The importance of using multi-scale and multi-organ approaches to understand host-pathogen dynamics in TB

Denise Kirschner, PhD

(The University of Michigan Medical School)



NIH support funding this work

- **Systems Biology** (Pls: Kirschner, Linderman, Flynn, Kunkel)
- R33HL092853, "A multi-scale and multi-system approach to understand granuloma formation in *Mycobacterium tuberculosis*", 7/15/2008 – 5/30/2012
- RENEWAL submitted (A1 status)

- **MSM**-(PIs Kirschner, Linderman, Flynn)
- **2**R01EB012579-04A1 "Multi-scale methods to predict outcomes of immuno-modulation and drug therapy during TB" 8/2011-8/2016.
- **MSM** (completed): R01 LM 10020661: "A multi-scale approach to understanding antigen presentation in human immunity" 9/05-8/09

Infection Outcomes Associated with Exposure to the bacteria *M. tuberculosis*



Flynn Lab: Non-human primate model of tuberculosis



Spectrum of granulomas in macaques: Immune and bacterial microenvironments



From granulomas at necropsy: obtain data on cell types, cytokines, chemokines in different granulomas at a specific time point



Flow cytometry, intracellular cytokine staining, boolean gating, SPICE analysis

PET/CT: Imaging modality for serial tracking of lesions and disease

CT: structural map of lesions in organs PET: functional map of lesions in organs





BSL3 imaging suite Regional Biocontainment Lab (RBL), Flynn Lab University of Pittsburgh

Understanding dynamics at the level of a granuloma using systems biology

- To this end, necessary to build/refine a model of granuloma forming in lungs of infected primates –integrate data
- Add relevant organs/compartments that feed into and out of the lung-integrate data
- Add relevant scales (genetic, molecular, cellular, tissue)
- Build and validate model on NHP and other data
- Test model against different data
- Perform analysis, make predictions



We apply tuneable resolution to toggle between detail and none as appropriate



D:

1930

950



Snapshot of a 3D ABM simulation of a granuloma at 200 post-infection. Shown is a 'transparent front-end' granuloma. We can see inside the granuloma because we can control the transparency level of different cell types from a transparency level of 0 (opaque) to 100 (invisible). The colors correspond to cells as follows: Resting M Φ (green), activated M Φ (blue), infected M Φ (orange), chronically infected M Φ (red), Treg (teal), Tgamma (pink), Tcyt(purple). Necrotic regions



It takes 60 hours to generate one 200 day simulation in the right dimension of tissue (2 mm x 2mm x 2mm)



Parameter estimates and analysis: how do we begin to distinguish mechanisms driving observed differences?

- <u>Uncertainty Analysis</u> determines how much variability in outcome is induced by variability in parameter values **Latin Hypercube Sampling (LHS)*
- <u>Sensitivity Analysis</u>— measures which parameters induce this variability and ranks the correlations **Partial Rank Correlation (PRC)*
- KEY FEATURE can quantify relationships over time
- Simeone Marino, Ian B. Hogue, Christian J. Ray, Denise E. Kirschner. A Methodology For Performing Global Uncertainty and Sensitivity Analysis in Systems Biology Journal of Theoretical Biology, Vol 254, pp 178-196, 2008, NIHMS ID #68202.

(programs available on our website)

Understanding granulomas is a Multi-scale problem in both space and time: multi-organ scale





Mark Miller, Wash U Collaborator



LN image of a NHP by Flynn Lab

Conical simulation area



⁷⁰ compartments



CD4+ T cell CD8+ T cell Dendritic cell T cell exit

3D ABM Design for LN

CD4+T cells (active, effector) CD8+ (active, effector) DCs (naïve, antigen-bearing and licensed) HEV, AL, EL—simulate acute infection 500 DCs Simulated over 7 days

Need to optimize size of cone to be sure We are capturing all relevant dynamics Without having to simulate the entire T zone, which is computationally prohibitive





Fibroblastic Reticuluar Cell Network, red football T cell, DC is green sphere

Summary of points for Theme 3

- We build single scale models of a variety of types and link them in different ways
 - Link multi-scale, Link multi-organ
- We use tuneable resolution to turn on and off at will the different scales and organs
- We developed and use a detailed uncertainty and sensitivity analysis for determining parameters and indentifying model features
- We are currently focusing on 2-D versus 3-D representations of the ABMs





- Collaborators: Jennifer Linderman, (Univ of Mich)
- JoAnne Flynn (Pitt)
- Steve Kunkel, (Univ of Mich)

Website: http://malthus.micro.med.umich.edu/