Predictive Virtual Infection Modeling of Pathogenic Immune Evasion in Human Whole-blood

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Introduction: the State-based Model of Whole-blood Infection

- rising incidence of microbial infections, e.g. by Candida albicans, Candida glabrata and Staphylococcus aureus - data collected from whole-blood infection assays to investigate innate immune response

- a fraction of pathogenic cells exhibit immune evasion (IE), *i.e.* remain extracellular

- mathematical modeling allows for hypothesis testing by changing single parameters or mechanisms



Modification of the SBM

- it is unknown why pathogenic cells are able to evade the immune response
- possible reason are polymorphonuclear neutrophils which secrete proteins into extracellular space
- proteins could mask pathogenic cells or shave certain PAMPs
- spontaneous IE mechanism changed to a PMN-mediated IE mechanism





Immune Evasion

Spontaneous IE alive pathogenic cell killed pathogenic cell evasive pathogenic cel neutrophili neutrophilic evasion-inducing proteins proteins polymorphonuclear neutrophil (PMN)

PMN-mediated IE





References [1] Hünniger and Lehnert et al. (2014), PLOS comp Biol. 10(2), e1003479 [2] Lehnert and Timme et al. (2015), Front Microbiol. 6

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