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The role of neutrophils in Mycobacterium tuberculosis infection

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Tuberculosis remains a widespread and deadly disease, infecting approximately two billion people worldwide. Gaining a better understanding of the immune response to *Mycobacterium tuberculosis* is crucial, and the increased prevalence of multi-drug resistant strains, the current complexity and length of treatment, and the inherent difficulties of experimental work each highlight the need for new approaches. Computational modelling of the complex immune response which results in the formation of lung granulomas can enable analysis of what is currently a relatively black box for scientists. In particular, the role of neutrophils in the granuloma response to *M. tuberculosis* infection remains largely unknown, as neutrophils are easily activated and short-lived, and thus pose unique experimental challenges to wet lab study. Through the incorporation of a neutrophil cell type into our existing hybrid agent-based computational model, we investigate the spatiotemporal dynamic formation of lung granulomas in response to *M. tuberculosis* infection. We are interested in determining how neutrophil presence induces both global and localized features of granulomas, the dynamics of neutrophil interactions with other cells and *M. tuberculosis*, whether the neutrophil response to *M. tuberculosis* is beneficial or detrimental to the host, and how that response can be harnessed to aid in therapies. Our goal is to not only identify the sufficient biological assumptions necessary to reproduce experimental datasets from our collaborators, but to shed insights on the mechanistic basis for neutrophil-directed immunopathogenesis in *M. tuberculosis* that are beyond current experimental capabilities.

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