

MSc Computational Science  
joint programme UvA/VU



# MODELLING DIFFUSIVE SIGNALLING IN *ASPERGILLUS* SPP. GERMINATION INHIBITION



INTERMEDIATE PRESENTATION - APRIL

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April 4, 2025

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# OUTLINE

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## 1 Introduction

Effect of spore clusters on inhibitor decay

## 2 Clusters across model scales

Implicit vs. explicit solving

Comparison setup

Comparison results

## 3 Adjustment of the high-resolution model

Correction of the high-resolution model

## 4 Next steps

Putting together a universal model

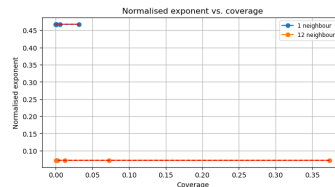
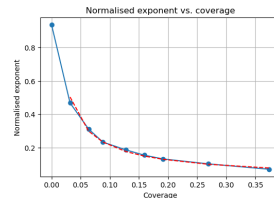
To do

# INTRODUCTION



## Effect of spore clusters on inhibitor decay

- » Previously the **high-resolution model** showed that
  - the **number of neighbours** influences the inhibitor decay from the spore wall,
  - the **distance between neighbours** did not influence the inhibitor decay from the spore wall.
- » The latter result was likely due to the **tight spatial constraint** (large high-resolution lattices are hard to compute).
- » Furthermore, the high-resolution model uses an **implicit solver**, while the low- and medium-resolution models use an **explicit solver**.
- » The cluster effect needs to be **verified across all model resolutions**.



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# CLUSTERS ACROSS MODEL SCALES



## Implicit vs. explicit solving

» The **implicit method** (backward Euler) [1] updates the lattice concentrations by solving a system of linear equations (matrix operations).

- **unconditionally stable**
- **first-order accurate** (the global error scales linearly with the simulation timestep  $\Delta t$ )
- **large time steps** are possible, leading to shorter simulation time
- **small time steps** may cause changes smaller than the computer accuracy, leading to simulations standing still

$$\frac{\partial c}{\partial t} = D \nabla^2 c \quad (1)$$

» The **explicit method** (forward Euler) [1] updates the lattice concentrations by "depositing" concentrations from a lattice node to its neighbours.

- only **stable for small enough simulation timesteps**
- **first-order accurate** (the global error scales linearly with  $\Delta t$ ).
- **large time steps** are not possible due to stability issues
- **small time steps** may cause standstill of simulations

# CLUSTERS ACROSS MODEL SCALES



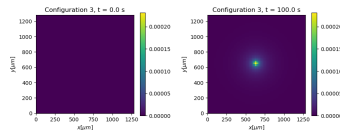
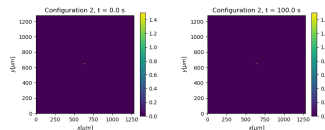
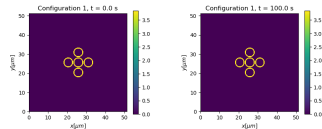
## Comparison setup

» Clusters of 2, 3, 6 and 7 spores are simulated with

- spore-to-spore distance  $2R < d < 5R$  in **high-resolution** simulations;
- spore-to-spore distance  $4R < d < 40R$  in **medium-resolution** simulations;
- spore-to-spore distance  $8R < d < 40R$  in **low-resolution** simulations;

» Measuring the exponent  $\alpha$  in the inhibitor decay relationship

$$c_{\text{in}}(t) = c_0 e^{-\alpha \frac{t}{\tau}}, \quad (2)$$

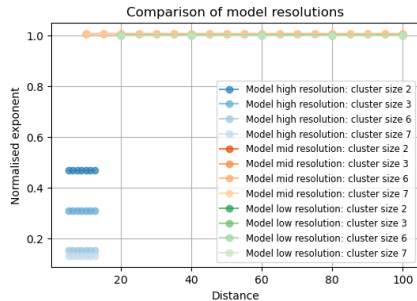


# CLUSTERS ACROSS MODEL SCALES



## Comparison results

- » The blocking effect of neighbours is not detectable beyond  $d > 4R$  using the **explicit method** (medium and low resolution).
- » In contrast, the blocking effect is persistent over the range  $2R < d < 5R$  using the **implicit method** (high resolution).
- » Despite being stable at large timesteps, the **error** of the implicit error might be high and the **narrow boundary** of the high-resolution lattice may bias the results.



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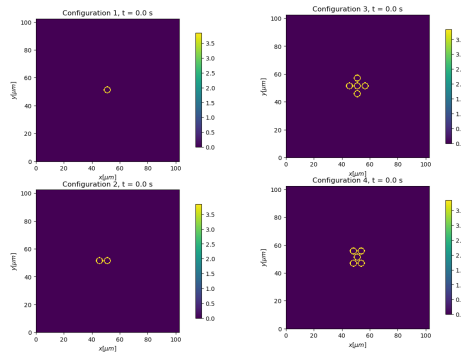


# ADJUSTMENT OF THE HIGH-RESOLUTION MODEL



## Overview of adjustment

- » Examining the potential errors in the high-resolution model, a step is made to bridge its gap toward the medium-resolution model.
- » The spatial subdivision is changed from  $\Delta x = 0.2 \mu\text{m}$  to  $\Delta x = 0.4 \mu\text{m}$ .
- » Clusters of size 1, 2, 7 and 13 are simulated using both an **implicit** method and an **explicit** method with varying spore-to-spore distance.
- » Pending results: the goal is to confirm whether the **neighbour-blocking effect persists at longer ranges**.



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# NEXT STEPS



## Putting together a universal model

- » If a spore is surrounded by adjacent neighbours, the effective cell wall area for inhibitor permeation is reduced by a factor  $\alpha$ .
- » The characteristic time for inhibitor permeation is

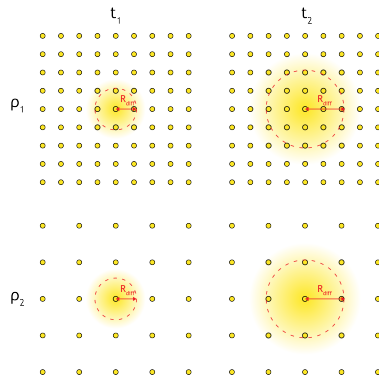
$$\tau = \frac{P_s A_{\text{eff}}}{V} = \frac{P_s A_{\text{spore}}}{V \alpha}. \quad (3)$$

- » The inhibitor concentration in the spore is

$$c_{\text{in}}(t) = (c_0 + c_{\text{out}}) e^{-\frac{t}{\tau}}, \quad (4)$$

where, at a moderate spore density  $\rho_s$ ,

$$c_{\text{out}} = \rho_s \frac{AP_s c_0}{4\pi D^{3/2}} \int_0^{R_{\text{diff}}} dr r^2 \int_0^t t'^{-3/2} e^{\left(\tau t' - \frac{r^2}{4Dt'}\right)} dt'. \quad (5)$$



# NEXT STEPS



To do

1. Verify the dependence of the decay exponent  $\alpha$  on the number of spore neighbours.
2. Identify whether  $\alpha$  only applies for close or adjacent neighbours.
  - If it does, the neighbour-blocking of cell wall permeation can be **decoupled** as a phenomenon from the effect of the general inoculum density  $\rho_s$ .
  - If it doesn't, then the two phenomena could potentially be **reduced** to a single relationship.
3. Refine the formula for  $c_{\text{out}}$  so it becomes valid for higher spore densities.
4. Fit combinations of  $\rho_s$ ,  $P_s$  and  $\langle N_{\text{neighbours}} \rangle$  to empirical data.
5. Interpret what the fitted  $P_s$  means in terms of molecular properties.

# BIBLIOGRAPHY I



- [1] Michael T. Heath and Eric M. Munson. “Scientific Computing: An Introductory Survey”. In: 1996. URL: <https://api.semanticscholar.org/CorpusID:267834859>.