

SOUMYA BANERJEE

Department of Computer Science, 1,
University of New Mexico office: (505)
277-3122, Albuquerque, NM, 87131,
USA

Office: (505) 277-3122

Email: neel.soumya@gmail.com

Website: <http://sites.google.com/site/neelsoumya/>



Biography

- Soumya Banerjee has a PhD in Computer Science from the University of New Mexico, USA. He worked in Los Alamos National Laboratories while he was in graduate school. Prior to graduate school, he was a software engineer working in the financial services sector for Fortune 500 clients.
- His work is at the intersection of computer science and biological systems – he uses tools from computer science to study biological systems and takes inspiration from biological systems to design more efficient human-engineered systems. He is skilled in machine learning techniques and mathematical modelling using spatially explicit agent-based models and computationally tractable differential equation models.
- He works closely with people from other domains, especially experimentalists. His work has been recognized with a University of New Mexico Student Award for Innovation in Informatics in 2010.
- He takes pride in writing industrial-strength software, which he attributes to years working in industry and skills honed in academia. As of August 2014, he was ranked within the top 500 worldwide on MATLAB Central (an online repository for Matlab code contributed by

Research Interests, Skills and Projects

Skills

- Machine Learning and Data Science
- Bioinformatics (Analysis of Next-Generation Sequencing data)
- Wet-lab techniques (cell biology and microscopy techniques)
- Biostatistics (statistical analysis of sequencing data from human clinical trials)
- Computer Languages

Projects

- Stage Structured Hybrid Model
- Non-Linear Dynamical Systems and Complex Systems
- Modular RADAR and Scale Invariance of Immune System Rates and Times
- Modelling Activated T cell Homing and Recirculation
- Applications for Immune System Inspired Distributed Systems
- Statistical Analysis and Automated Cell Tracking for Cell Biology Experiments
- An Immune System Inspired Approach for Automated Program Verification (undecidability in immunocomputing)
- Modelling Within-Host and In-Vitro Viral Dynamics for Emerging Pathogens

Major Publications

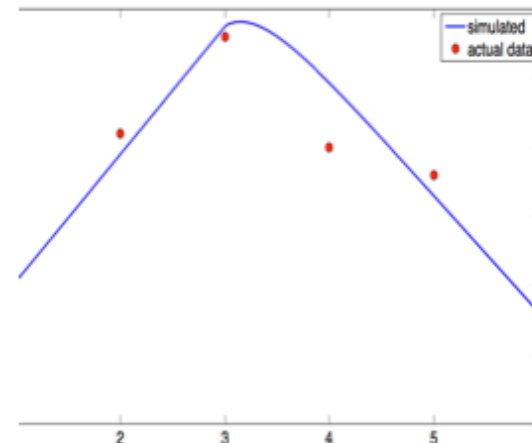
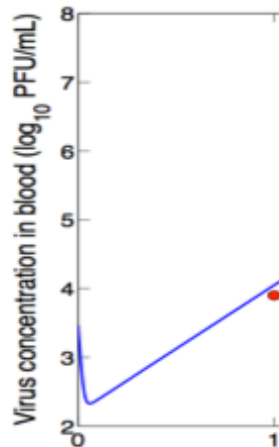
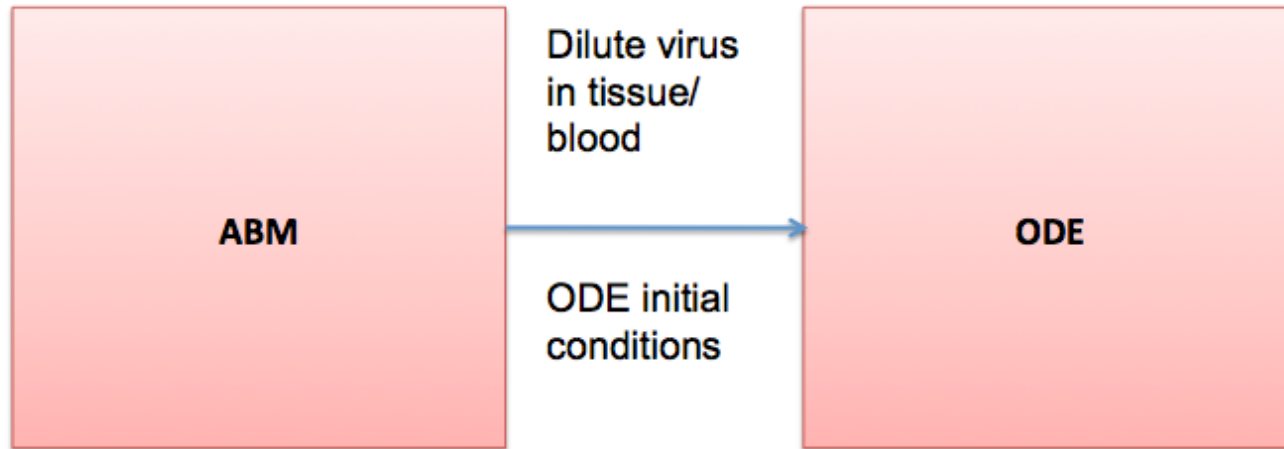
- 1) Immune System Inspired Strategies for Distributed Systems**, S. Banerjee & M. Moses. *6th Annual Computer Science at UNM Student Conference (CSUSC) 2010*
- 2) Modular RADAR: An Immune System Inspired Search and Response Strategy for Distributed Systems**, S. Banerjee & M. Moses. *The 9th International Conference on Artificial Immune Systems (ICARIS)*, 2010, Lecture Notes in Computer Science, Volume 6209/2010, 116-129, DOI: 10.1007/978-3-642-14547-6_10
- 3) Scale Invariance of Immune System Response Rates and Times: Perspectives on Immune System Architecture and Implications for Artificial Immune Systems**, S. Banerjee & M. Moses, *Swarm Intelligence*, Vol. 4(4), pp. 301-318.
- 4) A Hybrid Agent Based and Differential Equation Model of Body Size Effects on Pathogen Replication and Immune System Response**, S. Banerjee & M. Moses. *The 8th International Conference on Artificial Immune Systems (ICARIS)*, Volume 5666-014, 14-18, 2009
- 5) An Immune System Inspired Approach to Automated Program Verification**, S. Banerjee, 2009
- 6) The Value of Inflammatory Signals in Adaptive Immune Responses**, S. Banerjee, D. Levin, M. Moses, F. Koster and S. Forrest. *The 10th International Conference on Artificial Immune Systems (ICARIS)*, 2011, Lecture Notes in

Stage structured hybrid model

- Stochasticity and spatial distribution of the pathogen play a very critical role in determining the outcome of an infection. 1 in 10^6 B-cells are specific to a particular pathogen. The serendipitous encounter of such a rare cognate B-cell with its fated antigen can determine host mortality. Mosquito vectors inject an average of 10^5 PFU of WNV into an animal however there is a lot of variation around this mean. If a mosquito injects into a vein, the pathogen can spread systemically instead of being localized in tissue, leading to faster progression disease progression but possibly faster recognition by immune system cells. If a mosquito only injects into tissue, the pathogen will remain localized in a small volume of tissue and will probably be able to evade immune recognition while proliferating.
- Such stochastic and spatial aspects of pathogenesis likely play a role in other diseases also. For example, macaques experimentally inoculated with HIV became infected with a very low probability in a dose dependent manner suggesting the role of initial stochastic events in shaping the trajectory of pathogenesis.

- Current efforts at investigating the effect of stochasticity and space in modeling of host immune response and pathogens uses agent based models (ABMs). An ABM represents each entity or agent (each cell or virion in our case) explicitly, and a computer program encodes each rule or behavior for interacting with other agents. The agents move about in space and interact with other agents in their neighborhood according to the encoded rules. ABMs emphasize local interactions based on first principles, and these interactions give rise to the complex high-level phenomena of interest.
- Due to the level of detail at which individual components are represented, ABMs can be computationally expensive and sometimes intractable. Population level approaches like ordinary differential equations (ODEs) are computationally tractable and can scale up to simulate host pathogen dynamics in large organisms . However they make simplifying assumptions. For example they subsume individuals into a homogeneous compartment. They also assume that populations are homogeneously mixed. For example, the implicit assumption is that at initialization, a population of injected virions and normal cells would be “well-mixed” i.e. each virion has the opportunity to come in contact with every normal cell. This is unlikely to be satisfied during the initial stage of infection, when inoculated virions localize at the site of infection. Such spatial effects assume more importance during the onset of infection, when the number of virions is low, and we need an ABM to address this.
- We proposed an approach that aims to strike a balance between the detail of representation of an ABM and the computational tractability of an ODE model. We call this a *stage-structured hybrid model* ([paper](#)). It uses a detailed and spatially explicit, but computationally intensive ABM in the initial stage of infection, and a coarse-grained but computationally tractable ODE model in the latter stages of infection (when the assumptions of homogeneous mixture of population are likely to be satisfied and spatial effects can be ignored)

Such an approach might hold promise in modeling of other pathogens where the initial stochasticity of the pathogen and host response dictates the trajectory of pathogenesis. A general schematic of the approach is shown below



Thank
You