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Population-based modeling of infection processes

Infection processes can in many cases be viewed from a macroscopic perspective, i.e. as being an interplay of different constituents that are present in large numbers. In such cases, differential equations represent the adequate mathematical modeling approach and allow exploring solutions by analytical and numerical methods. The current project will start from differential equation models of various infection scenarios, such as: (i) comparing strategies of clearance versus tolerance of pathogens in the context of sepsis, (ii) modeling antibiotic treatment and resistance development in microbial communities, and (iii) identifying optimized treatment protocols of immunoglobulin substitution for patients with primary immune deficiency agammaglobulinemia. The biomathematical modeling will include analytically and/or numerically solving differential equations - including analyses of the stability of solutions and the identifiability of parameters - and may be extended to computer simulations of state-based models where appropriate.

Publications

Tille A, Lehnert T, Zipfel PF, Figge MT (2020) Quantification of Factor H Mediated Self vs. Non-self Discrimination by Mathematical Modeling. *Front Immunol* 11, 1911. [Details](#) [PubMed](#)

Supervisor

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Start of PhD

January 9, 2017

Doctoral Disputation

June 1, 2023