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Modeling the distribution of colonial species to improve estimation of plankton concentration in ballast water

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A B S T R A C T

The International Maritime Organization (IMO) has set limits on allowable plankton concentrations in ballast water discharge to minimize aquatic invasions globally. Previous guidance on ballast water sampling and compliance decision thresholds was based on the assumption that probability distributions of plankton are Poisson when spatially homogenous, or negative binomial when heterogeneous. We propose a hierarchical probability model, which incorporates distributions at the level of particles (i.e., discrete individuals plus colonies per unit volume) and also within particles (i.e., individuals per particle) to estimate the average plankton concentration in ballast water. We examined the performance of the models using data for plankton in the size class ≥ 10 µm and < 50 µm, collected from five different depths of a ballast tank of a commercial ship in three independent surveys. We show that the data fit to the negative binomial and the hierarchical probability models equally well, with both models performing better than the Poisson model at the scale of our sampling. The hierarchical probability model, which accounts for both the individuals and the colonies in a sample, reduces the uncertainty associated with the concentration estimation, and improves the power of rejecting the decision on ship's compliance when a ship does not truly comply with the standard. We show examples of how to test ballast water compliance using the above models.

1. Introduction

The global transfer of nonindigenous species by ship ballast water and their associated risks and impacts have been known for decades (Carlton, 1996). The International Maritime Organization (IMO) proposed performance standards for ballast water discharge to reduce the transfer of harmful aquatic organisms in ballast water (IMO, 2004). Regulation D-2 of the International Convention for the Control and Management of Ship Ballast Water and Sediments states that ballast water discharged by ships shall contain (i) fewer than 10 viable organisms per m^3 for size class ≥ 50 µm in minimum dimension, and (ii) fewer than 10 viable organisms per ml for size class < 50 µm and ≥ 10 µm in minimum dimension. It is important to establish statistically sound protocols for compliance monitoring, acknowledging that there will be variability in organism concentrations between point samples and resultantly measured concentrations need to be considered in context of the underlying probability distributions at the scale of the sampled volumes (Bierman et al., 2012; Costa et al., 2015). For example, a measurement of 20 viable organisms per ml for size class ≥ 10 µm and < 50 µm in minimum dimension may not necessarily be evidence for noncompliance with Regulation D-2 as such sample could be drawn by chance alone from a heterogeneous population with an overall mean concentration of < 10 organisms per ml.

The distribution of plankton in ballast water may take various forms, from random to patchy (Fig. 1); this influences how much variation is expected between random samples collected from the tank and dictates the appropriate sampling distribution. When individuals are distributed homogeneously, the Poisson distribution is appropriate, however, if individuals are aggregated, a negative binomial distribution could be used (Fig. 1). Few empirical studies have examined the distribution of plankton inside ballast tanks. Murphy et al. (2002) assessed the vertical distribution of zooplankton on a ship and showed that the likelihood of large abundances of crustacean to occur near the tank surface is high. In a land-based macrocosm study, First et al. (2013) examined the stratification of taxa ≥ 50 µm during simulated tank discharges, and found weak evidence for stratification. Plankton may become aggregated as a response to light, food, predators, or similar biotic and abiotic stimuli within the ballast water (Murphy et al., 2002; First et al., 2013). Clumping occurs when individuals of the same species are physically attached to each other forming colonies (Fig. 1), for example, in genera such as *Asterionella* and *Oscillatoria* (Illustration 1). If colonial taxa are present in ballast water, selection of an individual

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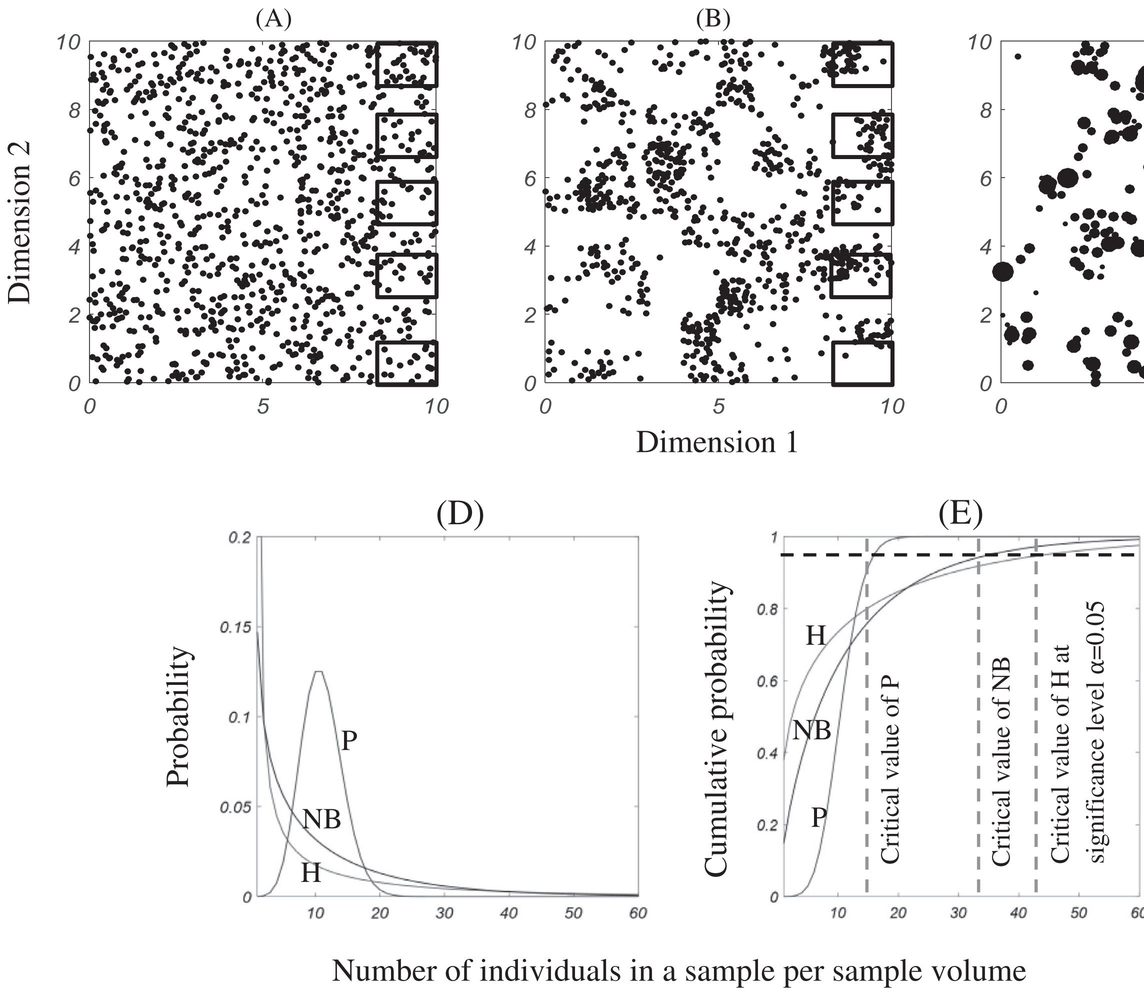

Fig. 1. Simulation of particle distributions in 2-dimensional space (shown by dots) under three scenarios (A) homogenous (random), (B) heterogeneous (with aggregation of individuals), and (C) heterogeneous aggregation of particles (i.e., individuals plus colonies), having the same average concentration of individuals per square unit. The size of the dot in (C) indicates the size of the colony. The simulations were based on (A) Poisson (P), (B) negative binomial (NB), and (C) hierarchical (H) models (H with NB probability distributions at two levels: across particles and within colonies) using Matlab. Boxes in panels (A–C) suggest spatially distributed samples: Panel (A) would yield a more accurate estimate of the mean plankton concentration, even with few samples, due to low variability, compared to that in (B) and (C). Panel (D): probability mass functions assuming a mean of 10 individuals/sample volume, and Panel (E): cumulative concentration functions of P, NB and H probability models. Samples from Panel (C) have a higher probability of either containing zero individuals than (A) or (B) and a higher probability of containing a much higher concentration than the true population mean compared to (A). This demonstrates the expected variation between samples collected from ballast water where the mean concentration of individuals per tank is equal but the spatial aggregations of individuals within those tanks differs.

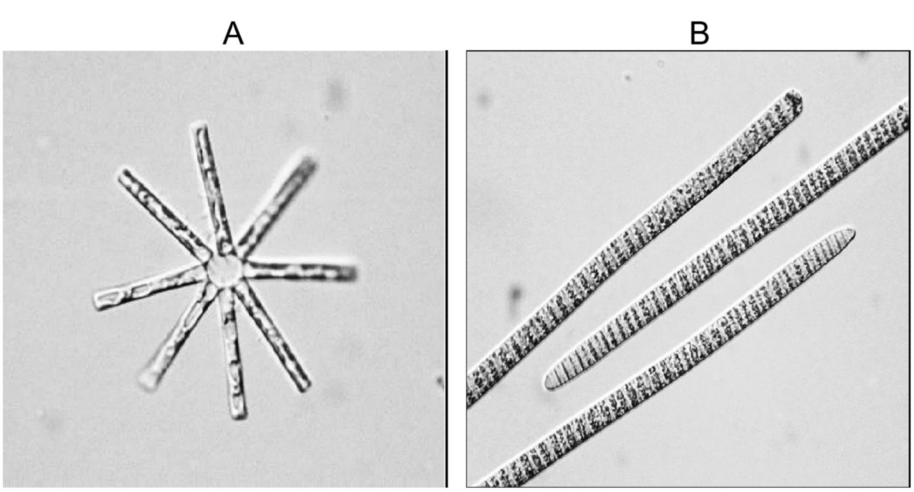

Illustration 1. Examples of colony-forming species within the genera (a) *Asterionella*, (b) *Oscillatoria*.