

AGH University of Science and Technology



Fungi growth simulation

PAWEŁ PYCIA, PRZEMYSŁAW ROMAN, MATEUSZ WRONKA

Contents

1	Literature overview	2
1.1	Sources	2
1.2	Key points	2
2	Work schedule	4
3	Model construction	5
3.1	Basic model	5
3.2	Possible extensions	6
3.3	Final model description	6
3.4	Technical details	8
4	Results	10
4.1	Great branching factor	10
4.2	Abnormal nutrition spots	12
4.3	Big lattice	14

1 Literature overview

1.1 Sources

1. "A Hybrid Mathematical Model of Fungal Mycelia: Tropisms, Polarised Growth and Application to Colony Competition." - Steven Hopkins
2. "The dynamics of hyphal growth" - Graham W. Gooday
3. "Bioreactor model of the mushroom growth — Production process and its computer aided simulation" - Zs.Viczián, E.László, Zs.Füstös
4. "A Model for Hyphal Growth and Branching" - J. I. Prosser, A. P. J. Trinci
5. "Modelling mycelial networks in structured environments" - Graeme P. Boswell

1.2 Key points

- Cells should be hexagons with triangles as subcells.
- First model is going to be a single hypha on a random walk. Then it is going to be extended to represent a full mycelium with the option of anastomosis and branching.
- Continuous models generally aim to simplify the extremely complex structure of a mycelial network into a biomass density profile.

$$\frac{\partial \rho}{\partial t} = \eta v - d$$

$$\frac{\partial \eta}{\partial t} = \frac{\partial \eta v}{\partial x} + \sigma$$

$\rho(x, t)$ - change in biomass

$\eta(x, t)$ - density of tips in growing mycelium

v - constant tip velocity

d - hyphal death rate

σ - free parameter reflecting different combinations and types of branching and anastomosis

The equations describe a tip and trail system.

- When a new branch is created it forms an angle between itself and its parent which is normally distributed with a mean 56° and standard deviation a 17° .
- Fungi retrieve their required growth substances, such as carbon, nitrogen, phosphorus and other trace metals and elements, from the local environment through the process of uptake by secreting enzymes that reduce external matter to components that can be internalised. Once internalised these nutrients and wall synthesis materials are moved (translocated) to the apex of each hypha to fuel extension.
- Mycelial networks can continue to develop across hostile environments due to the translocative process. Translocation is the process through which internally located nutrients and growth materials are transported through the hyphal tubes to the hyphal tips. A nutrient-rich area can be excavated far beyond local needs and the excess nutrients transported to areas where there is a nutrient deficiency. Although translocation is usually modelled with a focus on the diffusive component, there is strong evidence to suggest that an active component can direct nutrients to specific regions.

2 Work schedule

1. Literature overview and work schedule plan	27.04.2022
2. Model construction	04.05.2022
3. Basic simulation	11.05.2022
4. More advanced simulation	18.05.2022
5. Additional features	25.05.2022
6. Documentation	01.06.2022

3 Model construction

3.1 Basic model

This model is lattice-free. We begin with an origin point P_0 and n children to spread out on a circle with radius r around P_0 . After this initialization the following steps are taken for each tip in a repeating manner:

1. pick a random direction based around the growth axis
2. growth axis changes with probability p_{cga}
3. there is a chance p_{db} for a branch to develop, based on the total hypha length and the number of hypha tips (2)
 - (a) branch starts growing from the tip
 - (b) the newly created branch forms an angle between itself and its parent that is sampled from $\mathcal{N}(56^\circ, 17^\circ{}^2)$
4. extend from the current tip by a length $\Delta l \sim \mathcal{N}(E, \sigma^2)$ (1)
 - (a) if there's nutrition in the destination there's a chance p_g to repeat previous points in this iteration
 - (b) if there's a branch on a way stop at the intersection and forward the remaining growth length to the nearest tip

Hypha growth speed is based on the relation:

$$E = \mu * G \tag{1}$$

where:

E = the average hypha growth speed

μ = max growth speed specific for the fungus

Growth speed increases until it reaches a near constant value.

$$G = \frac{L_t}{N_t} \tag{2}$$

where:

L_t = total mycelium length

N_t = number of hypha tips

New branches appear to keep G close to 1.

3.2 Possible extensions

- The direction growth of hyphal is based on resources flow in the fungi. When a specified critical level of resources in a tip is achieved hyphal extends from that point.
- Take into account speed of resources spread and uptake.
- Introduction of the face-centered cubic lattice.
- Distinguish 3 types of fungus structures: active hyphal, passive hyphal and tip.

3.3 Final model description

The model presented below is of type most commonly-know as cellular automata (CA) but modelled with continuous variables making it of discrete-continuum type. Time was divided into the series of discrete steps. The environment was modelled using body-centered cubic (BCC) lattice. Except at the boundaries, each cell has 14 neighbours; 4 from its own layer; 5 from layer above and 5 from layer directly below. 3D cell models were used to denote location of hyphae with different colors representing each of possible hyphal types (i.e. red - hyphal tips; green - active hyphae). It was assumed that external substance was equally accessible to all the hyphae and hyphal tips that were neighbours of that element.

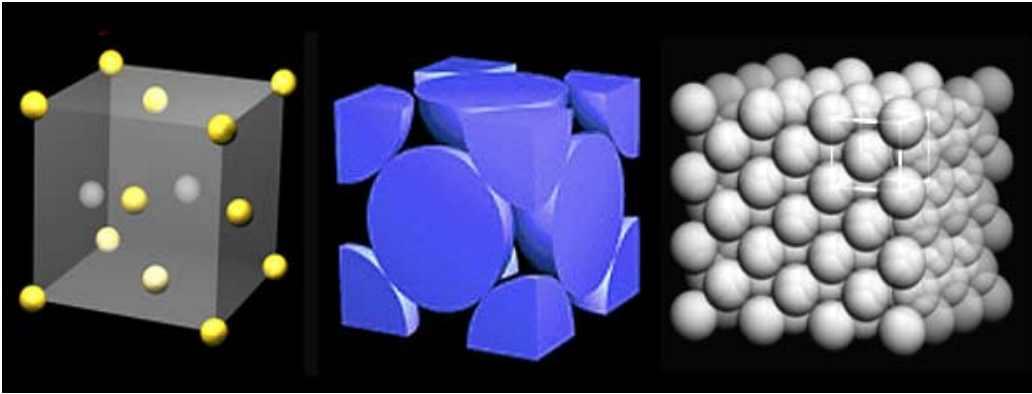


Figure 1: Body centered cubic lattice.

Transition rules for our model:

Δx defines the distance between the centers of adjacent elements in the BCC lattice and represents the maximum distance moved by hyphal tip during a time of Δt . The value for Δx is stated below and the value of Δt varies depending on the size of modelled environment.

The probability of tip movement during Δt :

$$P(\text{same direction}) = v s_i \frac{\Delta t}{\Delta x} + D_p s_i \frac{\Delta t}{\Delta x^2}$$

$$P(\text{acute angle}) = D_p s_i \frac{\Delta t}{\Delta x^2}$$

$$P(\text{do not move}) = 1 - P(\text{same direction}) - P(\text{acute angle})$$

where

D_p = non-negative parameter describing the strength of the diffusive movement
 v = non-negative parameter describing the strength of the advective movement

Consequently, when hyphal tip moved, the internal substance in the corresponding element was reduced by an amount $c_2 \Delta x$.

In our model we assumed that fungi exhibit lateral branching, whereby hyphal tips emerge from active hyphae walls and branching was related to internal substance concentrations and the probability of hyphae branching during time interval Δt was

$$P(\text{branching}) = b s_i \Delta t$$

where:

b = non-negative constant describing branching rate

The direction of branching was uniformly distributed from all the possible directions.

The amount of internal substance moving from cell k to cell m over time Δt was:

$$\Delta_{passive} = \begin{cases} D_i \Delta t \frac{s_i(k) - s_i(m)}{\Delta x^2}, & \text{if } k \text{ and } m \text{ were hyphae} \\ 0, & \text{otherwise} \end{cases}$$

D_i = non-negative coefficient of diffusion

Each active hyphae and hyphal tip acquires nutrients from all its neighbours. The uptake process was modelled as depending on the amount of internal substance s_i and external substance s_e :

$$\Delta_{uptake} = c s_i s_e \Delta t$$

where:

c = non-negative parameter c

Since the acquisition of substance is not perfect and some of the nutrients are lost the external substance level was reduced by $c_3 s_i s_e \Delta t$ and internal substance was increased by an amount $c_1 s_i s_e \Delta t$ where $c_1 < c_3$

External substance was uniformly distributed across the whole environment. Few tests with asymmetric distribution were also run.

3.4 Technical details

The CA was written using C# programming language and Unity game engine.

The results presented below were obtained on a machine with given specification:

- Model: HP DL380 Gen8
- CPU: 2 x Intel Xeon CPU E5-2680 v2
- RAM: 256GB DDR3 ECC
- OS: Windows Server 2019 Datacenter
- Storage: 6 x 1TB Samsung 970 Evo Plus, ZFS RAIDZ2

Parameter	Physical description	Value
Δx	Minimal distance	$2 * 10^{-5}$ cm
s_{i0}	Initial internal substance	10^{-6} mol
s_{e0}	Initial external substance	10^{-6} mol
v	Directed tip velocity	10^{-2} cm day $^{-1}$ mol $^{-1}$
D_p	Diffusive tip velocity	10^{-3} cm day $^{-1}$ mol $^{-1}$
b	Branching rate	0.3456 cm 2 day $^{-1}$
c_1	Net uptake rate	$9 * 10^7$ mol day $^{-1}$
c_2	Cost of growth	10^{-7} mol cm $^{-1}$
c_3	Gross uptake rate	10^8 mol day $^{-1}$
c_4	Translocation cost	10^{-11} mol cm $^{-1}$ day $^{-1}$
c_5	Maintenance cost d	10^{-11} mol cm $^{-1}$ day $^{-1}$

Table 1: Calibrated parameter values

4 Results

4.1 Great branching factor

In this test we wanted to see how the branching factor affects the results of the simulation.

The following changes were made:

$$b = 10^6 \text{ cm}^2 \text{ day}^{-1}$$

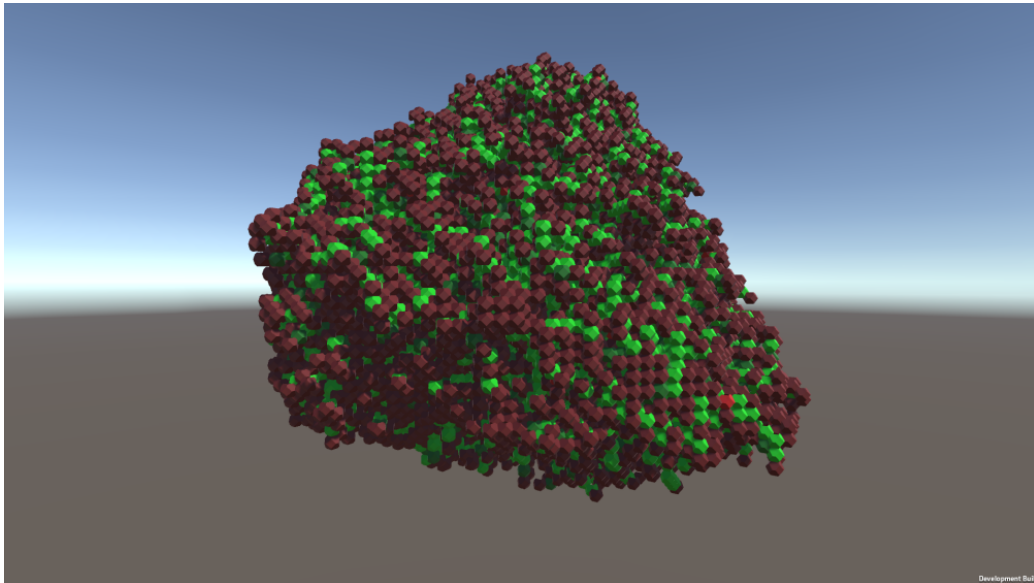


Figure 2: Simulation

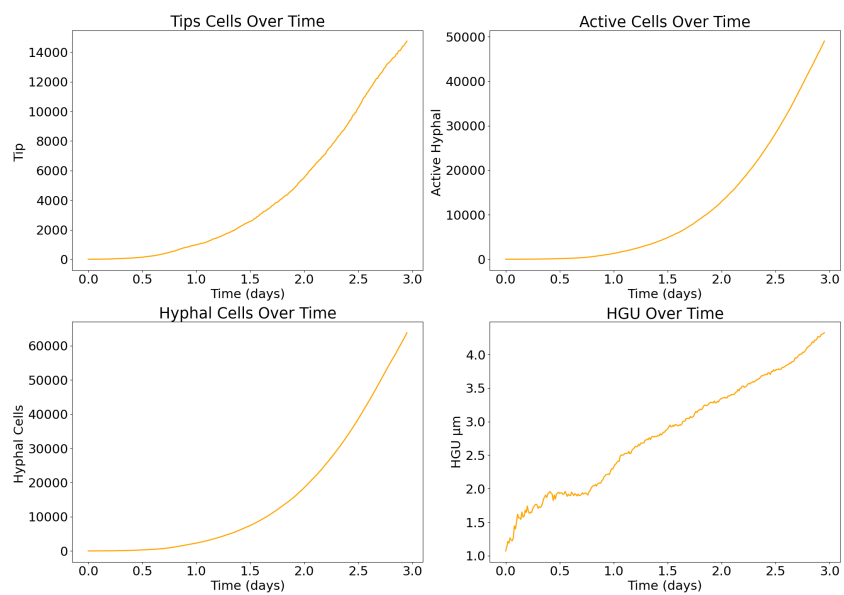


Figure 3

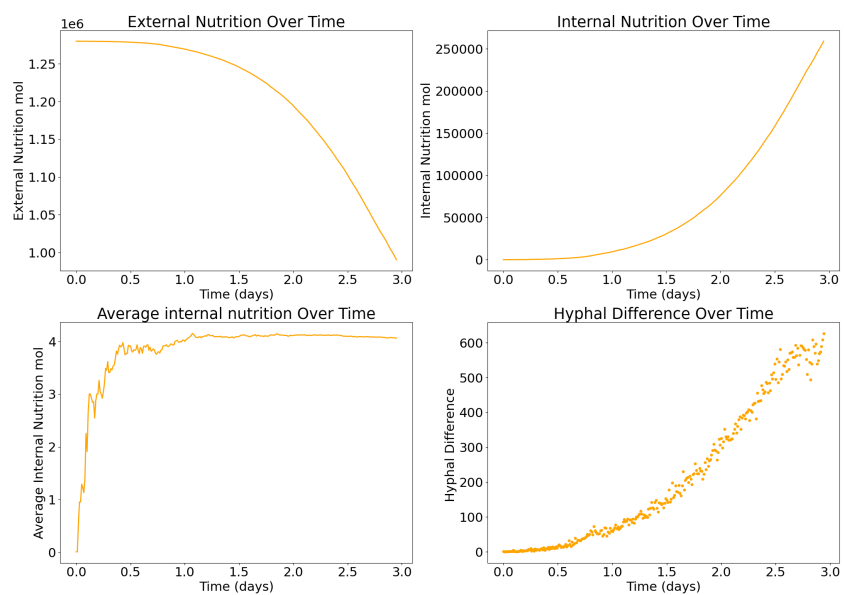


Figure 4

4.2 Abnormal nutrition spots

In this test we wanted to see how the fungi would behave in an environment with a non-uniform nutrition distribution.

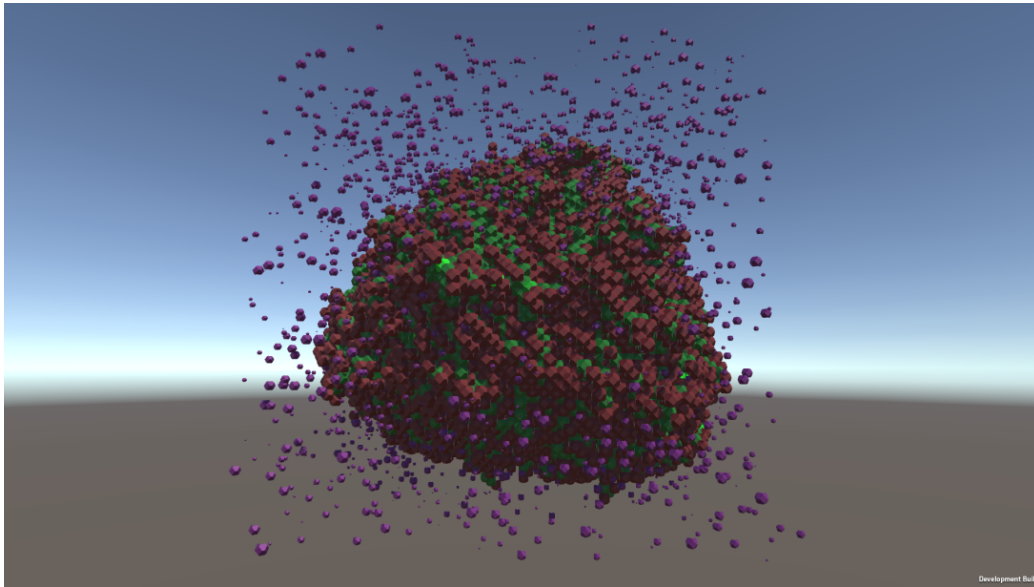


Figure 5: Simulation

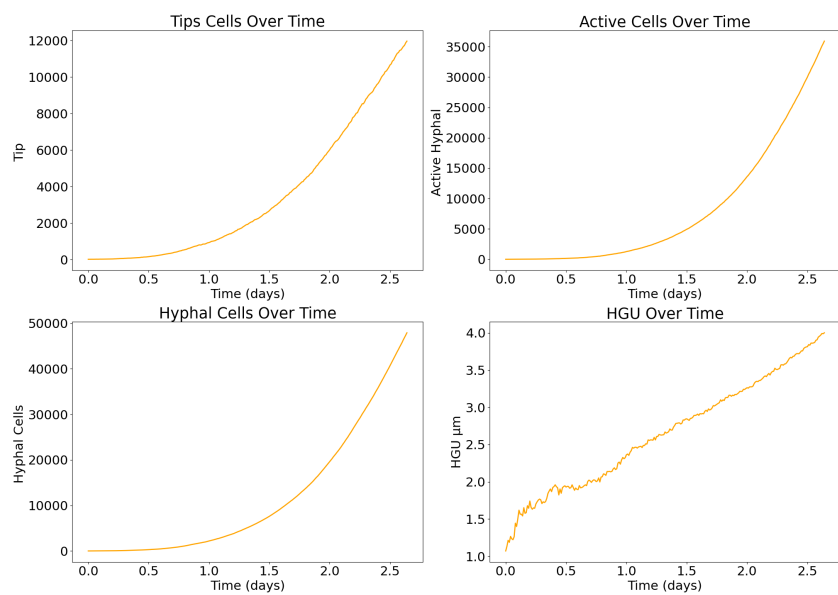


Figure 6

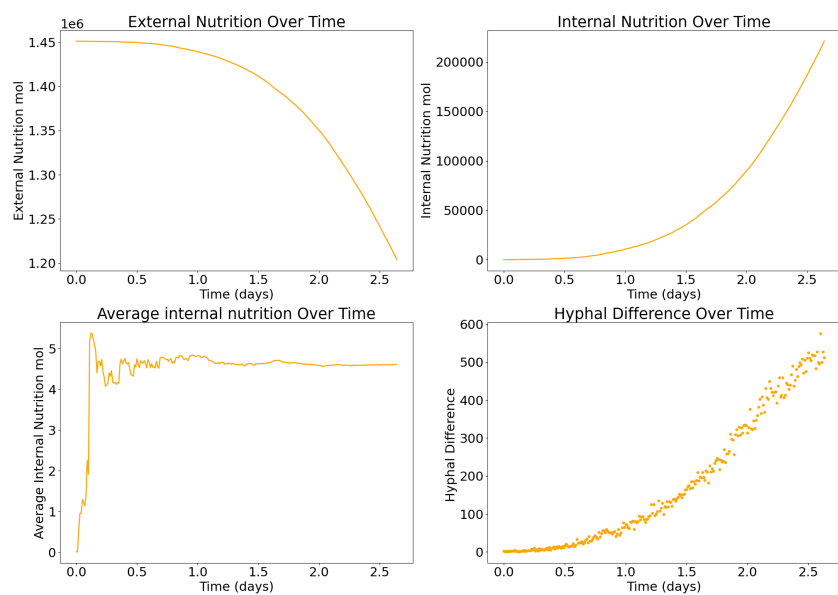


Figure 7

4.3 Big lattice

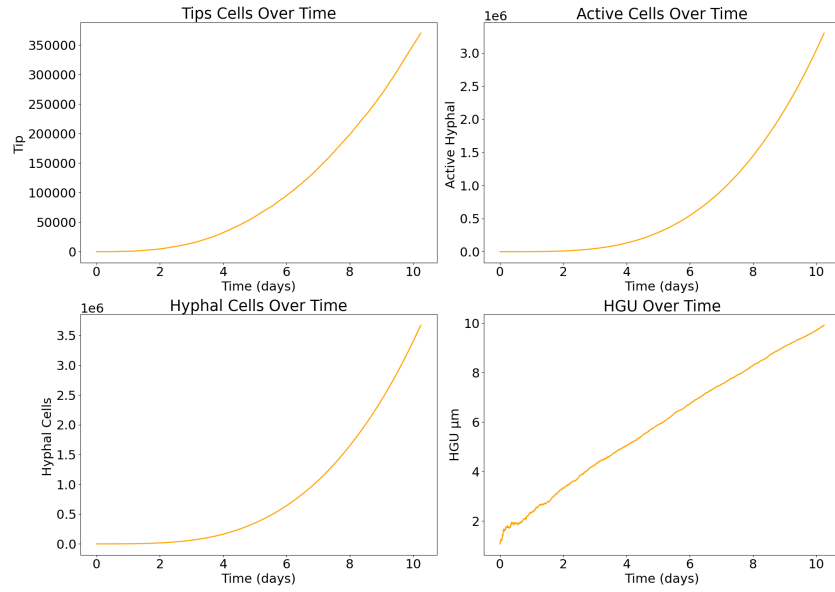


Figure 8

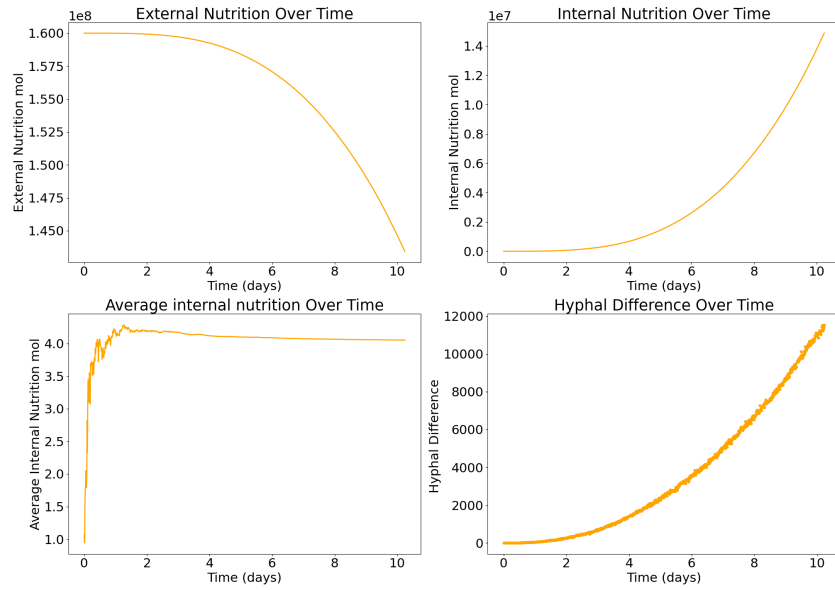


Figure 9