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Summary

The carbon cycle is a significant component of life on the earth. Decomposition of plant material and woody fibers, conducted by fungi, is a process of great importance in this cycle. Research has done recently identified fungi traits determining decomposition rates and figured out links between certain traits.

For Model 1, we begin with the mathematical models aimed at describing the decomposition process of a certain type of fungi by figuring out the formula, which relates decomposition rate to extension rate linearly. Finally, the plots of 34 species are put forward.

For Model 2, it is determined that extension rate and moisture tolerance are the only two factors to be analyzed. We first take the extension rate into consideration. Since temperature and moisture are the key factors affecting extension rate-moisture graph are drawn and piecewise linear function are figured out, fitting the curves. Then a multiple linear regression is done to figure out the relation of decomposition rate and the features of different fungi.

For Model 3, we are intended to analyze the interactions of different types of species in both the short and long term. Firstly, we set up an equation set to describe the microcosmic situation concerning single species action. Then we use cellular automaton to simulate the situation of multiple species interaction in the short term.

For Model 4, we are required to compare different species of fungi and reasonable combinations of species and describe their relative advantages and disadvantages in a different environment. So we select multiple niche widths as the index to measure the advantages and disadvantages and use a formula to calculate the niche width.

For Model 5, we are supposed to figure out the relation of diversity and decomposition efficiency. Then a model showing the significance of diversity in different environments that differ in rate of change is required. So we build a model simulating the real world fungi community by plotting digraph. Then we abstract the model and put forward a matrix equation. Finally, based on outcomes in the previous sections, we figure out the formula of the efficiency related to diversity and decomposition factors. It is showed that decomposition efficiency have positive correlation with the diversity. Also, use the variance as an evaluation of stability, it turns out that the stability is positively related to diversity.

Keywords: Carbon Cycle; Fungi; Decomposition; Linear regression; Cellular automata; Differential equation model

Contents

1	Introduction	3
1.1	Problem Background	3
1.2	Restatement of the problem	3
1.3	Our Approach	3
1.4	The Data	4
2	General Assumptions	4
3	Model Preparation	4
4	Model 1	5
4.1	A linear model of decomposition rate and extension rate	5
4.2	Result	5
5	Model 2	5
5.1	lot fungal growth rate versus humidity and temperature	6
5.2	Linear Fitting	6
6	Model 3	7
6.1	Single species model in microcosmic level	8
6.2	Cellular Automaton	8
6.3	The interactions of long term	8
6.4	The analysis of Model 2	9
6.5	Result	9
7	Model 4	9
7.1	Multiple niche width	9
7.2	Result	9
8	Model 5	9
8.1	Result	11
9	Strengths and Weaknesses	11
9.1	Strengths	11

9.2 Weaknesses	11
10 The Article: Recent developments in the understanding of the roles fungi play in ecological systems	11
Appendices	13
Appendix A First appendix	13

1 Introduction

1.1 Problem Background

The carbon cycle refers to the whole process of the exchange of carbon on the earth, which is a significant component of life around the world. Being part of the process of decomposition of compounds, breakdown of plant material and woody fibers, conducted by fungi, is of great necessity in this cycle. The research did recently identified fungi traits determining decomposition rates and figured out associations between certain traits. It turns out the growth rate of fungi is negatively connected to the resilience to changes. While a great number of traits concerning fungi are examined in the research mentioned above, two traits are laid importance in the extension rate of fungi and the tolerance to moisture.

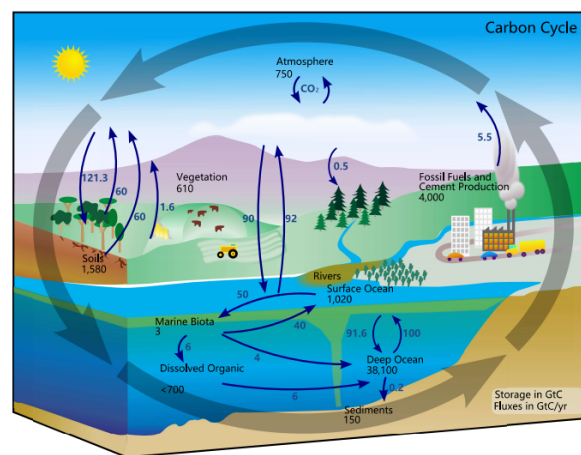


Figure 1: Carbon Cycle

1.2 Restatement of the problem

Build a mathematical model to identify the relation between the decomposition of ground litter and woody fibers caused by fungal activity and the amount of a certain type of fungi. Based on the model above, figure out a comprehensive model that takes the interactions between different types of fungi into consideration. make an analysis of the mutual effect between different types of fungi in both the short-term and long-term. Figure out the sensitivity of fungi to rapid change, and evaluate the comprehensive influence of atmosphere variation on fungi based on the model in the previous section. Compare different species of fungi and reasonable combinations of species and describe their relative advantages and disadvantages in a variety of environments, including arid, semi-arid, temperate, arboreal, and tropical rain forests. Measure the effect of the diversity of certain fungal communities on the decomposition of ground litter and woody fibers. Figure out the significance of biodiversity in different environments with different changeability.

1.3 Our Approach

The topic requires us to figure out the relation between extension rate, moisture tolerance, and decomposition rate of fungi and describe the mutual effect of different species of fungi in a community, also the effect of the diversity of fungi. Our work mainly includes the following: A mathematical model is built to identify the relation between the decomposition of ground litter and woody fibers caused by fungal activity and the amount of a certain type of fungi.

Based on the model above, a comprehensive model is figured out in respect of the interactions between different types of fungi. An analysis of the interaction between different types of fungi in a short and a long period was made. The environmental sensitivity of fungi and the impact of atmosphere variation on fungi are figured out. Different species of fungi and reasonable combinations of species are compared and their relative superiority and inferiority in a variety of environments are measured. The effect of the diversity of certain fungal communities on the decomposition of ground litter and woody fibers is measured. The significance of biodiversity in different environments with different changeability is figured out.

1.4 The Data

We got the data from the PNAS and Nature paper in the reference.



Figure 2: Data FFlow

genus	name	rate.05	decomposition.rate	slope	temp.slope	temp.b1	temp.slope	temp.b2	moist.slope	moist.b1	moist.slope	moist.b2
Armillaria	gallica.FP1025a.gal.s	0.25	17.12	0.22495277	68.48	0.0131	0.127	-0.064	2.2	0.088496	0.516881	-0.70303
Armillaria	gallica.FP1025a.gal10.n	0.25	15.42	0.164398987	44.06	0.04	-0.405	-0.2647	8.85	0.069287	0.379133	-1.94118
Armillaria	gallica.FP1025a.gal.s	0.21	11	0.22495277	52.38	0.0086	0.12	-0.0441	2.112	0.057371	0.430793	-0.75
Armillaria	gallica.FP1025a.gal.s	0.25	12.3	0.22495277	49.2	0.0089	0.097	-0.0511	1.729	0.045161	0.366129	-0.6
Armillaria	gallica.FP1025a.gal.s	0.25	9.2	0.387670311	38.9	0.0116	0.033	-0.0023	1.977	0.144482	0.742195	-1.1099
Armillaria	gallica.HH8125a.gal.n	0.49	39.51	0	80.63	0.0282	-0.136	-0.0797	2.751	0.056154	0.422615	-0.675
Armillaria	gallica.DC1.AA.gal.n	0.25	9.26	0.164398987	37.04	0.0279	-0.169	-0.1843	6.421	0.140385	0.640308	-1.09125
Armillaria	gallica.DH1.AA.gal.n	0.76	10.78	0.452936333	14.18	0.0857	-1.029	-0.2448	7.637	0.189931	0.803361	-3.37333
Armillaria	sinapina.F99 .a.sin.n	0.77	8.28	0.387670311	10.76	0.0444	-0.108	-0.2825	8.815	0.031202	0.227422	-3.78667
Armillaria	tabescens.FP1a.tab.n	0.5	13.38	0.387670311	26.56	0.0506	-0.181	-0.1648	6.053	0.090614	0.552014	-1.05261
Armillaria	tabescens.FP1a.tab.s	1.07	12.75	0	11.92	0.1036	-0.808	-0.1341	5.07	0.512782	1.291865	-5.7
Formes	fomentanus.TV1010m.n	4.71	47.24	0.284747399	10.03	0.5838	-7.724	-3.2583	100.264	2.680228	6.192523	-30.4
Hypodermia	crustacea.HH1crust.n	1.96	13.62	0.58484797	6.95	0.0509	0.907	-0.3383	10.981	1.075843	3.518725	-1.27
Hypodermia	serigenum.H1seri.n	4.11	12.45	0.753770804	3.03	0.447	-3.3209	-2.56	76.5	0.008842	3.18284	-26.4615
Hypodermia	serigenum.H1seri.s	4.7	18.82	0.16484797	1	0.448	-3.3208	-2.5	76.4	0.089931	3.989901	-13.9331
Laetiporus	conifericola.H1conf.n	5.16	7.6	0.284747399	1.47	0.4625	-5.38625	-2.3	68.97	3.142857	7.491429	-14.6538
Leitium	crinitus.PK2058.com.s	6.38	16.01	0.58484797	2.51	0.69114	-3	-4.09	124.87	2.57037	7.494615	-31.9667
Mycosia	mentibovis.FP1m.ment.s	1.3	7.96	0.58484797	6.12	0.61679	-6.42385	-1.49231	66.43769	0.807143	4.83	-0.1
Merulius	tremulosus.FP1m.trem.n	10.82	53.5	0.78842848	5.04	0.10358	-0.55831	-0.82462	24.09	5.660377	13.84264	-58.0625
Merulius	tremulosus.FP1m.trem.s	9.62	43.91	0.832776444	4.56	0.506407	-1.98635	-4.29375	152.9525	6.837396	15.68154	-59.7625
Phlebotomus	flavidoalba.FP1p.flav.n	8.04	27.84	0.582748978	3.48	0.452174	-0.74809	-2.8625	102.4025	3.278788	8.647939	-42.3333
Phlebotomus	flavidoalba.FP1p.flav.s	10.9	25.93	0.988393524	2.4	0.619549	-4.17995	-2.82903	105.171	2.894029	9.156705	-39.7619
Phellinus	gihvus.HH81197.p.gihv.n	4.04	42.09	0.464905555	10.42	0.638423	-3.00577	-1.88605	67.79271	1.971014	6.658116	-12.3158
Phellinus	harpagus.DM94.p.har.n	1.54	17.39	0.491196962	11.29	0.16242	-0.41299	-1.02222	38.37333	0.762609	2.462609	-9.33333
Poreobolus	pendulus.H1p.pend.n	4.06	4.36	0.464905555	1.07	0.76053	-0.12392	-0.0796	2.825	2.536364	3.92777	-11.6364
Phellinus	robinae.FP1357.p.rob.n	2.3	8.28	0.518675245	3.6	-0.036	1.196	-0.05799	2.889317	1.133333	3.293333	7.31579
Phellinus	robinae.A215.p.rob.s	2.14	26.29	0.22495277	12.29	0.246148	-2.53037	-1.20909	40.25638	1.903445	3.133103	-5.61111
Plebia	acarina.MR4280.p.plebia.n	8.75	16.18	1	1.85	0.440476	-0.19929	-2.5037	83.67037	5.467213	12.68574	-54.3571
Plebia	acarina.DM90.AB.p.plebia.s	8.51	73.39	0.972597525	8.62	0.361955	0.507293	-2.85	91.84	5.65	14.795	-20.4167
Porroponax	serquensis.Es.sanga	4.97	37.42	0.691488582	7.55	0.578947	-5.14777	-3.79952	161.051	1.688025	6.472765	-23.125
Schizophyllum	commune.s.comm.n	4.41	12.69	0.687958949	2.88	0.359504	-1.76331	-1.83333	71.49	2.167421	9.17095	-39.6667
Schizophyllum	commune.s.comm.s	2.57	6.67	0.671488718	2.97	0.581237	-1.40968	-3.88333	139.3417	1.967363	4.126272	-6.86
Tyromyces	chioneus.HH84.chion.n	3.88	29.06	0.805387266	7.49	0.448276	-3.47621	-2.47619	87.37619	1.829932	4.168571	-22.7778
Xylodolus	subroseus.FP1a.sub.s	0.77	8.55	0.493196962	1.11	0.037008	0.385197	-0.06889	2.887896	0.114567	1.11104	-1.39394

Figure 3: Data

2 General Assumptions

- The 'S' shape growth curve of fungi under laboratory conditions is of the greatest accuracy in the middle of the curve.
- The relation of the decomposition rate and the features of the species is a multiple linear relation.
- The multiple species situation in the short term can be described by discrete model.
- The multiple species situation in the long term is a resource and space limited situation.
- Temperature and moisture are the two main factors affecting the state of fungi.

3 Model Preparation

sdafsdfadfasd

4 Model 1

It is required that a mathematical model be set to figure out the relation of the breakdown of ground litter and important factors. As stated in the topic, the decomposition rate can be set as an index representing the breakdown situation. Since extension rate is one of the two factors for consideration, a model concerning decomposition rate and extension rate is therefore built to satisfy the needs.

4.1 A linear model of decomposition rate and extension rate

As Some microbiological academic papers stated, there is a law concerning the change of fungi biomass through time under standard laboratory condition, in the middle of fungus growth, which is shown in figure(number3235156161565) below:

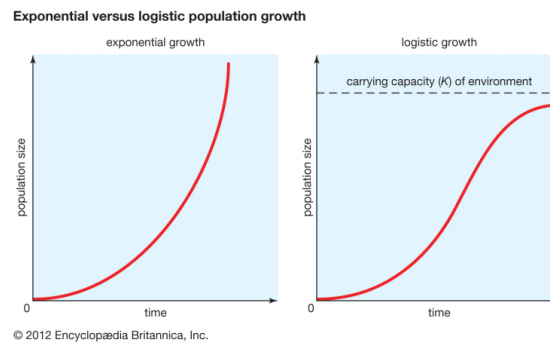


Figure 4: Logistic population growth, John N. Thompson. Eric Post

$$N = kt \quad (1)$$

k: the fungi's growth rate

Also, according to the basic biological knowledge, if the amount of ground litter and woody fiber is sufficient, the decomposition rate V satisfies the formula:

$$V = \lambda N \quad (2)$$

So, it turns out that $V = (\lambda t)k$ is a straight line passing the original point.

4.2 Result

The linear model concerning decomposition rate and extension rate is figured out as: There are 34 types of species altogether, so the graph of each species:

5 Model 2

The interactions between different species of fungi are required to be taken into consideration. Extension rate and moisture tolerance are the only two factors requiring an analysis. So,

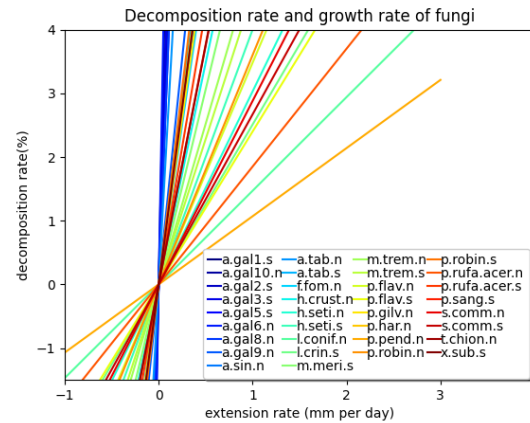


Figure 5: decomposition_growth_fungi

multiple linear regression is conducted to measure the connection between decomposition rate and the features of different species.

5.1 lot fungal growth rate versus humidity and temperature

First, we select two significant factors, temperature, and moisture. Then we plot two scatter diagrams that relate temperature and moisture to extension rate separately and use the smooth curve to fit the data point. The two graphs are as follows.

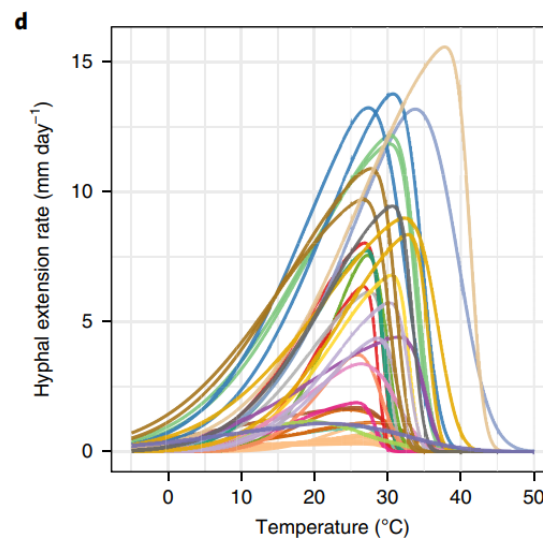


Figure 6: Hyphal extension rate-temperature

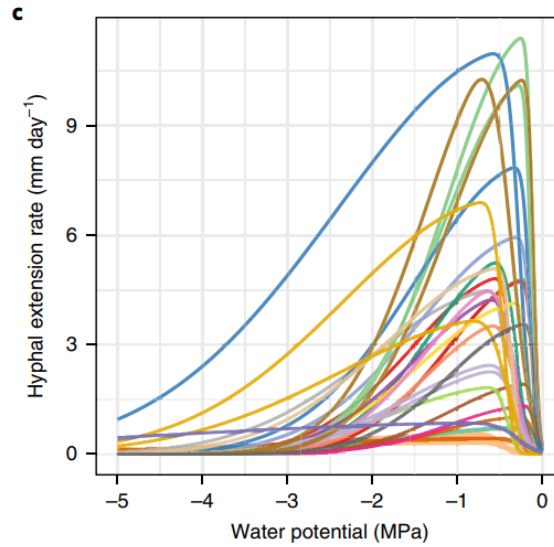


Figure 7: Hyphal extension water

5.2 Linear Fitting

From the graphs, it can be seen that both of the curves are highly identical to the piecewise linear function. In an attempt to figure out the functions, we set two functions with parameters:

$$k = \begin{cases} \alpha_1 T + b_1 \\ \alpha_2 T + b_2 \\ \beta_1 M + b_3 \\ \beta_3 M + b_4 \end{cases}$$

Then we select some points from the graphs as sample point, and conduct least square method with these sample points to search the best-fitted functions, the outcomes are as follow:

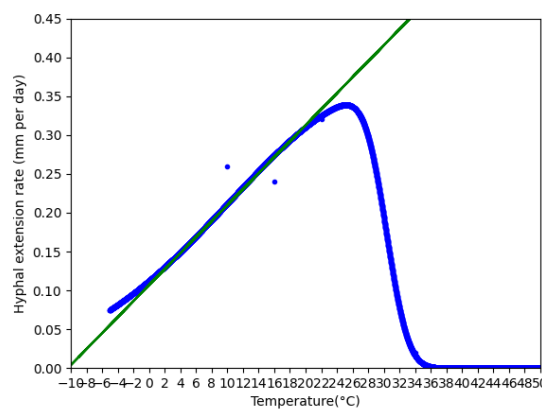


Figure 8: Hyphal extension rate - Temperature

multiple linear regression In order to figure out the connection between decomposition rate and the features of different species, the linear function is put forward. According to competitive

ranking, so we take ranking as the estimation of:

$$k_i = [T_i, \quad M_i] \begin{bmatrix} r_1 \\ r_2 \end{bmatrix} + [b_1 \quad b_2] \begin{bmatrix} r_1 \\ r_2 \end{bmatrix}$$

6 Model 3

We are required to make an analysis of the interactions between different types of fungi in both the short and long term. So partial differential equation is used first to model the situation of single species at the microcosmic level and the analysis of dynamic multiple species situations of short term is done by a cellular automaton. Then we put forward a partial differential equation set to analyze the interactions of the long term. Then an analysis of model 2 is needed. It is required that we examine the sensitivity to rapid environmental change and the impact of slower environment change.

6.1 Single species model in microcosmic level

Before analyzing the overall situation of the interactions of different species, it is proper to view on a smaller field. To fulfill the basic logic and increase the similarity to real situations, an equation set is put forward:

$$\begin{aligned} (1) \rho \mathcal{D}_t \vec{v} &= \nabla \cdot \sigma + \vec{f} \\ (2) \sigma &= \mu (\nabla \vec{v} + \nabla \text{vec} v^T) + (-\varepsilon + \zeta \text{div} \vec{v}) \mathbf{I} \\ (3) \mathcal{D}_t \rho &= \lambda R \rho (1 - \rho) - \rho \text{div} \vec{v} \\ (4) \vec{f} &= \rho \alpha \nabla R \\ (5) \frac{\partial R}{\partial t} &= -\beta \rho H(R) \end{aligned}$$

(1) is the dynamic equation, (2) is the constitutive equation, (3) is the proliferation equation, (4) is the motivation equation, (5) is the decomposition equation.

$$\begin{aligned} \mathcal{D}_t &= \frac{\partial}{\partial t} + \vec{v} \cdot \nabla \\ \vec{v} &=: u\vec{i} + v\vec{j} \\ \vec{f} &=: f_x\vec{i} + f_y\vec{j} \\ H(x) &= \begin{cases} 0, & x \leq 0 \\ 1, & x > 0 \end{cases} \\ \varepsilon &\sim T, W \end{aligned}$$

The above equations can be written in the form of components as follows.

6.2 Cellular Automaton

In the reality, many species of fungi spread, coexisting or competing with each other. To simulate the real fungi interactions, a cellular automaton with special rules is built. A grid group of $n \times n$ is set to represent the field of spread and the neighbor mechanism is set as Von Neumann. The rule of the automaton is set as follows: There are some fungi species named G_1, G_2, \dots, G_n and their competitive ranking is set as $R_1^\phi, R_2^\phi, \dots, R_n^\phi$ which range from 0 to 1. Von Neumann's form of neighbors will react to each other. The original value of the empty cellular is set as -1, and the change of cellular type follows this rule: The original type of cellular is $G_{i,0}$. The frequency of a certain cellular reacting to its neighbor of different types G_k is recorded as n_k . Set $n_j R_j^\phi = \max\{n_1 R_1^\phi, n_2 R_2^\phi, \dots\}$, and $G_{i,0}$ will transform to G_j .

6.3 The interactions of long term

Different from the situation of the short term, long term situation have to consider the limitation of resources and space, the change of environment condition and the self retardation.

$$\begin{aligned}\frac{dR}{dt} &= r_1 e^{-\lambda R} - \beta \rho H(R) \\ \frac{d\rho}{dt} &= \varepsilon r_2 R \rho (1 - \rho) \\ \varepsilon &= (1 + \xi) \varepsilon_T \varepsilon_W \\ \varepsilon_T &= \left(1 + \exp\left(\frac{\partial ER}{\partial T}\right)\right)^{-1} \\ \varepsilon_W &= \left(1 + \exp\left(\frac{\partial ER}{\partial W}\right)\right)^{-1} \\ T &= T_0 + \Delta T \sin(\omega_1 t + \varphi_1) \\ W &= W_0 + \Delta W \sin(\omega_2 t + \varphi_2)\end{aligned}$$

6.4 The analysis of Model 2

In this part, the sensitivity to rapid environment change and the influence of slower atmospheric change is evaluated. Based on the outcome of model 2, we make a linear regression and fitting. The result of fitting is as follows: (formula)<><><><> (figure)(figure)

6.5 Result

It can be seen from the model that the interactions of fungi is mainly consists of competition and self-organizing. If the fungi are almost equal in their competitiveness, it is likely that they will lead to the situation of vibration, causing a self-organizing pattern. If they differ in competitiveness, the most competitive one will invade the other, and occupy the whole field in the end.

7 Model 4

It is required that we compare different species of fungi and reasonable combinations of species and describe their relative advantages and disadvantages in a variety of environments. So, we use 'niche width' to save this problem. Niche width is a type of index that represents the adaptability and competitiveness of species in an environment with certain conditions. In regard to the five types of environment mentioned, temperature and moisture are the two most significant factors, for these environment types differ the most in these two aspects. Thus, we use temperature niche width and moisture niche width to evaluate the advantages and disadvantages.

7.1 Multiple niche width

To conduct an evaluation, we use an index named 'multiple niche width'. Nevertheless, considering that the two factors are of the great difference in the five types of environment, it is more reasonable that the two niche widths weigh differently in different environments. Thus, some modification is made to the original formula. The final formula is :

$$B^\phi = \sqrt{\mu_T B_T^{\phi^2} + \mu_M B_w^{\phi^2}}$$

The parameters are calculated with the equation set:

$$T^\phi = \left[1 + \exp\left(-0.1 \times \frac{T_{\max} + T_{\min}}{2}\right)\right]^{-1}$$

$$W^\phi = \left[1 + \exp(-0.05 \times \text{Rainfall})\right]^{-1}$$

$$\frac{\mu_T}{\mu_M} = \frac{T^\phi}{W^\phi}$$

$$\mu_T + \mu_M = 2$$

$$B_T^\phi = \left[1 + \exp(-0.1 \times B_T)\right]^{-1}$$

$$B_W^\phi = \left[1 + \exp(-0.35 \times B_W)\right]^{-1}$$

7.2 Result

gen.name2	name3	CAIRO(Ord)	XIAN(Ord)	LONDON(temperature)	NY(Ord)	SING (Ord)
1) <i>Armillaria gallica</i> FP102531_C4D	aga1 s	1.177087963	1.14400914	1.17566002		
2) <i>Armillaria gallica</i> EL8_A6F	aga10 n	1.060543885	1.0354063	1.0316354	1.028256064	1.033131902
3) <i>Armillaria gallica</i> FP102534_A5A	aga2 s	1.234095781	1.205118959	1.200772111	1.196877023	1.202497825
4) <i>Armillaria gallica</i> FP102535_A5D	aga3 s	1.249028948	1.227201358	1.22239591	1.221018334	1.225333396
5) <i>Armillaria gallica</i> FP102542_A3B	aga5 s	1.143372301	1.111155093	1.10630917	1.101963448	1.10822272
6) <i>Armillaria gallica</i> HHB13557_C0C	aga6 n	1.161942681	1.162627399	1.16185024	1.161121476	1.16244642
7) <i>Armillaria gallica</i> SH1_A4E	aga7 n	1.101161713	1.072575427	1.069433002	1.065717995	1.071075546
8) <i>Armillaria gallica</i> SH1_A4A	aga8 n	0.990665069	0.980709021	0.979227514	0.977802539	0.979813079
9) <i>Armillaria sinapii</i> H8B	as10 n	1.080520868	1.048231987	1.042273392	1.038923163	1.044829050
10) <i>Armillaria tabescens</i> FP102622_A3C	atab n	1.170662967	1.150729877	1.147763062	1.14509804	1.148944625
11) <i>Armillaria tabescens</i> TV93_261_A1E	atab s	1.070139043	1.024264581	1.017202204	1.011042844	1.020067906
12) <i>Fomes fomentarius</i> TV95_1_A3E	f10 n	0.957499161	0.926554897	0.929131117	0.926810358	0.930601383
13) <i>Haplophragma crustosum</i> HHB13392_B7B	h10 n	1.146234358	1.081678292	1.071797655	1.062899999	1.075723583
14) <i>Haplophragma sinapii</i> HHB1336_B0H	h10 s	0.913094401	0.977969999	0.972051169	0.968491231	0.974629136
15) <i>Haplophragma sinapii</i> FP150363_B0C	h10 s	0.972471457	0.949505056	0.945997954	0.942950289	0.947368512
16) <i>Leitporus carbonatus</i> GDL1_A1A	lcamb s	1.042650035	1.015888775	1.011835004	1.008227954	1.013432013
17) <i>Leitporus confusus</i> HHB15411_C8B	lconf n	1.005944654	0.97403083	0.968688465	0.963924355	0.970818021
18) <i>Leitporus cinnam</i> P62056_C1B	lcinn s	1.104034685	1.056552871	1.049345922	1.042867572	1.052208797
19) <i>Leitporus gilbertsonii</i> C4A_C2D	lgib s	1.023364923	0.992839871	0.98796022	0.981563898	0.989950435
20) <i>Leitporus hirsutus</i> LMJ1_C2H	lhun n	0.973777791	0.94645177	0.942106691	0.938993547	0.944748433
21) <i>Mecocacia meridionalis</i> FP150352_C4E	mmet s	1.021656483	0.982890463	0.977024762	0.971756401	0.979334239
22) <i>Marasmius formicivorus</i> FP102381_C4E	mmet s	1.089212503	1.056250283	1.028155561	1.020897989	1.031362585
23) <i>Marasmius formicivorus</i> FP150849_C3F	mmet s	0.98189987	1.044543812	1.036371549	1.029018353	1.039618872
24) <i>Phaeoglossum flavidoaba</i> FP102185_B7D	pf10 n	1.043684444	1.041543409	1.035056212	1.029229087	1.037632313
25) <i>Phaeoglossum flavidoaba</i> FP150451_A5D	pf10 s	1.129138132	1.098847315	1.09431722	1.090245656	1.095975335
26) <i>Phellinus gilvus</i> HHB11977_C4H	pgilv n	1.108312063	1.056368794	1.04846574	1.041337127	1.051805764
27) <i>Phellinus hartigi</i> DMH94_4A_A1B	phar n	1.114113565	1.064968088	1.057504235	1.050815722	1.060488889
28) <i>Pseudotsuga pendula</i> HHB13375_B7C	ppend n	1.059564439	1.011120051	1.004317249	0.998207738	1.007118905
29) <i>Phellinus robinae</i> FP135708_A1G	probin n	1.024264313	0.993521302	0.988911985	0.984739323	0.990729721
30) <i>Phellinus robinae</i> AT15_A101 Bark/Mark	probin s	1.017955654	0.984272294	0.979750251	0.973720004	0.981329574
31) <i>Phlebia acerina</i> MH4280_B9D	pf10 s	0.990446523	1.037205156	1.029094823	1.021797385	1.032317525
32) <i>Phlebia acerina</i> DRG1_ABA	pf10 s	1.104220798	1.050289556	1.042066548	1.034674708	1.043333533
33) <i>Porosporus sanguineus</i> PRC_9C_9L_A1C	psang s	1.110741843	1.05647426	1.058115025	1.052671976	1.061327574
34) <i>Schizophyllum commune</i> TV93_A1G	scomm n	1.143187244	1.102583428	1.09644877	1.090940981	1.098884761
35) <i>Schizophyllum commune</i> W1177	scomm s	0.979765135	1.056074965	1.052549492	1.049344438	1.053933662
36) <i>Uromyces chesteri</i> HHB11353_B1F	uchest n	1.049225647	1.030387792	0.997048579	0.991032946	0.999722843
37) <i>Xyllobolus subglauces</i> FP102567_A11A	x10 s	1.288080852	1.268183789	1.265103936	1.262347084	1.266325744

Figure 9: Multiple niche width

In the table, within the same type of region, a certain species have advantages over species with a lower niche width than it, and have an disadvantage to species with a higher niche width than it.

8 Model 5

According to the statement of model problem 5, a model describing the relation of fungi community diversity and the decomposition efficiency is to be set. Also, we are asked to figure out the significance of biodiversity in different environments with different changeability. Since temperature and moisture are two significant factors which affect fungi greatly and are possible to witness rapid change or form trends, it is proper to take them into consideration. In order to satisfy the needs, we ought to build a model of a fungi community to describe the mutual effect in a multiple fungi species system. The graphic model is put forward as follows: Based on the graphic model, a mathematical model of matrix is set up:

$$\begin{bmatrix} T_{n+1} \\ W_{n+1} \\ A_{n+1} \\ B_{n+1} \\ C_{n+1} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ \tau_A & W_A & K(AA) & K(AB) & K(AC) \\ \tau_B & W_B & K(BA) & K(BB) & K(BC) \\ \tau_C & W_C & K(CA) & K(CB) & K(CC) \end{bmatrix} \begin{bmatrix} T_n \\ W_n \\ A_n \\ B_n \\ C_n \end{bmatrix} + \begin{bmatrix} \tilde{T}_n \\ \tilde{W}_n \\ 0 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} TP_n \\ WP_n \\ AP_n \\ BP_n \\ CP_n \end{bmatrix}$$

According to the models in the previous section, the mass loss of woody fiber and ground litter is related to the temperature and moisture. The relation can be represented by the formula:

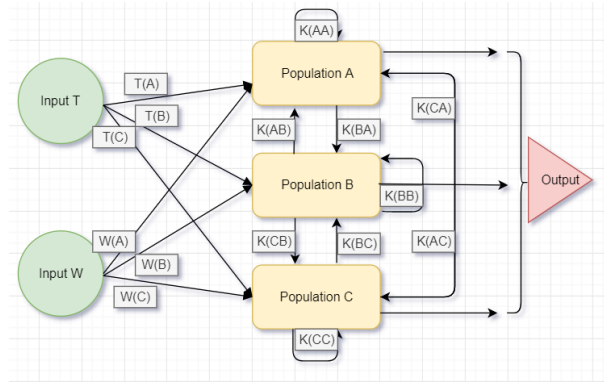


Figure 10: work flow

(ML)

All species of fungi contributes to the decomposition process and their contribution is positively related to their proportion in the community. So the efficiency can be viewed as:

$$\eta = \frac{1}{A_n + B_n + C_n} \left(A_n \Delta ML_n^{(A)} + B_n \Delta ML_n^{(B)} + C_n \Delta ML_n^{(C)} \right)$$

$$\Delta ML_n^{(A)} = ML_{n+1}^{(A)} - ML_n^{(A)}$$

It is a common sense in the biology that diversity can improve the stability of the community. So, when mention the significance of diversity, stability is a vital related factor. To measure the stability of the community, we choose the variance of species, and the stability is viewed as weighed sum of all variance. Thus, the formula is put forward as:

(In sdfasdfs)

We start with single species, then we gradually add more species to the community and calculate the decomposition efficiency and stability to figure out the relation of diversity and efficiency and the importance of diversity.

8.1 Result

As is calculated, the diversity is positively related to the decomposition efficiency. Also, the diversity is of huge importance to the environment, for the diversity is positively related to the stability, a community of diversity is of more stability and resilience.

9 Strengths and Weaknesses

9.1 Strengths

1. Different situation is carefully divided and different model are set to satisfy the needs.
2. Models take most of the rules in real life into consideration. They can simulate real life situation better.

9.2 Weaknesses

1. The temperature curve and moisture curve in model 2 is simplified to piecewise linear function, which have turning point and contradicts with real life situation.

2. Many of the models require a large amount of accurate data and is hard to calculate, which add to the difficulty of data collecting and analysis.

10 The Article: Recent developments in the understanding of the roles fungi play in ecological systems

The carbon cycle, which refers to the circulation of carbon on the Earth, is well known as a vital process for life on the planet. There is a crucial part of the cycle, the decomposition of compounds, in which carbon is absorbed and produced periodically. The decomposition of plant material and woody fibers is a component of the necessity of the whole decomposition part.

Recently, a group of researchers from MCM conducted research to explore the effect of fungi on the environment. First, they focus on the relation between the decomposition rate of fungi and its extension rate. A single species situation is viewed first, then a multiple species situation is figured out based on the single one. It was found that the decomposition rate is positively correlated to the extension rate. The single system relation can be described briefly as: $V = (\lambda t)k$ The multiple systems are fungi break down the ground litter and woody fibers. A higher decomposition rate means fungi can be more efficient in carbon transportation. So the extension of fungi can have a positive effect on the ecological systems.

Researchers then adjust the environment settings of the model to examine the sensitivity of the model to rapid fluctuations and the impact of certain atmospheric trends.

Following the impact evaluation, researchers attempt to figure out the interactions between different types of fungi in the short and long term. An equation set was first put forward as the basis and detail supply of the study, describing the microcosmic situation of single species: 00000

Researchers then use cellular automaton to imitate the fungi community in real life. The imitation model contains the spread, competition, and invasion behavior of fungi. According to the result of the simulation,

Besides, an evaluation of the advantages and disadvantages of different species is conducted. Researchers use multiple niche width as the index to compare the competitiveness of different species. As is shown in the table below, environmental conditions can pose great effect on the competition and survival of fungi. It seems that fungi are also affected by the ecological environment. 00000

Finally, researchers examine the influence of the diversity of fungal communities on the decomposition aspect in an environment of different degrees of variability. As can be seen from the resulting series calculated by matrix. Diversity is positively related to the overall efficiency of decomposition. 0000 Also, according to the sensitivity test model, a fungi community of diversity perform better in the stability and resilience facing rapid and long-time change in environment. 0000 To sum up, it can be seen from the research results that fungi play an important role in ecological systems. The growth and prosperity of fungi can facilitate carbon circulation. In turn, the ecological systems can pose an effect on fungi.

- **Applies widely**

This system can be used for many types of airplanes, and it also solves the interference during the procedure of the boarding airplane, as described above we can get to the

optimization boarding time. We also know that all the service is automate.

- **Improve the quality of the airport service**
Balancing the cost of the cost and the benefit, it will bring in more convenient for airport and passengers. It also saves many human resources for the airline.
-

References

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- [3] <https://www.weather.gov/>

Appendices

Appendix A First appendix

some more text **Input Python source:**

```
"""
Cellular Automata are used to simulate the relationships between fungi
"""
import bidict
import numpy as np
import matplotlib.pyplot as plt

class GameOfLife(object):

    def __init__(self, cells_shape, fungi_data):
        """
        Parameters
        -----
        fungi_data: [[(color1, weight1), [(x11, y11), (x12, y12), ...]],
                    [(color2, weight2), [(x21, y21), (x22, y22)], ...]
        -----
        cells_shape: a tuple
        """

        self.cells = np.zeros(cells_shape)
        self.fungi = dict([fungi[0] for fungi in fungi_data])
        for fungi in fungi_data:
            for coordinate in tuple(fungi[1]):
                xPos = coordinate[0]
```

```
        yPos = coordinate[1]
        self.cells[xPos, yPos] = fungi[0][1]
    self.timer = 0

    def update_state(self):
        """update a state"""
        buf = np.zeros(self.cells.shape)
        cells = self.cells

        for i in range(1, cells.shape[0] - 1):
            for j in range(1, cells.shape[0] - 1):

                if i == 1 and j == 1:
                    if cells[i + 1, j] == cells[i, j + 1]:
                        if cells[i, j] < 2 * cells[i + 1, j]:
                            buf[i, j] = cells[i + 1, j]
                        else:
                            buf[i, j] = cells[i, j]
                    else:
                        buf[i, j] = max(cells[i, j],
                                         cells[i + 1, j], cells[i, j + 1])

                elif i == 1 and j == cells.shape[1] - 2:
                    if cells[i + 1, j] == cells[i, j - 1]:
                        if cells[i, j] < 2 * cells[i + 1, j]:
                            buf[i, j] = cells[i + 1, j]
                        else:
                            buf[i, j] = cells[i, j]
                    else:
                        buf[i, j] = max(cells[i, j],
                                         cells[i + 1, j], cells[i, j - 1])

                elif i == cells.shape[0] - 2 and j == 1:
                    if cells[i - 1, j] == cells[i, j + 1]:
                        if cells[i, j] < 2 * cells[i - 1, j]:
                            buf[i, j] = cells[i - 1, j]
                        else:
                            buf[i, j] = cells[i, j]
                    else:
                        buf[i, j] = max(cells[i, j],
                                         cells[i - 1, j], cells[i, j + 1])

                elif i == cells.shape[0] - 2 and j == cells.shape[1] - 2:
                    if cells[i - 1, j] == cells[i, j - 1]:
                        if cells[i, j] < 2 * cells[i - 1, j]:
                            buf[i, j] = cells[i - 1, j]
                        else:
                            buf[i, j] = cells[i, j]
                    else:
                        buf[i, j] = max(cells[i, j],
                                         cells[i - 1, j], cells[i, j - 1])

                elif i == 1 and 1 < j < cells.shape[1] - 2:
                    dic = {}
                    if cells[i, j - 1] in dic.keys():
                        dic[cells[i, j - 1]] += 1
                    else:
                        dic[cells[i, j - 1]] = 1
```

```
        if cells[i, j + 1] in dic.keys():
            dic[cells[i, j + 1]] += 1
        else:
            dic[cells[i, j + 1]] = 1

        if cells[i + 1, j] in dic.keys():
            dic[cells[i + 1, j]] += 1
        else:
            dic[cells[i + 1, j]] = 1

        if cells[i, j] in dic.keys():
            dic[cells[i, j]] += 1
        else:
            dic[cells[i, j]] = 1

        for key in dic.keys():
            if buf[i, j] < key * dic[key]:
                buf[i, j] = key

    elif i == cells.shape[0] - 2 and \
         1 < j < cells.shape[1] - 2:
        dic = {}
        if cells[i, j - 1] in dic.keys():
            dic[cells[i, j - 1]] += 1
        else:
            dic[cells[i, j - 1]] = 1

        if cells[i, j + 1] in dic.keys():
            dic[cells[i, j + 1]] += 1
        else:
            dic[cells[i, j + 1]] = 1

        if cells[i - 1, j] in dic.keys():
            dic[cells[i - 1, j]] += 1
        else:
            dic[cells[i - 1, j]] = 1

        if cells[i, j] in dic.keys():
            dic[cells[i, j]] += 1
        else:
            dic[cells[i, j]] = 1

        for key in dic.keys():
            if buf[i, j] < key * dic[key]:
                buf[i, j] = key

    elif 1 < i < cells.shape[0] - 2 and j == 1:
        dic = {}
        if cells[i - 1, j] in dic.keys():
            dic[cells[i - 1, j]] += 1
        else:
            dic[cells[i - 1, j]] = 1

        if cells[i + 1, j] in dic.keys():
            dic[cells[i + 1, j]] += 1
        else:
            dic[cells[i + 1, j]] = 1
```



```
    if cells[i, j + 1] in dic.keys():
        dic[cells[i, j + 1]] += 1
    else:
        dic[cells[i, j + 1]] = 1

    if cells[i, j] in dic.keys():
        dic[cells[i, j]] += 1
    else:
        dic[cells[i, j]] = 1

    for key in dic.keys():
        if buf[i, j] < key * dic[key]:
            buf[i, j] = key

elif 1 < i < cells.shape[0] - 2 and\
     j == cells.shape[1] - 2:
    dic = {}
    if cells[i - 1, j] in dic.keys():
        dic[cells[i - 1, j]] += 1
    else:
        dic[cells[i - 1, j]] = 1

    if cells[i + 1, j] in dic.keys():
        dic[cells[i + 1, j]] += 1
    else:
        dic[cells[i + 1, j]] = 1

    if cells[i, j - 1] in dic.keys():
        dic[cells[i, j - 1]] += 1
    else:
        dic[cells[i, j - 1]] = 1

    if cells[i, j] in dic.keys():
        dic[cells[i, j]] += 1
    else:
        dic[cells[i, j]] = 1

    for key in dic.keys():
        if buf[i, j] < key * dic[key]:
            buf[i, j] = key

else:
    dic = {}
    if cells[i - 1, j] in dic.keys():
        dic[cells[i - 1, j]] += 1
    else:
        dic[cells[i - 1, j]] = 1

    if cells[i + 1, j] in dic.keys():
        dic[cells[i + 1, j]] += 1
    else:
        dic[cells[i + 1, j]] = 1

    if cells[i, j - 1] in dic.keys():
        dic[cells[i, j - 1]] += 1
    else:
        dic[cells[i, j - 1]] = 1
```

```
        if cells[i, j + 1] in dic.keys():
            dic[cells[i, j + 1]] += 1
        else:
            dic[cells[i, j + 1]] = 1

        if cells[i, j] in dic.keys():
            dic[cells[i, j]] += 1
        else:
            dic[cells[i, j]] = 1

        for key in dic.keys():
            if buf[i, j] < key * dic[key]:
                buf[i, j] = key

    self.cells = buf
    print(buf)
    self.timer += 1

def plot_state(self):
    """Draw a graph of the current state"""
    plt.title('Iter :{}'.format(self.timer))
    plt.imshow(self.cells)
    plt.show()

def update_and_plot(self, n_iter):
    """
    Parameters
    -----
    n_iter: Number of updated rounds
    """
    plt.ion()
    for _ in range(n_iter):
        plt.title('Iter :{}'.format(self.timer))
        plt.xlim(0, self.cells.shape[0])
        plt.ylim(0, self.cells.shape[1])
        plt.imshow(self.cells)
        self.update_state()
        plt.pause(0.1)
    plt.ioff()

if __name__ == '__main__':
    fungi_data = [(('blue', 0.62), [(2, 3), (2, 4)]),
                  (('green', 0.57), [(27, 27), (25, 27)])]
    game = GameOfLife(cells_shape=(30, 30), fungi_data=fungi_data)
    game.update_and_plot(200)
```
