Mathematical models of virus infections

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Short Abstract — **Motivated by recent experimental data, we investigate mathematical models regarding the evolutionary outcomes of viral infections, specifically human immunodeficiency virus (HIV), in humans. We analyze how the interplay between multiplicity of infection, synaptic cell-to-cell transmission of the virus, and free virus transfer can affect the dynamics of an infection taking place. Finally, we will discuss how recombination between virus strains can change the evolutionary outcomes of infection and influence the course of disease. The overall goal of the project is to better understand the dynamics of viral infections, specifically HIV, and to help design more effective healthcare and vaccination approaches.**

Keywords **— HIV, recombination, synaptic cell-to-cell transmission, free virus transmission, multiplicity of infection.**

I. Extended Abstract

Motivated by recent experimental data [1,2,4], we investigate mathematical models regarding the evolutionary outcomes of viral infections, specifically human immunodeficiency virus (HIV), in humans [5]. We will analyze how the interplay between synaptic cell-to-cell transmission of the virus and free virus transfer can affect the dynamics of an infection taking place.

We consider models that take into account multiplicity of infection, where a cell can be infected multiple times by different strains of the virus. Further, we also consider models with competition between virus strains, characterized by different mutations, to see how each strain's infection strategy can affect outcome.

Finally, we will discuss how recombination between virus strains can change the evolutionary outcomes of infection and influence the course of disease. Multiple mathematical models for HIV including synaptic cell-to-cell transmission have been put forth [3], however we now make use of an agent based model to study recombination and the dynamics of recombinant strains of the virus in the presence of both transmission modes. We show that a combination of both free virus transmission and synaptic cell-to-cell transmission minimizes the time to recombinant virus formation. This is because non-spatial free virus transmission ensures different strains will meet in the same cell and spatial synaptic cell-to-cell transmission then repeatedly transmits the different strains together, resulting in more opportunities for recombination to occur.

The overall goal of the project is to better understand the dynamics of viral infections, specifically HIV, and to help design more effective healthcare and vaccination approaches.

Acknowledgements: This work was funded by grant NSF DMS

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References

[1] Hüber W, et al. (2009) Quantitative 3D Video Microscopy of HIV Transfer Across T Cell Virological Synapses. *Science* **323.5922** 1743-1747.

[2] Komarova, N.L. et al. (2012) Relative contribution of free-virus and synaptic transmission to the spread of HIV-1 through target cell population. *Biology Letters* **9** 20121049.

[3] Komarova, N.L. and Wodarz, D. (2013) Virus dynamics in the presence of synaptic transmission. *Mathematical Biosciences* **242** 161-171.

[4] Levy, D.N. et al. (2004) Dynamics of HIV-1 recombination in its natural target cells. *PNAS* **101** 4204-4209.

[5] Nowak, M. and May, R.M. (2000) *Virus Dynamics: Mathematical Principles of Immunology and Virology*. Oxford University Press, UK