Research papers

How well do we know the infaunal biomass of the continental shelf?

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ARTICLE INFO

ABSTRACT

Benthic infauna comprise a wide range of taxa of varying abundances and sizes, but large infaunal taxa are infrequently recorded in community surveys of the shelf benthos. These larger, but numerically rare, species may contribute disproportionately to biomass, however. We examine the degree to which standard benthic sampling gear and survey design provide an adequate estimate of the biomass of large infauna using the Atlantic surfclam, *Spisula solidissima*, on the continental shelf off the northeastern coast of the United States as a test organism. We develop a numerical model that simulates standard survey designs, gear types, and sampling densities to evaluate the effectiveness of vertically-dropped sampling gear (e.g., boxcores, grabs) for estimating density of large species. Simulations of randomly distributed clams at a density of $0.5–1\ m^{-2}$ within an 0.25-km^2 domain show that lower sampling densities (1–5 samples per sampling event) resulted in highly inaccurate estimates of clam density with the presence of clams detected in less than 25% of the sampling events. In all cases in which patchiness was present in the simulated clam population, surveys were prone to very large errors (survey availability events) unless a dense (e.g., 100-sample) sampling protocol was imposed. Thus, commercial quantities of surfclams could easily go completely undetected by any standard benthic community survey protocol using vertically-dropped gear. Without recourse to modern high-volume sampling gear capable of sampling many meters at a swath, such as hydraulic dredges, biomass of the continental shelf will be grievously underestimated if large infauna are present even at moderate densities.

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1. Introduction

Benthic infauna comprise a wide range of taxa of varying abundances and sizes. The literature records a rich and diverse record of benthic surveys in which abundance and biomass are reported, only a few of which will be referenced herein. Generally speaking, large animals contribute substantially more to community biomass than to community abundance (e.g., Staff et al. (1985)). This trend suggests that estimates of benthic biomass should be designed to adequately sample the larger, but numerically rarer, infauna. We ask these questions here. How well do we achieve that goal? Do we really know the biomass of infauna on the continental shelf? We examine this question by using the Atlantic surfclam, *Spisula solidissima*, on the continental shelf off the northeastern coast of the United States as a test organism. This clam supports a major commercial fishery in this region (Weinberg, 1999, 2005). The density of these clams is well described based on stock surveys using hydraulic dredges with known and high efficiency of capture (Weinberg et al., 2005; Hennen et al., 2012). Dredge tows reported in Weinberg et al. (2005) typically sampled $1375\ m^2$. High density populations typically exist at densities of $0.5–2\ m^{-2}$. Taking an 140-mm surfclam as a typical individual, this density contributes $14–56\ g\ m^{-2}$ (Marzec et al., 2010) to benthic biomass, a biomass that is representative of typical samples obtained in many benthic surveys (e.g., Josefson and Hansen, 2004; Dubois et al., 2009; Bolam et al., 2010; Schonberg et al., 2014). Thus, successful sampling of these large clams, were they to be present in these densities, would constitute an important component of macroinfaunal biomass.

2. Methods

To examine the potential for sampling and adequately quantitating clam density and hence biomass using gear and sampling densities typically employed in benthic survey designs, we developed a numerical model that simulates standard survey designs, gear types, and sampling densities. The model evaluates the effectiveness of vertically-dropped sampling gear (e.g., boxcores, grabs) for estimating density of large species such as surfclams. The model establishes a two-dimensional grid in which particles

(clams) are dispersed either randomly or patchily. In the case of patches, the patches are distributed randomly, and the clams are distributed in a biased random fashion so that clams are more likely to be within a given distance from another clam than otherwise. The basic unit of the domain is cm. Simulations for this study were conducted using a domain of 500-m × 500 -m. For the purposes of this exercise, clams were sampled using either a 25-cm × 25-cm or 50-cm × 50-cm sampling device, representing typical boxcore or grab sampling gear.

Simulated sampling locations within the domain are chosen randomly using Knuth's Ran1 random number generator (Press et al., 1986). Initial trials showed that small-scale autocorrelation (2–4 numbers in a row) occurred often enough to generate biased results in some cases. Thus all random numbers were re-randomized using an independent set of random numbers. We assume that surfclams expose an 8-cm × 8-cm surface to the sampling gear; that is, clams are oriented vertically in the anterior-posterior dimension, so that the exposure is expressed by the width and height of the clam rather than the length. Chosen sampling locations defined the northwest corner of the sample. By convention, any clam falling $> 50\%$ within the sampled area was considered sampled. For each simulation, the domain was seeded with enough clams to provide an average density of 0.5, 1, or 2 clams m^{-2}, representative of typical and high densities for surfclams in the Mid-Atlantic Bight (NEFSC, 2010).

All simulated sampling was conducted using a random sampling protocol. We recognize that many biological surveys use fixed station designs (e.g., Van der Meer, 1997; Petitgas and Lafont, 1997; Morehead et al., 2008) and are often transect based (e.g., Young and Rhoads, 1971; Flint and Holland, 1980; Dauer et al., 1984). King and Powell (2007) show that the uncertainties posed by insufficient sampling density, as discussed herein, plague sampling designs of the transect kind as they do random sampling designs.

For patchy distributions, patchiness was defined in terms of the maximum distance permitted between one clam and a second. The domain was seeded with a given number of clams that defined the initial set of patches. Further clams were placed into patches if distance requirements were met by means of the drawing of a limited number of random numbers. If distance requirements were not met in the allotted number of draws, a new patch was initiated at a random location. This permitted expansion of the number of patches, while also permitting enlargement of and increased density in established patches. Patchiness was determined by estimating the variance-to-mean ratio of the number of clams in a complete series of non-overlapping, but contiguous, samples of "sample-size" dimension (e.g., 50-cm × 50-cm) covering the entire domain (Taylor, 1961; Elliott, 1977). The two example scales of patchiness used in this study are shown in Figs. 1 and 2. Variance-to-mean ratios for simulations using these cases were about 1.6 and 2.5, respectively, based on contiguous sampling of the entire domain with a 25-cm x 25-cm sampling gear ($n=4,000,000$). Clam densities inside patches reached about 80 clams m^{-2} within a domain where average clam density was 1 clam m^{-2}. Patches this dense have been observed during surveys (Mann, unpubl. data).

Edge effects were minimized by using a domain at least 1 million times larger than the sample volume. Choice of the northwest corner of the sampling gear to establish the location of sampling assured that samples would not overlap the northern and western domain boundary, limiting edge effects to the southern and eastern boundary. On occasion some fraction of a sample would lie beyond one of these latter boundaries. Examination of the difference between simulations excluding or including such samples revealed few and always minor differences, confirming that edge effects were inconsequential with the
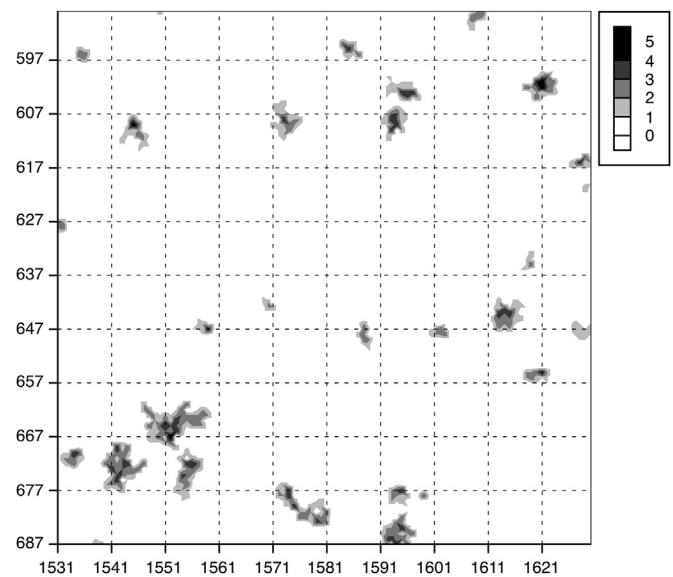

Fig. 1. A selected portion of the 0.25-km^2 domain for the case of a highly patchy population (variance-to-mean ratio=2.5). Each grid square is 25-cm x 25-cm, the size of a typical boxcore or grab sample. Axis labels are arbitrary locations in the entire 2000 × 2000-grid domain (2000 grids × 25 cm=500 m). Gray scale defines clam density. Highest densities reach about 80 clams m^{-2}; overall density average is 1 clam m^{-2}.
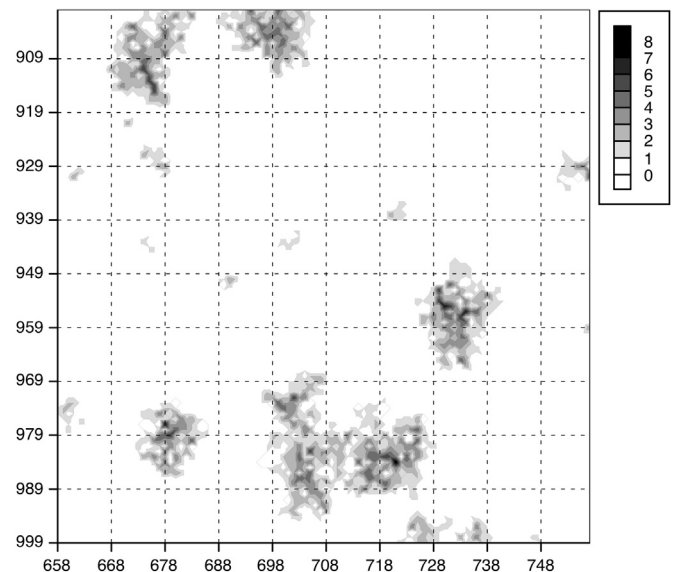

Fig. 2. A selected portion of the 0.25-km^2 domain for the case of a moderately patchy population (variance-to-mean ratio=1.6). Each grid square is 25-cm x 25-cm, the size of a typical boxcore or grab sample. Axis labels are arbitrary locations in the entire 2000 × 2000-grid domain (2000 grids × 25 cm=500 m). Gray scale defines clam density. Highest densities reach about 80 clams m^{-2}; overall density average is 1 clam m^{-2}.

domain size employed. Similarly, simulation results varied little with variation in the seed number for the random number generator. Thus, only single results for each spatial distribution and sampling intensity are presented.

Each simulation included 1000 trials. Clam density was calculated from the samples obtained by each of these trials and the trials ranked by the density estimated. Simulation results are presented as the clam density obtained for a series of percentile ranks obtained from the 1000 trials. Thus, the 90th percentile value represents the density obtained in the trial ranked as the 900th by clam density.