

During my short term visit we worked on Mtb infection data in mouse from the lab of David Sherman that was partly published in<sup>1</sup>. Additionally to infection dynamics in mouse, also the bacterial load in the spleen was measured. The aim of the project is to include this additional compartment in the modeling and analyze differences between lung and spleen and the role of migration in the dynamics. Therefore, we firstly analyzed the noise on the data using bootstrapping. We further developed several different models and hypothesis for the dynamics of Mtb especially incorporating various mechanisms for the migration of bacteria from lung to spleen. Those models were fitted to the data using parameter estimation as implemented in the MATLAB toolbox PESTO (<https://github.com/ICB-DCM/PESTO>). Using statistical model comparison like the F-test and AICc we could rank the models identifying models that can not describe the data sufficiently well. The corresponding hypotheses can be rejected. The results were compiled in a preliminary manuscript.

<sup>1</sup> Gill, W., Harik, N. S., Widdon, M. R., Liao, R. P., Mittler, J. E., and Sherman, D. R. (2009). A replication clock for Mycobacterium tuberculosis. *Nat. Med.* 15, 211–214.

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