The mathematical modeling of the microbial loop

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Abstract

Computer-based simulations, employed at the Parsons Laboratory to understand the foraging abilities of planktonic microbes in spatial and temporal variability of key limiting resources, are used to evaluate the ecological dynamics in microbial food web studies. A mathematical model of the microbial food web has been developed to model the individual-level foraging behaviors in a great variety of chemotaxis, diffusivity and dimensionality. This model can provide how these abilities significantly influence the overall ecological dynamics in the view of resource turnover rate and individual patchy distribution.

Introduction

Several researches have been done lately on the ecological dynamics of marine microorganisms to study the influence of resource patchiness on their consumers in time and space. The speed and accuracy of allocating concentration of resources depends on a list of different factors such as chemotaxis, diffusion, dispersion of resource, dimensionality, etc. Chemotaxis is the phenomenon in which consumers direct their movements to regions of high resource density. Taxis is facilitated by both directional behavior-change of velocity, and turning angle, and nondirectional behavior-change of speed or turning rate in response to stimulus (Okubo and Levin, 2000). Diffusion, on the other hand, determines the stay of a consumer in attractant abundant regions. And dimensionality specifies the position of the microorganism patches with respect to one another.

Many studies emphasize spatially explicit approaches, but still consider resource homogeneity in their calculations. In this paper, we developed formulas and simulations that apply to resource heterogeneity in order to study population dynamics. Individual-level responses, which usually occur on relatively small time and space scales, are then used to formulate population-level models that predict spatial distribution of resources and consumers at much longer time and space scales characterizing ecological dynamics (Okubo, 1980). If the resource distribution is considered homogenous, then the consumer would move at a constant velocity considering the fact that it depends on the resource gradient. One consequence of this heterogeneity is increased viability of the prey population, compared to the equivalent homogenous model, and increased consumption (Arditi, 2001).

This paper is structured as follows: In the ‘Methods’ section, I talk about the model that we assumed for the microbial food web, the resource distribution and the consumer movements, and talked briefly about the degree of patchiness of microorganisms. In the ‘Results and Discussion’ section, I present simulation results beginning with the individual-level foraging behaviors as background information on the trophic cascade behavior of the microbial loop. I also discuss the implications of chemotaxis, diffusivity, and dimensionality on nutrient and zooplankton for the study of complex spatial dynamics in ecological systems.

Methods

Model of a microbial food web

To analyze how microscale patch of resource influences on the degree of aggregations and populations of consumers in spatiotemporal distributions, the diffusion-reaction equations including both random and directed movements in dimensionless form were employed (Grunbaum, 2002). For simplicity, it is assumed that multiple competitors for the same resources don’t exist. Nutrient (N), phytoplankton (P), bacteria (B), and zooplankton (Z) were simulated as individual organic substances in a one-dimensional domain [-L, L] with zero
flux boundary condition. Under the assumption, population dynamics obey the following model:

\[
\begin{align*}
\frac{\partial N}{\partial t} &= D_N \nabla^2 N - \beta_N \cdot (NP) \\
\frac{\partial P}{\partial t} &= D_P \nabla^2 P + \gamma_P \beta_N \cdot (NP) - \beta_P \cdot (PB) - \nabla \cdot (P \nabla N) \\
\frac{\partial B}{\partial t} &= D_B \nabla^2 B + \gamma_B \beta_P \cdot (PB) - \beta_B \cdot (BZ) - \nabla \cdot (B \nabla P) \\
\frac{\partial Z}{\partial t} &= D_Z \nabla^2 Z + \gamma_Z \beta_B \cdot (BZ) - \nabla \cdot (Z \nabla B)
\end{align*}
\]

Resource Distribution

\[
\frac{\partial N}{\partial t} = \nabla^2 N - C_{\gamma_1} NP
\]

The release of a point source obeying Gaussian distribution was simulated at the middle of domain. The terms on the right-hand side of the equation for the nutrient represent molecular diffusion known as Fick’s Law and consumption by phytoplankton, respectively.

Movement of Consumers

\[
\begin{align*}
\frac{\partial P}{\partial t} &= D_P \nabla^2 P - \nabla \cdot (P \nabla N) + C_{\gamma_1} NP - C_{\gamma_2} PB \\
\frac{\partial B}{\partial t} &= D_B \nabla^2 B - \nabla \cdot (B \nabla P) + C_{\gamma_1} PB - C_{\gamma_2} BZ \\
\frac{\partial Z}{\partial t} &= D_Z \nabla^2 Z - \nabla \cdot (Z \nabla B) + C_{\gamma_1} BZ
\end{align*}
\]

The right-term of equations which consists of molecular diffusion, biased random walks (Chemotaxis), and interaction between prey and predator can be explored for a great variety of foraging behaviors in terms of each microorganism’s degree of patchiness and amount of biomass transfer.

Degree of patchiness

To check the degree of patchiness of each microorganism and that of interaction between two microorganisms, the expressions (Grunbaum, 1999) below can be applied for our model.

\[
\begin{align*}
C_i(t) &= \mathbb{E} \left[ \frac{\Delta i}{\Delta t} \right]_i \\
C_{ij}(t) &= \mathbb{E} \left[ \frac{\Delta i \Delta j}{\Delta t \Delta j} \right]_{i j}
\end{align*}
\]

\[\tilde{i} = E[i], \quad \tilde{i} = i - i, \quad \tilde{j} = E[j], \quad \Delta j = j - j\]

Where \(E[]\) is the spatial average over all points in the domain at time \(t\), \(\tilde{i}\) and \(\tilde{j}\) are average amounts of \(i\) and \(j\) compartments at the given time, \(t\), and \(\Delta i\) and \(\Delta j\) are the spatial deviation from those averages.
Results and Discussion

Individual-level foraging behavior

**Fig 1:** Change in the overall amount of nutrient, phytoplankton, bacteria, and zooplankton in a 1D four compartments domain.

A very basic case that helps studying the individual-level behavior of the different components of a microbial loop, is the 1D base model, which means all chemotactic and diffusional variables of P, B and Z are unities. The microbial loop which consists of the nutrient (N), phytoplankton (P), bacteria (B), and zooplankton (Z); acts as a trophic cascade. Starting with an overall amount of 1.0 at time 0, N starts to decrease as time passes by due to its consumption by P which increases with time. On the other hand, B consumes P thus increasing with time. And finally, Z, the final consumer feeds on B thus increasing. Different factors come into role in determining the consumption rate and thus the overall amount of different individuals in the microbial loop.

Chemotactic effect

**Fig 2:** Effect of chemotactic sensitivity on the overall amount of bacteria in a 3D three compartments domain.

To study the chemotactic effect on how efficiently N transfers to the final consumer B in a 3D three compartments domain, multiple simulations had to be run holding all coefficients constant and varying chemotaxis. Such a case study starts with varying the chemotactic coefficient of phytoplankton (P), plotting it for four different values: 0, 0.1, 1 and 10 and comparing them. Fig 2 indicates that the resource turnover rates to the final consumer, bacteria (B), are enhanced according to the increase of chemo ability of P (CChemo). Increasing the chemotactic sensitivity of P allows it to more efficiently catch N, thus decreasing its overall amount; P’s overall amount increases which leads accordingly to an increase in the overall amount of B. Note that the square solid lines in blue represent base model which means all chemotactic and diffusional variables of P and B are unities.
Fig 3: Effect of random diffusivity on the overall amount of bacteria in a 3D three compartments domain.

Fig 4: Increase of consumer amount with respect to dimensionality in a three compartments domain.

Same procedure as above has to be done to study the diffusion effect on the overall amount of B in a 3D three compartments domain, but in this case, diffusivity varies. The three different diffusion coefficients of P used were: 0.1, 1 and 10. Fig 3 indicates the molecular random diffusion effect on the overall transfer turnover rate to the final consumer, B. It shows that lower diffusivity of P (C_Diff) contributes to the enhancement of resource transfer to the final consumer in the microbial loop. Lower diffusion coefficient lengthens the stay of P in the attractant’s (N) abundant region; it results in increasing the probability of reacting with it. The decrease of P’s overall amount with the increase of diffusivity applies accordingly to B, the final consumer. Note that the square solid lines in blue represent base model which means all chemotactic and diffusional variables of P and B are unities.

Three cases of dimensionality are considered in the study on the microbial loop: 1D, 2D, and 3D. A point source nutrient (N) is released at the middle of the domain in each case. The one-dimensional case can be described as a line that spreads over a domain of [-L, L], where 0 is the release point for N and thus studying the behavior of the other individuals accordingly. The two-dimensional domain consists of a circle of radius r where the center represents the N release point. And the three-dimensional domain is a sphere of radius r where once again the center of that sphere is the release point for N. Higher dimension holds steeper resource gradient in space, thus triggering the effective consumer’s moving toward it at short time period. Fig 4 shows us that the ability of P uptaking N increases with the increase in dimensionality. The overall amount of P increases, and that also applies to bacteria (B).
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**References**


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**To check the degree of patchiness of the bacteria as a function of chemotactic ability in a 3D three compartments domain, Grunbaum’s expression, that was previously stated in the ‘Methods’ section, had to applied to our model. Fig 5 shows the degree of patchiness of the bacteria as a function of its chemotactic ability (CChemo_B). The overall degree of patchiness increases gradually with the increase of bacteria’s chemotaxis. Note that little or no patchiness was formed without chemo ability, and slight patchiness with CChemo_B=0.1 compared to higher values of 1 and 10.**

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**Fig 5:** Degree of patchiness of bacteria as a function of its chemotactic ability in a three compartments domain.

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