

CARRYING CAPACITY EVALUATION FOR BIVALVE SUSPENSION-FEEDERS

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Abstract

Bivalve culture is an important economic activity in several regions and it should be carefully managed towards its sustainability. In this context, carrying capacity (CC) evaluation of coastal ecosystems for bivalve culture became an important topic. Mathematical modelling is a common approach for CC estimation. The objective of this work is to evaluate the importance of spatial resolution of mathematical models for CC evaluation. Obtained results suggest that low resolution models may lead to CC overestimates.

1. INTRODUCTION

Aquaculture is a rapidly growing activity, being responsible for nearly half of the world production of aquatic organisms (Rheault and Rice, 1995; FAO, 2001; Watson et al., 2001). Western countries, especially China, have a large contribution to this rapid growth (Watson e Pauly, 2001). In this context, the cultivation of bivalve suspension-feeders, such as mussels and oysters, gained relative importance over time.

In opposition to finfish culture that demands large inputs of artificial food, with negative impacts on environmental quality, suspension-feeders capture organic particles such as detritus, bacteria and phytoplankton, though their filtering activities and depend entirely on natural food items. Over the last decades, bivalve densities and cultivation areas increased rapidly. This may have negative environmental impacts though the accumulation of metabolites and faecal material, oxygen consumption and intensive bivalve filtering activities, leading to water and sediment quality degradation and negative effects over biodiversity. Ultimately, these impacts may lead to an increase on bivalve mortality (Zhang and Yang, 1999a, b) and a decrease on growth and production (Yang et al., 1998a,b, 1999; Zhang et al., 2001).

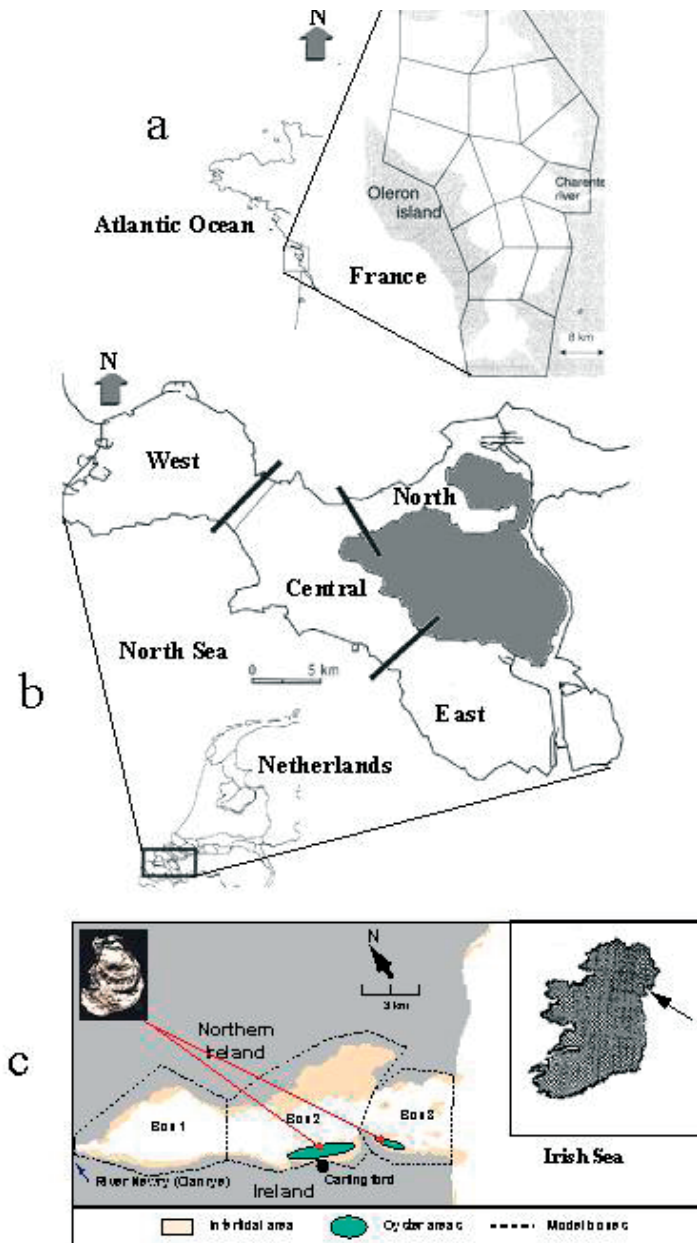
The success of bivalve cultivation depends mostly on water renewal and food input that should be faster than filtration, excretion and oxygen consumption rates of cultivated organisms. Therefore, bivalve density should be kept below environmental carrying capacity (CC) (Dame and Prins, 1998). CC may be defined as the bivalve biomass or abundance that may be kept within a particular ecosystem without affecting negatively

their production and ecosystem health (Duarte, 2003). Ecosystem health may be understood as ecosystem structural and functional integrity, i.e., its biodiversity and functioning in terms of nutrient recycling, primary and secondary production (Rapport et al., 1998).

CC evaluation may be viewed as a dimensioning process. Its complexity stems from the need to integrate hydrodynamic phenomena, responsible for water and food renewal, with biogeochemical processes, responsible for local food production and the recycling of bivalve metabolites and faeces. Furthermore, bivalve physiological processes such as food filtration, ingestion, absorption and metabolic losses, must also be considered namely (Dame, 1993). This complexity justifies the usage of mathematical models (Duarte, 2003).

The general approach in a CC model is dividing the study area in several compartments or cells to account for ecosystem spatial heterogeneity. Cell dimension and shape are variable among different models, with important effects on model spatial resolution. Hydrodynamic, biogeochemical and bivalve physiologic processes are calculated at each model cell, with several feedbacks between them. For example, bivalves remove phytoplankton from the water column, affecting the variable representing phytoplankton biomass. Each variable is represented by a mass-balance differential equation. Some variables may be “transported” in the water, such as phytoplankton and dissolved substances excreted by the bivalves, as a function of current velocity and turbulent mixing. For a revision on CC models see Duarte (2003). In Figure 1 a layout of three CC models is presented, showing the geographic domain and model cells.

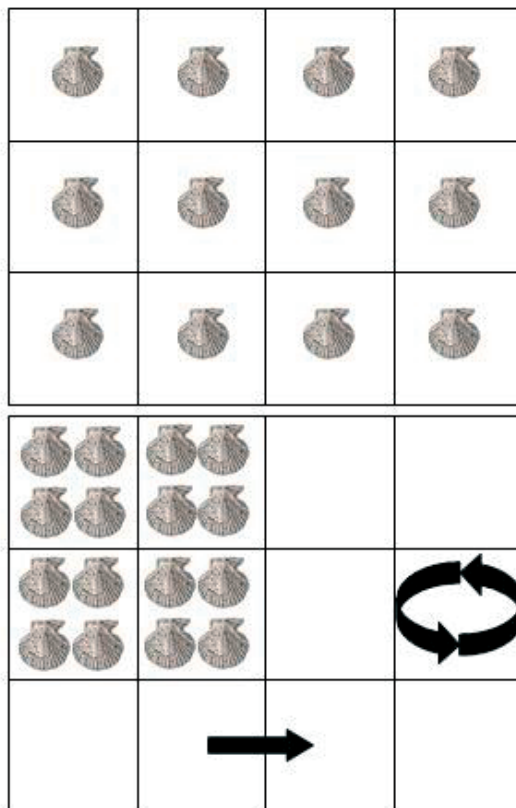
Figure 1. Examples of CC models including geographic domains and compartments or cells. Cell spatial dimension is in the order of several km. Models of: (a) Mar  nnes-Ol  ron bay (adapted from Bacher et al. 1998), (b) Oosterschelde estuary (adapted from van der Tol and Scholten (1998) and (c) Carlingford "lough" (adapted from Ferreira et al. 1998).



The spatial resolution used to represent cultivation systems is a critical issue in CC models (Duarte et al. 2005). These authors advanced the hypothesis that when bivalve abundance is integrated over areas larger than the cultivation zones, models tend to underestimate local food depletion effects, overestimating CC. Therefore, it is important that model spatial resolution is higher than the spatial scale of cultivation areas.

Some of these ideas are synthesized in Figure 2, with two examples of CC model grids, applied to an ideally simple rectangular domain. In one of the grids (A), bivalves are uniformly distributed over all cells. Although, in principle, such a distribution may occur, most frequently, cultivation zones are concentrated in part or parts of the domain. Therefore, the bivalve distribution

presented in grid B is a more realistic example – the same total number of bivalves as in A, but concentrated in part of the domain. Models assume that properties in each cell are homogeneous i.e., cell dimensions (length) correspond to their spatial resolution. In the grid A case, it is less likely that bivalves become food limited than in grid B case, as a result of their higher local density in the latter (one bivalve per cell against four per cell, respectively), everything else being equal. Sometimes, due to the low spatial resolution of CC models, bivalve distribution is “homogenized” over large areas. In an extreme case, all cells of Figure 2 grids could be lumped together in one large cell that could be part of a low resolution grid, covering a larger domain than the one represented in Figure 2. In such a situation, details on bivalve spatial distribution would be lost.



A

B

Figure 2. A and B represent two possible calculation grids of a CC model with a rectangular domain. The arrow on the lower panel stands for a flux of a generic property, calculated between grid cells as a function of its upstream concentration and current velocity. The rounded arrows stand for local regeneration/consumption processes. Panel A represents a homogeneous distribution of bivalve abundance. Panel B exemplifies a distribution where bivalves are concentrated in part of the model domain (see text).

The loss of these details corresponds to a dilution of local bivalve density. When this happens, it is more likely that local food regeneration processes, computed by models, are faster than bivalve consumption, leading to a CC overestimation. Considering these arguments, one might ask why not simply using the proper spatial resolution in CC models?

There are several possible answers to this question: (i) Increasing spatial resolution implies more computing time; (ii) Limited knowledge on bivalve spatial distribution and abundance; (iii) Lack of knowledge of the effects of “diluting” bivalve abundance on CC estimates. Model grids shown in Figure 1 are examples of spatial resolutions that do not allow distinguishing between cultivated and non-cultivated areas. For example, in case b, cultivation areas are mainly located along the margins, in the intertidal zone, not resolved by the grid. In case c, cultivation areas occupy only a very small part of cells 2 and 3. Therefore, bivalve density integrated over the whole area for each of these cells leads to an important dilution effect.

The objective of this work was to test empirically the hypothesis mentioned earlier: CC is overestimated

when model spatial resolution is inadequate to represent the spatial details of bivalve abundance.

This study is part of a larger work including a similar analysis for several ecosystems, to test the mentioned hypothesis. Obtained results may be relevant for future CC evaluations, in order to avoid methodological bias.

2. METHODS

2.1 STUDY AREA

This work is based on a previous case study described by Duarte et al. (2003) about Sungo bay, located in the Shandong province, in the People's Republic of China ($37^{\circ}00' - 37^{\circ}10'N$, $122^{\circ}25' - 122^{\circ}35'E$) (Figure 3). The bay has an area of c.a. 180 km² and a depth range from zero till nearly 20 m at the sea boundary. This bay has been used for mariculture for more than 20 years (Guo et al., 1999). Main cultivated species are kelps (*Laminaria japonica*), oysters (*Crassostrea gigas*) and scallops (*Chlamys farreri*) with yearly productions of c.a. 40,000, 60,000 and 13,000 tons, respectively. Figure 4 synthesizes bivalve distributions and respective densities at cultivation sites.

Figure 3. Sungo bay location. The insertion on the upper left corner shows part of the model grid (500 m squares) used to represent spatial details.

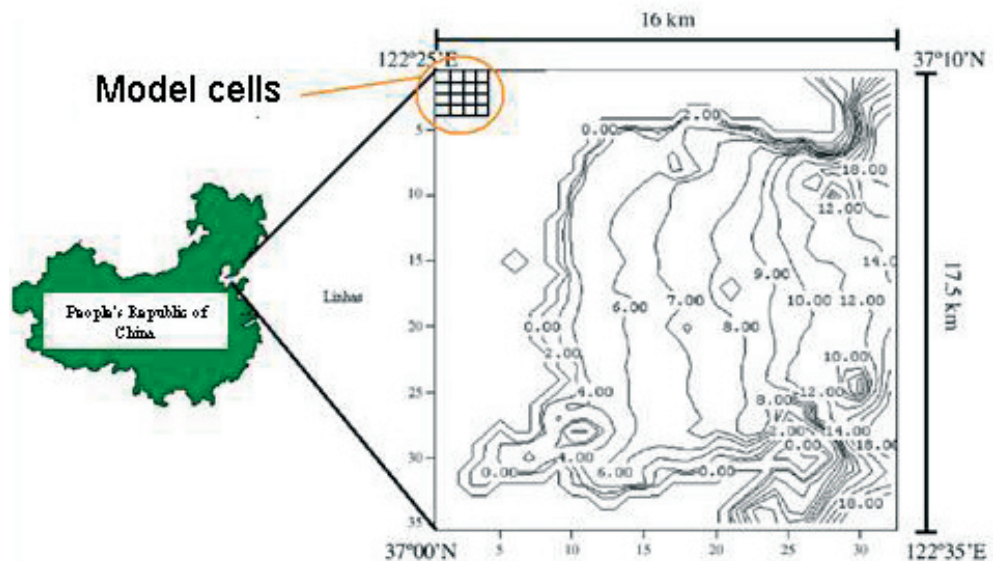
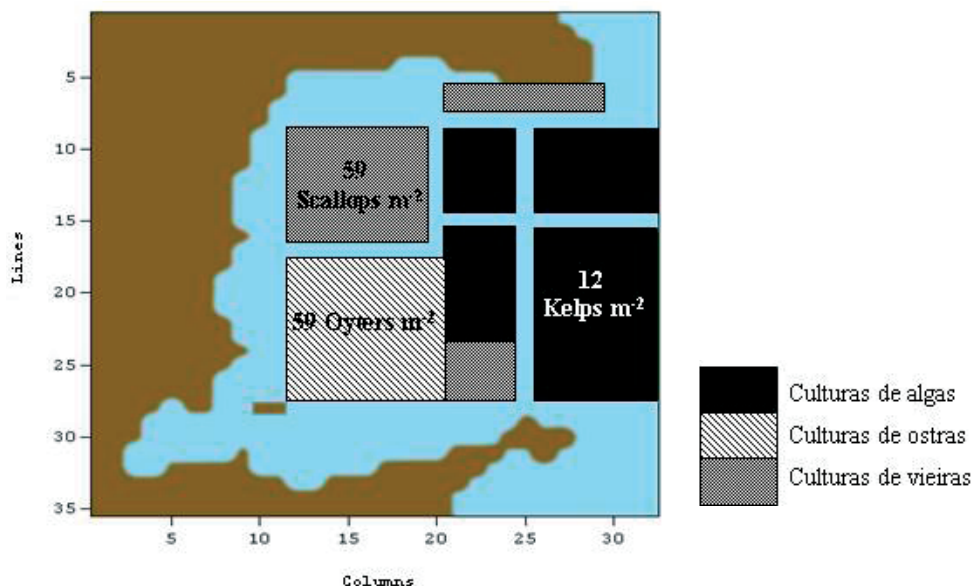


Figure 4. Sungo bay aquaculture with the location of kelp, oyster and scallops cultures and respective densities. Numbers indicating "columns" and "lines" correspond to the coordinates of the 1120 calculation cells (32 X 35).



2.2. MODEL IMPLEMENTATION

The model used in this study was described by Duarte et al. (2003), including details on state variables, equations, parameter values, calibration and validation. The present model version has some (small) differences that will be discussed below. It is a two dimensional vertically integrated model (spatial variability is considered as a function of longitude and latitude and vertical homogeneity is assumed), with sea and land boundaries. The first version of this model was implemented with EcoWin (Ferreira, 1995). The current version was implemented with EcoDynamo – a modelling software developed at Fernando Pessoa University (Pereira and Duarte, 2005).

Regarding calculations, the only difference between the current version and the one described by Duarte et al. (2003), is in the way phytoplankton nutrient limitation is computed. In the original version, calculations were based on inorganic nitrogen availability in the water. In the present version, calculations are made according to Jørgensen and Bendorichio (2001), following a three stage process: (i) Nutrient uptake is computed as a function of nitrogen concentration in the water and assuming a

Michaelis-Menten kinetic; (ii) Internal phytoplankton cell nutrient concentrations are updated; (iii) Photosynthesis is limited by internal nutrient concentrations, assuming a Michaelis-Menten type limitation. Necessary parameters were taken from the literature or estimated by model calibration. For a detailed description on equations and parameters see Duarte et al. (2006) and Duarte et al. (in press). After these changes were introduced in the model, calibration and validation were confirmed to guarantee that model performance remained similar to the original version.

2.3. MODEL SIMULATIONS

Given the objective of this work, several model simulations were carried out for CC estimation in Sungo bay, following the methodology described in Ferreira et al. (1998) and using several spatial resolutions to represent bivalve distribution and abundance. The methodology used by the mentioned authors, consists in evaluating bivalve production as a function of bivalve abundance. A set of simulations is performed, for a period corresponding to the cultivation cycle (c.a. 1.5 years), chan-

ging bivalve abundance every new simulation. The expected result is a parabolic response of production, with a maximum, after which any further increase in bivalve abundance reduces production. This pattern was explained in Bacher et al. (1998). The initial increase in production is explained by the larger abundance of bivalves. When abundance increases over a certain level, individual bivalve growth becomes food limited and overall production decreases. At this stage, food regeneration rate is lower than food consumption by the bivalves.

In this work, several simulation sets were undertaken, using the following bivalve abundances relative to reference values (Figure 3): 0.5X, 1X (reference values), 2X and 3X. This procedure was performed for both bivalve species: oysters and scallops. Different spatial resolutions were used to represent bivalve distribution and abundance in each simulation set: 500X500 m (reference resolution), 1000X1000 m, 1500X1500 m and the whole bay. Hereafter, these sets will be referred as simulations 1, 2, 3 and 4. The larger the spatial scale, the larger the area over which bivalves are distributed, in order to simulate the effects of spatial resolution on CC evaluation. Another simulation set was carried out with the reference resolution but distributing scallops over the areas already occupied by kelps (Figure 3), keeping everything else equal. For this simulation set the following abundances were tested relative to the reference values: 1X, 2X e 3X. Hereafter, this simulation set will be referred as simulation 5. In all simulations, bivalve "seeding" and harvest timings are in accordance with current farmer practices (Duarte et al., 2003).

3. RESULTS AND DISCUSSION

Expected and model predicted oyster and scallop production per cultivation cycle are presented in Table 1 for the reference abundance (cf. – Figure 4) and a spatial resolution of 500X500 m. As it may be seen, predicted values are well within expected ranges - 37636 and 10735 tons of fresh weight (meat + shell) for the oysters and the scallops, respectively.

Table 1. Oyster and scallop production predicted by the model for the reference scenario (simulations 1 with a normal bivalve density (cf. – Figure 4)) and expected values (Tones of fresh weight), described in Duarte et al. (2006).

| | Oysters | Scallops |
|------------------|---------------|---------------|
| Expected values | 34000 - 46000 | 10000 – 19000 |
| Predicted values | 37636 | 10735 |

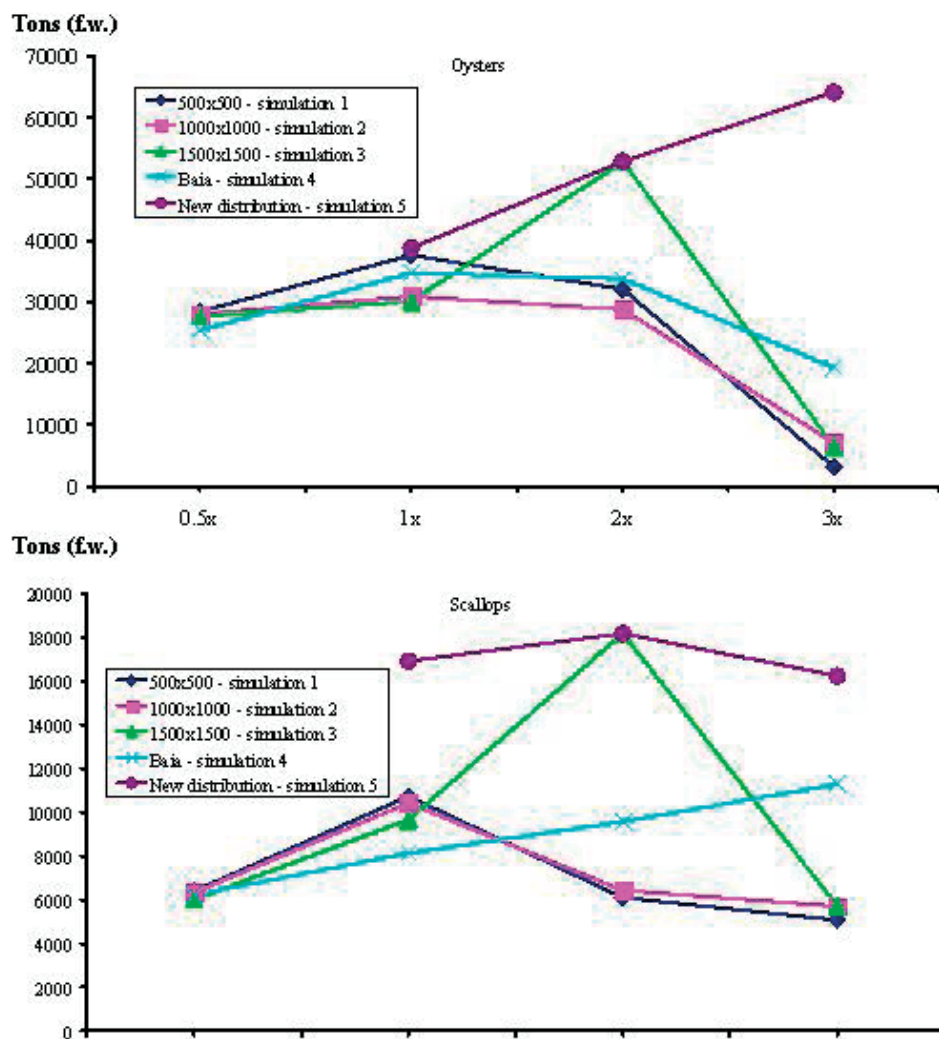
Figure 5 synthesizes bivalve production results of all simulations as a function of bivalve abundance and for the simulation sets described above (cf. – 2.3, Bacher et al., 1998; Ferreira et al., 1998). Obtained results exhibit the usual parabolic pattern. The exceptions to this behavior are simulations 5 results, for the oysters, and simulations 4 results, for the scallops, meaning that larger abundances could be tested. In the former case, results suggest that when scallops are distributed over a larger area there is more food available for the oysters, allowing a more intense cultivation. In the latter case, obtained results suggest that when model spatial resolution is lowered, distributing bivalve abundance over the entire bay, production may increase until abundances 3X the normal values, due to a reduction on local food depletion. This result raises the following question: Why then, under lower abundances, higher productions are obtained for simulations 1, 2 and 3? The answer may be on bay habitat qualities, i.e., food distribution and quality is not homogeneous, reason why a linear increase in production with bivalve "dilution" over larger areas may not occur, although this pattern may be observed for certain bivalve abundance ranges. In fact, considering simulations 1 to 4, larger productions for both species were obtained when bivalve abundance is doubled and spatial resolution is 1500X1500 m (simulations 3). Another interesting result is that under abundances 3X than normal ones, predicted production increases with the reduction in spatial resolution in the sequence 500X500, 1000X1000, 1500X1500 and the whole bay. This suggests that the hypothesis being tested in the present work is correct, especially under large bivalve abundances, when local food depletion effects are more likely to occur and being underestimated if spatial resolution is not adequate.

From the results above, it follows that it is important to compare several models for the same ecosystem with different spatial resolutions, in trying to get some fur-

ther empirical evidence for the hypothesis being tested. Nunes et al. (2003), implemented a zero dimensional ecological model for the Songo bay (the same ecosystem analysed in the present study), i.e., a model where the bay is viewed as a homogeneous water body, without any type of spatial resolution. They estimated that the bay CC is 2X and 15X the actual rearing density for scallops and oysters, respectively. Duarte et al. (2003), using a two dimensional model with a 500X500m resolution (similar to the one used in the present work with the differences listed above (cf. – 2.2)), concluded that Songo bay is already being exploited at its CC for scal-

lops, whereas for the oysters, cultivation density might be increased c.a. 2X, assuming that cultivation areas remain unchanged. In the present study, as a result of the minor modifications introduced in the model implemented by Duarte et al. (2003) (cf. – 2.2), it is suggested that, at normal cultivation densities, oysters are also being exploited close to bay CC. These comparisons, in spite of the differences between the models employed, provide some additional evidence for the hypothesis being tested, suggesting that massive CC estimates may be erroneously obtained with low resolution models.

Figure 5. Oyster (upper panel) and scallop (lower panel) production predicted by the model as a function of bivalve abundance relative to the reference values and for each of the simulation sets (cf. – 2.3).



4. CONCLUSIONS

From the results obtained, the hypothesis that CC is overestimated when model spatial resolution is inadequate to represent the spatial details of bivalve abundance is empirically confirmed. However, results are not always consistent. In fact, CC overestimates are apparent mostly under high bivalve abundances, when food limitation is more important. Furthermore, there is not always a monotonous relationship between the mentioned overestimate and the reduction in spatial resolution, except under higher abundances. These "irregularities" may be explained by the fact that when bivalves are distributed over larger areas, part of them may be confined to low food concentration zones, leading to a local reduction on predicted production that may be not compensated by the decrease in local food depletion. Obtained results demonstrate the importance of representing in detail cultivation areas and suggest that part of the models described in the literature may overestimate CC. This is quite relevant, since overestimating CC may be environmentally more damaging than its underestimation.

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