# Small-scale spatial structure in plankton distributions

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Understanding the interaction of nutrients and plankton species is of vital importance for comprehending the $CO_2$ interchange between the atmosphere and the ocean. Considering they are passively advected by the flow and given that their population numbers are big, Advection-Diffusion-Reaction (ADR) equations have frequently been employed to comprehend the spatial structures arising from the biological and fluid coupling.

The observed filamental nature of the corresponding populations suggests that stirring plays an important role in determining the spatial structure. One approach to understanding the small-scale behaviour of the interacting species is to consider flows that are smooth functions of space, i.e. with finite spatial scale, and to focus on the spatial variations of the biological species at spatial scales smaller than the flow scale. (In some contexts this is referred to as the Batchelor regime.) Trajectories in such a regime can be chaotic – what is known as Lagrangian Chaos. A further simplifying assumption is to neglect the effects of diffusion. The concentrations of different biological species within a fluid parcel are then determined by time history of that parcel, e.g. in determining the time history of biological forcing functions experienced by the parcel.

In such systems the induced spatial structure has been shown to be a result of competition between the rate of convergence of the biological processes involved and the rate of divergence of the distance of neighbouring fluid parcels. It has also been argued that, except under rather special conditions, the small scale behaviour should be the same for all interacting species (Neufeld et al 1999). However Abraham et al (1998) have presented results for a system in which the biological evolution equations are delay-differential equations that show different small-scale spatial structure for different species (specifically different structure for zooplankton and phytoplankton).

In the work to be presented we examine a class of models involving a nutrient, a prey and a predator, coupled to a Batchelor-regime flow. A wide range of numerical simulations seem to be in good agreement with the results attained by Neufeld et al. Allowing the possibility of delay-differential equations does not change these conclusions, provided sufficiently small spatial scales are considered. However, under certain conditions, there is decoupling of the spatial structure of zooplankton on the one hand and phytoplankton and nutrient on the other, at scales larger than a particular characteristic length scale. The factors that determined this lengthscale will be discussed. By theoretically investigating the relevant mechanisms, we hope to obtain a further insight into the phenomenon on of plankton patchiness in more realistic systems.