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Summary Sheet

In this article, we construct a model of a wood being corrupted by one or more fungus in different types of environments. We set up a logistic growth, competition, and mutation model as a start point for models in the next sections. We modify the model with stochastic parameters representing temperature and moisture levels. Then we use evolution simulation to model the progress of the long-term wood-decay process. At last, we illustrate how different climates can change the behavior of different fungus, and how the bio-diversity of fungus can change the decay process and their significance in the research.

Key Words: Fungus; Decomposition; Hyphal Extension Rate; Moisture Tolarence; Temperature Tolarence; Logistic Growth, Stochastic Differential Equations, Genetic Evolution

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1 Abstract

In this article, we construct a model of a wood being corrupted by one or more fungus in different types of environments. We set up a logistic growth, competition, and mutation model as a start point for models in the next sections. We also modify the model in section 1 with stochastic parameters representing temperature and moisture levels. In addition, we use evolution simulation to model the progress of the long-term wood-decay process. At last, we illustrate how different climates can change the behavior of different fungus, and how the bio-diversity of fungus can change the decay process and their significance in the research.

Keywords: Logistic Growth, Ordinary Differential Equations, Stochastic Differential Equations, Genetic Evolution

2 Introduction

2.1 Background

The fungus is one of the most vital decomposition agents in the carbon cycle. They consume any dissolved molecules by inserting different enzymes into their host and gather the nutrition they need to grow. One of the most common hosts of fungus is wood and usually fallen dead wood and the fungus that decomposing woods are called a wood-decay fungus.

The wood-decay fungus can be a severe disaster in the wood industry, as replacing rotten wood furniture or house parts with new woods or attempting to reconstruct rotten woods cost a huge amount of capital. We would like to analyze the process of how fungus decomposes wood material, including how different fungus species and environmental conditions can affect its corruption, and create a mathematical model for different situations so that researchers can use these as references to find a possible solution of preventing wood-decay.

2.2 Problem Restatement

In this paper, we need to:

1. build a mathematical model to illustrate the process of wood-decay from the breakdown of ground litter and woody fibers through the fungal activity of multiple fungal species.
2. analyze the interaction between different species of fungus in short term and long term and consider the system sensitivity to environmental fluctuation.
3. evaluate the advantages and disadvantages of different species of fungus and the combination of different species in different climates.

4. discuss how diversity of fungus affect the breakdown of ground litter and the importance of its role in the environment.

2.3 Assumptions

Assumption 1: The fungus growing process is deterministic in large scale.

Assumption 2: The Growth Rate and Environment Tolerance of different species of fungus are dominated by different genes.

2.4 Notation

Symbol used for Logistic Growth	
Symbol Name	Description
P_j	Population of a specific fungus population j
W	The remaining fraction of the wood
K	Natural capacity of fungus by the wood
k	Proportionality coefficient between wood surface area and wood capacity of fungus
r_j	Natural reproduction rate of j
v_j	Benefit from wood consumption by j
s_j	Rate of decay of the wood caused by fungus j
i_{jk}	The interaction effect on population j by population k

Symbol for Stable and Stochastic Environment model	
Symbol Name	Description
T	Current Temperature
T_j^*	Optimal Temperature for a fungus
M	Current Moisture
M_j^*	Optimal Moisture for a fungus
τ	Moisture Growth Limit Function
θ_T, θ_M	Parameters for Growth limit functions (GLF)
$\alpha_{temp,j}, \beta_{temp,j}, \alpha_{moi}, \beta_{moi}$	Parameters to represent a single population's tolerance to temperature and moisture
γ_T, Γ_T	The environment conductivity factor
Ψ, ψ	Population Penalty Index due to Moisture or Temperature
$\tilde{T}_{ext}(t), \tilde{M}_{ext}(t)$	Variate temperature and moisture using Stochastic Differential Equation (SDE)
$B_T(t)$	One-dimensional Brownian motion

Symbols for Genetic Evolution Model	
Symbol Name	Description
G	the Gene Space
g_j	population j 's gene
d_G	the metric for gene space
c_E	the metric for gene space

3 Starting From Logistic Growth

3.1 Logistic Model of Single Population in Isolated Environment

3.1.1 Background

The Logistic Growth Model is a very fundamental model in ecology. It serves as a simple function representing how one species' population reaches its capacity, and how the population will bounce back and reaches stability. We use the Logistic Growth Model from (1) to simulate the natural growth and the population capacity of our fungus.

background for the predator & prey model

The predator & prey model, also known as the Lotka-Volterra model, is widely used in many species. It simulates the competition between two species with unique growth rate and decay rate. The original prey predator model can be written as:

$$\frac{dx}{dt} = Ax - Bxy \quad (1)$$

3.1.2 Model Construction

We want to model the situation where a single fungus species parasite on a block of deadwood. For simplicity, we do not consider environmental effects at this point.

The fungus will parasite on the wood and spreading enzymes into it to decompose the wood, which causes the wood to rot and the fungus to grow. However, the more wood that rots, the less wood there will be for the fungus to decompose, which will restrict the growth of the population of the fungus species. The fungus will grow slower and slower until it reaches maximum capacity. This behavior is described by a typical logistic growth model

$$P' = rP(1 - P/K)$$

$$P(0) = P_0$$

Since we want to model the interaction between fungus and wood, we introduce a typical predator prey model. For mycorrhizal fungus, we can consider the fungus as a predator and the wood as the prey, and according to the predator prey model, their relationship can be written as:

$$P' = rP + vPW$$

$$W' = uW - sPW$$

Where W is the fraction of remaining wood, v is the additional growth by decomposing the wood, and s is the rate of wood consumption per unit wood per unit fungus, and vPW and sPW are **interaction terms** which consider the effect of the interaction of two species on one of them.

However, this simulation uses deadwood as a host, which means it will not reproduce, making $u = 0$. We will apply the logistic growth model on our fungus reproduction to make it more realistic, and we can do that by replacing rP with $rP(1 - P/K)$.

By appending the terms to the equation, we obtain the following model:

$$P' = rP(1 - P/K) + vPW \quad (2)$$

$$W' = -sPW$$

$$W(0) = 1$$

We notice that K is actually not a constant, from the fact that fungus live on the wood surface. Hence the natural capacity of fungus depends on the surface area available. Hence $K \propto A$, where A is the surface area of the wood.

A consists of the outer surface area, A_{out} , and the inner surface area, A_{in} . From geometry we know that $A_{out} \propto V^{2/3}$, and $V \propto W$ if we assume uniform density of the wood.

The internal surface area is more complicated, but it largely depend on the porosity of the wood. We may take that $A_{in} \propto V$.

To simplify the model, we apply the approximation $A \propto W^{3/4}$. We let k be the proportionality constant, hence $K = kW^{3/4}$.

3.1.3 Model Sensitivity Analysis

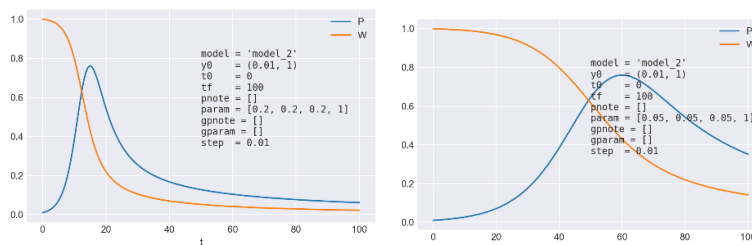


Figure 1: Result of Simulation

We try to half, double, and triple the growth rate r of the fungus and observe that the population grows faster if we increase the reproduction rate and the wood decays faster

at the beginning. After the fungus population reaches its maximum, the lack of resources forces it drastically decrease until it approaches zero. When we half the reproduction rate, the wood decays much slower at the beginning but eventually gets dominated by the fungus species with the same shape.

The overall trend is the same between the two cases, proving that this model is not much sensitive to changes and can be applied to many fungus species.

3.2 Logistic Model for Two Populations

3.2.1 Model Construction

Now we need to take in the situation of multiple fungus species living on the same wood. As multiple species living in one ecosystem, they will have some mutualism relationship, either positive or negative. Let's first consider two fungus populations.

We will refer to how (3) build his mutualism model in his journal,

By considering each pair of interaction between the two populations, we obtain the following ODE model with three variables:

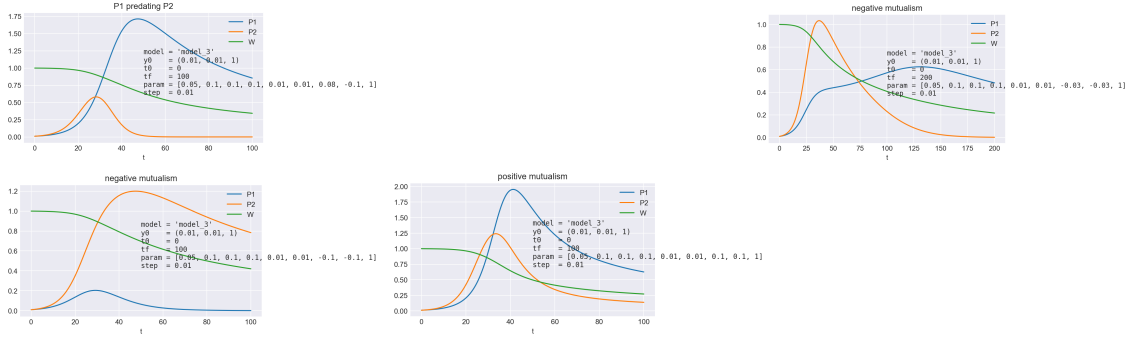
$$\begin{aligned}P_1' &= r_1 P_1 (1 - (P_1 + P_2)/K) + v_1 P_1 W + i_{12} P_1 P_2 \\P_2' &= r_2 P_2 (1 - (P_1 + P_2)/K) + v_2 P_2 W + i_{21} P_1 P_2 \\W' &= -s_1 P_1 W - s_2 P_2 W \\W(0) &= 1\end{aligned}$$

Where P_1 and P_2 represents the population of two different types of fungus. i_{12} and i_{21} are interaction coefficients, as i_{12} expresses the effect of fungus type 2 on fungus type 1 and i_{21} represents the effect of fungus type 1 on fungus type 2.

3.2.2 Implementation and Results

We simulate all situations, including positive, negative mutualism, and one preda-ting the other. And as Figure 3.2.2 "visualization" illustrated, the curve seems to fit the situation of two fungus species' competition.

This simulation shows that no matter the relationship between the two types of fungus on the wood, they will eventually reach a stable status given enough time. Only with positive mutualism will the weaker fungus survive with a small number. In the negative mutualism and predating model, the weaker fungus will reach a natural death and the other will have a significant drop in the population before reaching stability.



4 Stable Environment and Stochastic Environment

We now extend our model by adding two variables: temperature T , and moisture, M , into our model. Our goal in this section is to determine how fungus populations interact with temperature and moisture, and how temperature and moisture themselves are related.

4.1 Getting Hot and Humid

4.1.1 Environment Modeled as Growth Constraint

The growth of the fungus is heavily affected by the local environment. According to Jone, "temperature and humidity are the key agents of the fungus' growth" cite . Different fungus species will prefer different temperatures and humidity, and thus their interaction and effect on the rate of wood-decay will be different according to the environment.

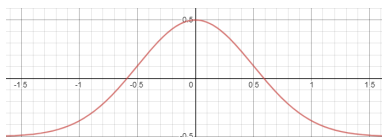
We begin by making the reasonable assumption that each species of fungus j has a favorite temperature T_j^* and favorite moisture M_j^* . We then assume that the less "favorite" the environment is, the fungus grows slower. With this in mind, we consider that temperature and moisture level to be growth constraints. We first define the **maximum growth function** τ as:

$$\tau(T, T^*, \alpha_{\text{temp}}, \beta_{\text{temp}}) = -\alpha_{\text{temp}} + \exp \left[-\beta_{\text{temp}} |T - T^*|^{\theta_T} \right] \quad (3)$$

Where T, T^* represents the current temperature and the optimal temperature of a specific fungus, and α_{temp} and β_{temp} are arbitrary constants for the model.

We further define the function $\tau_j(T)$ to be the partial function $T \rightarrow \tau(T, T_j^*, \alpha_j^{(T)}, \beta_j^{(T)})$ where T_j^* is optimal temperature for that fungus.

figure graph of $\tau_j(T)$, where $T_j^* = 0, \alpha_j = 0.5, \beta_j = 2$



Now we let τ be an upper limit for the growth rate. (2) becomes:

$$P' = \min(\tau, r(1 - P/K) + vW)P \quad (4)$$

4.1.2 Generation and Conduction of Heat and Moisture

However, when the fungus is decomposing the wood, it will generate or absorb a certain amount of heat depending on the specific fungus species. According to (2), certain types of fungi can generate great with certain types of woods. Hence, we assume that the rate of thermal exchange between the environment and the fungus is proportional to the rate of wood consumption. We thus define the parameter γ_T as the unit heat production due to each unit of wood consumption, given by

$$T' = -\gamma_T W'$$

We also consider the thermal exchange between the environment surrounding the fungus, and the **exterior environment** which has a large thermal capacity. Hence the thermal conduction equations are:

$$Q = \Gamma_T(T_{ext} - T)$$

where Q is the rate of heat flow from exterior environment to interior environment, and Γ_T is the thermal conductivity coefficient.

Let the thermal capacity of inner environment be 1 and the thermal capacity of exterior environment be C , we have

$$T'_{ext} = -Q/C, T' = Q$$

Since the exterior environment has huge thermal capacity, we take $C \rightarrow \infty$ and yield $T'_{ext} = 0$. Thus the surrounding environment cannot affect the exterior environment in any manner.

Combining the effect of generation and conduction, we obtain the equation describing change of temperature:

$$\begin{aligned} T(0) &= T_{ext} \\ T' &= -\gamma_T W' + (T_{ext} - T)\Gamma_T \end{aligned}$$

We ran the simulation of this model at different temperatures, and the result is in Figure 3: "visualization effect of different conduction factor Γ_T ".

Here, we assume humidity's effect on P' is symmetric to temperature's effect on P' , since they are two important factors of fungal growth. Therefore, we model moisture's effect on fungal growth symmetrically in the following equations:

$$\mu(M, M^*, \alpha_{moi}, \beta_{moi}) = -\alpha_{moi} + \exp\left[-\beta_{moi}|M - M^*|^{\theta_M}\right]$$

$$M(0) = M_{ext}$$

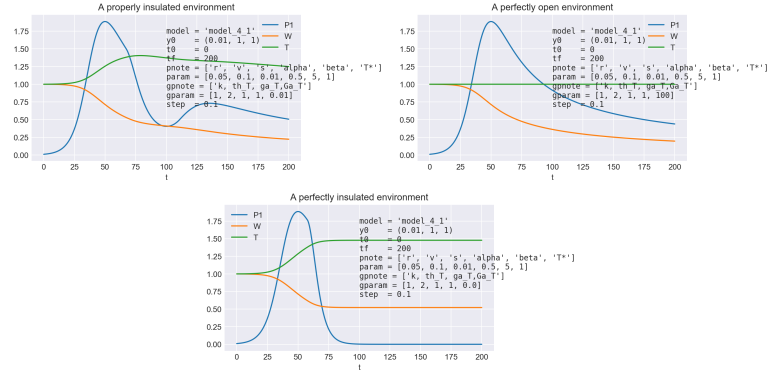


Figure 2: Caption

$$M' = \gamma_M W' + (M_{ext} - M)\Gamma_M(5)$$

Where $\mu(\cdot)$ is the **maximum growth function** in regards to humidity, and M, M^* represents the current and the optimal moisture level for a specific fungus. The current model for humidity is completely symmetrical to the temperature model.

4.1.3 Interaction Between Temperature and Humidity

According to the concept of relative humidity, different temperature levels can affect the relative humidity level, as colder air does not require as much moisture to become saturated as warmer air. Also, temperature affects the movement of water vapors, while humidity affects the conduction of heat. We summarize these mechanics in two phenomena:

The Green House Effect. The higher the moisture, the more difficult for heat to transfer.

The Condensation Effect. The lower the temperature, the more difficult for water vapor to transfer.

We can mathematically describe the concept as a conduction penalty index Φ , which will only range from 0 to 1. It can be calculated as follows:

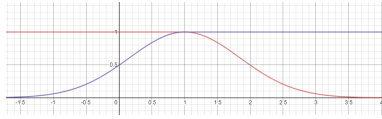
$$\Phi_M(M) = \begin{cases} 1, M < 1 \\ \exp[-\psi_M |M - 1|^2], M \geq 1 \end{cases} \quad (6)$$

$$\Phi_T(T) = \begin{cases} 1, T > 1 \\ \exp[-\psi_T |T - 1|^2], T \leq 1 \end{cases} \quad (7)$$

Where Φ_T is the moisture conductivity penalty due to temperature decrease and Φ_M is the temperature conductivity penalty due to moisture level increase.

reference

figure plot of the two functions



The red line represents Φ_M 's trend and the purple line represents Φ_T 's trend. As we can see, both the temperature and the moisture will start to affect each other once within the range of 1 and 0, which justifies our model's accuracy.

After integrating this concept, we obtain the following ODE model describing the interaction of temperature, moisture, wood, and a single fungus population.

$$P' = \min(\tau P, \mu P, rP(1 - P/K) + vPW) \quad (8)$$

$$W' = -sPW \quad (9)$$

$$M' = \gamma_M W' + (M_{ext} - M)\Gamma_M \Phi_T \quad (10)$$

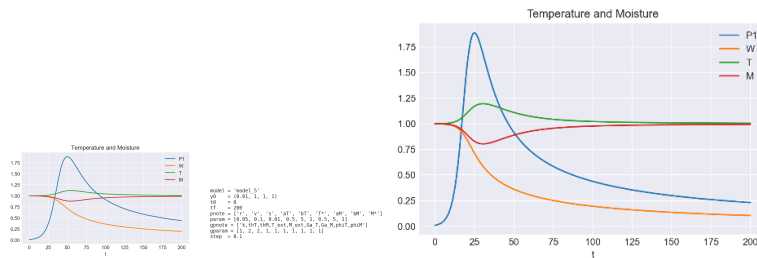
$$P(0) = P_0 \quad (11)$$

$$W(0) = 1 \quad (12)$$

$$T(0) = T_{ext} \quad (13)$$

$$M(0) = M_{ext} \quad (14)$$

4.1.4 Simulation and Results



According to our simulation in Fig. 4.1.4, the effect of temperature and moisture on the fungus' population growth is very significant. In a constant environment, the growth of fungus will affect the local environment, causing the temperature to rise and moisture to drop. However, this will reduce the population of the fungus and reduce the activity of decomposition. With less decomposition, the temperature and moisture will slowly bounce back to normal with a decrease of fungus growth rate. At the end, the growth rate of the fungus will be stable, and so does the temperature, moisture and wood-decay rate.

4.2 Getting Chaotic

The temperature and the moisture are never consistent and will often change unpredictably and rapidly due to many other aspects hard to be modeled. In the long run, too many unexpected situations may occur such as extreme weather.

To model real-world random disturbances of temperature and moisture, we extend our ODE model to **Stochastic Differential Equation (SDE)**.

4.2.1 Model Construction

We add a disturbance to temperature by directly summing T_{ext} with a Brownian motion:

$$\tilde{T}_{ext}(t) = T_{ext}(t) + B_T(t)$$

where $B_T(t)$ is one-dimensional Brownian Motion.

We symmetrically define

$$\tilde{M}_{ext}(t) = M_{ext}(t) + B_M(t)$$

where $B_M(t)$ is one-dimensional Brownian Motion.

We will use this to replace and adjust the model we used in the previous section, replacing T_{ext} by \tilde{T}_{ext} and M_{ext} by \tilde{M}_{ext} in all previous equations. We obtain the SDE model:

$$P' = \min(\tau P, \mu P, rP(1 - P/K) + vPW)$$

$$W' = -sPW$$

$$\tilde{T}_{ext}(t) = T_{ext}(t) + B_T(t)$$

$$\tilde{M}_{ext}(t) = M_{ext}(t) + B_M(t)$$

$$T' = -\gamma_T W' + (\tilde{T}_{ext} - T)\Gamma_T \Phi_M$$

5 Genetic Evolution

5.1 Genes? Geneious!

We now develop a model of Genetic Evolution of the fungus populations. Doing so allow us to discuss long-term tendency of a fungus colony, i.e. a large collection of fungus populations cohabitating in a single area.

5.1.1 Structure of a Gene

We define gene, or **gene vector**, g_j as a complete description of the population p_j . Formally it's an element of the **gene space** G that covers all possible parameters a fungus population can have.

The gene space is defined as the cartesian product of the bounds of each population parameter. Let $G = \prod G_n$ where each G_n describes a bound. We list all the bounds here:

Besides the 11 population parameters listed earlier, we also add additional 4 **formal parameters** " $\zeta_{j1}, \dots, \zeta_{j4}$ " that range between -1 and 1. By doing this we can model the

complex behavior of fungus mutualism. Note that i_{jk} is *asymmetric*, such that i_{jk} in most cases $\neq i_{kj}$.

To measure difference between two genes, We define the distance function $d_G : G^2 \rightarrow$ of the gene space, such that $d_G(g_1, g_2) = d_2(c_E \odot (g_1 - g_2))$, where d_2 is 2-D Euclidean Metric and \odot is element-wise multiplication, where c_E is **evolution cost vector** that weights the different genetic components. By adjusting c_E we can encode the **evolution difficulty** of each parameter.

Since we don't have valid source to determine c_E , we simply let $c_E = \mathbf{1}$ for the rest of the paper. In this case, d_G is equivalent to d_2 .

5.1.2 Stochastic Mutation of Genes

- Model of One Genetic Mutation

Each evolution step will traverse $g_j \rightarrow g_{j'}$ in G , where the distance, $d = \|g_{j'} - g_j\|$, follows normal distribution $d_{E,j} \sim N(\Lambda, \Lambda^2)$ where Λ is the **evolution intensity** encoded by its gene.

$$ev(g, d_E) = \text{choice}\{h \in G : \|g - h\| = d_E\}$$

- Model of single-population genetic evolution

Num of evolutions in unit time should follow poisson distribution $n_{E,j}(\Delta) \sim \text{Po}(\lambda_j P_j \Delta)$ where the expectation is proportional to size of population. λ_j is the **evolution likelihood** of the population, encoded by its gene.

- Algorithm for multi-population evolution

Let $\Omega = (J, P, g)$ be the population set that encode all populations and their genetics. J is the population index set. P_j is population variable. g_j is gene vector. Let $ev(j, \Omega) \rightarrow (j', P_{j'}, g_{j'})$ be the process that randomly generates a new population.

The process The process $EV(\Omega, \Delta) \rightarrow \Omega$ is defined in Fig. 3.

5.2 Fungus Evolution

Now that we have set up a rigorous algorithm to describe genetic mutation of the fungus populations, we can proceed to incorporate that into the SDE model, and then run some simulations to observe the performance of the model.

Before moving on to implementations, we want to make a few remarks:

The evolution is described by a stochastic difference equation while the other equations are stochastic differential equations. This sounds intimidating at first, but since we are using numerical simulation which is discrete in nature, the notational difference doesn't affect the implementation of the model. We will run the EV algorithm in each discrete time step.

```

Let population_threshold be a constant.
Let  $J' = \{j \in J : P_j(t) \geq \text{population\_threshold}\}$ 
for each  $j$  in  $J$ :
    repeat for  $\lfloor n_{E,j}(\Delta) \rfloor$  times:
        Let  $j'$  be the index of new population  $ev(j)$ 
        add  $j'$  to  $J'$ 
Let  $\Omega' = \{(j, P_j, g_j) : j \in J'\}$ 
return  $\Omega'$ 

```

Figure 3: Algorithm for Fungus Evolution

The choice of population_threshold. If we set the threshold to be 0, we never delete a population even if its magnitude is astronomically small. This can bring extra burden to computing. Hence we set it to some constant that is orders of magnitude smaller than the magnitude of a thriving population. Some sensitivity analysis have shown that removing the threshold doesn't affect the model performance much.

5.2.1 Biostatistical Measurements of Fungus Populations

We define the temperature survival interval $\text{TSI}_j = [T_j^* - \epsilon, T_j^* + \epsilon]$ where $\epsilon = \left(\frac{\ln \alpha}{-\beta}\right)^{1/\theta_r}$

We define the **moisture survival interval** MSI similarly.

We define the **survival interval** $\text{SI}_j := \text{TSI}_j \times \text{MSI}_j \subset \mathbb{R}^2$

Species Diversity can be measured by the Shannon-Wiener diversity index $H = -\sum_{j \in J} P_j \ln P_j$.

Species Richness is the total number of species observed. $S = |J|$

Species Evenness can be measured by the Pielou Index $E = H / \ln S$. When all species have even number of observations, the value is close to 1; when one species dominates, the value is close to 0.

5.3 Modeling Climates

5.3.1 Model Structure

We now take manual control of the T_{ext} and M_{ext} functions, and observe how the multi-population genetic SDE model behaves as we input different environment patterns to it.

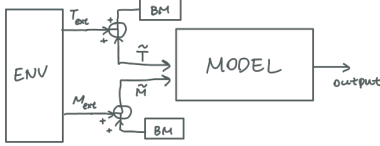


Figure 4: Signal Flow Diagram

5.3.2 Modeling Short and Long-Run Climate Change

We define short-run environment change as the activities with some periodicity Δ_{st} . For example, the change of temperature and humidity during seasons can be regarded as short-run, which has a period of one year.

Instead of letting the trend to be determined by a Brownian Motion, we now want to take more control of T_{ext} in its short and long-term tendencies. Splitting T_{ext} into short-term, long-term and noise allow us to perform simulations on the environments that we design.

$$T_{ext}(t) = T_{st}(t) + T_{lt}(t) + B_T(t)$$

where T_{st} is the short-term fluctuation, with the periodicity $T_{st}(t + \Delta_{st}) = T_{st}(t)$ for $\forall t$.

where T_{lt} is the long-term tendency.

Similarly we define

$$M_{ext}(t) = M_{st}(t) + M_{lt}(t) + B_T(t)$$

5.3.3 Tools for Visualization and Analysis

- Representation of Climate Pattern using "Environment Phase Curves (EPC)"
- Representation of environment adaptations using the EPP The intersection of the orange lines represents (M_{ext}, T_{ext}) , while the center of the orange rectangle represents (M, T) .

5.4 Short and Long Run Climate Response and Evolution Preferences

5.4.1 Short-term Environment Shock

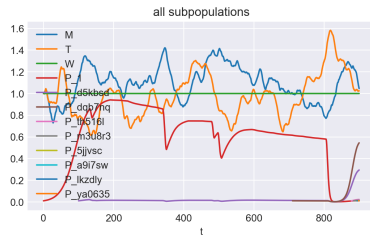


Figure 5: Simulation Result

Around $t = 800$ we observe "Sudden Shift of Dominator." The direct cause is the temperature spike at the same time up to 1.6. The spike lasted so long that P_1 almost died out, allowing other species to take this opportunity to become dominant.

In order for environment shock to tear down the dominator, three conditions must suffice:

The temperature and moisture must be outside the SI of the dominating population

The shock must last long enough not to let the population regain its dominance after the shock

There exists genetically superior populations with the potential to outcompete the dominating population when they have comparable magnitude.

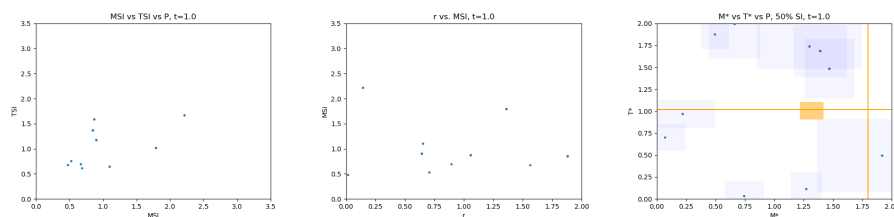


Figure 6: t=4

5.4.2 Robustness-Growth Rate Tradeoff

Less Growth Rate may lead to solving resource scarcity when there's limited amount of wood. Hence, the species are not trying to evolve for large growth rate. In fact they prefer slow growth rate, so that the resource scarcity term in the equation is minimized.

We can observe the movement to the top-right corner of SI graph. When a population has larger survival interval, it can survive in a more variety of temperature-moisture environments and withstand short-term climate changes.

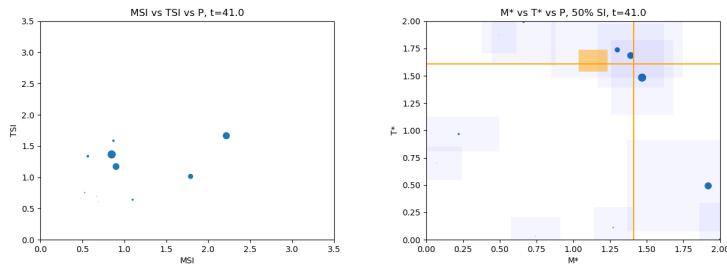


Figure 7: t=41

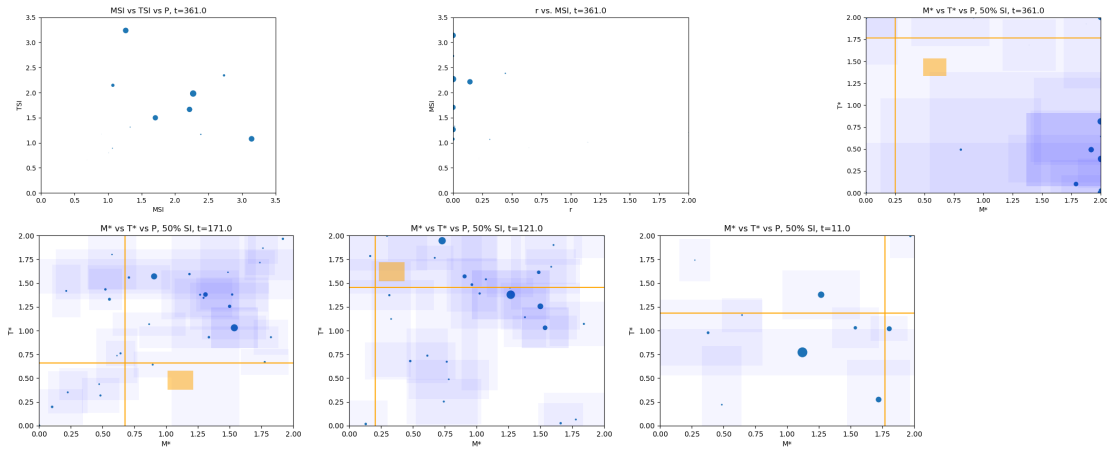


Figure 8: t=361

5.5 Evolution in Different Climates

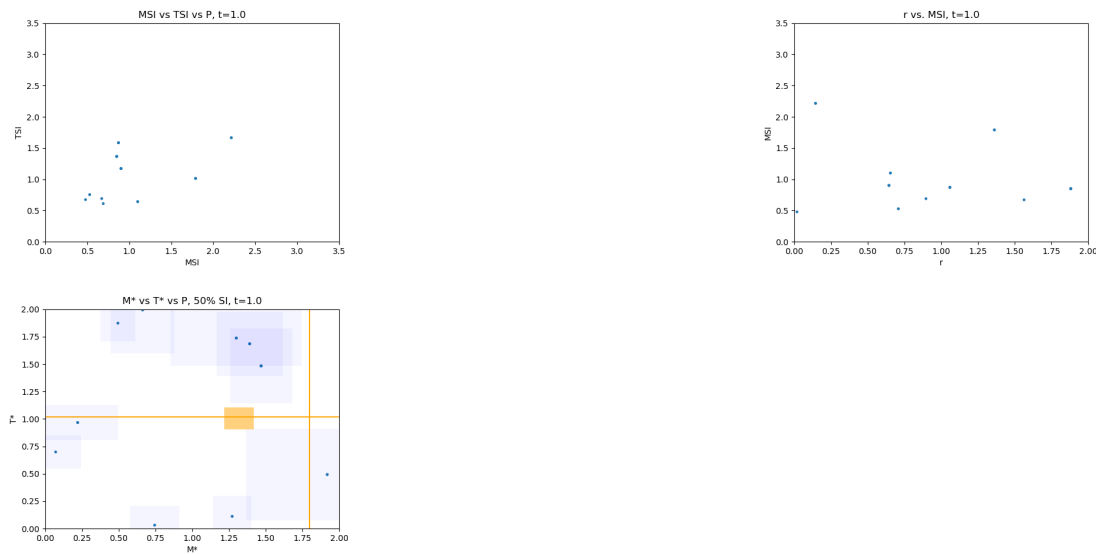
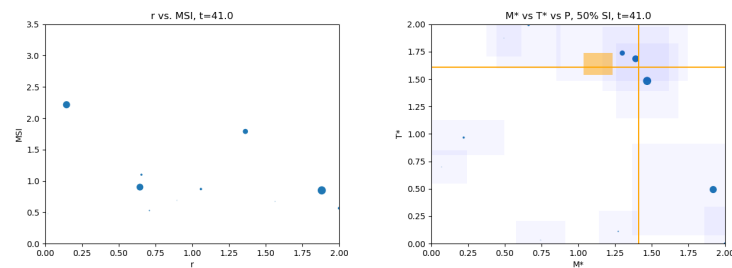
The **Köppen Climate Classification System** classifies climates into these types:

- **A-** Tropical Moist Climates: all months have average temperatures above 18° Celsius.
- **B-** Dry Climates: with deficient precipitation during most of the year.
- **C-** Moist Mid-latitude Climates with Mild Winters.
- **E-** Polar Climates: with extremely cold winters and summers.

We choose one climate from each type to perform analysis. For each climate we research its typical temperature and precipitation tendency, design T_{ext} , M_{ext} that encodes the climate profile, and run simulation for 1 year. After that, we analyze biostatistics and determine successful genes and combination of genes for that climate.

5.5.1 Tropical Moist Climate

- General Pattern

Figure 9: $t=1$ Figure 10: $t=41$

- EPC
- Simulation and Biostatistics

We can see that the evolved species generally cluster around the EPC in the EPP. This validates the trivial claim that tropical fungus, which better adapts to the temperature and moisture of the tropical area, tend to thrive in tropical climates.

A lot of species are evolved and they take turn to be the dominant fungus before $t = 100$. The Species Richness soon exceeds 30, while the species evenness is still low, since several fungus species consist of the whole population.

Right After $t = 100$ we see an unexpected spike of fungus populations, followed by sudden fluctuation of temperature and moisture that soon kills the whole population. This Environmental Catastrophe is possibly caused by self-induced overgrowth and competition that depletes the environment and triggers a series of environmental crisis.

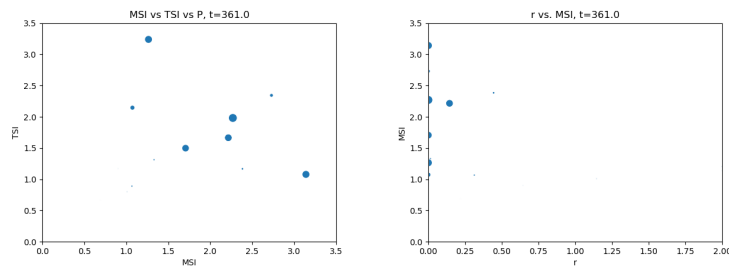
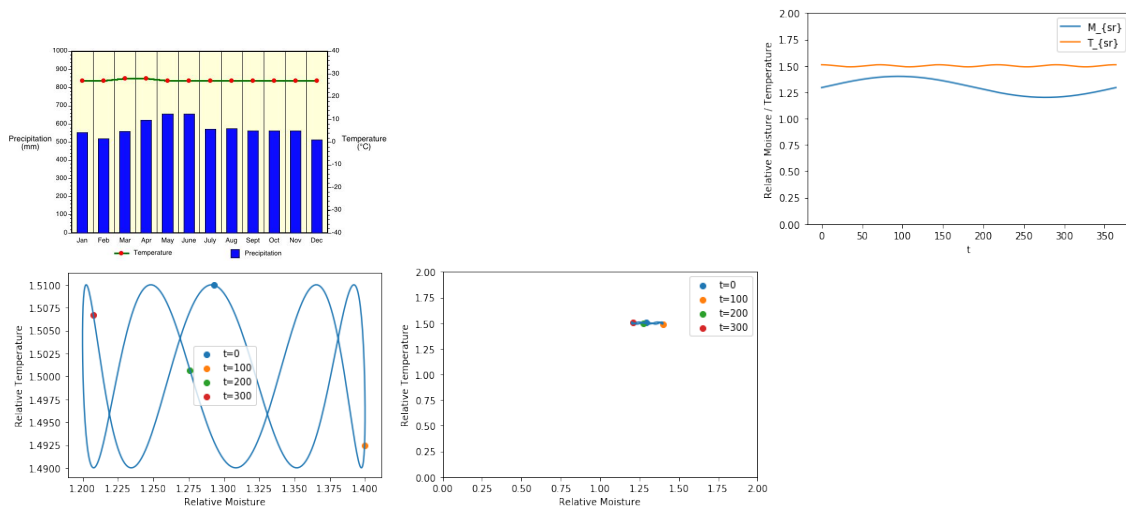


Figure 11: t=361



5.5.2 Dry Climate

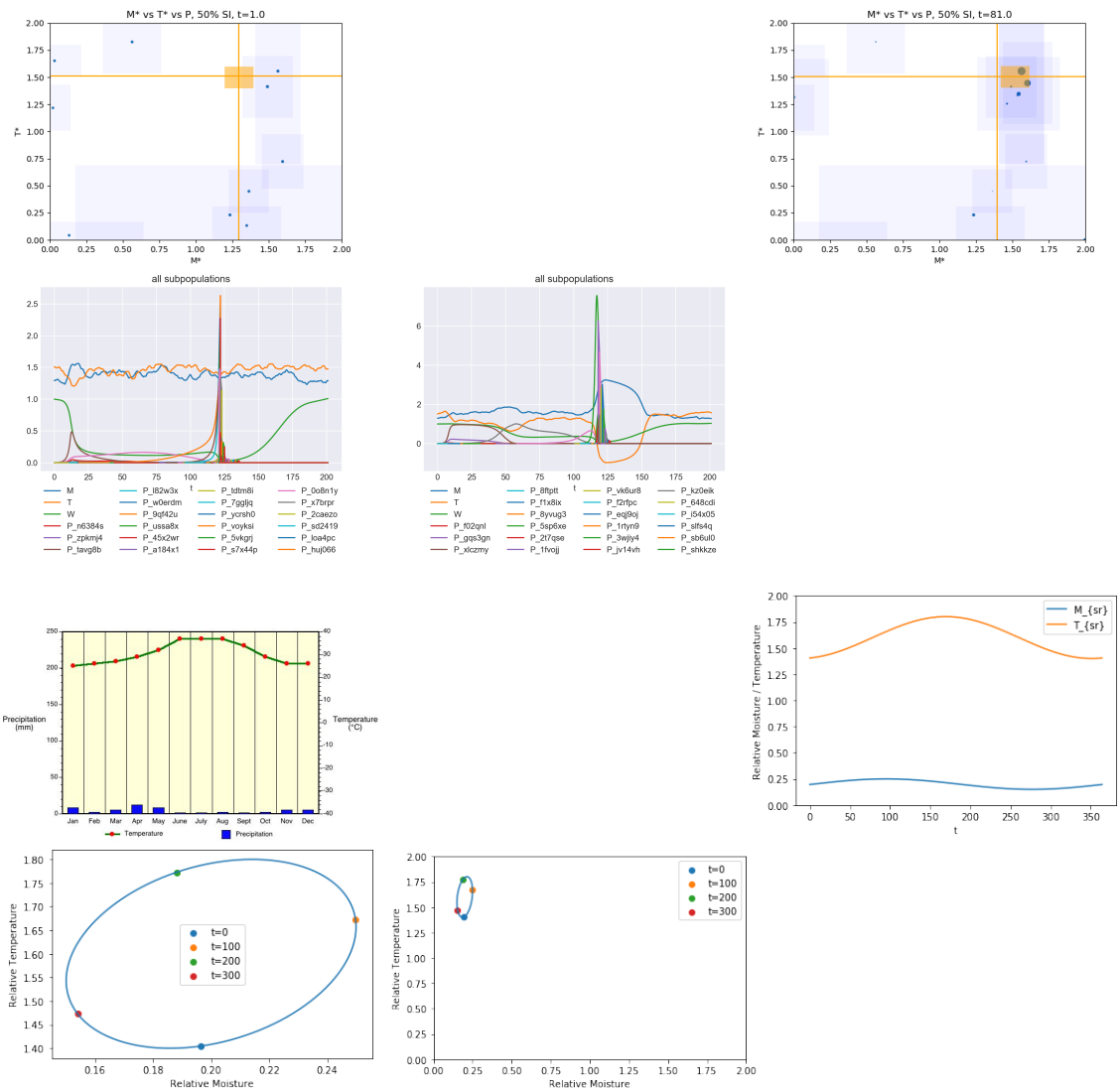
- General Pattern
- EPC
- Simulation and Biostatistics

In this harsh environment, fungus populations strive and compete to survive. Hence we can see that only the one species with optimal temperature and moisture preference get to survive in this scenario, and all other populations soon become extinct.

We can see that species with low growth rates tend to be larger. This is possibly because the starvation of resources. Having a low r_j value can reduce the negative penalty of resource limitation in the SDE model.

Since there's no enough room for population diversity, one species dominates the whole district for a long period of time. Dominant Genes are the ones with enough moisture tolerance and grow slowly.

Interestingly, we see fast-growing small subpopulations surrounding the slow-growing dominant populations. Since the small **satellite populations** are fed by positive mutualism with the dominant population, they do not need to have the optimal SI. Hence their SI can spread out and cover more of the CPP, and improve the survival chance of the population as a whole.



5.5.3 Moist Mid-Latitude Climate with Cold Winter

- General Pattern
- EPC
- Simulation and Biostatistics

First, there's no dominance by a single gene. Since the temperature and moisture is fluctuating significantly, no one population can have a large enough Survival Interval in order to thrive throughout the year. Any species, take P_{jky1k4} as an example, would start growing when its favorite weather

5.5.4 Moist Mid-Latitude Climate with Mild Winter

- General Patterns
- EPC

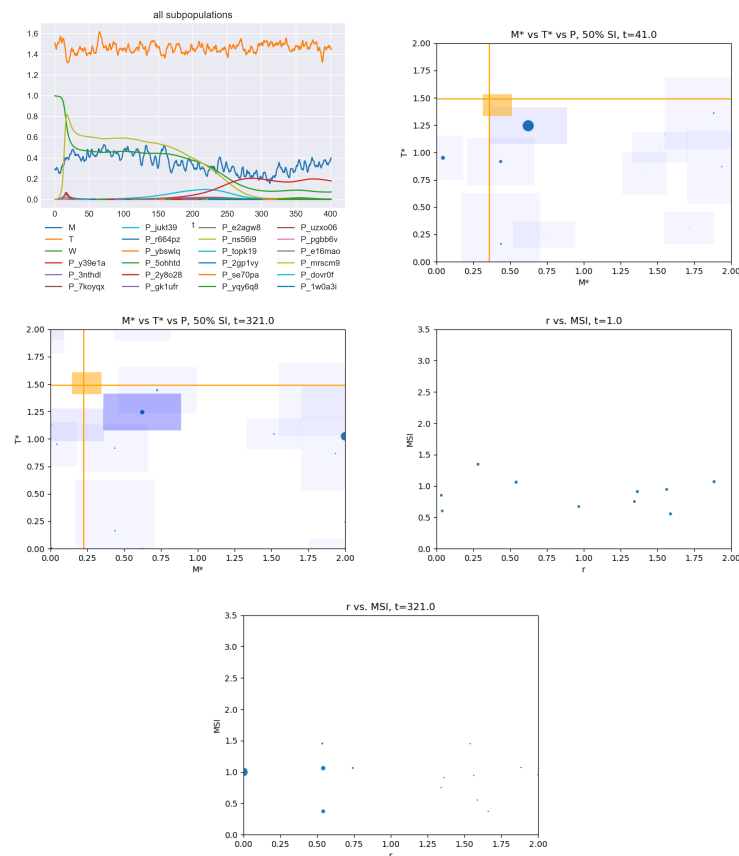


Figure 12: Dfa- Omaha, Nebraska, USA

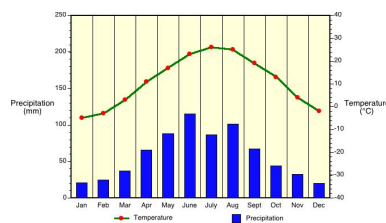


Figure 13: General Pattern, Omaha, Nebraska, USA

• Simulation and Biostatistics

This There's only small variation in temperature and moisture, so the transition between fungus populations are smooth and stable. This implies that the cause of **dominator shift** is usually new population out-competing old populations, and sudden, drastic environmental changes are not involved in this process.

The species diversity is constantly high. The species evenness is relatively high, because several species can take dominance together for an extended period of time (see the interval $t=75-150$). This is only possible in stable and friendly climate like this one.

As all genes converge to a similar configuration, there's no more relative advantage among them, so each specie start taking the same share of population. The Species

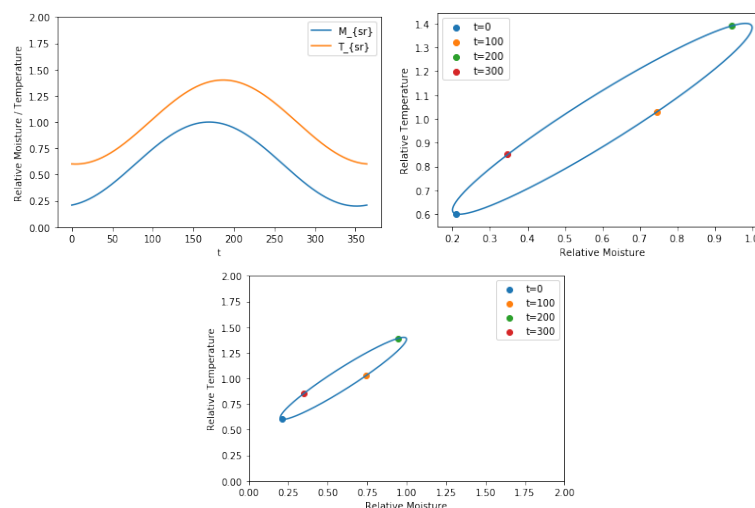


Figure 14: EPC

Evenness now become very high and approaches 1.

We observe a set of genes with zero growth rate but very high positive mutuality. Therefore, their growth and survival completely depend on the presence of other species. It's surprising that some fungus develop the ability to live together as a whole. This strategy turns out to be very effective, as it allows each population to steadily grow.

5.5.5 Polar Climate

- General Pattern
- EPC
- Simulation and Biostatistics

The harsh environment poses a strict constraint on the environment adaptability and robustness of the fungus populations. Only the populations close to the bottom-left corner of the EPP tend to survive and thrive.

Since the environment is unstable, we can see rapid and sudden shift of dominators. The ultra-low temperature posts a constant threat to all species, that urges them to evolve quickly..

Green-house and Condensation effect compound each other, further fluctuation of temperature and moisture

Before implosion, a cluster of genes with varied growth rate and similar environment adaptations. After implosion, a single specie that has medium growth rate, with a large temperature tolerance.

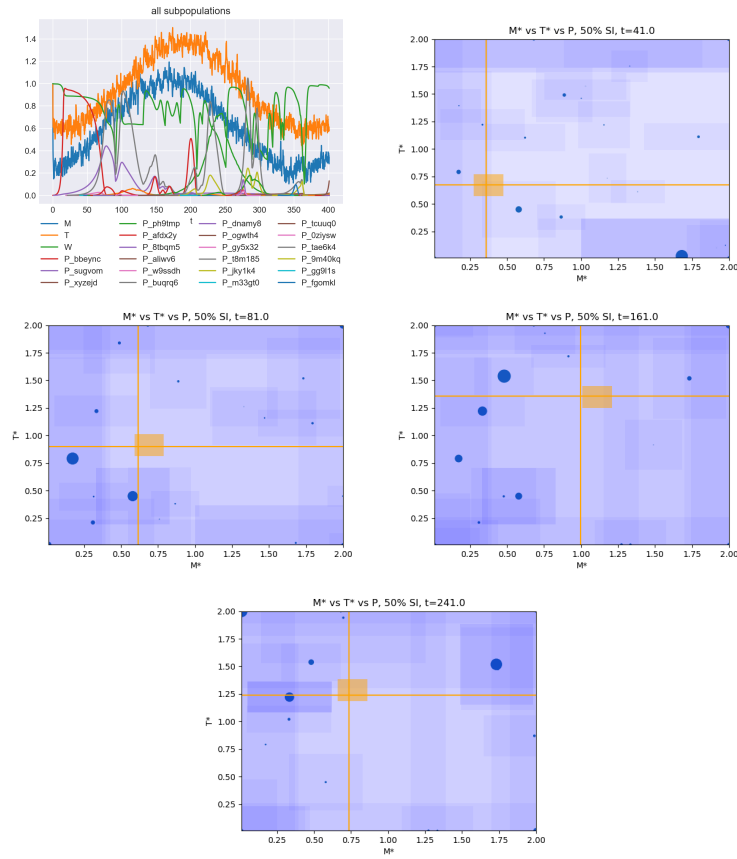


Figure 15: Simulation and Biostatics

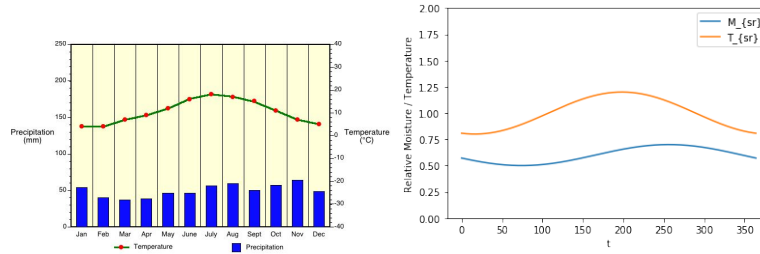


Figure 16: General Patterns

6 Conclusion

6.1 Advantages

- Our model successfully provides qualitative representation of fungal growth, mutation and interaction between the environment.
- Our model is highly extensible.
- Our model is a white-box, which means it's equations and parameters are explainable and match our common intuition.

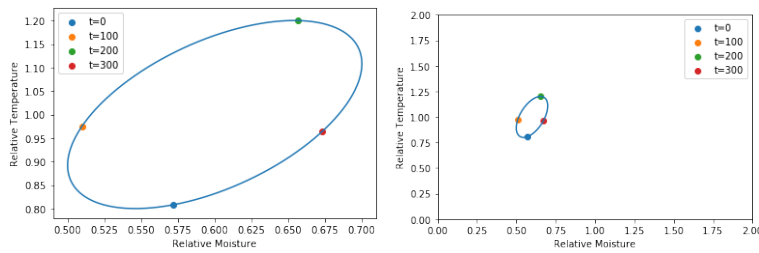


Figure 17: EPC

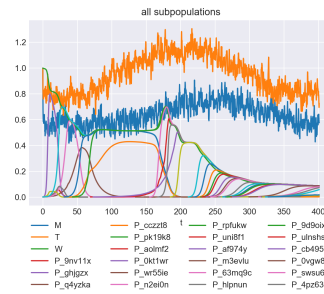


Figure 18: Simulation and Biostatistics

- Although our model follows a simplistic bottom-up design, it's able to generate very complex dynamics of fungus evolution, and was able to let complex behaviors like **dominator shift** and **implosion** to emerge. We even discovered the possibility of **fungal communism** where multiple fungus populations act together like a single species.

6.2 Limitations

- We only consider temperature and moisture, while there are a lot of other parameters like exposure to sunlight, latitude and longitude, existence of other plants and activity of wild lives.
- Since we are using relative metric instead of real-life units for all variables, we do not have a solid procedure to specify the parameters. Our choice of parameters and bounds of the gene space is somewhat arbitrary. Luckily, it is shown earlier that the model is stable under small variations of parameters.
- The **implosion effect** the we encountered in the simulation might be introduced by technical error in coding implementation, nevertheless it has brought some interesting inspirations.

References

- [1] Elizabeth S Allman, Elizabeth S Allman, and John A Rhodes. *Mathematical models in biology: an introduction*. Cambridge University Press, 2004.

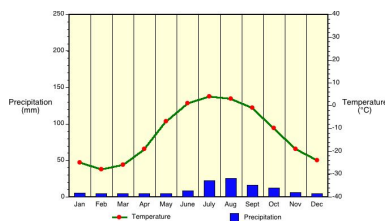


Figure 19: General Patterns

- [2] Leire Caizan Juanarena, Annemiek Ter Heijne, Cees JN Buisman, and Annemieke van der Wal. Wood degradation by thermotolerant and thermophilic fungi for sustainable heat production. *ACS sustainable chemistry & engineering*, 4(12):6355–6361, 2016.
- [3] Antony M Dean. A simple model of mutualism. *The American Naturalist*, 121(3):409–417, 1983.

Appendices

Some Appendix The contents...

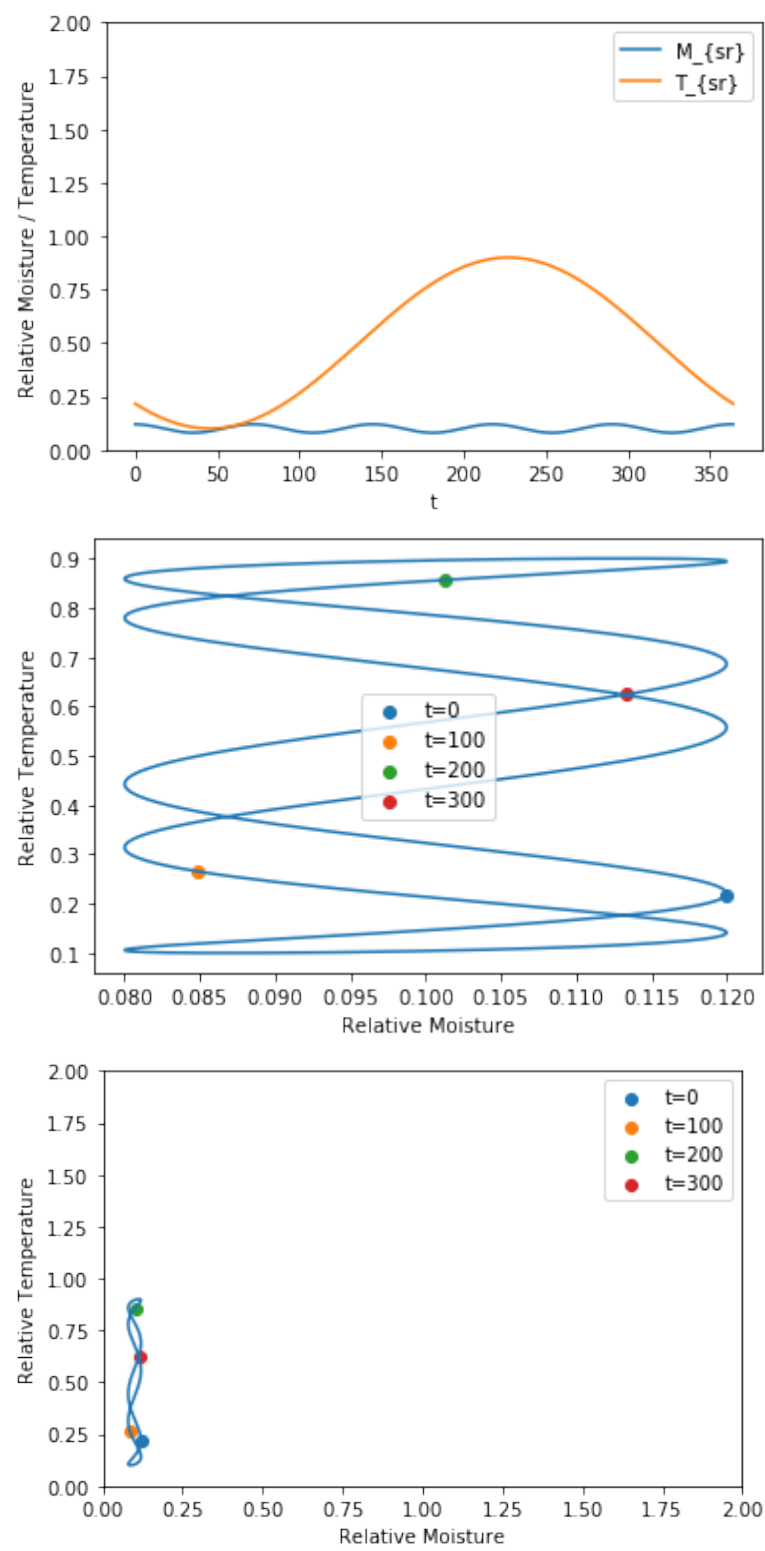


Figure 20: EPC

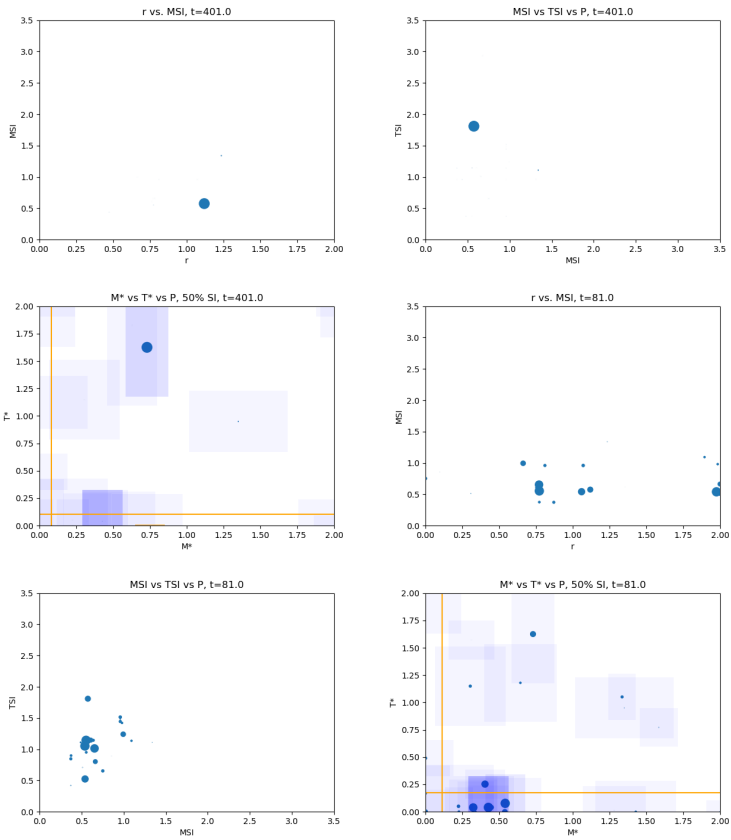


Figure 21: Simulation and Biostatics