A Diffusion-Based Model of Spatial Interactions in *Aspergillus* Species From Germination to Outgrowth

Thesis Proposal MSc Computational Science

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Abstract

The development of filamentous fungi from spores to mycelial colonies is driven by complex biochemical pathways through multiple stages of structural transformation. During these stages, the concentrations of spores and hyphae are both cause and effect of the diffusive transport within the organism and in the surrounding medium. The current proposal aims to incorporate such interactions in a spatial lattice-based model, tracing mycelial morphologies back to the incoculation state and enabling valuable predictions in industrial, medical or microecological applications.

1 Research Context

Research on *Aspergillus* spp. has revealed variable responses to the density and consistency of the conidial inoculum - expressed both in the distribution of germination times[7] and in the morphology of the resulting mycelia[13]. Spatial interactions during these life-cycle phases include carbon sensing in inducing media[7], competitive self-inhibition among conidia[16], spore agglomeration[6], apical growth through targeted deposition of proteins to the cell wall[15, 1], hyphal branching[3, 10] and concentration gradients through hyphal formations of different density[14, 13]. Diffusion - both intra- and extracellular - links all these phenomena and invites a unifying modelling approach that explains observed statistical measurements through simulated spatial interactions.

2 Research Methods

The proposed framework aims to represent spatial and morphological phenomena spanning temporally from inoculation to outgrowth and spatially from microscopic scale (single conidia and agglomerates thereof) to mesoscopic scale (free fillaments and hyphal pellets). The well-studied model species *Aspergillus*

niger will be taken as a starting point, beyond which the applicability of the model to other species can potentially be explored.

A minimal outcome of the research would be to investigate hyphal growth patterns under different germination parameters (aligned with the data obtained by Ijadpanahsaravi et al.[8, 7, 9]). In this case, known distributions of germination time and incidence can be used to control the simulated time lag[5] of individual spores prior to their hyphal extension. As spore agglomeration is a key component in coagulative mycelium growth in *A. niger*[11], the mechanics of conidial clumping should be investigated and represented appropriately in the model.

The focus on intra- and extracellular diffusion as driving morphogenetic principles suggests the implementation of a lattice-based PDE solver of the diffusion equation with respect to substance concentrations of interest (e.g. carbon, dissolved oxygen or vesicles). The growth and motion of fungal cells can be implemented through either neighbourhood-based Monte Carlo perturbations[1] or through vector-based operations on points in space[3], resulting in line segment networks superimposed over the lattice.

The resulting morphologies can be analysed with respect to volume and branching distribution and thus compared to data from synchrotron tomography of fungal pellets[12] or from other sources, based on microscopic imaging.

As a potential extension of the model, the spatial implications on the germination itself can be closely reviewed. Factors such as carbon source type and density of the inoculum[7] have a quantifiable effect on germination, so they could be used as primary parameters informing the germination time and incidence, instead of taking the latter as a given input. This would not only relate germination factors to the same spatial framework used in hyphal modelling, but could also yield more informative explanations of the established statistical models related to germination[4].

Finally, the model can be extended to account for characteristics of other fungal species and even to mixtures of fungal cultures[9], exploring further levels of complexity.

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 their life-cycle and predicting the extents of their developmental stages therefore enables more advanced control over their effects.

4 Tentative Timeline

A tentative overview of some key milestones includes:

1. Week 43, 2024 - Submission of Thesis Proposal;
2. Week 49, 2024 - Completed literature review (biological principles and existing models);
3. Week 3, 2024 - Minimal model completion and data access setup;
4. Week 9, 2024 - Validation, verification and potential correction of the model;
5. Week 13, 2024 - Analysis of model results;
6. Week 17, 2024 - Model extensions;
7. Week 22, 2024 - Documentation (writing of Thesis).

References

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