# Quantification of the dynamics of fungal confrontation assays

<sup>1</sup> Applied Systems Biology, Leibniz Institute for Natural Product Research and Infection Biology – Hans-Knöll-Institute, Jena, Germany
<sup>2</sup> Faculty of Biological Sciences, Friedrich-Schiller-University Jena, Germany

#### Introduction

- Confrontation assays of polymorphonuclear neutrophils (PMNs) and Candida glabrata [1,2]
- Quantification of the population dynamics using a minimal state-based-model with 8 unknown parameters
- Why does the *C. glabrata* population survive the confrontation with the PMN and how can we stimulate the immune response to defeat the fungal infection?



### Workflow

- (1) Determine the parameters of the PMN dynamics
- (2) Use the results from (1) to determine the parameters of the PMN-*C.glabrata* dynamics of the complete system
- Fit the simulation data to individual experimental data: two migration parameters can be directly determined from the data
- Fit the simulation data to the ensemble of experimental data: models master equation is correctly represented and we can fit the model to the experimental data distribution





### **PMN** Dynamics

- The simulation data summarizes the results of 500 simulations
- Experimental data of each experiment fits to the corresponding simulation data within the standard deviation
- The system is very sensitive to the PMN-outflow parameter
- The optimal parameter set varies from experiment to experiment
  - Due to the high sensitivity of the model to the PMN-outflow parameter, there is no parameter set that fits to all experiments
  - The mean of all optimal parameter value of the single experiment fits to the mean of the ensemble fittings
  - Even though there are differences in the total population sizes of the PMN, there is no correlation to the PMN-outflow parameter

## C. glabrata Dynamics

- The mean of the ensemble of experimental data can be reproduced by our simulation for all fungi clusters
- The fluctuation of the experimental data are not reproduced by the simulations
- The fitted optimal parameters are so far only be determined in a very large interval (not shown)

#### Conclusion

- By fitting the PMN dynamics separately, we can determine the models parameters of the PMN very accurately
- The fitting of the remaining parameters has to be refined
- We are going expand our model to test hidden immune evasion mechanism that might explain the surviving *C. glabrata* population

[1] Essig F. *et al.*, Fungal Genet. Biol. (2015)[2] Brandes S. *et al.*, Medical Image Analysis (2017)

CONTACT Alexander.Tille@hki-jena.de Research Group Applied Systems Biology

