## Host immune parameters varied to capture granuloma variability for tissue PK calibration

calibrate tissue PK parameters <sup>1,2</sup>		
Host Immune Parameters	Unit*	Range (min – max)
Time to heal caseation	Days	8 – 12
TNF threshold for causing apoptosis	Molecules	900 - 1400
Rate of TNF induced apoptosis	s <sup>-1</sup>	$1.3x10^{-6} - 2x10^{-6}$
Minimum chemokine concentration allowing chemotaxis	Molecules	0.4 - 0.6
Maximum chemokine concentration allowing chemotaxis	Molecules	380 - 570
Initial macrophage density	Fraction of grid comp.	0.03 - 0.05
Time steps before a resting macrophage can move	Timesteps	2-4
Time steps before an activated macrophage can move	Timesteps	15 – 24
Time steps before an infected macrophage can move	Timesteps	135 - 200
TNF threshold for activating NFkB	Molecules	60 – 90
Rate of TNF induced NFkB activation	s <sup>-1</sup>	$8 \times 10^{-6} - 1.5 \times 10^{-5}$
Probability of resting macrophage killing bacteria		0.1 - 0.15
Adjustment for killing probability of resting macrophages with NFkB activated		0.15 – 0.25
Number of extracellular bacteria in the Moore neighborhood that can activate NFkB	Bacteria	200 - 300
Threshold for intracellular bacteria causing chronically infected macrophages	Bacteria	10 – 15
Threshold for intracellular bacteria causing macrophage to burst	Bacteria	18 – 30
Number of bacteria activated macrophage can phagocytose	Bacteria	4 - 6
Probability of an activated macrophage healing a caseated compartment in its Moore neighborhood		0.004 - 0.007
Number of host cell deaths causing caseation		4 (Caseous granulomas) 15 (Cellular granulomas)
Probability of a T-cell moving to the same compartment as a macrophage		0.035 - 0.055
IFN $\gamma$ –producing T-cell probability of inducing Fas/FasL mediated apoptosis		0.03 - 0.04
IFN $\gamma$ –producing T-cell probability of producing TNF		0.04 - 0.05
IFN γ -producing T-cell probability of producing IFN		0.3 - 0.45
Cytotoxic T-cell probability of killing a macrophage		0.007 - 0.01
Cytotoxic T-cell probability of, when it kills a macrophage, also killing all of its intracellular bacteria		0.6 – 0.9
Cytotoxic T-cell probability of producing TNF		0.04 - 0.06
Regulatory T-cell probability of deactivating activated macrophage		0.006 - 0.01
Time before maximum recruitment rates are reached	Timesteps*	790 – 1180
Macrophage maximal recruitment probability		0.25 - 0.4
Macrophage chemokine recruitment threshold	Molecules	0.7 – 1
Macrophage TNF recruitment threshold	Molecules	0.009 - 0.015
Macrophage half sat for TNF recruitment	Molecules	1.3 – 2
Macrophage half sat for chemokine recruitment	Molecules	1.8 - 2.6
IFN γ –producing T-cell maximal recruitment probability		0.12 - 0.18
IFN γ –producing T-cell chemokine recruitment threshold	Molecules	0.0.06 - 0.09
IFN γ –producing T-cell TNF recruitment threshold	Molecules	1 – 1.6
IFN $\gamma$ –producing T-cell half sat for TNF recruitment	Molecules	1 – 1.6
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Table S1: Host immune parameter ranges used to generate collections of test granulomas to calibrate tissue PK parameters  $^{1,2}$ 

IFN γ –producing T-cell half sat for chemokine recruitment	Molecules	1.5 – 2.5
Cytotoxic T-cell maximal recruitment probability		0.1 - 0.15
Cytotoxic T-cell chemokine recruitment threshold	Molecules	3.6 - 5.4
Cytotoxic T-cell TNF recruitment threshold	Molecules	1 – 1.5
Cytotoxic T-cell half sat for TNF recruitment	Molecules	1 – 1.5
Cytotoxic T-cell half sat for chemokine recruitment	Molecules	7 – 10
Regulatory T-cell maximal recruitment probability		0.02 - 0.04
Regulatory T-cell chemokine recruitment threshold	Molecules	1.5 – 2.5
Regulatory T-cell TNF recruitment threshold	Molecules	1.3 – 2
Regulatory T-cell half sat for TNF recruitment	Molecules	1.8 - 2.7
Regulatory T-cell half sat for chemokine recruitment	Molecules	1.2 – 1.8

\*Conversion factor: 10 min/timestep.

## References

- 1 Pienaar, E. *et al.* A computational tool integrating host immunity with antibiotic dynamics to study tuberculosis treatment. *J Theor Biol* **367**, 166-179, doi:10.1016/j.jtbi.2014.11.021 (2015).
- 2 Pienaar, E., Dartois, V., Linderman, J. J. & Kirschner, D. In silico evaluation and exploration of antibiotic tuberculosis treatment regimens. *BMC systems biology* **9**, 79, doi:10.1186/s12918-015-0221-8 (2015).