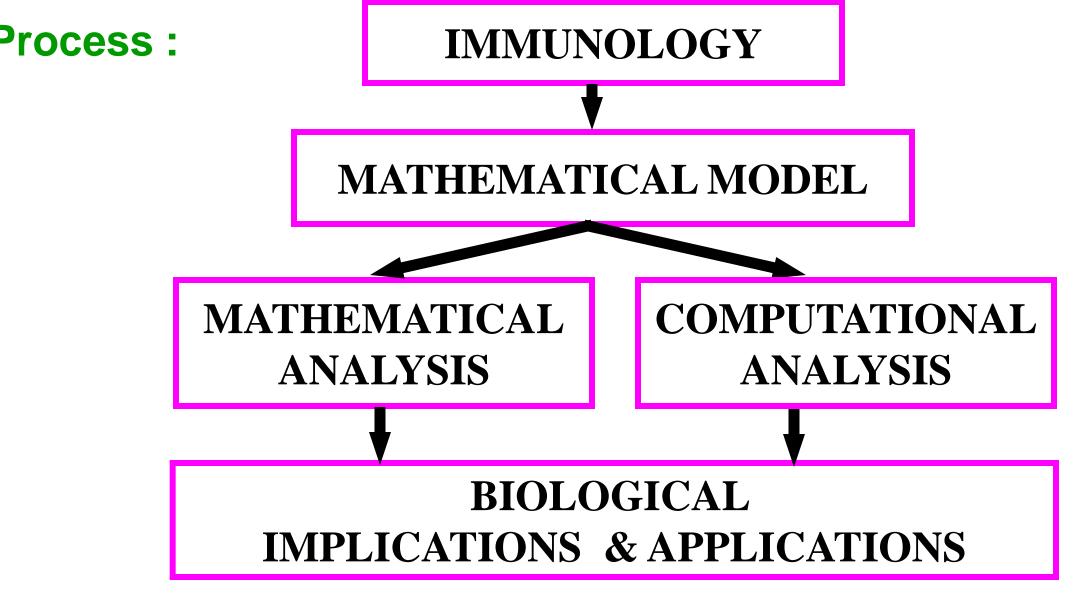
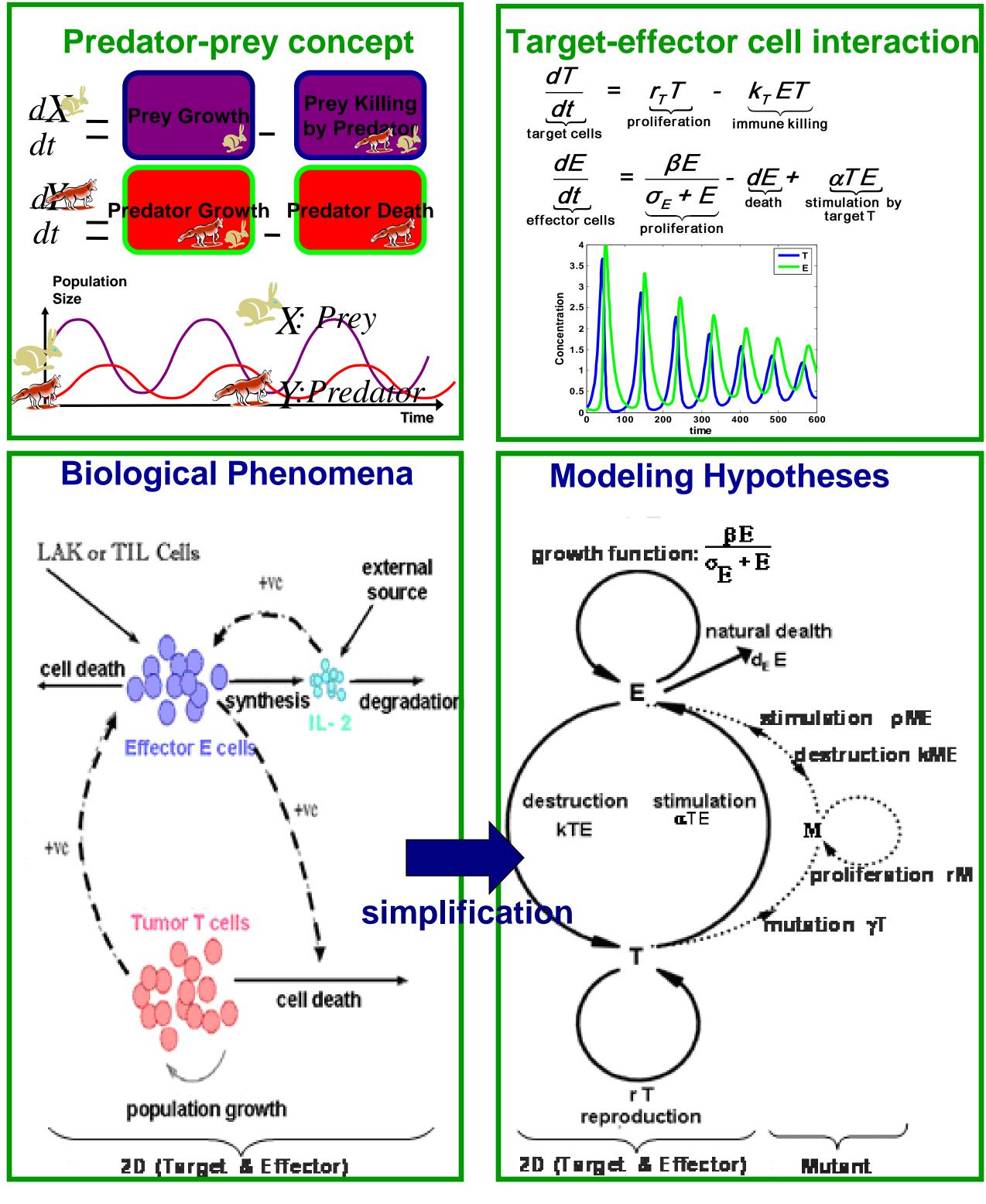
3. Mathematical Model **1. Introduction 3D ODE Model for target-effector-mutant interactions** (I) Verification of Equilibrium Stability Conditions **Goal**: develop a mathematical model to study the interactions b/w immune system, a target population (cancer cells or virus infection) & a mutative dT  $k_{\tau}ET$ target target cells **Process**: IMMUNOLOGY Mutant- usually more resistant & stronge  $k_{M}EM$ \_\_\_\_\_  $\smile$ MATHEMATICAL MODEL 0.5 COMPUTATIONAL MATHEMATICAL effector cells ANALYSIS ANALYSIS  $r_T$   $r_M$  = reproduction rate for target T & mutant M respectively 3.5  $k_T$  = contact rate between target T & effector E BIOLOGICAL  $k_{M}$  = contact rate between mutant M & effector E **IMPLICATIONS & APPLICATIONS**  $\gamma$  = mutation rate  $\beta$ , d = self generation & death rate of effector E respectively  $\alpha$  = stimulation of effector E by target / tumor T 2. Immune System Model Hypotheses  $\rho$  = stimulation of effector E by mutant M **Populations:**  $\sigma$  = critical threshold for cooperative & autocatalytic process •Target cells (T): infected (or tumor) cells surrounded by antigens 200 400 600 •Effector cells (E): immune system generates cells for fighting cells with specific antigen. 4. Mathematical Analysis — Е (I) Equilibria (i)  $(T_1, M_1, E_1) = (0, 0, 0);$ **Assumptions:** (ii)  $(T_2, M_2, E_2) = \left(0, 0, \frac{\beta - d\sigma_E}{d}\right)$  (target- & mutant-free cell population modeling • E cells - saturated growth, T & M cells -exponential growth equilibrium) non specific response of immune system (iii)  $(T_3, M_3, E_3) = \left(0, \frac{(d\sigma_E - \beta) k_M + dr_M}{\rho (\sigma_E k_M + r_M)}, \frac{r_M}{k_M}\right)$  (target-free, mutant endemic) different antigenity for target & mutant different stimulation of immune system by target & mutant different immune response on target & mutant predator-prey type interactions b/w target-mutant & immune system (iv)  $(T_4, M_4, E_4) = \left| \frac{(k_M E - r_M)M}{\sigma_E + E} \right|$  $r_T$  (target & mutant  $k_{T}$  endemic) **Target-effector cell interaction**  $\left| k_{M} \frac{r_{T}}{r_{T}} - r_{M} \right|$ **Predator-prey concept** ρ+ — Fitness factor of immune E cells :  $\beta - d\sigma_{E}$ -  $k_{\tau}ET$  $r_{\tau}T$ <u>dt</u> target cells dXproliferation immune killing (II) Local Stability Analysis of Equilibria Fitness factor of target T cells : de Pr Method:



- •Mutant cells (M) : infected cells that have undergone genetic changes (mutations)



## Mathematical Modeling of the Effects of Mutation on the Immune System Troy P.T. Teo

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- linearization of system (Jacobian Matrix)
- study of eigenvalues  $\lambda$  of the Jacobian J (e.g Routh Hurwitz Criteria)

### **Criteria for Locally Asymptotically Stability:**

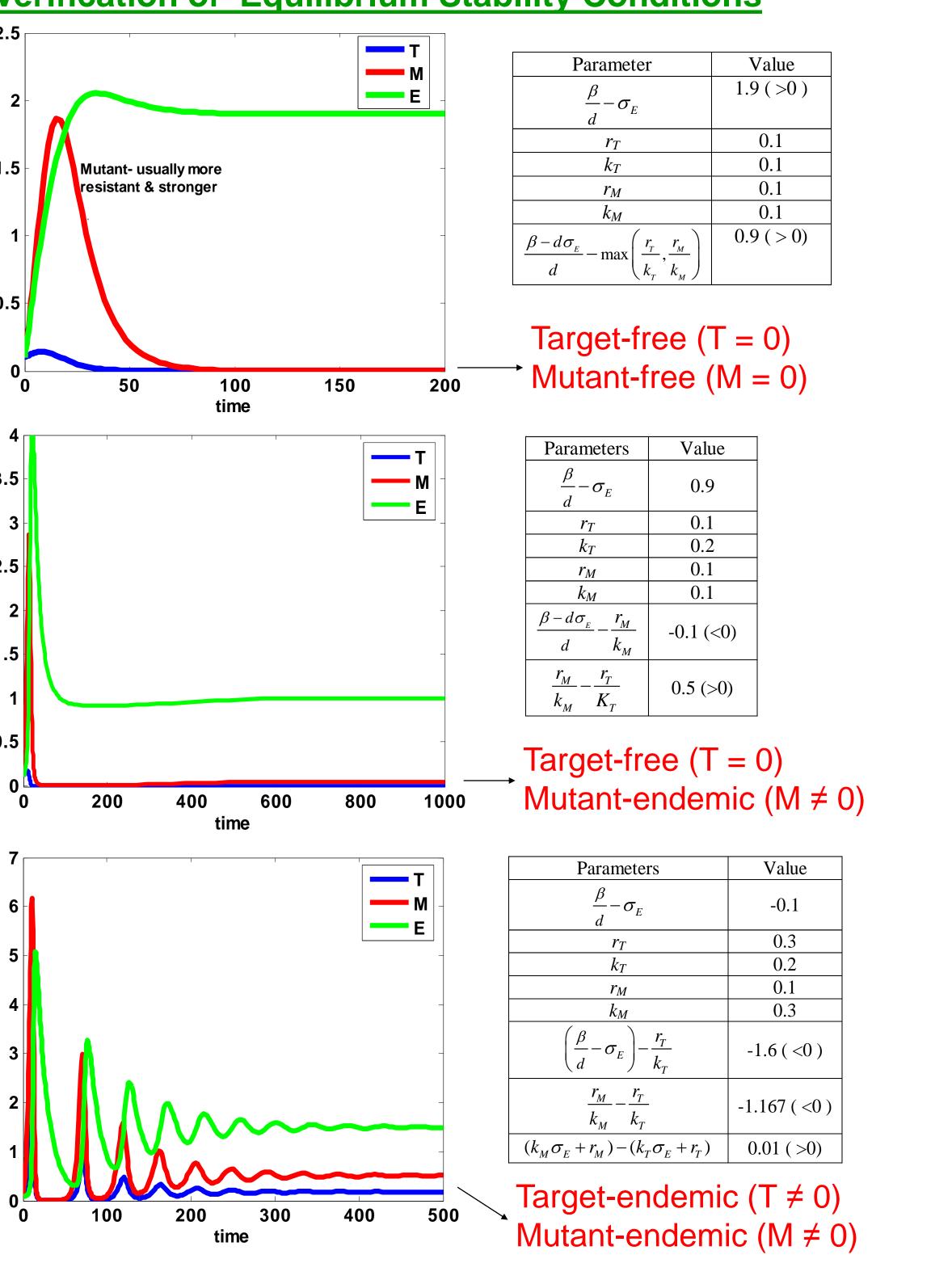
- If Re( $\lambda$ ) < 0; equilibrium is LAS
- If Re( $\lambda$ ) > 0; equilibrium is unstable

$$J = \begin{bmatrix} r_{T} - k_{T}E & 0 & -k_{T}T \\ \gamma & r_{M} - k_{T}E & -k_{M}M \\ \alpha E & \rho E & \frac{\beta}{\sigma_{E} + E} - \frac{\beta E}{(\sigma_{E} + E)^{2}} - d + \rho M + \alpha T \end{bmatrix}$$

### (III) Condition of Existence & Stability of Equilibria

Equilib rium	Condition of Existence	Condition of Stability	
(T1,M1,E1)	N.A.	Unstab le	
(T <sub>2</sub> ,M <sub>2</sub> ,E <sub>2</sub> )	<u>₿-do</u> d>0	$\frac{\beta - d\sigma_x}{d} > \max\left(\frac{r_x}{K_x}, \frac{r_y}{K_y}\right)$	
(T₃,M₃,E₃)	<u>β-do</u> r < rr d kr	$\frac{\boldsymbol{r}_M}{\boldsymbol{k}_M} > \frac{\boldsymbol{r}_T}{\boldsymbol{k}_T}$	
(T4,M4,E4)	$\frac{r_{r}}{k_{r}} > \max\left(\frac{r_{k}}{k_{s}}, \frac{\beta - d\sigma_{s}}{d}\right)$	$k_{\mu}\sigma_{E} + r_{\mu} \geq k_{T}\sigma_{E} + r_{T}$	

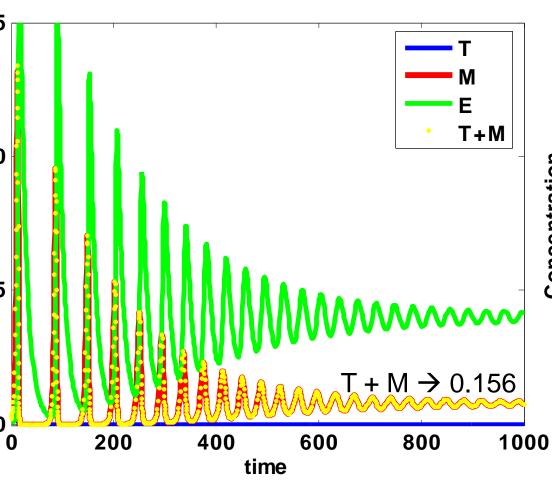
# **5. Computational Analysis**



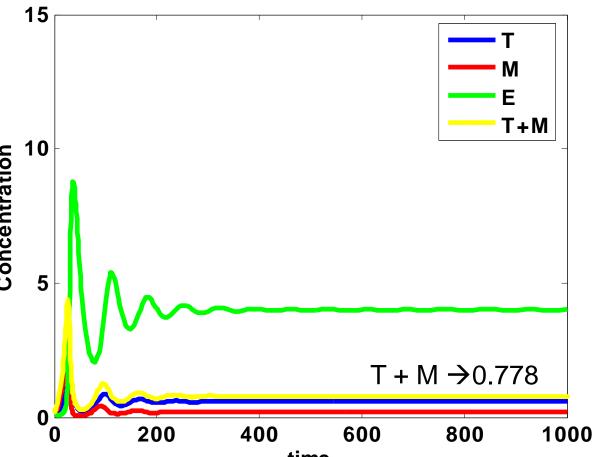
## (II) Effect of Difference b/w Target & Mutant Fitnesses

Fitness factor of mutant M cells:  $\frac{M}{A}$ 

	$\frac{r_T}{k_T}$	$\frac{r_{M}}{k_{M}}$	$rac{eta}{d} - \sigma_{_E}$	$\frac{\beta - d\sigma_{E}}{d} - \frac{r_{M}}{k_{M}}$	$\frac{r_M}{k_M} - \frac{r_T}{K_T}$	$ \begin{pmatrix} k_M \sigma_E + r_M \end{pmatrix} - \\ \left( k_T \sigma_E + r_T \right) $
$\frac{r_{M}}{k_{M}} > \frac{r_{T}}{k_{T}}$	1	4	-3	-7 ( < 0 ) (met existence cond. of (T <sub>3</sub> ,M <sub>3</sub> ,E <sub>3</sub> )	3 (>0) (met stability cond. of $(T_3, M_3, E_3)$	0.3
$\frac{r_{M}}{k_{M}} < \frac{r_{T}}{k_{T}}$	4	1	-3	$\begin{array}{c} -4 \ (\ < 0 \ ) \\ (met \ existence \\ cond. \ of \ (T_4, M_4, E_4) \end{array}$	-3 (<0) (met existence cond. of $(T_4, M_4, E_4)$	$\begin{array}{c} 0.375\\ (\text{met stability cond.}\\ \text{of }(T_4,M_4,E_4) \end{array}$



Case1: mutant 'fitter' than target - mutant pop. higher than target - target pop.  $\rightarrow$  zero eventually (i.e. target-free eventually)



Case2: target 'fitter' than mutant - target pop. higher than mutant - approaches equilibrium 4 (i.e. target & mutant both exist)

coexist.

To study the effect of introducing an engineered mutant cell (retrovirus) for treatment (eg. Retrovirus gene therapy to combat cancer cells)

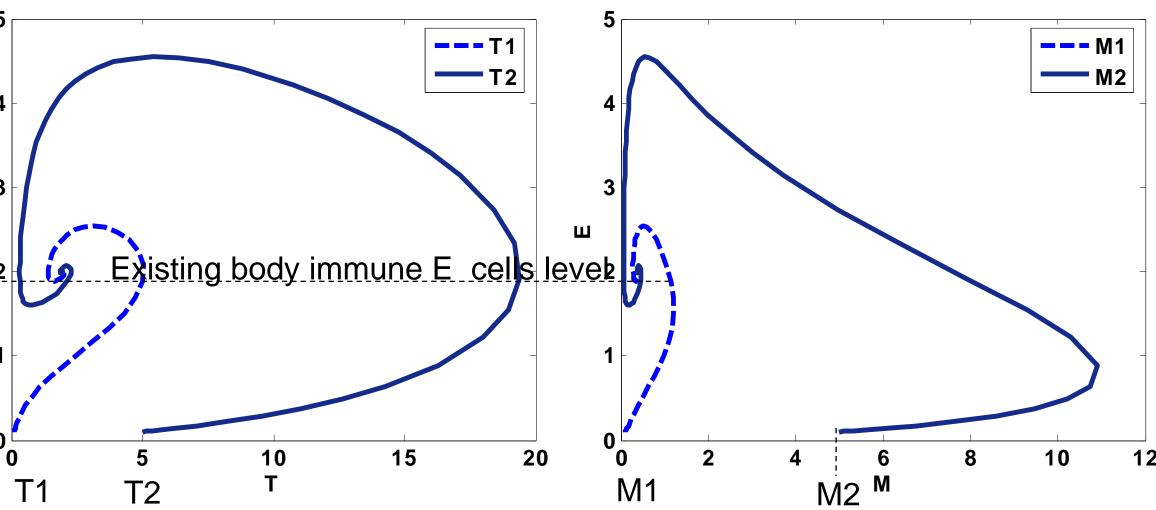


## 6. Applications & Biological Implications

(I) Treatment and Strength of Infection

To study the effect of treatment and/or different strengths of infection - Treatment yields a set of parameter values for T, M & E populations →Model can be used to predict the response of the populations to the treatment

- Different strength/stages of infection yields different initial conditions for T & M → Model can be used to predict the response of the populations



•Two trajectories correspond to infections of different strength started with initial conditions (T,E) = (T1, 0.1) and (T2,0.1). Strength of T2 >T1.

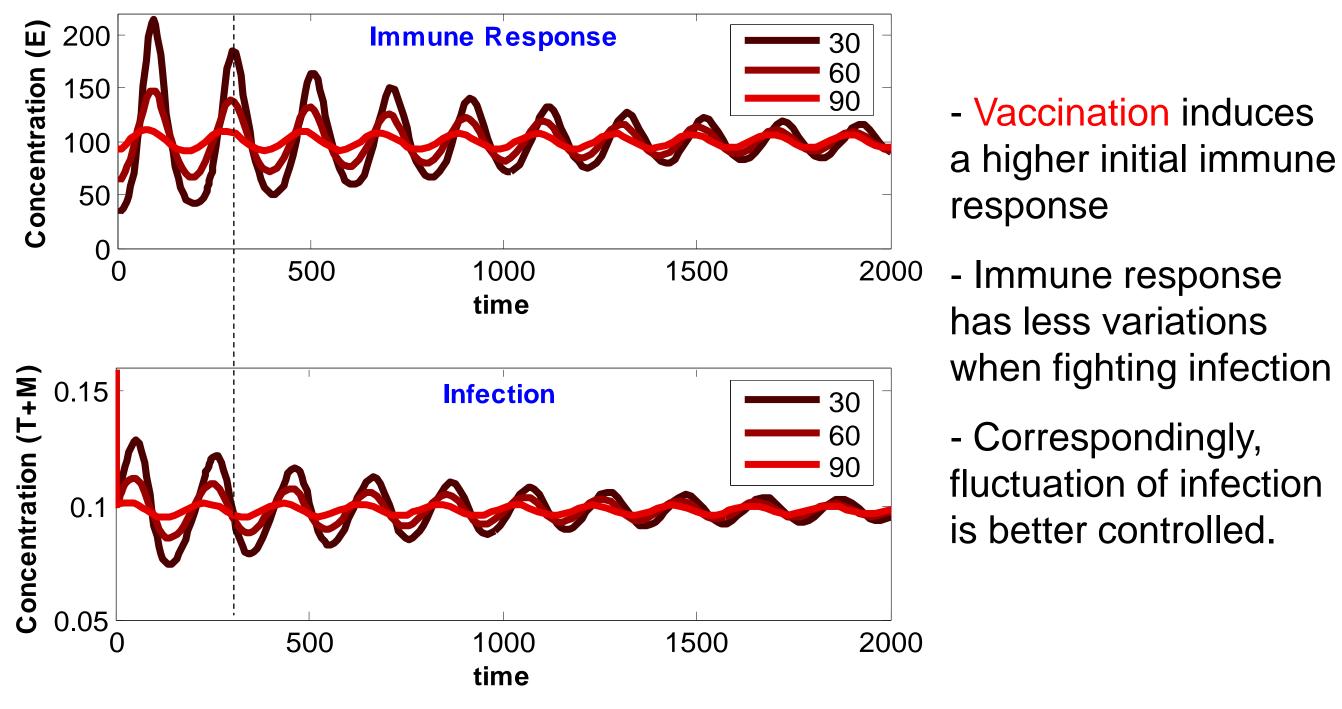
•As T increases, E increases correspondingly to combat infection.

•Complete extermination of T & M is impossible. Targets, mutants & effector cells

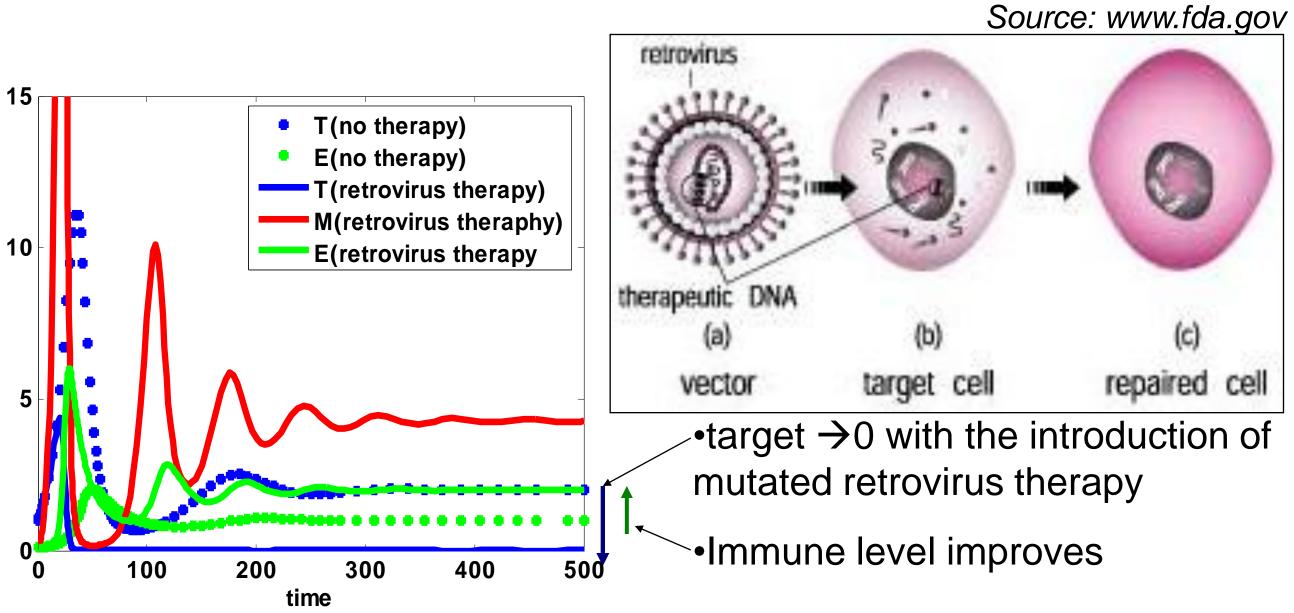
Example of diseases with mutation: HIV

### (II) Immune Memory of Effector Cell

To study the effect of immunological memory (acquired immune or vaccination)



(III) Mutative retrovirus therapy for cancer treatment



**Future Work** 

Validation of model with clinical data