A novel model of TB progression using CompuCell3D

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Outline

- IntroductionModel
- Results
- Discussion

Introduction

- TB is caused by airborne Mycobacterium tuberculosis (Mtb) transmission
 - 1.6 million died from TB in 2021
 - ► TB is treated with antibiotics (~6 months)
- Bowness et al. (2018)
 - Distance to nearest blood vessel is important
 - Dormant bacteria tend to remain after treatment
- CompuCell3D (CC3D) models biological cellular processes
- I'm developing a within-host TB model using CC3D

Model

Conceptual modelCompuCell3D



Conceptual model

Cells:

- Macrophages
- ► T cells
- Mtb bacteria
- Blood vessels



- Chemical fields:
 - Oxygen
 - Chemokine
 - Macrophage activating cytokine

Macrophages





Mtb bacteria

Slow-growing Fast-growing Intracellular extracellular extracellular





Caseum



Fields

Oxygen

Turns pandas into rabbits

Chemokine

Macrophage activating cytokine

Shia LaBeouf's voice

Biological processes

- Phagocytosis
- Immune cell recruitment
- Mtb bacteria state transition
- Chemotaxis
- Macrophage activation
- Killing of (chronically) infected macrophages
- Bursting of chronically infected macrophages
- Replication



Immune cell recruitment









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T cells kill (chronically) infected macrophages







Outcomes







CompuCell3D

Mixture of XML script and PythonCells:

live on a lattice

are assigned attributes

can interact with chemical fields

CompuCell3D

- Proposed cell configurations are accepted/rejected as follows:
- 1. Choose a random lattice site
- 2. Choose a neighbouring site to copy to
- 3. Calculate the proposed change in energy (ΔH)
 - a. If $\Delta H \leq 0$, accept the new configuration

 ΔH

b. If $\Delta H > 0$, accept with probability e^{-T_m}

CompuCell3D





Initial conditions



Slow-growing extracellular bacteria (6) **Fast-growing** extracellular bacteria (6) **Resting macrophage** (105)Blood vessel (49) Wall (1)

Results

► TBC!

- Expected results:
 - Containment in about 90% of simulations
 - Exponential growth in about 10% of simulations
 - Longer average distance to initial cluster
 - Predominantly slow-growing extracellular bacteria left

Discussion

- Easy to understand
- Can update states/parameters over time
- Allows for stochasticity and complex dynamics
- Open source, modular and easy to share
- Not analytically tractable
- Lots of parameters!
- Need to average over many (slow) simulations



Future work

- Finish parameterisation
 - Sensitivity and uncertainty analysis
- Test all model components in full
- Run 100 simulations and compare to original model
- Incorporate into a multi-scale TB model

Summary

First within-host TB model made using CC3D

- Cellular Potts approach plus cell-field interactions
- Results should validate Bowness et al. (2018)

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Thank you

Any questions?

