Ex vivo Immune Profiling in Patient Blood enables Quantification of innate immune Effector Functions

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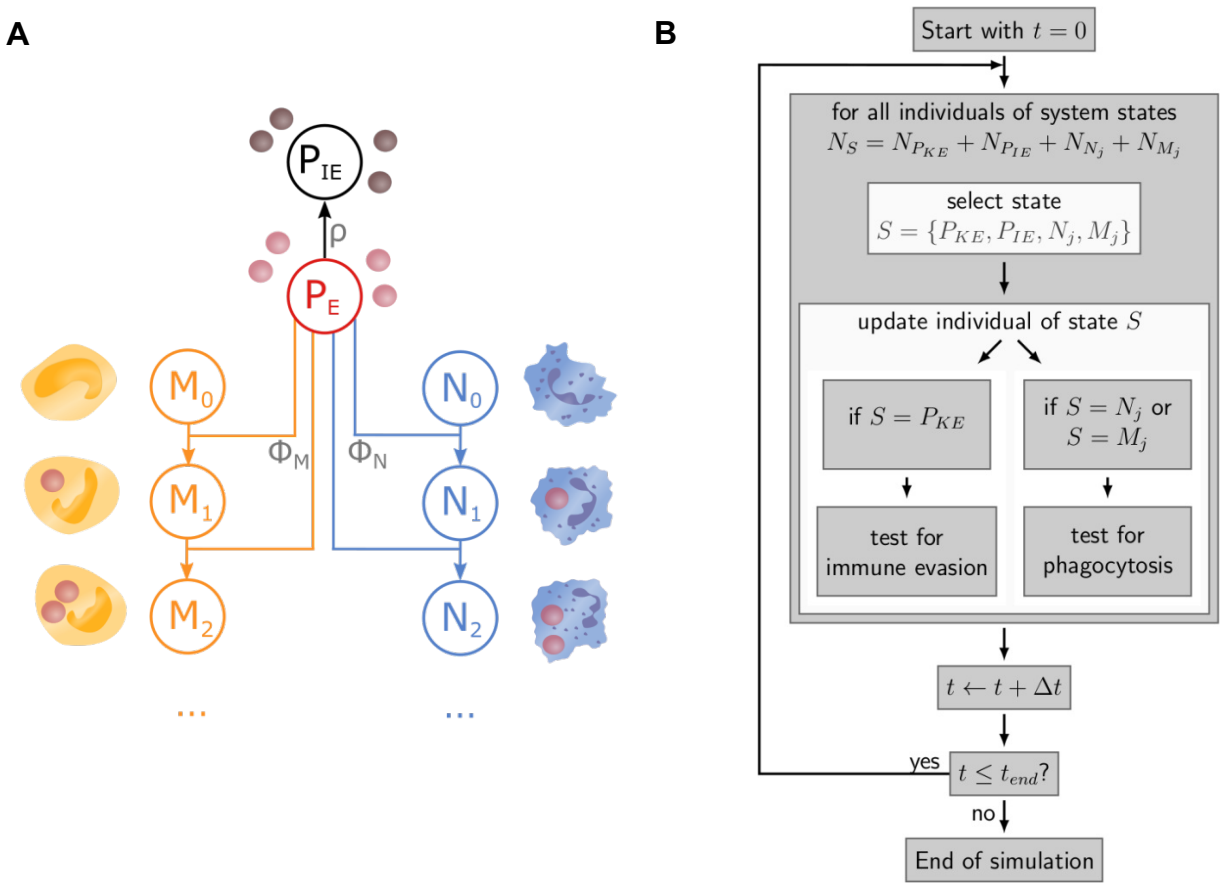

Fig S1. Schematic depiction of the state-based simulation algorithm (A) and the state-based virtual infection model for whole-blood infection (B). (A) The model is composed of different states that represent several cell populations during whole-blood infection (colored circles). The model contains states for killed pathogens in extracellular space (P_{KE}), immune evasive pathogens (P_{IE}) as well as two types of immune cells, neutrophils (N_j) and monocytes (M_j) with *j* phagocytosed pathogens. Connections between the states indicate possible state transitions that are characterized by transition rates (grey colored Greek letters): ρ for the acquisition of immune escape as well as ϕ_N and ϕ_M for phagocytosis by neutrophils and monocytes. The figure is adapted from Hünniger *et al.,* 2014. (B) For each simulation time *t*, an individual is randomly selected out of the number of individuals N_S. The current state of the individual can be left in dependence on the respective rate of the transition. After testing each individual for possible state transition, the simulation time is increased by the simulation time step Δt and the simulation algorithm ends if the simulation time t_{end} is reached. The Figure is adapted from Lehnert *et al.*, 2015.

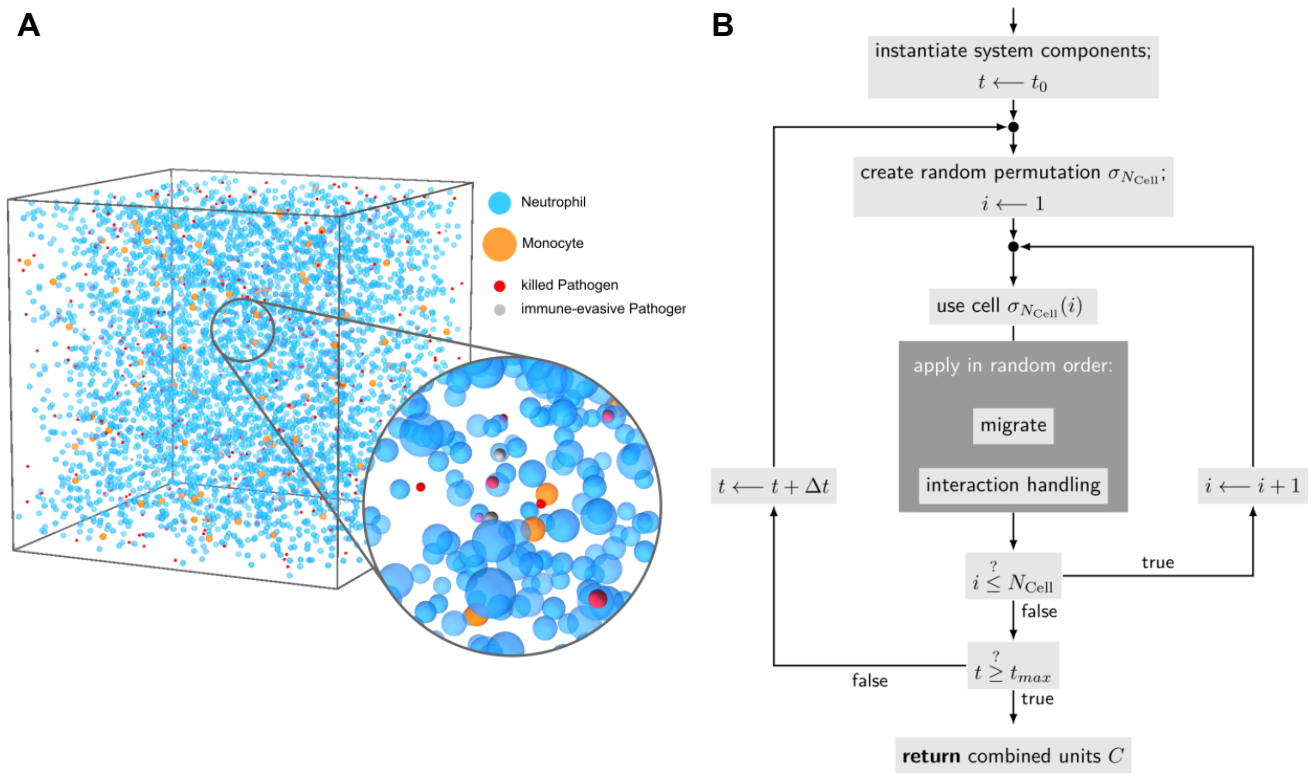

Fig S2. Schematic depiction of the agent-based virtual infection model for whole-blood infection (A) and its simulation algorithm (B). (A) Both immune cell types – monocytes (orange) and neutrophils (blue) – as well as the pathogenic cells (red: killed pathogens, grey: immune evasive killed pathogens) are modeled as spherical objects within a continuous three-dimensional environment representing 0.5 µl of blood. The figure is adapted from Lehnert *et al.,* 2015. (B) First, in the ABM all system components are instantiated. Afterwards, the interaction of monocytes and neutrophils with the pathogen is simulated for a time t_{max}. During each discrete time step t for all cells migration and interaction with other cells in the environment is simulated in random order. The Figure is adapted from Lehnert *et al.*, 2015.

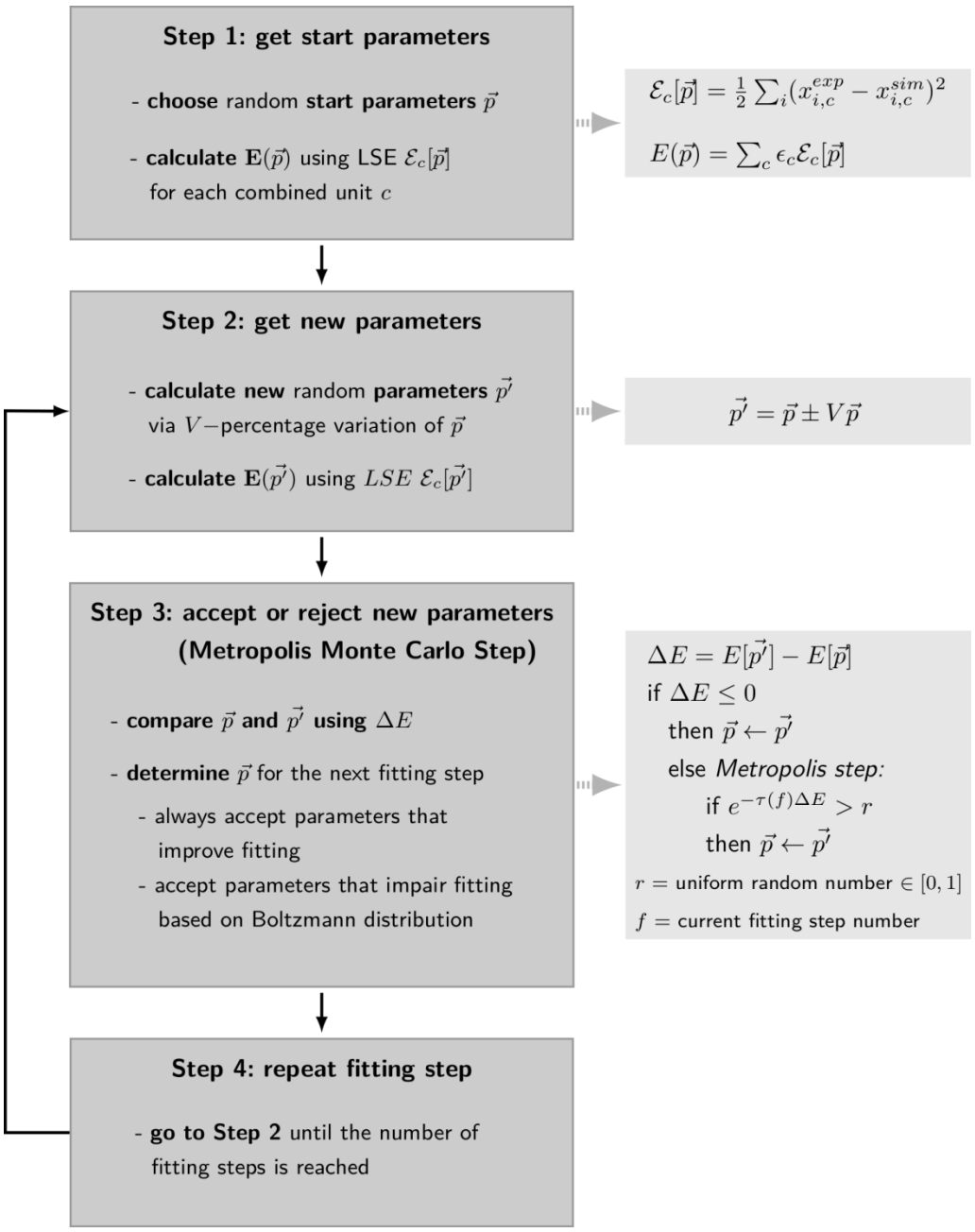

Fig S3. Flow chart of the SBM parameter estimation algorithm. Calibration of the SBM to the experimental data is realized by the Metropolis Monte-Carlo algorithm with simulated annealing. The algorithm is explained in detail in the Supplementary Material Section *SBM parameter estimation by simulated annealing*. The flowchart is adapted from Lehnert *et al.* 2015.

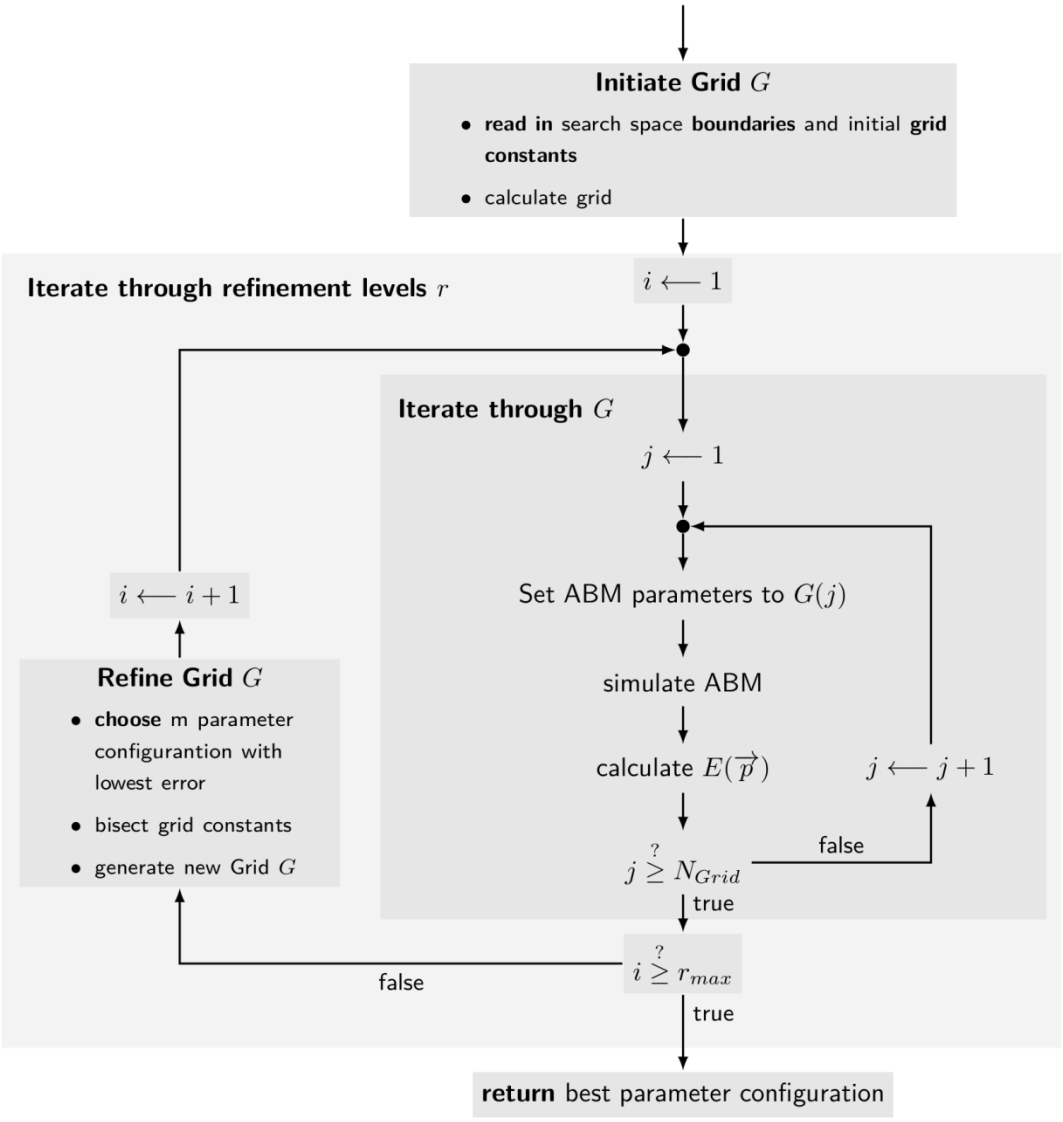

Fig S4. Flow chart of the ABM parameter estimation algorithm. For calibration of the ABM to the experimental data the local method of *adaptive regular grid search* is applied. First, a grid within the parameter space with predefined boundaries is initiated with a certain grid constant. Afterwards, the algorithm iterates through the grid and the model is simulated with the current parameter $\vec{p}$. The deviation of the simulation outcome and the experimental data is evaluated using the weighted least squares error. Furthermore, around the best parameters $\vec{p}$, *i.e.* the parameters with a low $E(\vec{p})$, the parameter space is screened with a more fine-grained grid by bisecting the current grid constant. The flowchart is adapted from Lehnert *et al.* 2015.