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Fungi

摘要

As an important part of the ecosystem, the decomposer is of great significance in the carbon cycle process. Fungi are the most important type of organisms among decomposers. How to predict the growth rate of fungi and the rate at which fungi decompose organic matter, as well as understanding the interaction between various fungal decomposers, is one of the important contents of our research on the carbon cycle.

Considering that the number of fungi in nature is in a dynamic equilibrium process, the decomposition rate of wood remains unchanged. On the basis of previous experience, we first established an exponential model for the rate of decomposition for fungi. Since the growth rate of fungi is closely related to the rate at which fungi decompose organic matter, we established a linear regression model of fungal hyphae growth rate and fungal decomposition rate in order to discuss the interaction of fungal later.

After that, we established an ordinary differential equation model of fungal interaction. Starting from the three inter-species relationships that may exist among fungi: "cooperation", "competition", and "parasitic", we constructed a differential equation model that reflects specific inter-species relationships, and pointed out their main occurrences. After that, we used the cellular automata model to simulate various inter-species relationships and determined the trend of the number of fungi under various inter-species relationships.

Environmental factors such as temperature and humidity also have a great influence on the activity of fungi. In order to analyze the impact of environmental factors, we established a generalized linear regression model of environmental factors on the growth rate of fungal hyphae through the annual average temperature and annual average precipitation data, and used this model to quantify the impact of environmental factors.

Combining the above four models, we comprehensively discussed the possible combinations of various fungi, and predicted the mycelial growth rate and wood decomposition rate of the fungi under various combinations. It is concluded that the wood decomposition rate is faster when there are more types of fungi. This reflects the positive impact of fungal biodiversity on the ecological environment.

Our paper systematically explained the decomposition rate of fungi and the relationship between fungal growth rate and environmental factors. And explained the interspecies relationship between fungi. It also further illustrates the importance of decomposers for maintaining the diversity of the ecosystem, and has certain reference value for studying the role of decomposers in the ecosystem.

Keywords: Ordinary Differential Equation Model, Cellular automata, Fungus, Interaction, Biodiversity

目录

1 Introduction

1.1 Background

The carbon cycle describes the process of the exchange of carbon throughout the geochemical cycle of the Earth, and is a vital component for life on the planet. And the decomposition of compounds, which allowing carbon to be renewed and used in other forms, is one of the most important part of the carbon cycle.

Some of the key agents in decomposing woody fibers are fungi. Recent research shows identified fungi traits that determine decomposition rates and also noted links between certain traits. Besides, the slow growing strains of fungi tend to be better able to survive and grow in the presence of environmental changes with respect to moisture and temperature, while the faster growing strains tend to be less robust to the same changes. [6] This may reveal some kind of interaction between fungi.

1.2 Problem Statement

- Build a mathematical model that describes the breakdown of ground litter and woody fibersthrough fungal activity in the presence of multiple species of fungi.
- In your model, incorporate the interactions between different species of fungi, which havedifferent growth rates and different moisture tolerances. And analyze the short-term and long-term trends of fungal interactions. Besides, for short-term interaction, we should examine the sensitivity to rapid fluctuationsin the environment to assess the impact of variation of local weather patterns.
- Based on the model established above, predict about the relative advantages and disadvantages for each species and combinations of species likely to persist, and do so for different environments.
- Describe how the diversity of fungal communities of a system impacts the overall efficiencyof a system with respect to the breakdown of ground litter. Predict the importance and role ofbiodiversity in the presence of different degrees of variability in the local environment.

2 Assumptions and Symbols

2.1 Model Hypothesis

1. The decomposers in the analyzed ecosystem are mainly fungi.
2. It is believed that the decomposition reaction of fungi is only the hydrolysis process of cellulose or lignin, without considering other reaction substrates
3. Ignore the influence of environmental factors other than temperature and humidity on the decomposition rate.
4. When discussing the interaction of fungi, only three interspecies relationships of "cooperation", "competition" and "parasitic" are considered.

2.2 Symbols and Definitions

表 1: Notation

Symbols	Definitions
R	The residual rate of dead wood
α	Correction coefficient of oison model
x_1	The annual average temperature($^\circ C$)
x_2	The annual average precipitation(100mm)
x_3	The moisture trade-off
$b_0, b_1, \cdots, b_7$	Parameters of linear regression model

Other variables not mentioned will be given in the text

3 Wood Decomposition Model

In this section, we will discuss the factors related fungal decomposition and establish a mathematical model about fungal decomposition rate and mycelial extension rate.

3.1 Exponential Model of Fungal Decomposition Rate

Since the number of different types of fungi in nature is in a dynamic balance, the decomposition rate of fungi can be considered to be a fixed value under the condition that other environmental factors remain unchanged. In this way, an exponential decomposition model is established. Olson [8] proposed such an exponential model in 1963. In his model, R represents the residual rate of dead wood, X_0 is the initial weight of dead leaves (kg), and X is the amount of dead leaves remaining after time t (kg).

$$R = \frac{X}{X_0} = e^{-kt} \tag{1}$$

However, the Olson model has a shortcoming: in reality, due to the accumulation of soil organic matter in the soil, the average turnover period of litter and the average lifespan of litter are often not equal. For example, the literature [12], based on calculations and ^{14}C isotope tracing analysis, shows that the average turnover period of woodland litter is 0.1-50a, and that in temperate areas is about 20a, while the average life span (average age of humus) of litter is more than 1000 years. The model is based on the assumption that the average turnover period of litter and the average lifespan of litter are completely equal, which causes a certain deviation. In order to eliminate the influence of this factor, we modify the model of 1 as follows:

$$R = \frac{X}{X_0} = ae^{-(kt)^\alpha} \tag{2}$$

In the formula, a is taken as 1, k and α are the parameters related to the average turnover period of litter and the average life of litter. Since the above two parameters are not given in the known data, we switch to using other known data (decomposition of the same fungus in 3 and 5 years) to determine α.Since k is related to fungal species, the data of *Celtis occidentalis*, a certain breed of fungal, with different years and same environmental conditions are taken here to solve the value of k and α.

Substitute the data to obtain the parameters of the model $k = 0.2178, \alpha = 2.1494$. The relationship between the weight of deadwood and time is shown in the figure below:

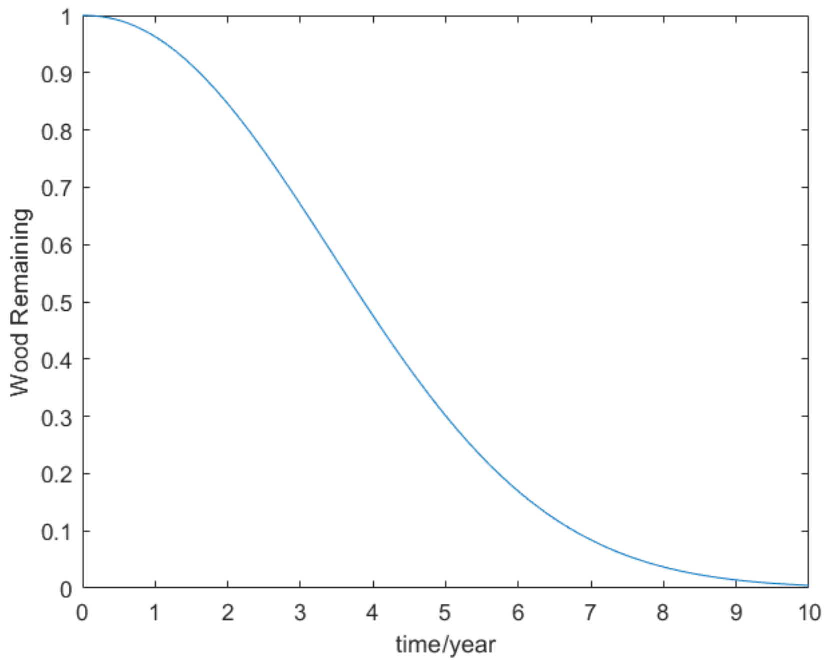


图 1: Relationship between the weight of deadwood and time

The decomposers in a specific ecosystem often contain a variety of fungi, so the α that we get related to the decomposition rate also involve the joint action of multiple fungi. The model 2 based on these data can simply reflect the relationship between the decomposition rate and time of many different fungi. Based on the analysis above, we have obtained the improved function relationship between litter mass and time. When $\alpha = 1$, the above relationship degenerates to Olson model.

3.2 The Relationship Between Hyphae Expansion Rate and Decomposition Rate

According to the correlation coefficient graph in the paper [6], the hyphae expansion rate is closely related to the decomposition rate of fungi. Mycelium is an important vegetative organ of fungi, and further study of the interactions between various fungi is inseparable from the analysis of mycelium. This requires us to determine the relationship between the rate of hyphae expansion and the rate of decomposition.

In this section, we use the hyphae growth rate and decomposition rate data in the paper [6] to determine the direct relationship between the hyphae growth rate and decomposition rate through linear regression analysis. The two data used are the geometric mean values at different temperatures.

Using x to represent the hyphae extension rate (mm/day) and y to represent the decomposition rate (% dry mass loss over 122 days), we get $y = 3.9145 + 2.5946x$. The model's $R^2 = 0.4998, r = 0.7070$, and the confidence interval of each variable does not contain zero,indicating that there is a strong correlation between the hyphae extension rate and the decomposition rate.

4 Fungal Interaction Models

4.1 The Frequency of Co-occurrence of Different Fungi

The interaction between species can be judged by how often they appear together. If two species often appear together, it means that they have a symbiotic relationship or a parasitic relationship, or have the same competitiveness. On the contrary, if two species with similar ecological niches rarely appear together, it means that they are in a competitive relationship and one of them is stronger. This phenomenon is more pronounced in the interaction of fungi [9].

We selected some data from the appendix of paper [9] to analysis, as shown in the following table:

表 2: List of Fungi, their code names used in the tables and figures, and some key ecological characteristics.

Code	Species name	Decay type	Fruit-body life span	Nutritional strategy
S1	Amylocystis lapponica	brown rot	annual	saprotrophi
S2	Antrodia serialis	brown rot	1-3 years	saprotrophic
S3	Byssoporia mollicula	brown rot	annual	mycorrhizal, saprotrophic
S4	Fomes fomentarius	white rot	perennial, long-lived	saprotrophic, parasitic
S5	Gloeophyllum sepiarium	brown rot	perennial, short-lived	saprotrophic
S6	Phellinus nigrolimitatus	white rot	perennial, long-lived	saprotrophic
S7	Phellinus viticola	white rot	perennial, short-lived	saprotrophic
S8	Trichaptum abietinum	white rot	annual	saprotrophic

These fungi have different decay types and different nutritional strategy. This means that they have different emphasis on using resources. For example, white rot fungi are better at decomposing lignin, and brown rot fungi are better at decomposing cellulose. These characteristics of fungi affect their interaction.

The correlation coefficient of the occurrence frequency reflects the interaction relationship of fungi. In order to explore this relationship, we calculated the correlation coefficient of the frequency of fungi. The frequency of each fungi is provided in Appendix G.

We use X_i to represent the frequency of fungus X in the i-th sample, Y_i represents the frequency of fungus Y in the i-th sample, $\bar{X}$ represents the average value of fungus X in all samples, and $\bar{Y}$ represents the average value of fungus Y in all samples, supposing the total number of samples is N, then the covariance of X and Y

can be expressed as:

$$Cov(X,Y) = \sum_{i=1}^{N} \frac{(X_i - \bar{X})(Y_i - \bar{Y})}{N} \tag{3}$$

The variance of the frequency of occurrence of fungus X can be expressed as:

$$Var(X) = \sum_{i=1}^{N} \frac{(X_i - \bar{X})^2}{N} \tag{4}$$

And the correlation coefficient of X and Y can be expressed as:

$$r(X,Y) = \frac{Cov(X,Y)}{\sqrt{Var(X)Var(Y)}} \tag{5}$$

We calculated the correlation coefficients of the frequency of occurrence among the 8 species in the table above, and the results are shown in the following picture:

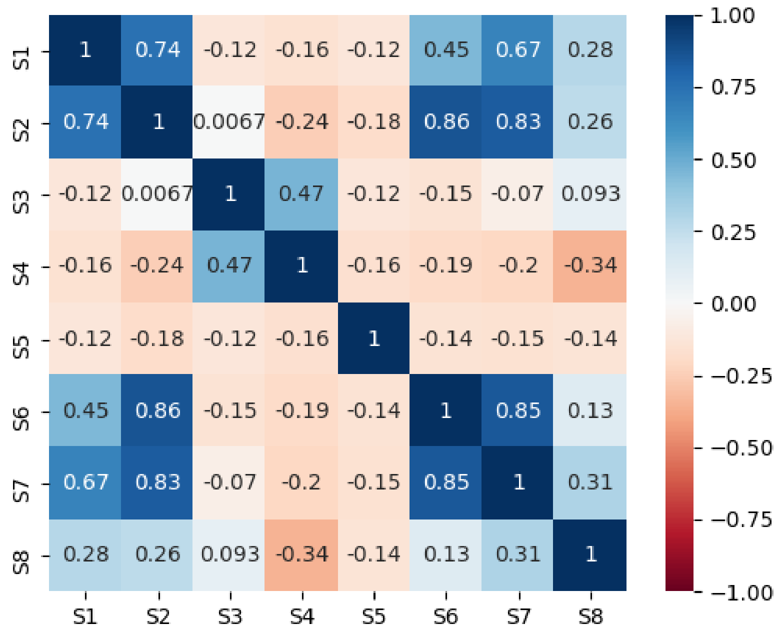


图 2: Correlation coefficient matrix between 8 species, blue indicates positive correlation, red indicates negative correlation.

From the above matrix, we can see that the species S2, S6 and S7 have a strong positive correlation, which shows that they often appear together. We can infer that they are in a symbiotic relationship or a competitive relationship with the same competition. Species S8 and S4 have a negative correlation, we infer that they may be a competitive relationship, and one of them is more competitive under certain circumstances.

Based on the above results, we summarized the interactions between fungi into **competition**, **parasitism**, and **symbiosis**.

4.2 Differential Equation Models of Fungal Interaction.

We summarized the interactions between fungi into three types. Based on the differential equation model of the biological population, we derived the differential equations for the interaction between fungi [10]. We only consider the interaction of two fungi in the following analysis.

4.2.1 Competition model

Competition appears to be the most common type of interaction between wood decay Fungi. Different hyphae living on the same piece of wood will not only compete for organic matter, water and space resources, but also produce chemical components that inhibit the growth of other hyphae. The antagonism between the hyphae varies with the spatial effect [4].

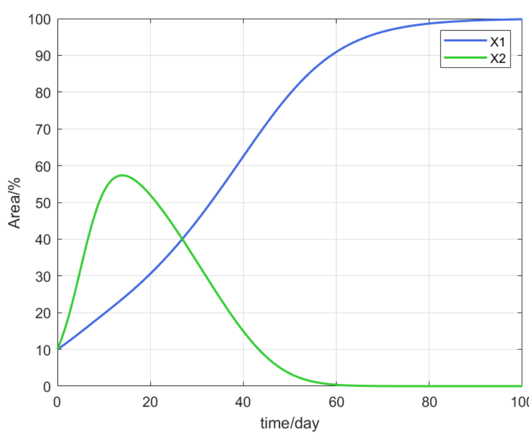
We assume that X_1 and X_2 are two kinds of fungi, and they are in a competitive relationship. We can get the following differential equation:

$$\frac{dS_1}{dt} = r_1 S_1 (1 - \frac{S_1}{S_m} - \frac{\sigma_2}{\sigma_1}\frac{S_2}{S_m}) \tag{6}$$

$$\frac{dS_2}{dt} = r_2 S_2 (1 - \frac{S_2}{S_m} - \frac{\sigma_1}{\sigma_2}\frac{S_1}{S_m}) \tag{7}$$

Where:S_m is the total surface area of wood, $S_i (i = 1, 2)$ is the surface area occupied by X_i, r_i is the growth rate of X_i, which is related to the expansion rate of mycelium, σ_i is the combative coefficient of X_i, which inhibits the growth of other fungi and reduces other fungi’ s influence.

In the two pictures below, we show two different competition results. In the first case, one fungus is more competitive than another, and the weaker one is eliminated. In the second case, the competition between the two fungi is the same, so they reach a dynamic equilibrium.



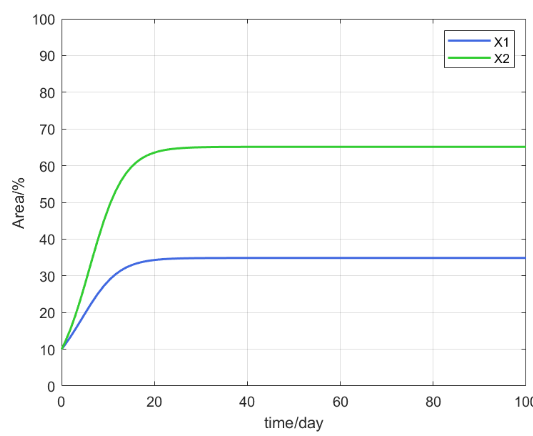


图 3: In the first picture, we set: $\sigma_1 = 1.8, \sigma_2 = 1, r_1 = 0.1, r_2 = 0.4$. Although X_2 grows faster than X_1, it is less competitive than X_1, so when the hyphae of X_1 and X_2 come into contact, X_2 is defeated. In the second picture, we set: $\sigma_1 = 1, \sigma_2 = 1, r_1 = 0.2, r_2 = 0.3$. X_2 grows faster and both X_1 and X_2 have the same competitive ability, so eventually they reach dynamic equilibrium.

4.2.2 Parasitism model

When one mycelium derives nutrients directly from another mycelium, a fungal parasitic relationship occurs. The host remains relatively healthy, but loses adaptability due to the absorption of nutrients by the fungus [5]. In some cases, fungal parasitism may be used as a temporary strategy for gaining competitor territory, and then the fungus will turn to wood decomposition to obtain nutrients [11]. For the sake of simplicity, we only consider the parasitic relationship when building the model here.

We assume that X_1 and X_2 are parasitic relations, and X_2 is parasitic on X_1 ,the following formula can be obtained:

$$\frac{dS_1}{dt} = r_1 S_1 (1 - \frac{S_1}{S_m} - \sigma_2 \frac{S_2}{S_m}) \tag{8}$$

$$\frac{dS_2}{dt} = r_2 S_2 (-1 + \rho_1 \frac{S_2}{S_m} - \frac{S_2}{S_m}) \tag{9}$$

Where: ρ_1 is embodied as the promotion effect of X_1 on the growth of X_2, and the meaning of other symbols remains unchanged.

We adjusted the parameters and drew the following two pictures:

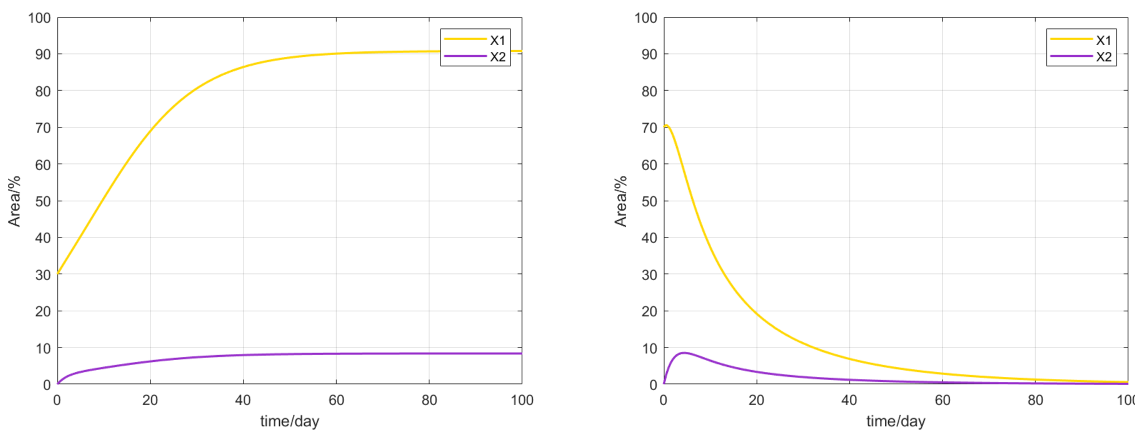


图 4: In the first picture, we set: $\sigma_1 = 1, \sigma_2 = 5, r_1 = 0.1, r_2 = 0.5$. The parasitic fungus X_2 and the host X_1 reache a balance. In the second picture, we set: $\sigma_1 = 8, \sigma_2 = 8, r_1 = 0.1, r_2 = 0.5$. In this case, the parasitic fungus destroyed the host and also caused its own demise.

The results show that X_1 can survive independently of X_2, X_2 cannot survive independently, and X_2 has an inhibitory effect on the growth of X_1.

4.2.3 Symbiosis model

There may also be symbiotic interactions between fungi. Symbiotic fungi can grow independently, but if they grow together, they will grow faster. This is because different fungi decompose and use different organic matter. For example, white rot fungi are better at decomposing lignin, and brown rot fungi are better at decomposing cellulose. But when a certain kind of resource is in short supply, such as water and space, then the growth-promoting interaction will turn into a growth-inhibiting interaction. Based on this principle, we established a fungal symbiosis model and simulated it in the case of sufficient resources.

We assume that X1 and X2 are symbiotic fungi, and obtain the following differential equation formula:

$$\frac{dS_1}{dt} = r_1 S_1 (1 - \frac{S_1}{S_m} + \rho_2 \frac{S_2}{S_m}) \tag{10}$$

$$\frac{dS_2}{dt} = r_2 S_2 (1 - \frac{S_2}{S_m} + \rho_1 \frac{S_1}{S_m}) \tag{11}$$

Where: ρ_i is embodied as the promotion effect of X_i on the growth of other fungi.

We adjusted the values of ρ_1 and ρ_2 and made the following two images:

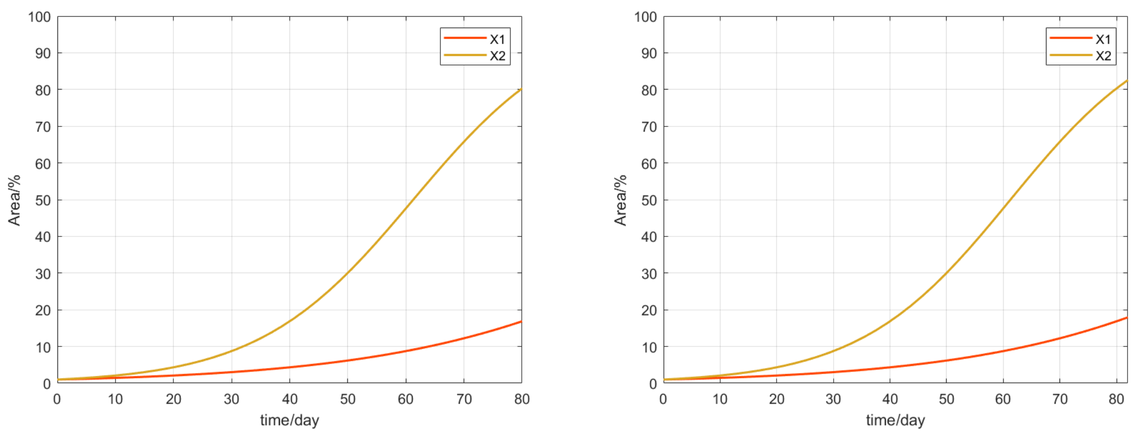


图 5: In the first picture, we set: $\rho_1 = 0.179, \rho_2 = 0.03, r_1 = 0.0375, r_2 = 0.075$. It takes 80 days for both fungi to occupy the entire area. In the second picture, we set: $\rho_1 = 0, \rho_2 = 0$,and the remaining parameters remain unchanged. In this case, it takes 82 days to occupy the entire area. This reflects the symbiotic interaction of the two fungi.

4.3 Cellular Automata Simulation

A cellular automaton consists of a regular grid of cells, and each cell has a finite number of states, such as on and off. The grid can be any finite number of dimensions. For each cell, relative to the specified cell, a group of cells called its neighborhood is defined. Select the initial state (time t = 0) by assigning a state to each unit. According to some fixed rules (usually a mathematical function), the new state of each cell is determined according to the current state of the cell and the state of neighboring cells, creating a new generation (increasing t by 1). Generally, the rules for updating the cell state are the same for each cell, do not change over time, and apply to the entire grid at the same time.

The growth of wood-rot fungi is similar to the growth of cells, so we use the cellular automata model to simulate the interaction of the two fungi. In the next iteration, the probability of cell expansion is related to the growth rate of the fungus, that is, the extension rate of the fungus. We assume that nutrients are evenly distributed in the fungal petri dish, so when there is sufficient space, the probability of fungus growing in the surrounding direction is the same, as shown in the following figure:

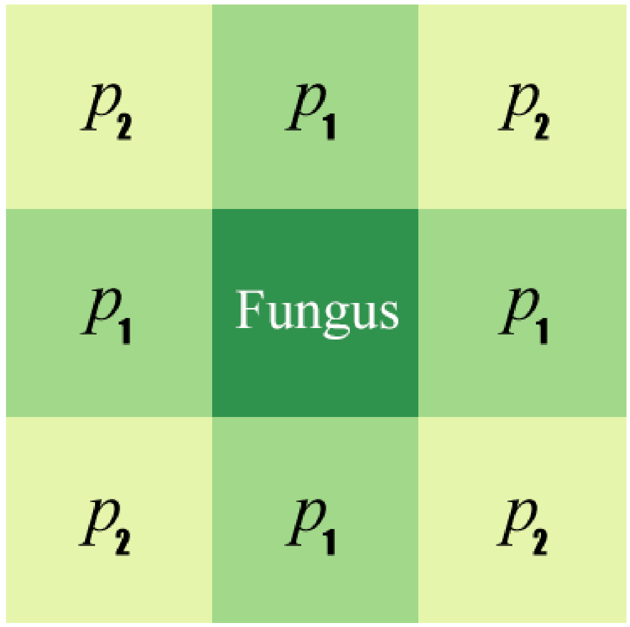


图 6: The middle grid has hyphae, so in the next iteration, the four adjacent grids have a probability of at least p_1 to produce hyphae, and the four diagonal grids have a probability of at least p_2 to produce hyphae.

It can be seen that when there is hypha in a grid, then the grids around it have a certain probability to produce hypha in the next iteration. The probability of a grid producing hyphae in the next iteration is the cumulative probability that the surrounding 8 grids will produce hyphae at this point. The formula can be expressed as:

$$p_{ij} = \sum_{a=-1}^{1} \sum_{b=-1}^{1} q_{(i+a)(j+b)} \tag{12}$$

Where: p_{ij} is the probability of hyphae in the grid $(i,\ j)$ in the next iteration, $q_{(i+a)(j+b)}$ is the effect of grid $(i + a,\ j + b)$ on the probability of generating hyphae on grid $(i,\ j)$.

Assuming that X_1 and X_2 are two kinds of fungi, and X_1 grows faster than X_2, we simulated three situations: X_1 destroys X_2, X_1 and X_2 maintain dynamic balance for a long period of time, and X_2 destroys X_1. There are a total of 300×300 grids. The probability of hyphae in each grid is:

4.3.1 X_1 destroys X_2

In this case, we did not set the fungus's combativeness, and the probability of the fungus expanding outward remained constant throughout the process. That is, the rate of mycelial growth remains unchanged. The formula can be expressed as:

$$p_{ij} = \sum_{a=-1}^{1} \sum_{b=-1}^{1} q_{(i+a)(j+b)}$$

The formula is the same as above.

We set the probability of the middle grid to the surrounding 8 grids to be the same, for X_1, we set it to 0.1, and for X_2, we set it to 0.3. The image below shows the result:

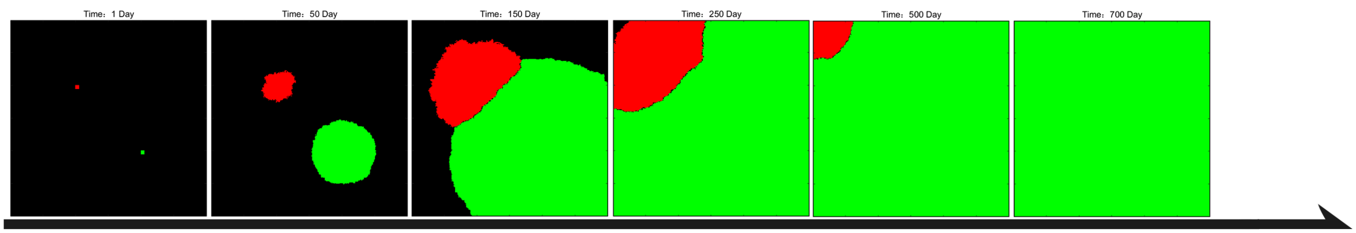


图 7: X_2 (green) grew faster than X_1 (red), and eventually X_2 defeated X_1.

We came to the conclusion that when environmental factors (space, moisture) are not considered, and the fungi are equally combative, the fungi that grow faster are more advantageous.

4.3.2 Maintaining dynamic balance

In the above model, we did not consider the inhibitory effect of the environment on the growth of fungi. According to the logistic model, the later growth rate of population growth should slow down. We think this rule is also applicable to the fungal growth model. The formula is rewritten as:

$$p_{ij} = (1 - \frac{N}{90000}) \sum_{a=-1}^{1} \sum_{b=-1}^{1} q_{(i+a)(j+b)} \tag{13}$$

Where:N is the number of cells occupied by the fungus in the current iteration. 90000 is the total number of grids.

We do not change other parameters and get the following image:

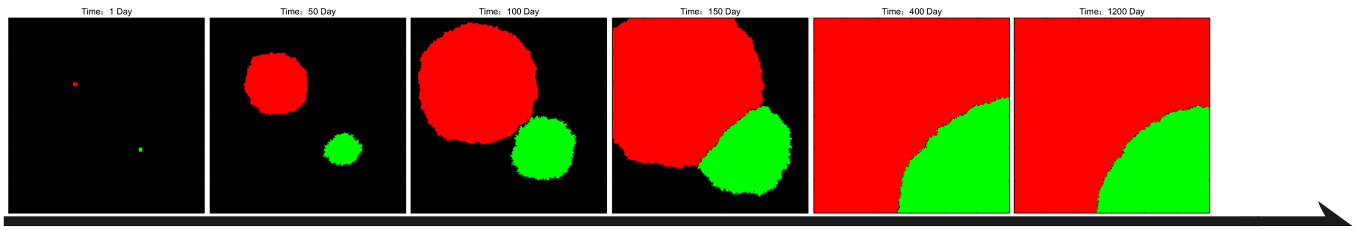


图 8: X_2 (red) grew faster than X_1 (green), but X_2 did not defeat X_1, they maintained a long-term balance.

We came to the conclusion that when considering environmental constraints, it is easier to achieve a balanced state between two fungi with different growth rates.

4.3.3 X_2 destroys X_1

In the above two models, we did not consider the combativeness of fungi. In this model, we introduce this situation. We add one more item to the above formula:

$$p_{ij} = (1 - \frac{N_1}{90000} - \frac{\sigma_2}{\sigma_1}\frac{N_2}{90000}) \sum_{a=-1}^{1}\sum_{b=-1}^{1} q_{(i+a)(j+b)} \tag{14}$$

Where:N_1 is the grid occupied by fungi, N_2 is the grid occupied by competitors, σ_1 is the combativeness of fungi, and σ_2 is the combativeness of competitors.

We adjust the size of the parameter so that the slow-growing fungus defeats the fast-growing fungus, as shown in the following figure:

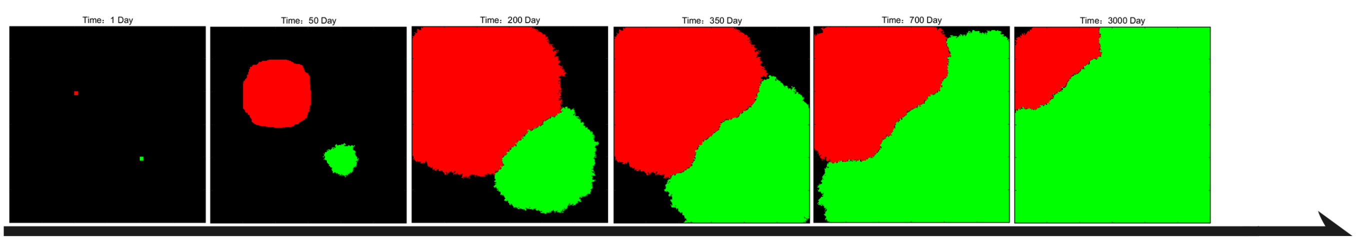


图 9: X_2 (red) grows faster than X_1 (green), but X_2 is defeated by X_1.

We have concluded that even fungi with a slow growth rate in the early stage may eventually become the dominant species.

5 Climate Model of Fungi

In this section, we mainly discuss the two main climatic factors, temperature and precipitation, and the influence of fungi's own factors on the extension rate of fungal hyphae. And established a statistical model to predict the effect of fungal hyphae extension rate and environmental changes.

5.1 Statistical Model of Fungal Hyphae Growth Rate

According to the paper [1], the hypha of fungi is the vegetative part of fungi, which has a certain functional differentiation, is an important structure for fungi to obtain nutrients. Since the interaction of fungi is closely related to the competition between fungi and various nutrients, in order to better reflect the interaction between fungi, we turn to analyze the relationship between the growth rate of fungal hyphae and environmental factors such as temperature and humidity.

5.1.1 Variable selection and data processing

According to the data in the paper [7], we have established a statistical model based on multiple linear regression. The variable selection and data processing process is as follows:

The paper [2] pointed out that *the distinction between fast-growing competitors and slow-growing stress-tolerant individuals may also apply to fungi and relate to changes in decomposer ability through successional time.* On this basis, Lustenhouwer et.al [6] puts forward the term dominance-tolerance trade-off. In their opinion *the moisture trade-off is the difference between each isolate's competitive ranking and their moisture niche width, both scaled to [0,1].* This explanation fully balances the trade-off between fungi's strong viability and strong competitiveness, and reflects the inherent differences in competitiveness (decomposition rate) and stress resistance of different fungal species. Under this interpretation, we first unitize the information of the water niche width in the data, and combine it with the unitized fungal competitiveness (competitive ranking in the data) as the first independent variable of the linear regression model.

The two natural environmental factors, temperature and humidity, may have a great impact on the activity of fungi. Therefore, we selected the two indicators of annual average temperature and annual average precipitation in the data as the other two independent variables of the linear regression model to represent temperature and humidity respectively. After that, we used the hypha extension rate in the data of the paper as the dependent variable, using the independent variables and dependent variable data mentioned above to establish a linear regression model.

5.1.2 Model establishment and solution

Based on the data above, $y$represents the hypha extension rate , x_1 represents the annual average temperature ($^\circ C$), x_2 represents the annual average precipitation (100mm), and x_3 represents the moisture trade-off (a constant between -1 and 1), b is a constant term, our multiple linear regression model is established as follows:

$$y = \omega_1 x_1 + \omega_2 x_2 + \omega_3 x_3 + b \tag{15}$$

Let $X = \begin{pmatrix} x_1 \\ x_2 \\ x_3 \end{pmatrix}, \omega = \begin{pmatrix} \omega_1 \\ \omega_2 \\ \omega_3 \end{pmatrix}$ the formula above can be matrixed as:

$$y = \omega X + b \tag{16}$$

According to the least squares method, when the mean square error of the linear model is the smallest, use m to represent the number of samples (here 37), and the values of ω and b are as follows

$$\hat{\omega} = (X^T X)^{-1} X^T \tag{17}$$

$$\hat{b} = \frac{1}{m} \sum_{i=1}^{m} (y_i - \omega X_i) \tag{18}$$

In order to consider the effects of all variables in pairs (x_1x_2,x_1x_3,x_2x_3) and their combined effects($x_1x_2x_3$) on our linear regression model, we improved our linear Regression model, adding x_1x_2, x_1x_3, x_2x_3 and $x_1x_2x_3$ items, the regression model at this time is:

$$y = b_0 + b_1x_1 + b_2x_2 + b_3x_3 + b_4x_1x_2 + b_5x_1x_3 + b_6x_2x_3 + b_7x_1x_2x_3 \tag{19}$$

Linear regression is performed through matlab software, and the code is shown in appendix C. In the process of solving the parameters, the data is further processed to remove the abnormal data with zero points in the residual confidence interval. The parameter results are as follows:

Regression coefficient	Coefficient estimate	Confidence interval
b_0	-1.1399	(-3.5390 , 1.2592)
b_1	0.2267	(0.0812 , 0.3722)
b_2	0.4608	(0.2125 , 0.7090)
b_3	-7.4617	(-13.8041 , -1.1194)
b_4	-0.0185	(-0.0307 , -0.0062)
b_5	-0.3505	(-0.0822 , 0.7832)
b_6	0.4299	(-0.2090 , 1.0689)
b_7	-0.0434	(-0.0775 , -0.0093)
$R^2 = 0.8691, F = 23.7062, p < 0.0001, s^2 = 1.4579$		

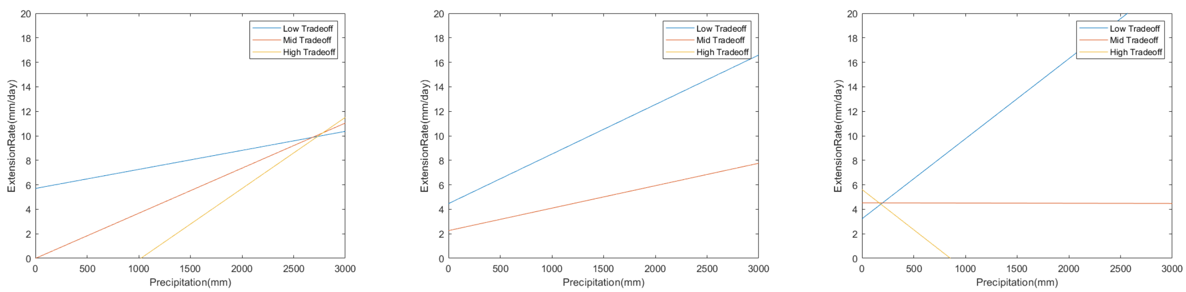
5.1.3 Model analysis

According to further calculations, the value of R^2 of the model is 0.8691, indicating that the model has a strong predictive significance. When the parameter $\alpha = 0.1$, only the constant item b_0 and cross item b_5, b_6 contains zero in the obtained confidence interval, which shows that the effect of the b_0 and b_5, b_6 item may not be significant. The confidence intervals of other variables do not contain zeros, and their influence on y is significant.

In summary, our linear regression model with cross-terms takes into account the three independent variables and their cross-effects on the hypha extension rate.

5.2 The Applications of Climate Model

Based on the above model, the influence of temperature, precipitation and fungi's own factors on the growth rate of fungal hyphae can be predicted. The following analysis respectively assumes that the annual average temperature is $y = 5°C, 15°C, 25°C$, and moisture trade-off is -1,0,1. Ignoring the influence of other climatic factors, analyze the relationship between precipitation and the growth rate of fungal hyphae as figures below :



(a) $5°C$ (b) $15°C$ (c) $25°C$

图 10: The relationship between fungal hyphae extension rate and precipitation

According to the above figure, when the temperature is low (as 10(a)) and the environment is harsh, the fungus with larger moisture trade off can better adapt to the environment with higher humidity, while the competitive fungus can adapt to other humidity conditions. However, when the temperature is high (as 10(c)) and the environment is more suitable, the water niche width of individuals with larger moisture trade off is larger, and the growth rate is higher under low precipitation, while the fungi with small moisture trade off have higher growth rate under high precipitation.

6 Integrated Models of Fungal Communities

6.1 Interactions Between Fungal Communities

Since the competition between fungi is the most obvious, in order to simplify the model, we only consider the competition between fungi here. We assume that the k fungi $X_1, X_2, \cdots X_k$ form a community, and these k fungi have mutual inhibition. Their combative coefficients can form a vector:

$$\sigma = \begin{bmatrix} \sigma_1, & \sigma_2, & \sigma_3 & \cdots & \sigma_k \end{bmatrix} \tag{20}$$

Their area can also form a vector:

$$S = \begin{bmatrix} S_1, & S_2, & S_3 & \cdots & S_k \end{bmatrix} \tag{21}$$

We can derive a differential equation model for the growth of the i-th fungus:

$$\frac{dS_i}{dt} = r_i S_i (1 - \sigma \frac{S^T}{S_m}) \tag{22}$$

The above equation reflects the inhibitory effect of other fungi on Fungus X_i and the inhibitory effect of environmental resources on Fungus X_i.

6.2 The Impact of Climate on Fungal Communities

Here we set the environmental parameters corresponding to dry and wet areas as follows:

Climate / Traits	arid	semi-arid	temperate	arboreal	rain forests
Temperature	15	15	15	15	25
Precipitation	150	300	600	1200	2500

The moisture trade-off is the difference between each Fungi's competitive ranking and their moisture niche width [6]. This is an important indicator to distinguish the nature of fungi. The fungi that make up the community have different moistrue-trade off. In order to simplify the model, we assume that the fungi X_1, X_2, X_3 have moistrue trade-off -0.1, 0, 0.1 respectively. We use the climate model to calculate the expansion rate of mycelium. Their corresponding growth rates in different environments are listed in the following table:

ExtensionRate / Climate / TradeOff	arid	semi-arid	temperate	arboreal	rain forests
-0.1	2.79	3.10	3.71	4.94	5.99
0	2.54	2.81	3.36	4.46	4.49
0.1	2.28	2.52	3.01	3.97	2.98

The probability of cell expansion is positively related to the rate of fungal extension. The expected value of the cell expansion distance is equal to the extension rate of the fungus. We assume that the side length of a cell is 6mm, we can get the probability in the following table:

P / Climate / TradeOff	arid	semi-arid	temperate	arboreal	rain forests
-0.1	0.465	0.517	0.618	0.823	0.998
0	0.423	0.468	0.560	0.743	0.748
0.1	0.380	0.420	0.502	0.662	0.497

The greater the value of Moistrue-trade-off, the stronger the competition. We set σ_1, σ_1, and σ_1 to 1, 1.5, and 3. σ is expressed as:

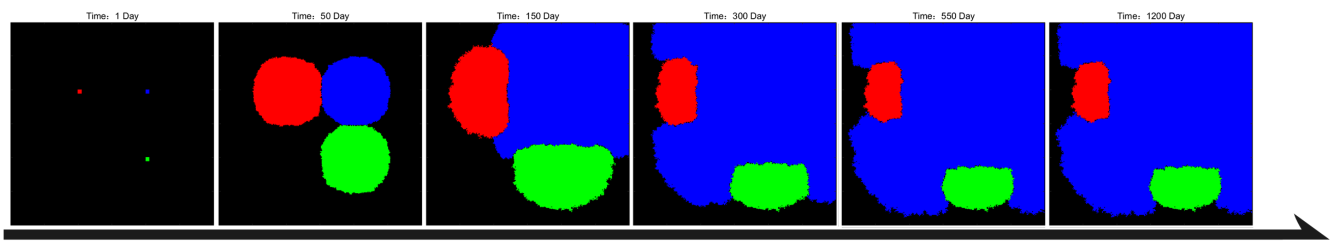
$$\sigma = \begin{bmatrix} 1, & 1.5, & 3 \end{bmatrix}$$

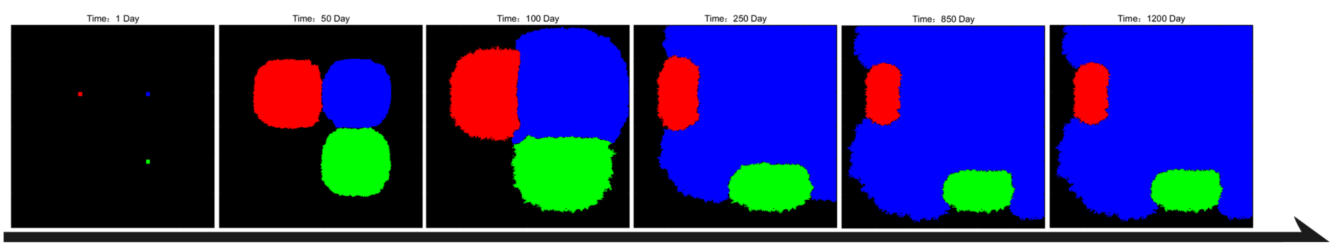
We set S_1, S_2, and S_3 to 36, and we can get the vector S:

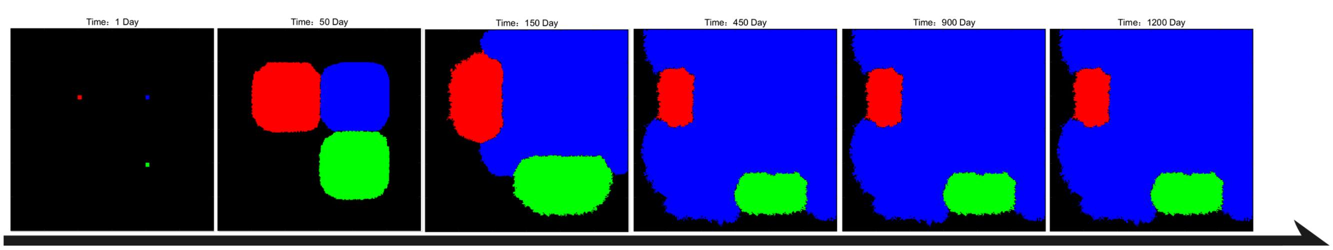
$$S = \begin{bmatrix} 36, & 36, & 36 \end{bmatrix}$$

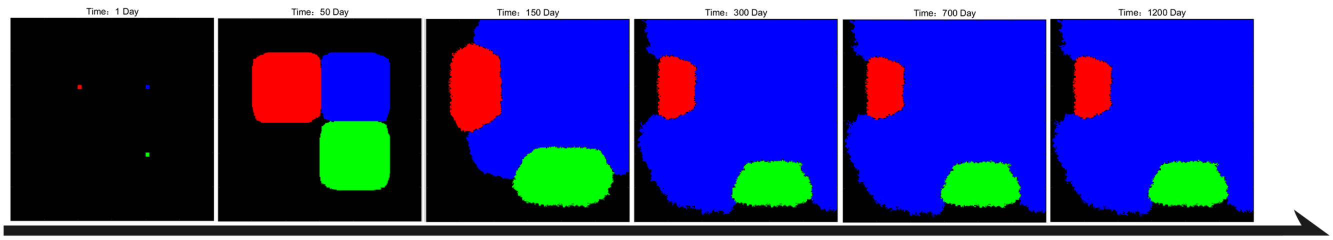
This means that each fungus initially occupies 36 grids.

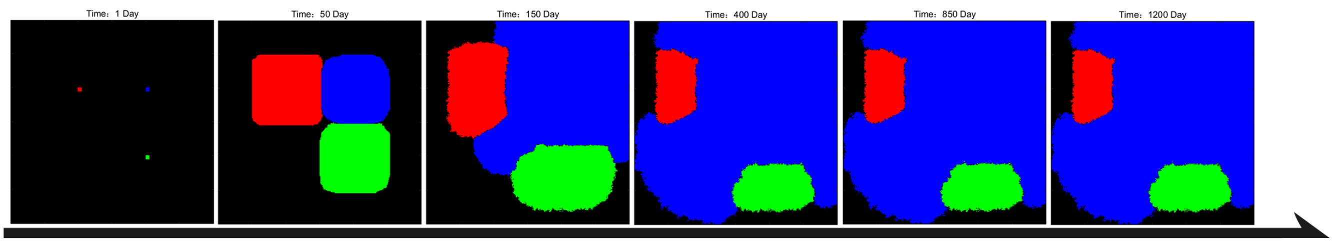
We used the above data to simulate each environmental situation, and the results are presented below. The pictures from top to bottom correspond to arid, semi-arid, temperate, arboreal and rain forests. Red, green, and blue correspond to X_1, X_2, and X_3 respectively.











6.3 The Composition and Decomposition Rate of Fungal Communities.

We have previously derived models of fungal extension rate and wood decomposition rate. The faster the fungal extension rate, the higher the wood decomposition rate. The interaction between fungi may promote the rate of fungal extension, and may also inhibit the rate of fungal extension. We use cellular automata to simulate the spread of different fungal communities and calculate the number of days it takes for them to fill the entire petri dish(We assume the climate condition is temperate). Then we calculate the average extension rate of different fungal communities, and the results are as follows:

In order to consider the relationship between hyphae extension rate and environmental factors. Here we set the environmental parameters corresponding to dry and wet areas as follows:arid area: $x_1 = 15°C, x_2 = 150mm$，semi-arid area: $x_1 = 15°C, x_2 = 300mm$,temperate area:$x_1 = 15°C, x_2 = 600mm$,arboreal area:$x_1 = 15°C, x_2 = 1200mm$,tropical rain forests:$x_1 = 25°C, x_2 = 2500mm$.

combinations	days	hyphae	k
-0.1	310	5.81	0.63
0	402	4.48	0.51
0.1	358	5.03	0.56
-0.1,0	300	6	0.65
-0.1,0.1	290	6.21	0.67
0,0.1	320	5.63	0.61
-0.1,0,0.1	270	6.67	0.71

The trends of the corresponding 7 curves are as follows:

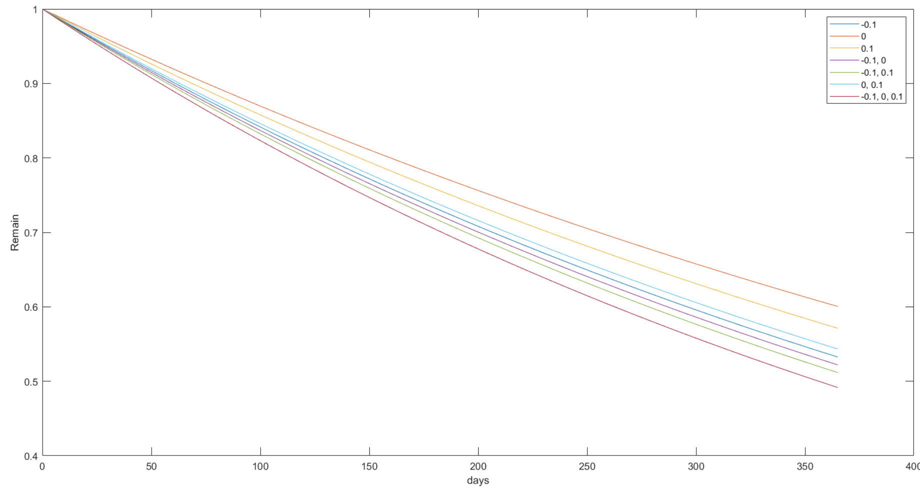


图 11: trends of 7 curves

The model of comprehensive moisture tradeoff=-0.1, 0, 0.1 has the largest parameter k and the fastest decomposition rate. It can be concluded that the biodiversity of the fungal community helps to increase the decomposition rate of the fungal community. Besides, according to the thesis [3], fungi have an important influence on the variability and productivity of the ecosystem.

7 Strengths and Weaknesses

7.1 Strengths

- The model predicts the relationship between the decomposition rate of fungi or the growth rate of fungi and environmental factors, which has certain practical value.
- The cellular automata model used when analyzing interspecies relationships can more intuitively reflect the properties of various inter-species relationships and the changing trends of various groups under different conditions.

7.2 Weaknesses

- The confidence interval of the parameters obtained by solving the linear model contains zero points, which means that there may be some terms that are not significant. And due to the limitation of the linear model, the model is not accurate enough to predict under extreme temperature and precipitation.
- The forms of differential equation models and comprehensive models are relatively complex.

8 A Chief Introduction

The carbon cycle describes the process of the exchange of carbon throughout the geochemical cycle of the Earth.As an important part of the ecosystem, the decomposer realizes the process of decomposing the organic matter accumulated in the remains of animals and plants into inorganic matter such as CO_2 and water, which is of great significance in the carbon cycle of the ecosystem. Fungi are the most important type of organisms among decomposers. How to predict the growth rate of fungi and the rate at which fungi decompose organic matter, as well as understanding the interaction of various fungi as decomposers, is one of the most important contents of our research on the carbon cycle.

Considering that the number of fungi in nature is in a dynamic equilibrium process, the decomposition rate of wood remains unchanged. In this way, an exponential model similar to the Olson model [8] is established. We realize that the Olson model does not take into account the problem that the average turnover period of litter and the average lifespan of litter are often not equal due to the accumulation of soil organic matter, and we added an index term to modify the Olson model.

Fungal hyphae are the vegetative body of fungi and the main organ for fungi to obtain nutrients from the outside world. Therefore, the growth rate of fungal hyphae is closely related to the rate at which fungi decompose organic matter. Based on this, we established a linear regression model between fungal hyphae growth rate and fungal decomposition rate.

After that, we started from the three species relationships that may exist between fungi: "cooperation", "competition", and "parasitic", and constructed a differential equation model that reflects the relationship between specific species. At the same time, we pointed out that competitive relationships often occur in poor environmental conditions, where living resources are insufficient, and the cooperative relationship is related to the types of hydrolysis enzymes controlled by genes. After that, we used the cellular automata model to simulate various inter-species relationships and determined the trend of the number of fungi under various inter-species relationships.

Environmental factors such as temperature and humidity also have a greater impact on the activity of fungi. In order to analyze the influence of environmental factors, we established a generalized linear regression model of environmental factors on the extension rate of fungal hyphae based on annual average temperature and annual average precipitation data to quantify the impact of environmental factors and the moisture trade-off with the fungi itself on the extension rate of fungal hyphae.

According to the thesis [3], fungi have an important influence on the variability and productivity of the ecosystem. Connecting all the four models mentioned above, we established a comprehensive fungal population model, and based on this model, we comprehensively discussed the possible combinationsof various fungi, and predicted the mycelial growth rate and wood decomposition rate of the fungi under various combinations. From the mathematical level, it is concluded that the wood decomposition rate is faster when there are more types of fungi. This reflects the positive impact of fungal biodiversity on the ecological environment.This also further reminds us of the important positive role of decomposers like fungi in the ecosystem.

Our model systematically explained the relationship between the decomposition rate of fungi or the growth rate of fungi and environmental factors. It also explains the interspecies relationship and interaction of fungi, and further illustrates the importance of decomposers for maintaining the diversity of ecosystems.In addition, this model still has certain unreasonable points in the establishment of linear regression model, but it still has certain reference value for the actual demand of analyzing the decomposition rate of fungi.

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Appendices

附录 A Python code for data processing

```
import pandas as pd
import numpy as np
from sklearn.linear_model import LinearRegression
from sklearn.model_selection import train_test_split
from sklearn import metrics
import matplotlib.pyplot as plt
from scipy.stats import pearsonr

file="\\Dataset\\Fungal_climate_data.csv"
pcsv=pd.read_csv(file)
#Standardization
pcsv['water.niche.width']=pcsv['water.niche.width'].apply(lambda x:x/4.96)
pcsv.insert(loc=len(pcsv.columns),column="MoistureTradeOff",
                    value=pcsv["water.niche.width"]-pcsv["ranking"])
pcsv=pcsv.sort_values(by="MoistureTradeOff",ascending=True)
pcsv.to_csv("Sorted.csv")
#PrepareDataset
X=pcsv.loc[:,('Annual.Mean.Temperature','Annual.Precipitation'
                                ,'MoistureTradeOff')].values
y=pcsv.loc[:,"rate.0.5"].values.astype(np.float)
X_train, X_test, y_train, y_test = train_test_split(X, y,
                         test_size=0.2, random_state=532)
#Train
model=LinearRegression()
model.fit(X_train,y_train)
print(model.coef_,model.intercept_)
y_pred=model.predict(X_test)
#Analyze
MSE=metrics.mean_squared_error(y_test,y_pred)
print(MSE)
print(metrics.r2_score(y_test,y_pred))
print(pearsonr(X_test[:,0],y_pred))
print(pearsonr(X_test[:,1],y_pred))
print(pearsonr(X_test[:,2],y_pred))
#Figure
plt.plot(np.arange(37),y,label="Actual",color="blue")
plt.plot(np.arange(37),model.predict(X),label="Predicted",color="orange")
plt.show()
```

附录 B Python code for data visualization

附录 C Matlab code for linear regression

```
clear
M1=dlmread('Sorted.txt');  %Read file
%for j=1:4
%    M(:,j)=M1(:,j+1);
%end
```

```
M=M1;
k=0;
for i=1:37
        k=k+1;
        x1(k)=M(i,1); % temp
        x2(k)=M(i,2); % humidity
        x3(k)=M(i,3); % tradeoff
        y(k)=M(i,4);  % out
end
k,
% Variable handling
X1=[ones(k,1),x1',x2',x3']; %Normal model
%Model added x1*x2,x1*x2*x3
X1=[ones(k,1),x1',x2',x3',x1'.*x2',x1'.*x3',x2'.*x3',x1'.*x2'.*x3'];
[b1,bint1,r1,rint1,s1]=regress(y',X1,0.1); %linear regress
b1,bint1,s1

pause
% Remove outliers
n1=k;
r0=0;
for n=1:n1
    if rint1(n,1)*rint1(n,2)>0 % Confidence interval does not contain zero
        r0=r0+1;
        rr(r0)=n;
    end
end
k=1;
for i=1:n1
    if i==rr(k)
        x1(i)=0; x2(i)=0;y(i)=0;
        k=k+1;
    end
if k>r0
break
end
end
nn1=0;
for i=1:n1
    if x1(i)>0;
        nn1=nn1+1;
        yn1(nn1)=y(i); % out
        xn1(nn1)=x1(i); % temp
        xn2(nn1)=x2(i);  % humidity
        xn3(nn1)=x3(i); % tradeoff
       end
    end
nn1
%XX1=[ones(nn1,1),xn1',xn2',xn3'];
%Model added x1*x2,x1*x2*x3
XX1=[ones(nn1,1),xn1',xn2',xn3',xn1'.*xn2',xn1'.*xn3',xn2'.*xn3',xn1'.*xn2'.*xn3'];
[bb1,bbint1,rr1,rrint1,ss1]=regress(yn1',XX1,0.1); % linear regress
bb1,bbint1,ss1
```

附录 D Matlab code for visualizing linear regression results

```
x1=25;%temperature
x3=-1;%tradeoff
x2=0:0.001:50;%precipitation
y=-1.1399+0.2267.*x1+0.4608.*x2-7.4617.*x3-0.0185.*x1.*x2+0.3505.*x1.*x3+
0.4299.*x2.*x3-0.0434.*x1.*x2.*x3;

plot(100*x2,y);axis([0 5000 0 20]);hold on
x3=0;

y=-1.1399+0.2267.*x1+0.4608.*x2-7.4617.*x3-0.0185.*x1.*x2+0.3505.*x1.*x3+
0.4299.*x2.*x3-0.0434.*x1.*x2.*x3;
plot(100*x2,y);axis([0 5000 0 20]);hold on
x3=1;

y=-1.1399+0.2267.*x1+0.4608.*x2-7.4617.*x3-0.0185.*x1.*x2+0.3505.*x1.*x3+
0.4299.*x2.*x3-0.0434.*x1.*x2.*x3;
plot(100*x2,y);axis([0 5000 0 20]);hold on
legend("Low Tradeoff","Mid Tradeoff","High Tradeoff")
xlabel("Precipitation(mm)")
ylabel("ExtensionRate(mm/day)")
```

附录 E Matlab code for ODE solving

附录 F Matlab code for cellular automata

```
%Wood surface area
m = 300;
n = 300;
%The direction in which the mycelium grows
d = {[1,0], [0,1], [-1,0], [0,-1], [1,1], [-1,1], [-1,-1], [1,-1]};

%The extension rate of fungi(Fungi A and Fungi B)
pa = [0.4, 0.4, 0.4, 0.4, 0.4, 0.4, 0.4, 0.4];
pb = [0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1];
pc = [0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1];

%Combative Ability
sigma_a = 1;
sigma_b = 1.5;
sigma_c = 3;

E = 0;
Fa = 1;
Fb = 2;
Fc = 3;

S = zeros(m,n);
for i = 100:105
    S(i,100:105) = 1;
end

for i = 200:205
```

```
    S(i,200:205) = 2;
end

for i = 100:105
    S(i,200:205) = 3;
end

%S(m/4, n/4) = 1;

imh = image(cat(3, S==Fa, S==Fb, S==Fc));
axis image;

for i = 1:3000
    %Calculate the cumulative probability of fungal A growth
    Fanum=length(find(S==Fa));
    Fbnum=length(find(S==Fb));
    Fcnum=length(find(S==Fc));
    Enum=length(find(S==0));

    suma = zeros(size(S));
    for j = 1:length(d)
        suma = suma + pa(j) * (circshift(S,d{j})==Fa);
    end

    ppa = 1-Fanum./90000-(sigma_b./sigma_a).*(Fbnum./90000)-(sigma_c./sigma_a).*(Fcnum./90000);
    suma = suma*ppa;

    sumb = zeros(size(S));
    for j = 1:length(d)
        sumb = sumb + pb(j) * (circshift(S,d{j})==Fb);
    end

    ppb = 1-Fbnum./90000-(sigma_a./sigma_b).*(Fanum./90000)-(sigma_c./sigma_a).*(Fcnum./90000);
    sumb = sumb*ppb;

    sumc = zeros(size(S));
    for j = 1:length(d)
        sumc = sumc + pc(j) * (circshift(S,d{j})==Fc);
    end

    ppc = 1-Fcnum./90000-(sigma_a./sigma_c).*(Fcnum./90000)-(sigma_b./sigma_c).*(Fbnum./90000);
    sumc = sumc*ppc;

    %the current state of S
    isE = (S==E);
    isFa = (S==Fa);
    isFb = (S==Fb);
    isFc = (S==Fc);

    %the new growing fungus A
    growa = rand(m,n)<suma;
    growb = rand(m,n)<sumb;
    growc = rand(m,n)<sumc;

    %the new state of S
```

```
    SE = zeros(m,n);
    SFa = isFa | growa;%Logical expression symbols used or
    SFb = isFb | growb;
    SFc = isFc | growc;
    %the new S
    S = SE + 1*SFa + 2*SFb + 3*SFc;

    S(1,1:300) = 0;
    S(300,1:300) = 0;
    S(1:300,1) = 0;
    S(1:300,300) = 0;

    Fanum=length(find(S==Fa));
    Fbnum=length(find(S==Fb));
    Fcnum=length(find(S==Fc));
    Enum=length(find(S==0));

    figure(1);
    set(imh, 'cdata', cat(3, isFa, isFb, isFc) )
    str1=['Fungi A: ',num2str(Fanum),' Fungi B: ',num2str(Fbnum),' Fungi C: ',num2str(Fcnum)];
    str2=['Time: ',num2str(i),' Day'];
    title({str1,str2});
    drawnow
    %pause(0.01);
end
```

附录 G　Frequency of co-occurrence of fungi

表 3: The abundances of the 8 species in the 18 sites. Species with less than 15 occurrences (shown by "0") were excluded from the analyses.

site	S1	S2	S3	S4	S5	S6	S7	S8
1	0	41	28	0	0	0	44	135
2	0	0	29	185	0	0	0	0
3	31	88	0	0	0	21	277	138
4	0	0	0	123	0	0	0	0
5	18	119	0	0	0	39	103	43
6	0	0	0	104	0	0	0	0
7	0	84	0	0	0	58	281	63
8	0	0	0	24	0	0	0	0
9	0	0	0	0	0	0	0	16
10	0	0	0	0	0	0	0	21
11	0	0	0	0	0	0	0	36
12	0	0	0	0	0	0	0	27
13	0	0	0	0	0	0	0	56
14	0	18	0	0	0	0	0	17
15	0	0	0	0	16	0	0	15
16	0	0	0	0	25	0	0	28
17	0	0	0	0	0	0	0	263
18	0	0	0	0	0	0	0	25