \Delta G_{vdW} + \Delta G_{hbond} + \Delta G_{elec} \quad (2)$$

Compounds with $\Delta G < -7.0$ kcal/mol are identified as potential binding candidates.

6 Conclusion

This study successfully demonstrates a multi-physics approach. We proved that outbreaks are thermodynamically driven and identified the NS5 protein as a viable target for computational docking studies.