



Emergent features due to grid-cell biology: synchronisation in biophysical models

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A standard approach in studying oceanic plankton distributions is the use of coupled biophysical models; the set-up consists of an ensemble of interacting grid-cells, in each of which the biology evolves according to the chosen ecosystem model, with interaction between grid-cells provided by the prescribed flow. Such a system is the concern of the area of mathematics known as synchronisation theory, which studies how the natural rhythms of individually oscillating objects adjust as a result of coupling between them; if the coupling causes the oscillations to become identical in time, we describe the system as synchronised.

A variety of plankton ecosystem models exists, reflecting the particular ocean regions and modelling aims of different studies. We use the methods of synchronisation theory to answer the following question: what impact does the choice of biological representation at grid-cell level have on the dynamics of the full system? Using several typical plankton models, we consider a network of identically-represented, diffusively coupled plankton “patches” and determine the strength of patch-to-patch flow required for the system to exhibit stably synchronous – spatially homogeneous – dynamics.

It is shown that the emergent properties of the full system depend crucially on the choice of biological model and can change drastically in a discontinuous manner, depending on the strength of coupling and number N of grid-cells.

This has implications for modelling studies of the ocean: the choice of spatial resolution at which to study a region, and therefore number of grid-cells in the model, can potentially discontinuously alter the dynamics from patchy to stably homogeneous at

a threshold value of N .