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Virtual whole-blood infection assays

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Background

Whole-blood infection assays (WBIA)

- Opportunistic human-pathogenic fungi: Candida albicans, C. glabrata
- Enter the bloodstream via the intestinal gut or medical devices (e.g. catheters)





- Cause systemic infections like sepsis in immunocompromised patients
- High mortality rates

[1,2]



Agent-based model (ABM)

[2]

State-based model (SBM)



Parameter Fitting:

- Least-Squares Error (LSE): $LSE = \sum_{i=0}^{n} (\mu_i^{exp} \mu_i^{sim})^2$
- Scheme
- •



Isotropic reaction diffusion equation with cells as source/sink:

$$\frac{dc(\vec{x},t)}{dt} = D \cdot \Delta c(\vec{x},t) - \lambda c(\vec{x},t) + Q(\vec{x},t)$$

periodic boundary condition

• Time discretization using the explicit Euler scheme: $c_{t+1} = Ac_t + Q(c_t)$

- A: three dimensional second order finite difference matrix
- $Q(c_t)$: discretized cell-molecule interaction

• Applications:

- Cytokine secretion of neutrophils
- Ligand-Receptor binding of chemokines
- Complement opsonization of pathogens

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References

[1] Hünniger *et al.* 2014. *PLOS Comput Biol*. 10:2 [2] Lehnert et al. 2015. Front Microbiol. 6:608





