

# A Diffusion-Based Model of Spatial Interactions in *Aspergillus* spp. Germination

Thesis Proposal MSc Computational Science

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## Abstract

The germination of conidia in filamentous fungi, in particular in the well-studied genus *Aspergillus*, is driven by complex signaling pathways in response to environmental stimuli. The density of spores thereby has a measurable effect on the percentual success of germination. The proposed project aims to explain the underlying spatial interactions of this phenomenon in terms of diffusive chemical signals between spatially distributed spores. The resulting model can therefore be used to provide insight about hypotheses that are difficult to verify experimentally, and to enable predictions in industrial, medical or microecological applications.

## 1 Research Context

Research on *Aspergillus* species has revealed that the density and composition of conidial inoculum has a distinct effect on germination time and incidence[6], with consequences extending to the characteristics of the vegetative mycelium[4, 9]. Spatial interactions during germination include carbon sensing in inducing media[6], resource competition among conidia[10], spore agglomeration[5] and quorum-sensing via chemical self-inhibitors or physical signals[7]. While existing models have focused on statistical observations of germination[3] and the mechanics of conidial swelling and germ tube formation[1], the factors leading to the activation of dormant spores have not been studied extensively as an interplay of spatially distributed concentrations.

## 2 Research Methods

The proposed project aims to represent and explain the interaction of such factors through a spatial model, expanded and revised in multiple iterations. The first set of numerical experiments will deal with the dispersal of self-inhibiting signals as a most likely culprit in initiating germination. This aims to test the hypothesis that the gradual decrease of an inhibitor concentration inside and

outside of the conidial wall has an effect on germination on a single spore or a group of spores within a time-frame comparable to empirical observations.

This question can be approached through a numerical solution of the time-based diffusion equation on a discrete lattice, given an initial non-regenerative quantity of the inhibitor inside a spore volume, which encompasses a single lattice node or multiple lattice nodes. Taking a sensible assumption for the diffusion coefficient, the time steps needed until reaching a predefined threshold for germination can be measured and compared to experimental data. The initial conditions for such simulations would start with a single spore, then extend to a regular (e.g. checkerboard) arrangement of spores and, finally, incorporate probabilistic spatial distributions of spores to account for realistic crowding conditions. An additional setup can illustrate the effect of an externally introduced inhibitor - a situation which can be easily reproduced through a physical experiment.

The basic numerical experiments are to be validated by parallel physical experiments using oCelloscope microscopic imagery analysis at the laboratory of Utrecht University, coordinated by Han Wösten. The results of more complex numerical experiments can either be compared with existing germination data on *Aspergillus niger*[8] or by conducting targeted physical experiments at the laboratory.

If this experimental stage does not outline a sufficiently clear or realistic picture of the role of the inhibitor concentration, additional components and assumptions can be incorporated in the model (e.g. heterogeneous spore sizes, adhesion of spores into agglomerates, diffusion of additional compounds, etc.) to address different hypotheses related to germination.

### 3 Significance of Research

Fungi of the genus *Aspergillus* are extensively used in fermentation for the food industry and in the industrial production of citric acid, enzymes and other biological molecules[2]. Concurrently, they are food spoilers and producers of harmful mycotoxins. Understanding the onset of their vegetative activity therefore enables more advanced control over their useful and pathogenic effects.

### 4 Tentative Timeline

A tentative overview of some key milestones includes:

1. Week 44, 2024 - Submission of Thesis Proposal;
2. Week 49, 2024 - Completed literature review (biological principles and existing models);
3. Week 3, 2025 - Minimal model completion and access to validation data;

4. Week 9, 2025 - Validation, verification and potential correction of the model;
5. Week 13, 2025 - Analysis of model results;
6. Week 17, 2025 - Model extensions;
7. Week 22, 2025 - Documentation (writing of Thesis).

## References

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