## Copper Contamination Effects on Phytoplankton-Zooplankton System within Deterministic and Stochastic Environments

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Abstract Since the aquatic organisms are very sensitive to the increasing copper contamination in water, this paper focuses on investigating the effects of copper contamination on the interaction between phytoplankton and zooplankton species within both deterministic and stochastic environments. We first construct a deterministic phytoplankton-zooplankton interaction model coupled with the copper concentration and analyze its dynamics, including existence and stability of equilibria, as well as the existence of Hopf bifurcation. A new stochastic model is derived in the form of continuous-time Markov chain (CTMC), and branching process theory is applied to the CTMC model to estimate the extinction probability of zooplankton species. Analytical and numerical findings show that the destiny of species is closely related to the copper concentration, and the predictions of the deterministic and stochastic models may be different in some cases.

**Keywords** Phytoplankton-zooplankton system, copper contamination, CT-MC model, extinction probability

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## 1. Introduction

Almost all aquatic life is based upon plankton, which is the most abundant form of life floating freely near the surfaces of all aquatic environments, namely, lakes, rivers, estuaries and oceans [1, 37]. The plant forms of plankton community are known as phytoplankton, which is a vital role in ecological systems since nearly half of the world's carbon dioxide is absorbed by them, and they also provide valuable oxygen resources and are important nutrients for a large number of aquatic species [31]. The animals in the plankton community are known as zooplankton. They consume the phytoplankton and can be a highly favourable food source for fish and other aquatic animals [37]. In past years, numerous works have been done towards analyzing the dynamics of phytoplankton-zooplankton system, see Refs. [7, 18–20,24,33,38] and the references therein. Besides, some researchers used Daphnia as the test organism on plankton ecosystem [27, 28, 34], because it constitutes a central component in aquatic food web structure and is sensitive to a multitude of xenobiotics (organophosphates, heavy metals, organochlorines, pyrethroids etc.) [5].

As a receptor of urban wastewater, industrial and mine effluents, agricultural

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runoff, and atmospheric pollution, aquatic ecosystems are prone to copper pollution. As an unusual micronutrient, copper is involved in many cellular reactions such as oxygen and iron acquisition [26] as well as denitrification [15], which results in bacteria and phytoplankton having an essential copper requirement. However, a high concentration of copper in water can also induce toxic effects with a deleterious impact on growth [8,35]. The copper with high concentration can inhibit the photosynthesis of phytoplankton (algae) [16], and then decrease the concentrations of glucides, proteins, amino-acids, chlorophyll and alkaline phosphatase activity in the algal cells [11,12,44]. The direct effects of copper on zooplankton (such as, Daphnia) include a decrease in fecundity, survival, body length, weight, and carbon uptake, as well as a delay in maturation [4,21,22]. Moreover, the Daphnia's swimming velocity, filtration rate, and ingestion rate are optimal for an intermediate copper range [14,41].

Mathematical modeling has already proved a useful tool to help predict the effects of pollutant (including copper) on aquatic ecosystems [5,6,10,32,40,42]. For example, in order to predict the effects of copper on a plant-herbivore interaction in a freshwater ecosystem Prosnier et al. [32] built a model that focuses on the interaction between algas and herbivores. Theoretical and numerical results showed that the herbivore may be more affected by copper pollution when community interactions are taken into account, and the copper pollution may stabilize the alga-herbivore interaction at the community level. More recently, based on the deterministic model in Ref. [32], Camara et al. [6] considered the environmental stochastic effects on the phytoplankton-zooplankton dynamics and proposed a stochastic alga-Daphnia model with white noises in Itô's sense. They supposed that the species lives in an environment subject to random fluctuations which affect the growth rate. The growth rate can be rewritten as an average growth plus an error term which can be approximated by a white noise (see Ref. [6] for more details).

We should point out that, except for the white noise, there are other tools which can be used to describe the environmental fluctuations. Specifically, some scholars formulated stochastic population or epidemic systems by using the continuous-time Markov chain (CTMC) [2,9,17,25,45]. For example, a CTMC model was developed for the dynamics of a viral infection and an immune response during the early stages of infection in Ref. [45]. It was found that the CTMC model can provide new insights, distinct from the basic deterministic model. In the case of  $R_0 > 1$ , the deterministic model predicts that the viral infection persists in the host, but for the CTMC model, there is a positive probability of viral extinction. Hu et al. [17] formulated a CTMC model for a predator-prey species system with disease in the predator. By applying the branching process theory to the CTMC model, the authors estimated the probabilities for disease outbreaks or successful invasions of prey species when the basic reproduction number is greater than the threshold value.

Motivated by the above works, we will devote ourself to investigating the copper contamination effects on phytoplankton-zooplankton system in deterministic and stochastic environments respectively. In Section 2, by considering that the maximum uptake rate of zooplankton is influenced by the copper contamination, we first construct and analyze a deterministic copper-dependence Scenedesmus-Daphnia model. In Section 3, we formulate a CTMC model based on the deterministic model and estimate the extinction probability of Daphnia species by applying the branching process theory. Our results are briefly summarized and discussed in