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# VIRUS AND BIOLOGICAL MODELING

# Introduction

- ① How is biological modeling used?
- ① Why do we need to estimate parameters?
- ① How does this apply to me?

## Variables

H = 1e6 ! healthy cells

V = 1e2 ! virus

I = 0, >=0 ! infected cells

End Variables

## Intermediates

kr1 = 1e5 ! Lambda production of healthy cells

kr2 = 0.1 ! d death rate of healthy cells

kr3 = 2e-7 ! beta infection rate of healthy cells

kr4 = 0.5 ! a death rate of infected cells

kr5 = 5 ! u death rate of virus

kr6 = 100 ! k production rate by infected cells

End Intermediates

## Equations

$$\$H = kr1 - kr2*H - kr3*H*V$$

$$\$I = kr3*H*V - kr4*I$$

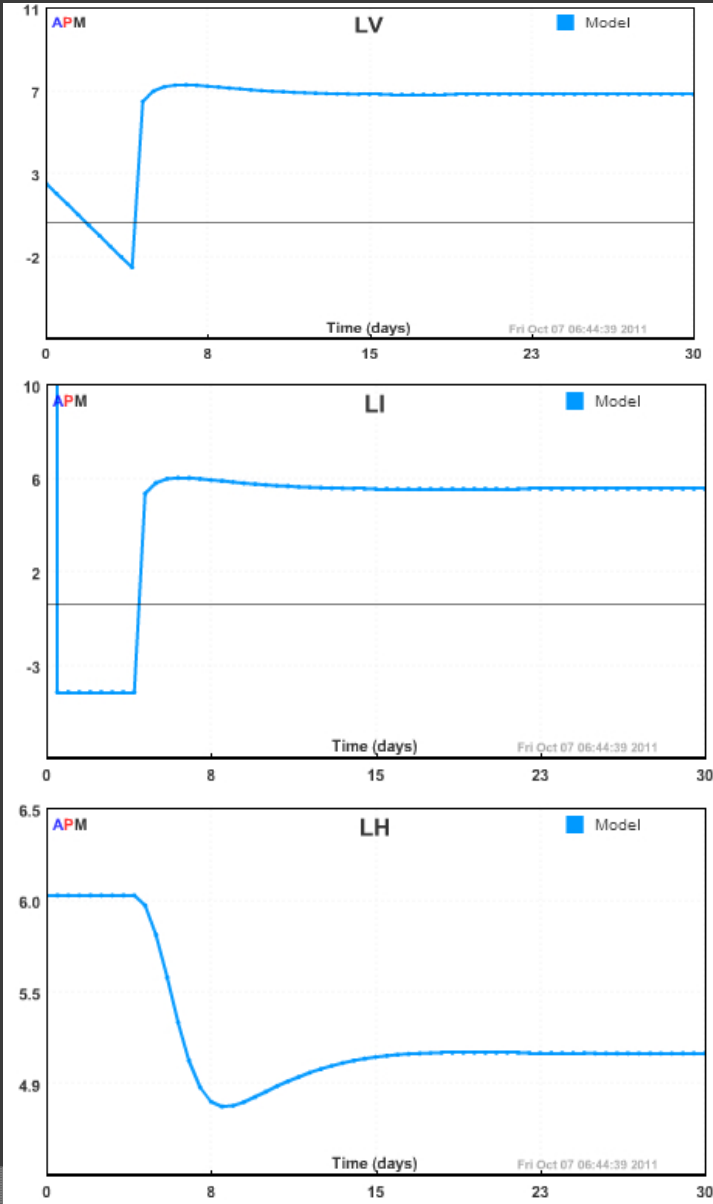
$$\$V = kr6*I - kr5*V$$

Parameters and equations obtained and based from

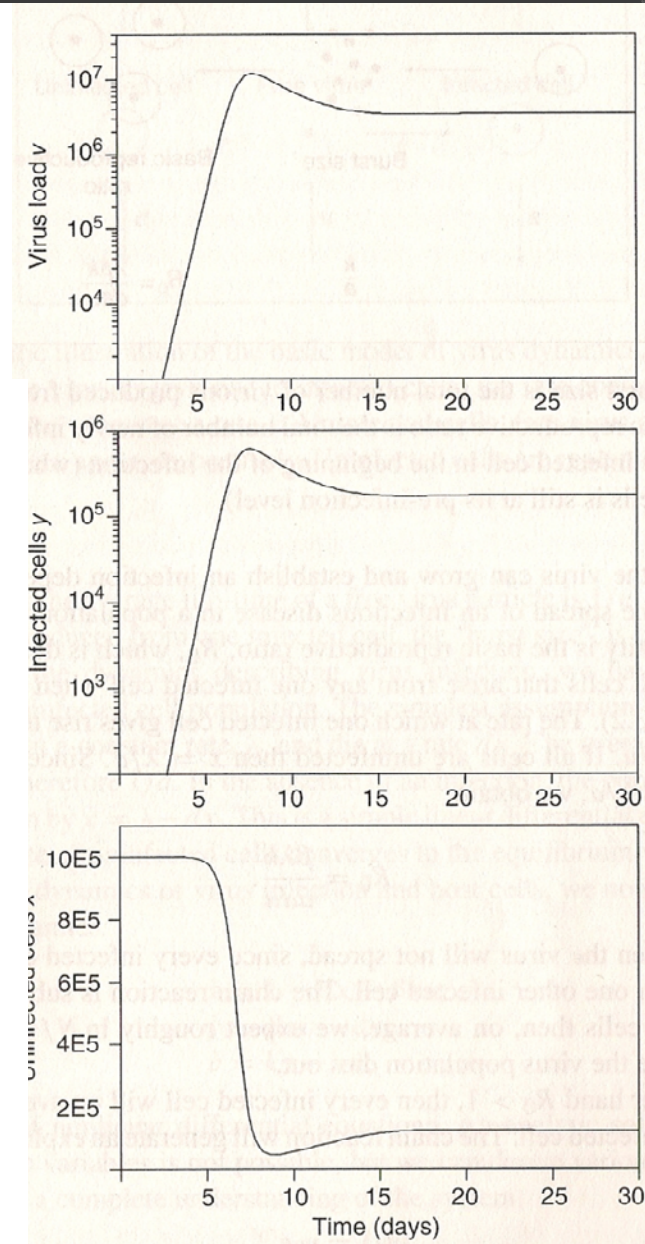
Nowak, M, & May, R. (2000). *Virus Dynamics Mathematical Principles of Immunology and Virology*.

Oxford, New York: Oxford University Press

# Graphs generated from my model



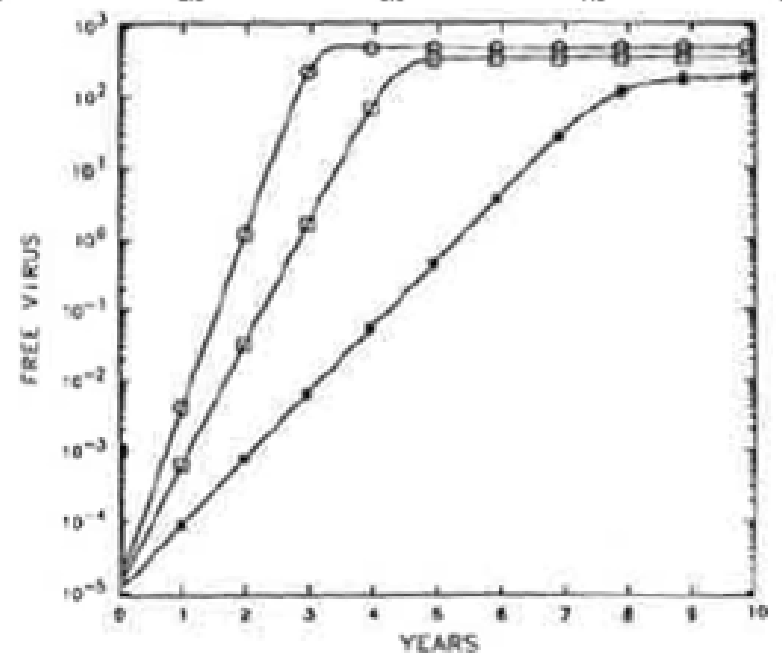
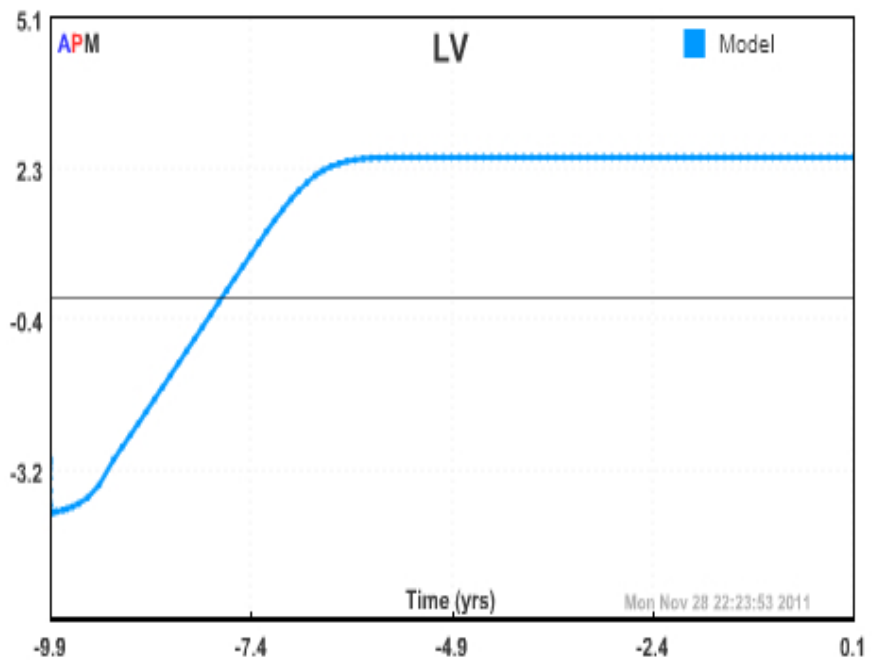
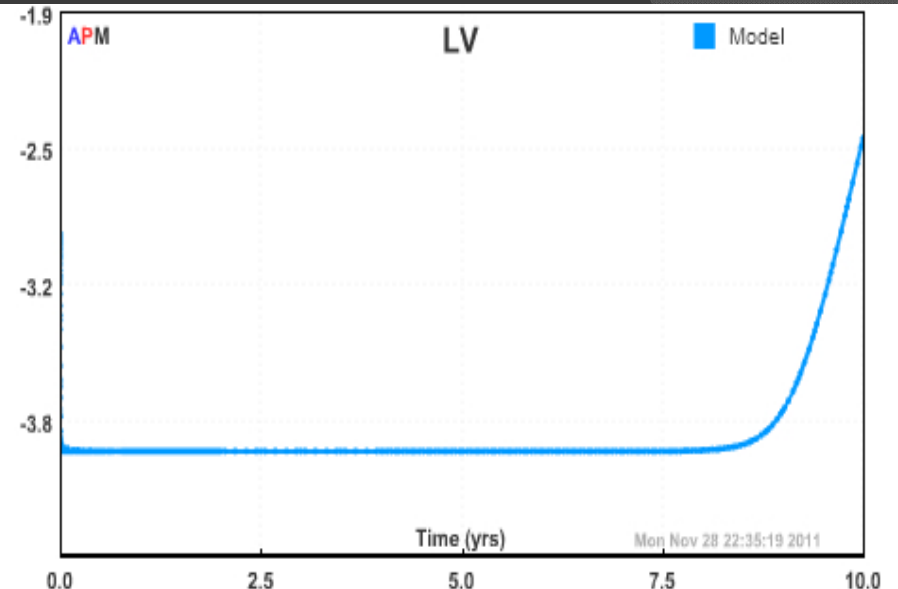
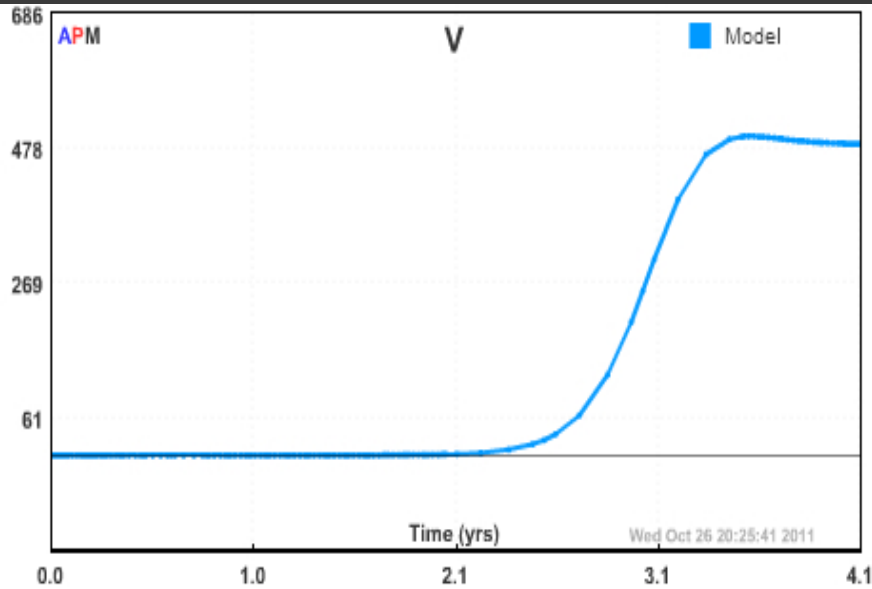
# Graphs from Virus Dynamics book



# Convert SBML to APMonitor

- ⦿ Convert SBML-XPP format by hand
- ⦿ Future have a program convert SBML to APMonitor
- ⦿ Problems with discretization

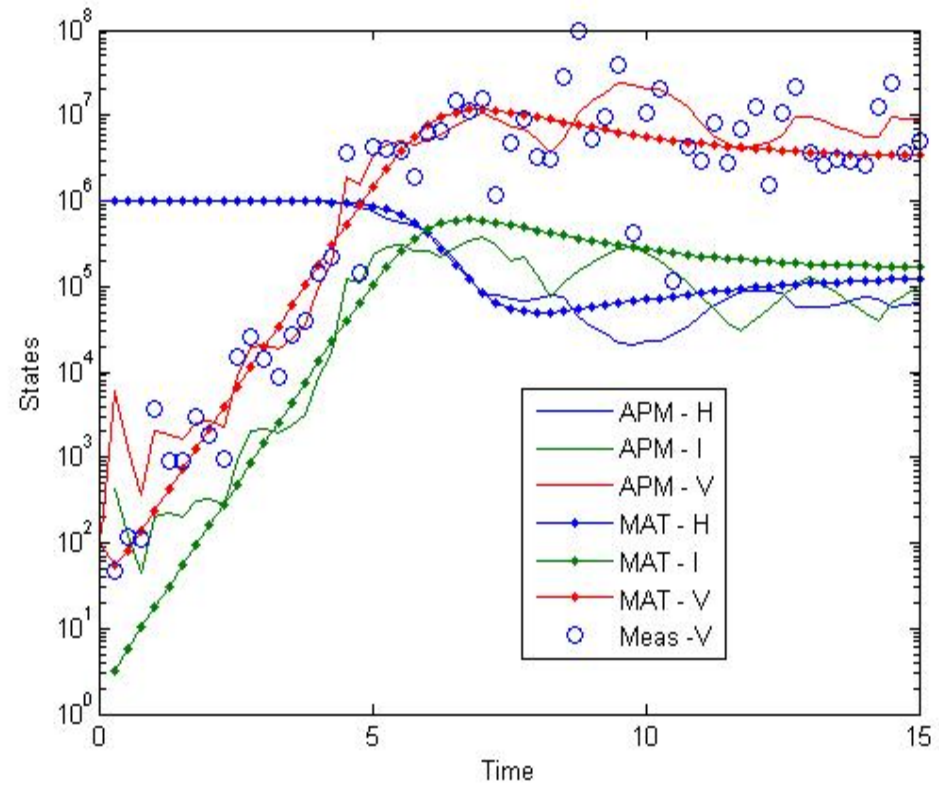
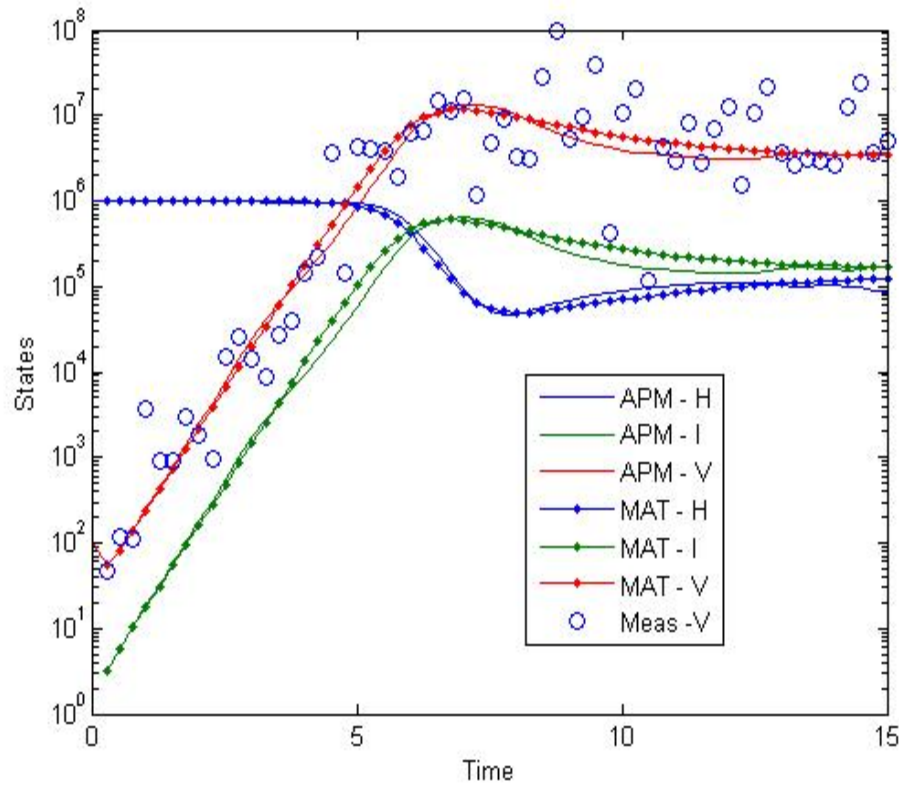
# Graphs from Dynamics of HIV Infection of CD4T Cells Article



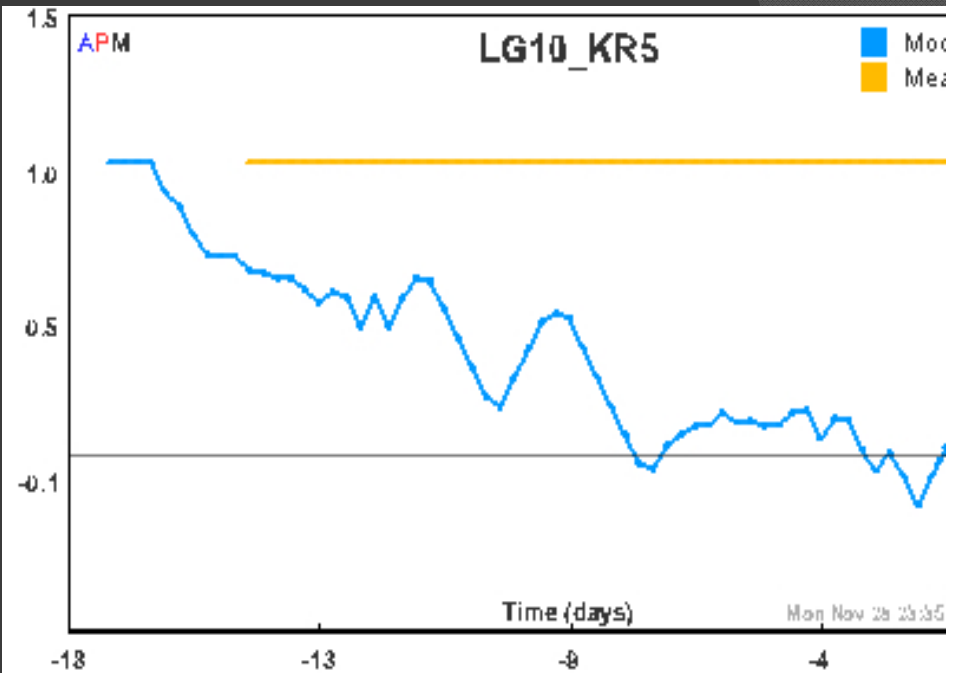
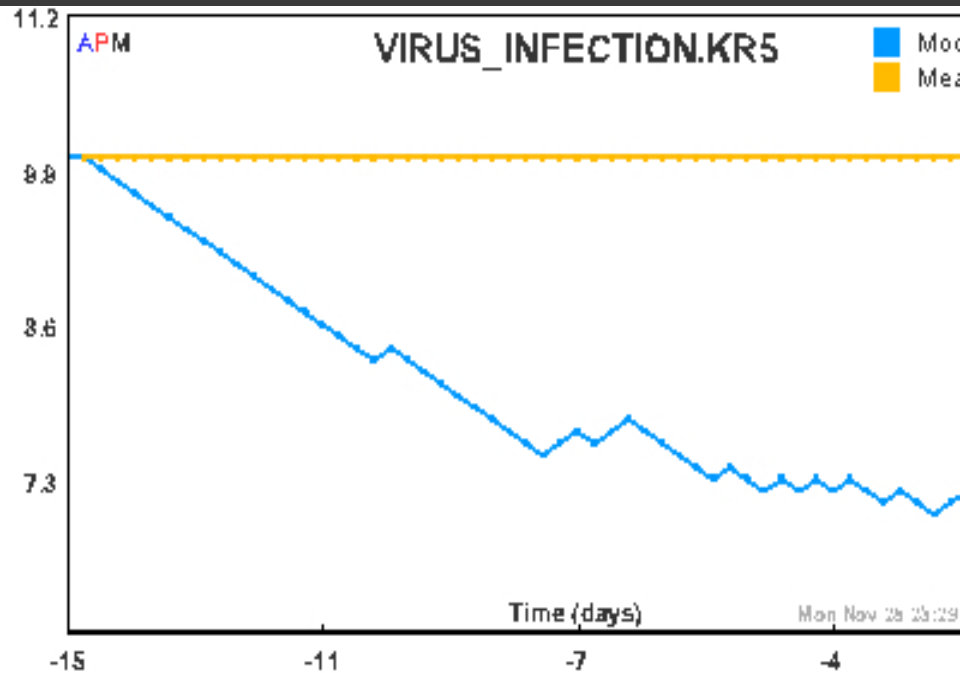
# Parameter Estimation

Normal parameters

Log parameters



# Parameter Estimation





# Future Work

- ⦿ Continue to learn how to use APMonitor software in parameter estimation
- ⦿ Solve larger models with over 800 reactions and 200 parameters

# Conclusion

- ① Discretization
- ① Forward stepping vs simultaneous
- ① Log parameter estimation