

Estimating habitat volume based on physical and biogeochemical models

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Abstract

We developed a program to translate habitat information from numerical models into metrics that can be used in fisheries stock assessments. Coupled 3D circulation and biogeochemical models predict changes in water properties that define fish habitat, including parameters such as temperature, salinity, and dissolved oxygen. When coupled with known physiological tolerances and habitat requirements of a species, model output can be used to estimate the volume of suitable habitat for the species over time. We are developing an open-source numerical model that calculates habitat volume from the predictions of the Regional Ocean Modeling System (ROMS) coupled to the RCA water quality model. We describe multiple approaches for calculating habitat volume from 3D model output and present results of an analysis that was used to select the most accurate and computationally efficient approach.

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Introduction

Coastal eutrophication is a widespread problem that is altering estuarine ecosystems and the habitat and nursery areas of many commercially and recreationally important fish species (Caddy 1993, Nixon 1995, Karlson et al. 2002, Kemp et al. 2005). Numerical biogeochemical models have played a central role in understanding water quality responses to nutrient loading (e.g., Kremer and Nixon 1978, Cerco 1995, Peeters et al. 1995). When linked to three dimensional hydrodynamic models, these coupled model systems can predict changes in various water properties, including temperature, salinity, and dissolved oxygen (DO), in three dimensions over time. Temperature, salinity, and DO are important characteristics in defining habitat suitability for fish species, which each have their own ranges of physiological tolerances (e.g., Funderburk et al. 1991; Brandt 1993; Breitburg 1994; Diaz and Rosenberg 1995; Secor and Gunderson 1998; Miller et al. 2002). Therefore, the physical and biogeochemical model output predicting these characteristics could be used to estimate the extent of suitable habitat in the model for a given species over time.

Our overall program objective is to create an essential fish habitat model that will compute the response of animal habitat and production potential under variable climate and nutrient loading using volume-based approaches and ecophysiological equations (e.g., Luo et al. 2001, Niklitschek and Secor 2005; in press, a, b). The volume-based model will be calculated from the intersection of water masses that encompass required temperature, salinity, DO and food conditions (Fig. 1), which will be defined by organism physiological requirements and avoidance behaviors. We will use output from the combined Row-Column Aesop (RCA) water quality model of biogeochemical processes (www.hydroqual.com/wr_rca.html) and the Regional Ocean Modeling System hydrodynamic model (ROMS, <http://www.myroms.org/index.php>) recently implemented for Chesapeake (Li et al. 2005, Zhong and Li 2006) and Delaware Inland Bays (J. Kirby and D. Di Toro, unpublished).

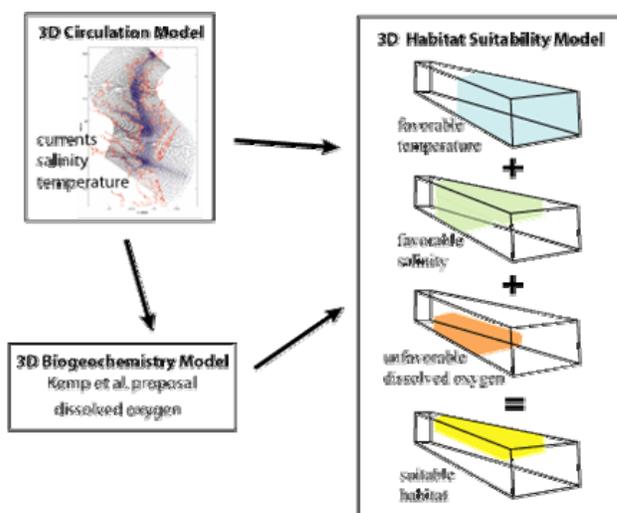


Fig. 1. Conceptualization of habitat suitability model

The objective of this paper is to describe multiple approaches for calculating habitat volume from 3D model output and to present results of an analysis that was used to select the most accurate and computationally efficient approach. Predictions of temperature, salinity, and DO from the ROMS-RCA model are defined at the model grid rho nodes, which are distributed non-linearly over the x- and y-directions and occur at multiple depths (at “s-levels”). We developed three different techniques to calculate the volume of suitable habitat using predictions at the rho grid nodes. We

compared the accuracy and efficiency of these techniques and chose the best technique to estimate grid cell volume in the model.

Methods

We investigated three methods for calculating the volume of a grid cell from ROMS-RCA model output: the “Step Method”, the “Triangle Method”, and the “Minimal Surface Method”. Once the volume of one grid cell is calculated, the technique is then applied to the entire model domain or to a subset of the model domain with water properties within an organism’s physiological tolerances.

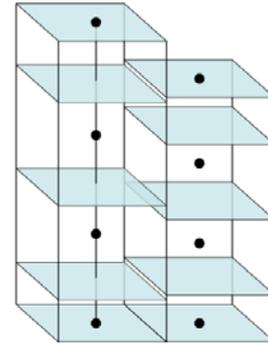


Fig. 2. Schematic of Step Method.

The Step Method uses a grid structure that places rho nodes, where depth and environmental parameters including temperature, salinity, and dissolved oxygen are defined, at the center of the grid cells (Fig. 2). In this method, the parameters are assumed to apply uniformly throughout their associated grid cell, and the top and bottom surfaces of the grid cells are flat and orthogonal to the vertical set of rho nodes. Although this technique is computationally simple, it does not preserve the implied smoothness of the s-levels in the model so we sought another technique that would allow calculation of smooth surfaces of temperature, salinity and DO across multiple grid cells.

The Triangle (Fig. 3) and Minimal Surface (Fig. 4) Methods placed the rho nodes at the vertices of the grid cells, which reflects the s-level structure of the model grid and preserves the implied smoothness of physical and chemical characteristics of the water across multiple grid cells. Because adjacent rho nodes may be located at different depths, the top and bottom faces of the grid cells are not necessarily planar. In the Triangle Method, the top and bottom faces are each divided into four triangles; the vertices of each of these triangles include two adjacent rho nodes in the face as well as the center point of the face. The grid cell can then be divided into four triangular “prisms” formed by joining the triangles of the top and bottom faces (Fig. 3). The total volume (V) of the grid cell can be calculated as the sum of the volume of each “prism” (v):

$$V = \sum_{i=1,4} v_i$$

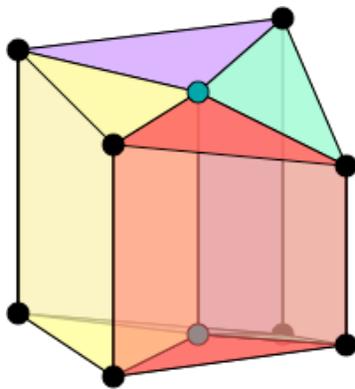


Fig. 3. Schematic of Triangle Method.

The volume of each “prism” is calculated using the x,y,z coordinates of the three points at the top [(x_{t1},y_{t1},z_{t1}), (x_{t2},y_{t2},z_{t2}), (x_{t3},y_{t3},z_{t3})]and bottom [(x_{b1},y_{b1},z_{b1}), (x_{b2},y_{b2},z_{b2}), (x_{b3},y_{b3},z_{b3})]of each “prism”:

$$v_i = \frac{A}{3} [(z_{t1} + z_{t2} + z_{t3}) - (z_{b1} + z_{b2} + z_{b3})]$$

where A is the cross sectional area of the “prism”:

$$A = \frac{1}{2} |x_{t1}(y_{t2} - y_{t3}) + x_{t2}(y_{t3} - y_{t1}) + x_{t3}(y_{t1} - y_{t2})|$$

In the Minimal Surface Method (Fig. 4), the top and bottom faces of the grid cell are assumed to be the minimal surfaces of the skew quadrilaterals formed by the four rho node vertices of the face. The minimal surface, the smallest surface area that can fit a given frame, is defined by drawing lines connecting midpoints of opposite sides of the skew quadrilateral, then drawing lines connecting matching quarter points, and so forth.

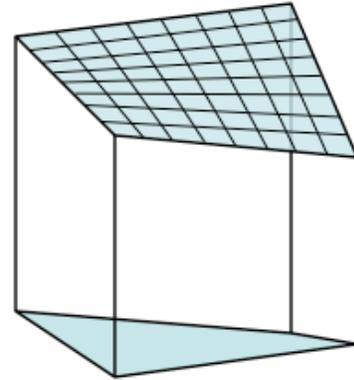


Fig. 4. Schematic of Minimal Surface Method.

We solved for the volume defined by this method numerically using the statistical programming language R (R Development Core Team 2005). First, a box defined by the x , y , and z extremes of the grid cell is drawn around the grid cell (outer box in Fig. 5). Then, evenly spaced points in x - y space in the box are sampled, with the height of the grid cell calculated at each of these x - y locations (dashed lines in Fig. 5). An x - y point in the box that is out of the bounds of the grid cell would have a height of zero. The volume of the grid cell is then calculated as the average of the heights times the x - y area (x - y area = A in Fig. 5) of the box. The accuracy of the numerical solution for the volume can be improved by using more closely spaced x - y points at which the height of the grid cell is calculated. Although we expected this technique to be more accurate than the Triangle Method, it is computationally intensive compared to that analytical approach.

To determine how the Minimal Surface Method compared with the analytical Triangle Method, we conducted multiple numerical simulations of the Minimal Surface model with varying numbers of x - y points for one model grid cell. Our goal was to determine the resolution (i.e., the number of x - y points) needed for the Minimal Surface model to converge on a stable volume, and then compare this volume to the analytical solution derived from the Triangle Method.

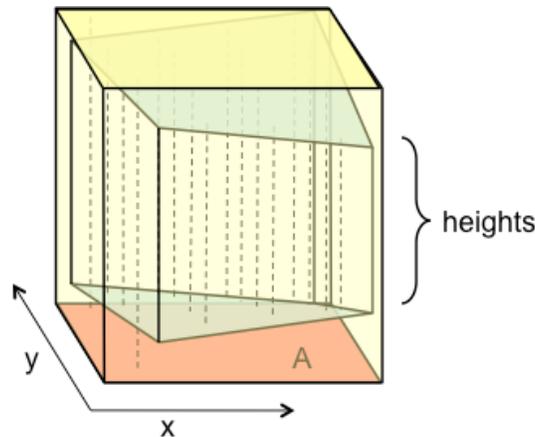


Fig. 5. Schematic of method to calculate volume of a three dimensional shape with a minimal surface.

Results

As the resolution of the Minimal Surface Method was increased, the volume calculated by the method converged with the volume calculated by the much simpler and faster Triangle Method (Fig. 6). Thus the more computationally intensive Minimal Surface numerical method is unnecessary. The method that preserves the implied smoothness of the s-levels and is both accurate and efficient is therefore the Triangle Method.

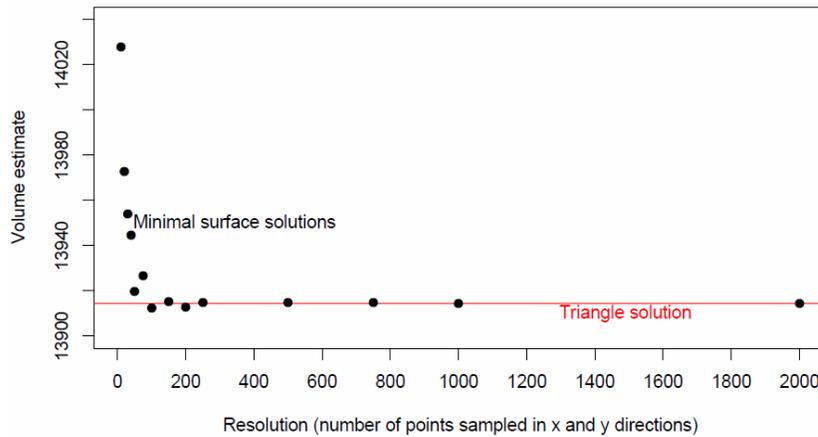


Fig. 6. Volume (m^3) of one model grid cell calculated with the Minimal Surface Method (filled circles) and the Triangle Method (red line). As the number of x-y points used for the Minimal Surface method increased (i.e. resolution increased), the solution for the two methods converged.

Discussion

The Triangle Method for finding the volume of the irregularly shaped model grid cells is being incorporated into a stand-alone open source Fortran program that can be applied to calculate habitat volume for species in multiple estuarine and coastal systems. This model will be applied to make habitat volume and associated bioenergetic calculations with ROMS-RCA output under a range of climatic and nutrient loading conditions to identify which species may be most sensitive to climate change and nutrient management in Chesapeake and Delaware Inland Bays. Particular focus will be placed on scenarios of variable freshwater inflow and temperature, which are known to affect estuarine fish recruitment and abundance (e.g., North and Houde 2003, Niklitschek and Secor 2005; Kraus and Secor 2005; Miller et al. 2006). In addition to providing predictions with high spatiotemporal resolution, spatially aggregated calculations will provide information suitable for use in stock-recruitment and Ecopath-Ecosim models for fisheries management.

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