

Interactive comment on “Small-scale spatial structure in plankton distributions” by A. Tzella and P. H. Haynes

A. Tzella and P. H. Haynes

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Interim Response to both Referees

We thank the referees for their reports. Both referees have suggested detailed technical corrections to which we will reply at the revision stage. Below we address, in brief, the more general comments.

Both referees question the realism of the model, e.g. with regard to the neglect of diffusion, buoyancy and locomotion (Referees #1 and #2) and with regard to the spatial independence of productivity (Referee #1).

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Interactive Discussion

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A first important point to note is that the main focus of the paper has been to resolve the discrepancy that arises between the theoretical and numerical work in Hernández-García et al. (2002) and the numerical work in Abraham (1998). Both investigations employ a similar biological model to describe the interactions among the species. Choosing that same model will allow the two investigations to be compared more easily, and the specific point of discrepancy to be located. Nevertheless it is important to be clear about the simplifying assumptions underlying this model.

First the model is intended only to represent larger scales (greater than $100m$ or so) on which the flow is quasi two-dimensional. This is one justification for the neglect of microscopic species motion, e.g. through locomotion or buoyancy, relative to the flow, which the referees rightly point out is a crude assumption in general.

Secondly, the biological model used is indeed highly simplified. The point made by referee #1, that the model could and probably should be extended by including a space-dependent productivity or death rate is very reasonable. However the general conclusions that follow from the biological model considered here follow for a wide class of biological models. As long as the biological system remains stable, with a single attractor, the emerging spatial patterns will still be characterised by a set of spectral exponents or Hölder exponents that are determined by the competition between the slowest decay rate associated with the biological processes (though when the biological model is space-dependent this decay rate will depend to some extent on the flow) and the Lyapunov exponent associated with the stretching properties of the flow.

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