



Politecnico
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DI TORINO

Agent-based and continuum models for spatial dynamics of infection by oncolytic viruses

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joint work with Marcello Delitala and Federico Frascoli

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Politecnico di Torino
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Università di Torino



Overview

- 1 Introduction and motivation
- 2 Modelling framework
- 3 Infection with standard diffusion
- 4 Infection with pressure-driven motion



Infection of oncolytic viruses

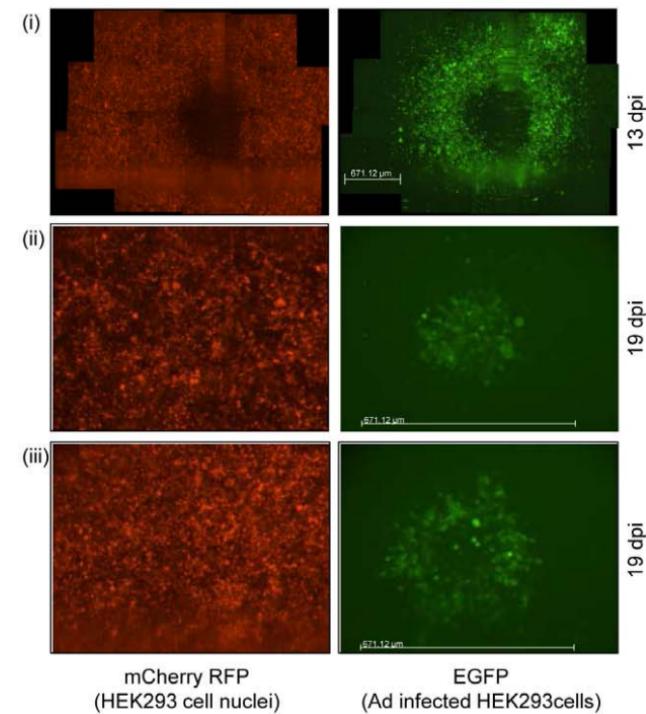
Oncolytic viruses can infect and destroy cancer cells, while preserving healthy tissues.

Thus, they could minimize side effects of cancer therapies.

PROBLEMS:

- insufficient diffusion of the virus in the cancer, due to stochastic events and physical obstacles (such as extracellular matrix);
- suboptimal features of viral infection (e.g., slow infection rate or fast killing rate);
- inhibition of infection due to hypoxia;
- clearance by the immune system.

We will focus on the first two problems.



D. Wodarz et al., *Complex spatial dynamics of oncolytic viruses in vitro: mathematical and experimental approaches*, 2012.

Which mathematical description is more suitable?

Discrete models

- ✓ track individual cells and allow to consider stochasticity
- ✗ limited in spatial and temporal scales, analytical results are harder

Continuum models

- ✓ track volume fractions, fast to solve numerically and often analytically tractable
- ✗ individual stochastic events cannot be described



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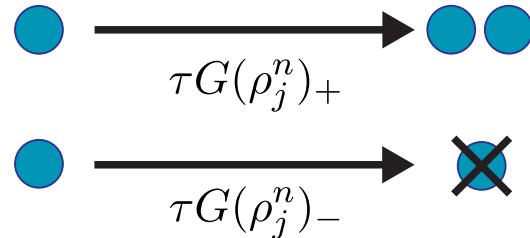


Derive a continuum model as the **appropriate limit** of an individual based model (large number of cells, small spatial and temporal discretizations). The comparison of the two models allows to:

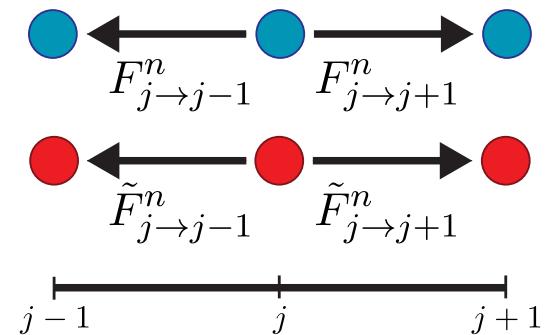
- understand more clearly **modelling assumptions** for the continuum model;
- gain some **theoretical intuition** on the behaviour of the individual-based model;
- understand the role of stochasticity;
- gain more robust **biological insight**.

Agent-based models

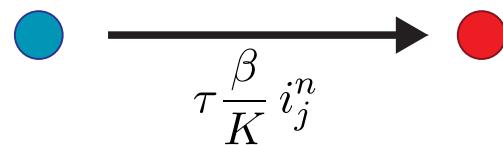
Proliferation of uninfected cells



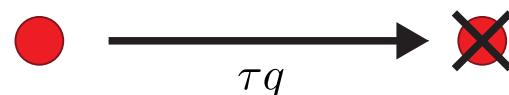
Cells' movement



Infection



Death of infected cells



Pressure: $\rho_j^n := u_j^n + i_j^n$

Growth probability: $G(\rho) = p \left(1 - \frac{\rho}{K}\right)$ (or also $G(\rho) = p$)

Cell's movement:
pressure independent

$$F_{j \rightarrow j \pm 1}^n := \frac{\theta_u}{2}$$

pressure dependent

$$F_{j \rightarrow j \pm 1}^n := \theta_u \frac{(\rho_j^n - \rho_{j \pm 1}^n)_+}{2K}$$

Formal derivation of continuum model (sketch)

At each time step t_n an uninfected cell at point x_j can **reproduce**

The “principle of mass balance” gives the equation

$$u_j^{n+1} = (1 + \tau p)u_j^n$$



Formal derivation of continuum model (sketch)

At each time step t_n an uninfected cell at point x_j can reproduce, move

The “principle of mass balance” gives the equation

$$u_j^{n+1} = \frac{\theta_1}{2}(1 + \tau p)u_{j-1}^n + \frac{\theta_1}{2}(1 + \tau p)u_{j+1}^n + (1 - \theta_1)(1 + \tau p)u_j^n$$



Formal derivation of continuum model (sketch)

At each time step t_n an uninfected cell at point x_j can reproduce, move and become infected.

The “principle of mass balance” gives the equation

$$u_j^{n+1} = \left[\frac{\theta_1}{2}(1 + \tau p)u_{j-1}^n + \frac{\theta_1}{2}(1 + \tau p)u_{j+1}^n + (1 - \theta_1)(1 + \tau p)u_j^n \right] (1 - \tau \beta i_j^n)$$



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$$u_j^{n+1} = (1 + \tau p) \left[u_j^n + \theta_1 \frac{u_{j-1}^n + u_{j+1}^n - 2u_j^n}{2} \right] (1 - \tau \beta i_j^n)$$



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which is equivalent to

$$\frac{u_j^{n+1} - u_j^n}{\tau} = \theta_1 \frac{u_{j-1}^n + u_{j+1}^n - 2u_j^n}{2\tau} + p u_j^n - \beta u_j^n i_j^n + \dots$$

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which is equivalent to

$$\frac{u_j^{n+1} - u_j^n}{\tau} = \theta_1 \frac{\delta^2}{2\tau} \frac{u_{j-1}^n + u_{j+1}^n - 2u_j^n}{\delta^2} + p u_j^n - \beta u_j^n i_j^n + \dots$$

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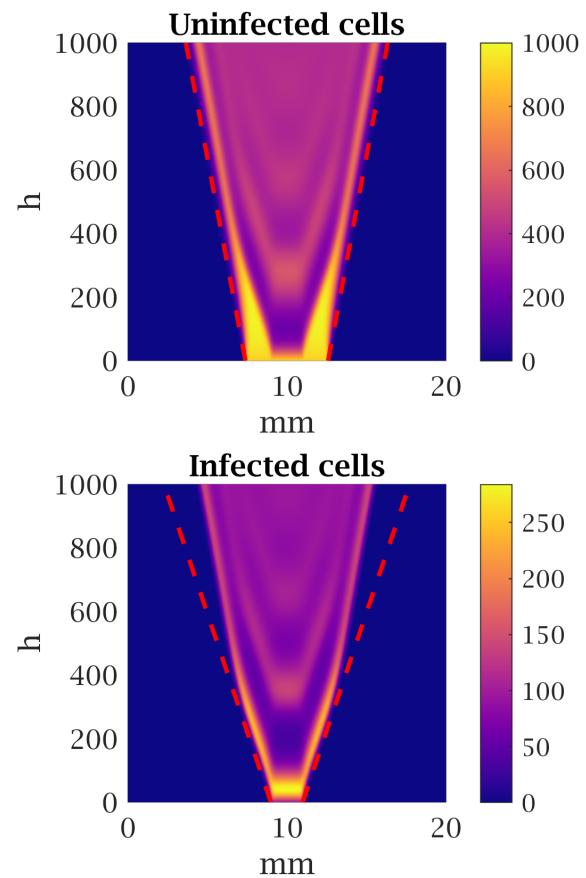
Letting $\tau, \delta \rightarrow 0$ in such a way that $\frac{\delta^2}{2\tau} \rightarrow D$ we obtain

$$\partial_t u(t, x) = \theta_1 D \partial_{xx}^2 u(t, x) + p u(t, x) - \beta u(t, x) i(t, x)$$

Continuum models with standard diffusion

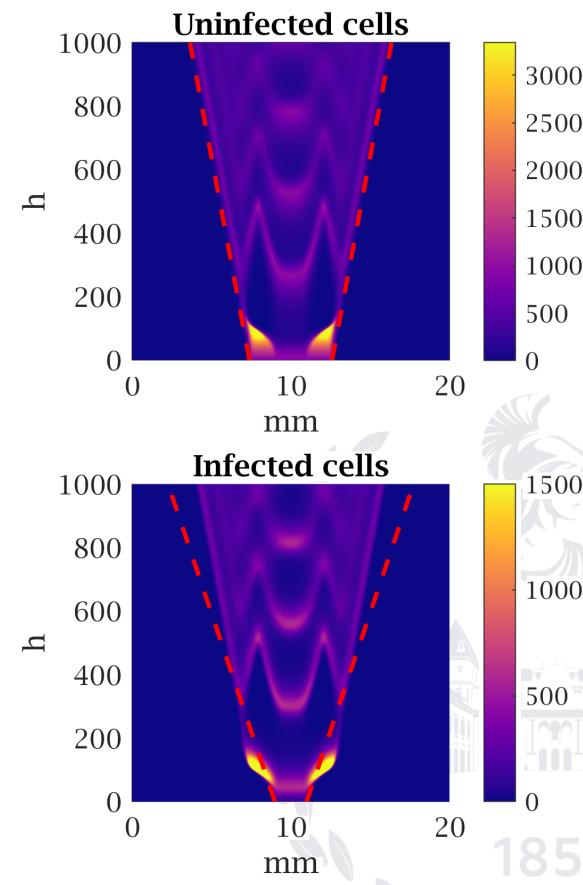
Logistic growth

$$\begin{cases} \partial_t u = D_u \partial_{xx}^2 u + pu \left(1 - \frac{u+i}{K}\right) - \beta ui \\ \partial_t i = D_i \partial_{xx}^2 i + \beta ui - qi \end{cases}$$

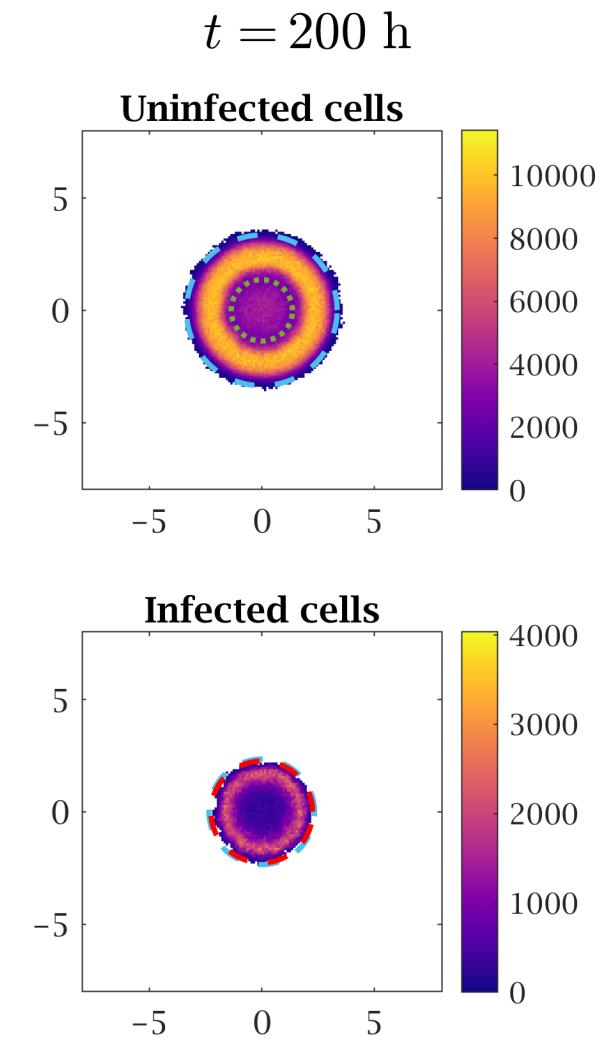
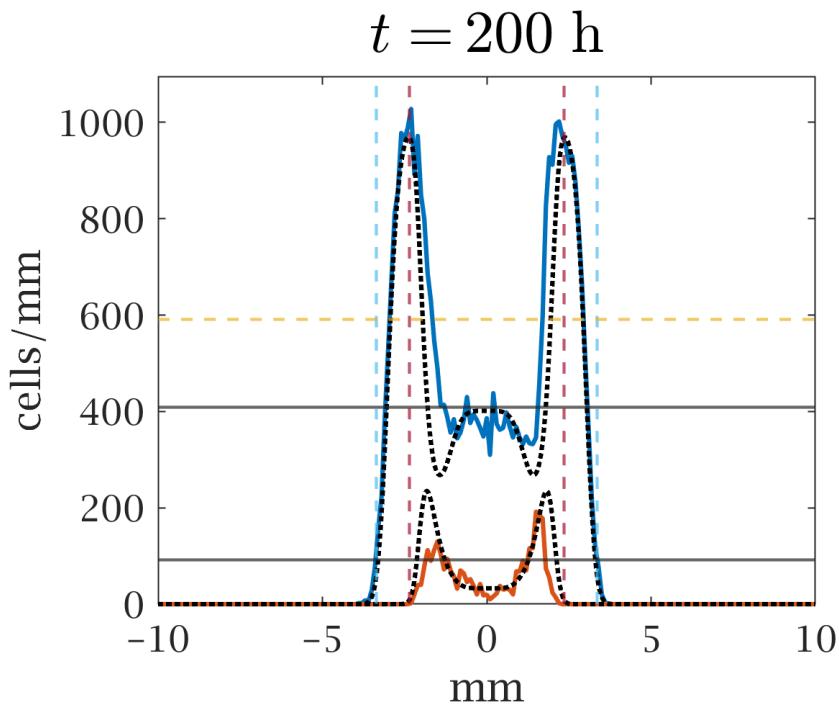


Exponential growth

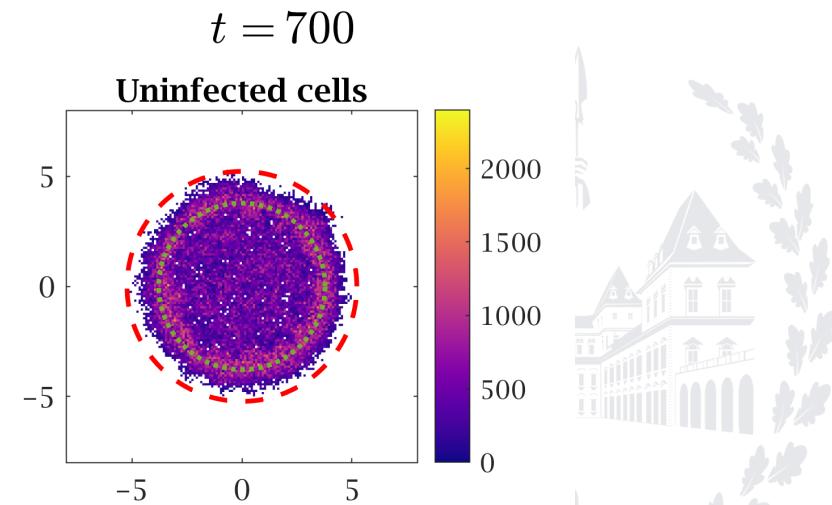
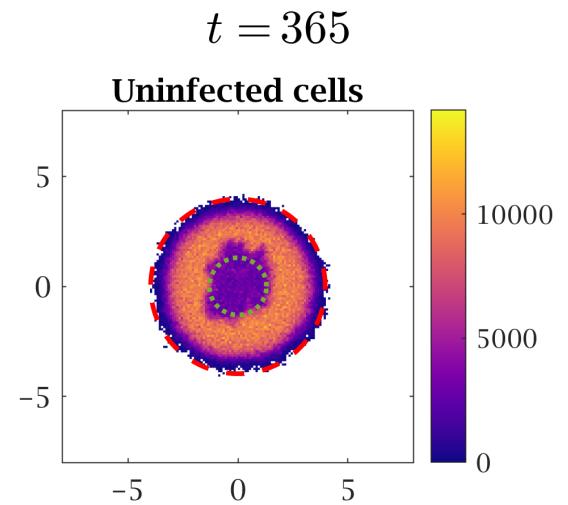
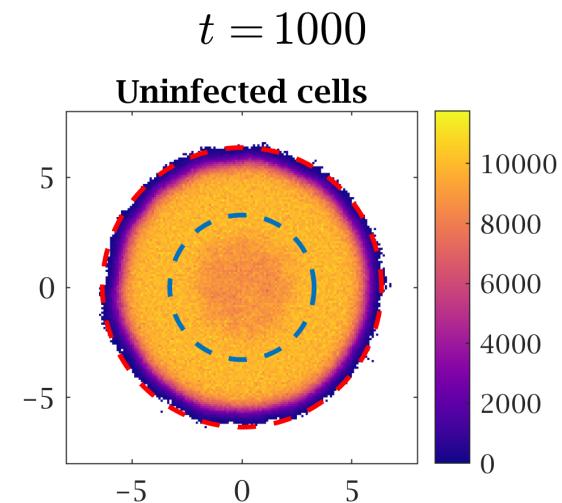
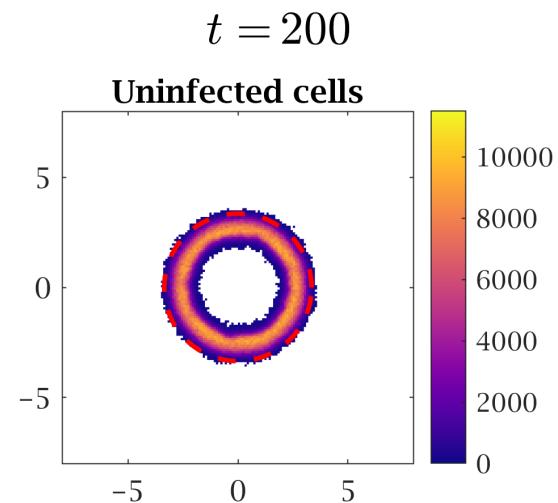
$$\begin{cases} \partial_t u = D_u \partial_{xx}^2 u + pu - \beta ui \\ \partial_t i = D_i \partial_{xx}^2 i + \beta ui - qi \end{cases}$$



Model with logistic growth and standard diffusion



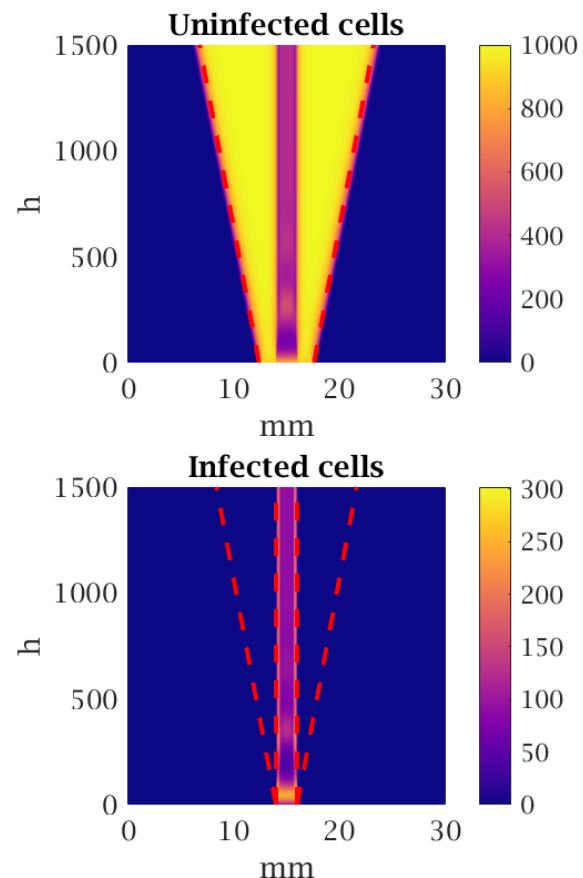
Other phenomena with logistic growth



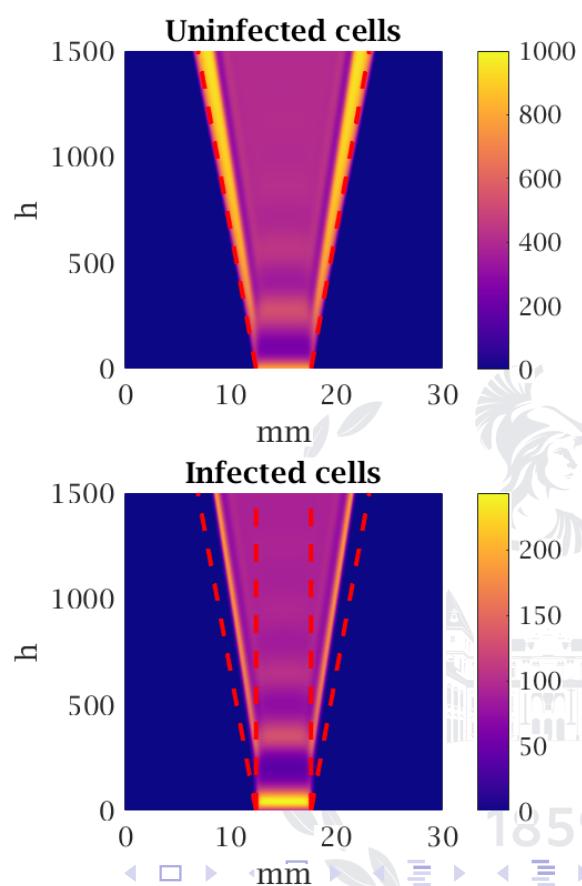
Continuum model with pressure-driven motion

$$\begin{cases} \partial_t u = D_u \partial_x(u \partial_x(u + i)) + pu \left(1 - \frac{u+i}{K}\right) - \beta ui \\ \partial_t i = D_i \partial_x(i \partial_x(u + i)) + \beta ui - qi \end{cases}$$

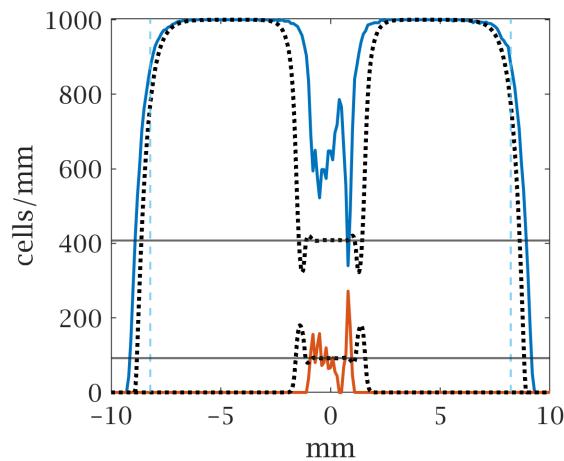
Initial infection localised



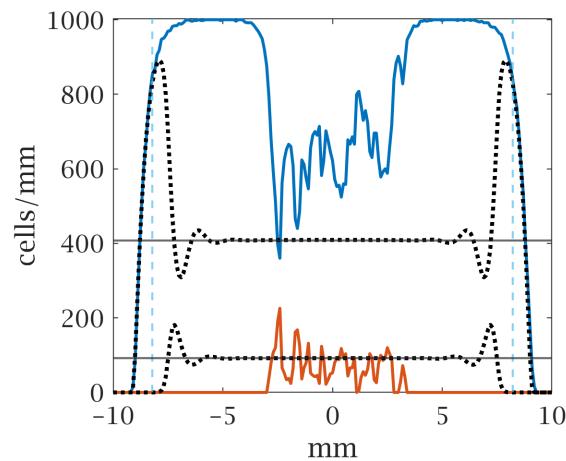
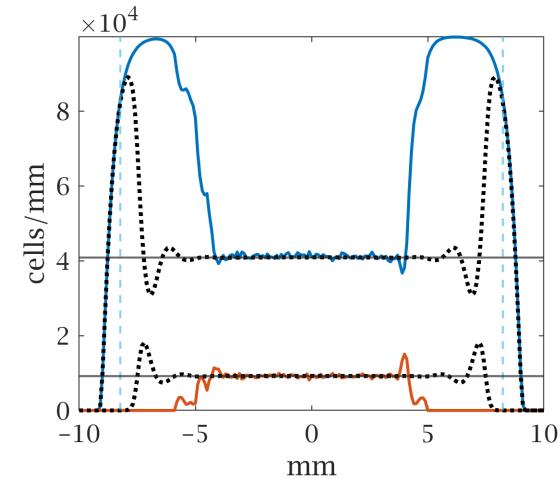
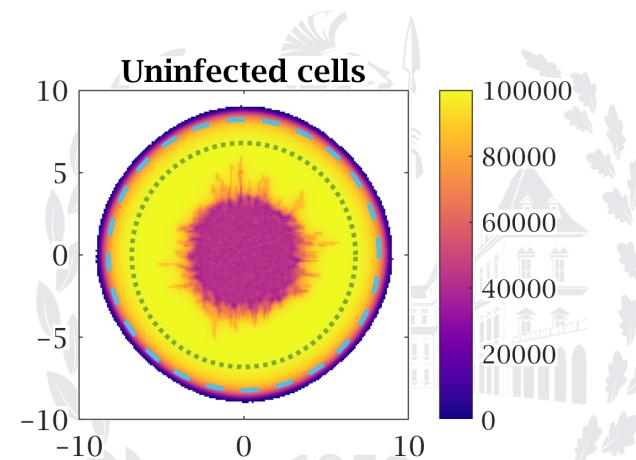
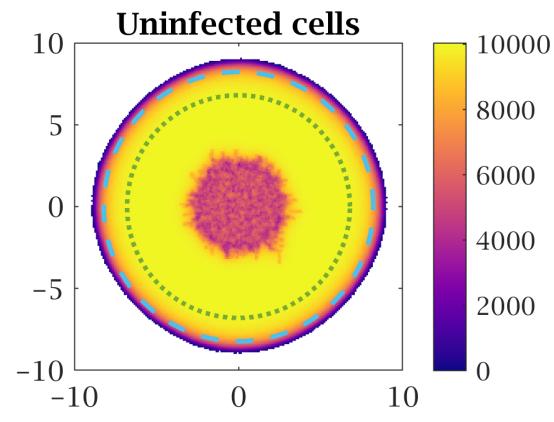
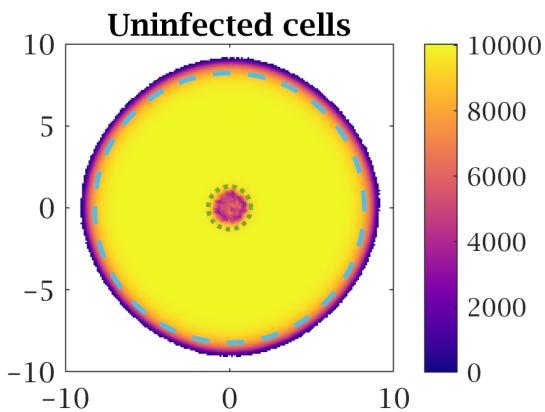
Initial infection spread



Ineffective infection

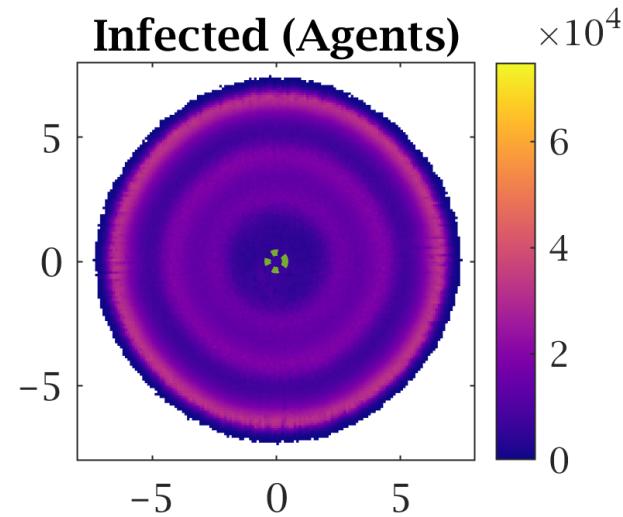
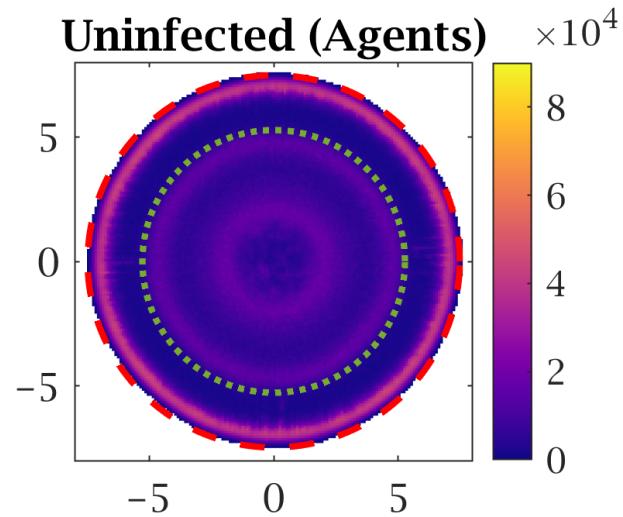
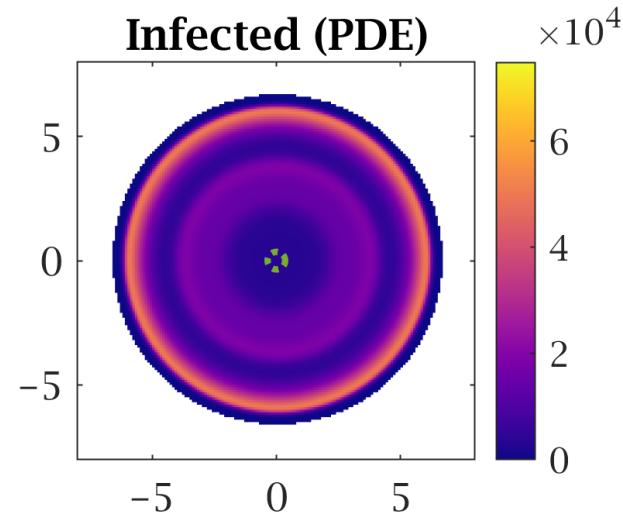
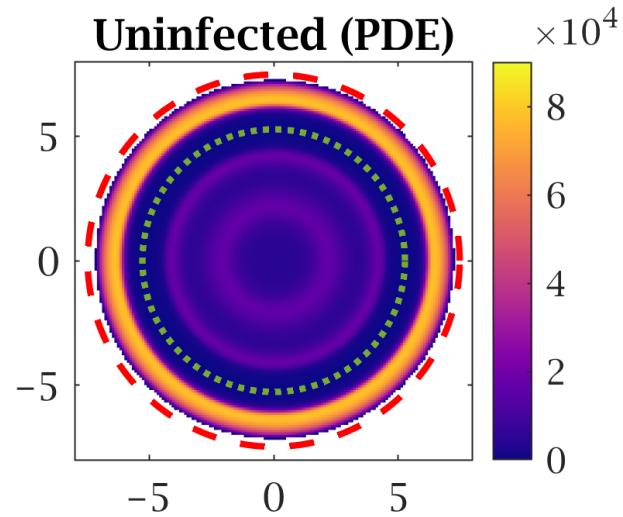


(a) reference

(b) $R_i = R_u$ (c) $R_i = R_u, K = 10^5$ cells/mm
(or cells/mm²)

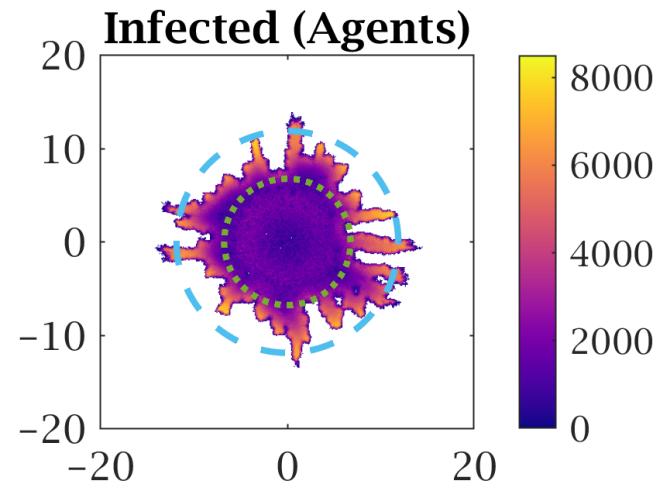
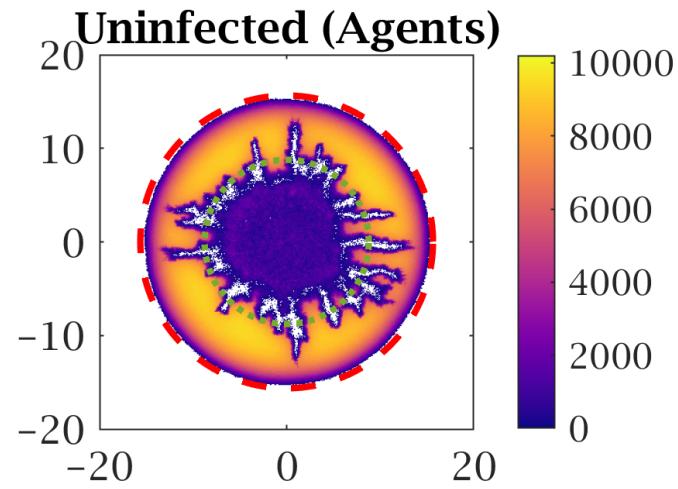
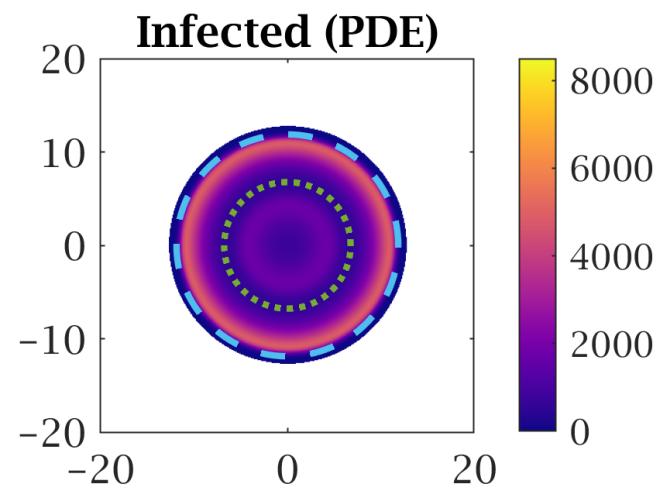
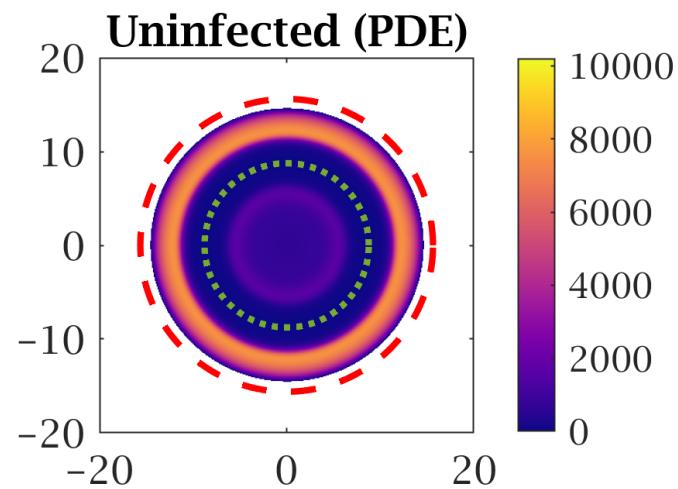
Successful infection

$t = 1300$



Partial failure

$t = 1100$



Conclusions and further perspectives

- Numerical simulations show **good agreement** between agent-based simulations with a sufficiently large cell number and the numerical and analytical results for the continuum model.
- Stochasticity may give rise to **asymmetric or disperse patterns** in the discrete model that cannot be described by the continuum model.
- The model is able to qualitatively reproduce ***in vitro* experiments**.

Further works could include:

- **explicit models of viral dynamics**, taking into account interactions with the extracellular matrix;
- interactions with the **immune system**;
- influence of **hypoxia**.



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Thank you for your attention!

