Direct Numerical Simulations of Phytoplankton Blooms

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Introduction

From satellite images, we see phytoplankton blooms in the North Atlantic from season to season. Scientists notice that these blooms take different behaviors in distinct flow topologies, such as vortices and filaments. Motivated by such observations, and the recent developments with objective extractions of flow topologies using Lagrangian Coherent Structures, we studied the Fisher-Kolmogorov equations inside a double-gyre system. We quantified the variabilities in biochemical reaction processes based on a natural coordinate system extracted from the Lagrangian topologies and examined how the initial placement of a biomass in this coordinate system correlated to its growth rate.

Mathematical Formulation

The governing equation for transport is given as:

$$\frac{\partial c}{\partial t} + \mathbf{u} \cdot \nabla c = -\frac{1}{Pe}\nabla^2 c + \eta c(1-c),$$

where

$$u = -\pi \sin[\pi(x-g)]\cos(\pi y), \; v = \pi\cos[\pi(x-g)]\sin(\pi y),$$

and

$$g(t) = 0.3\sin(4\pi t) + 0.1\cos(\pi t).$$

The governing non-dimensional parameters are Pe and η. Pe controls the diffusion time-scale versus the advection time-scale. η controls the reaction time-scale versus the advection time-scale.

The Lagrangian Coherent Structures (LCS) are characterized by finite-time Lyapunov exponents given as:

$$\sigma(x,t) = \frac{1}{2T}\log(\lambda_{max}(M)), \qquad M = \left[\frac{\partial x}{\partial x_0}\right]^T\left[\frac{\partial x}{\partial x_0}\right],$$

Where T denotes the integration time for Lagrangian trajectories, M is the deformation tensor, $[.]^T$ is the transpose of a matrix, and x is the end position for trajectories started at x_0.

Results

- We find strong correlation between the repelling LCS and the bulk growth rate.
- This can be explained by the early-time stretching history of a scalar in different flow topologies.
- The variability of the bulk reaction rate is non-Gaussian.
- The pure reaction process (homogenized) is the upper-bound for reaction speed, the non-flow case is the lower bound.
- The difference of the bulk reaction rate and the perfect logistic growth rate highlights the effect of stirring in homogenizing the scalar. At extended time periods, all of the cases approach this same reaction rate.
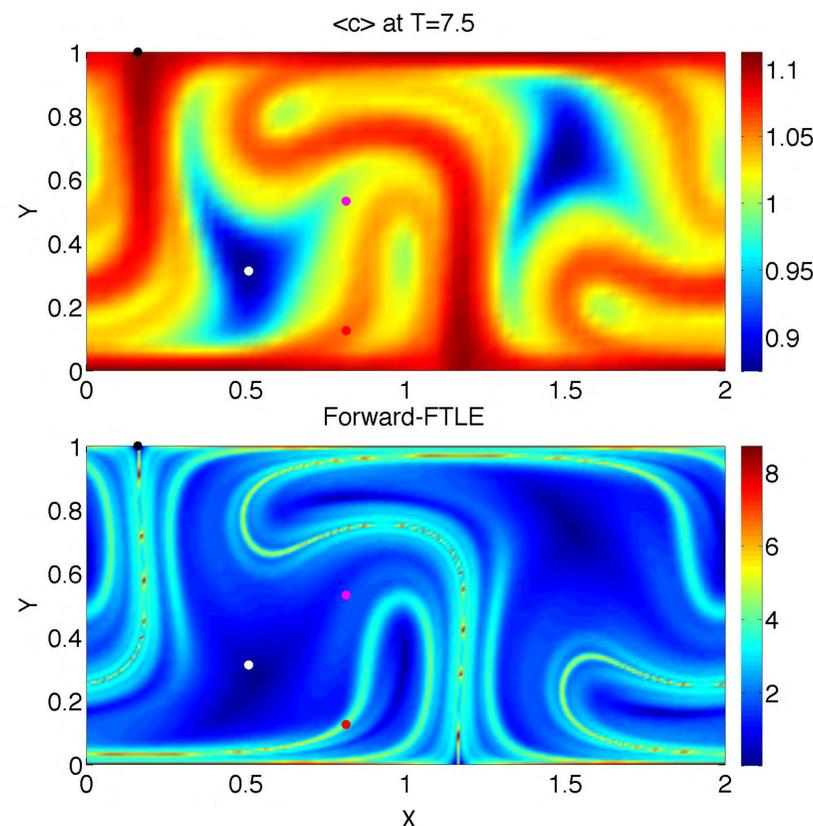

Figure 1: (Top) <c> at T=7.5, (Bottom) FTLE for repelling structures. The four dots indicate initial release locations of the cases considered later.

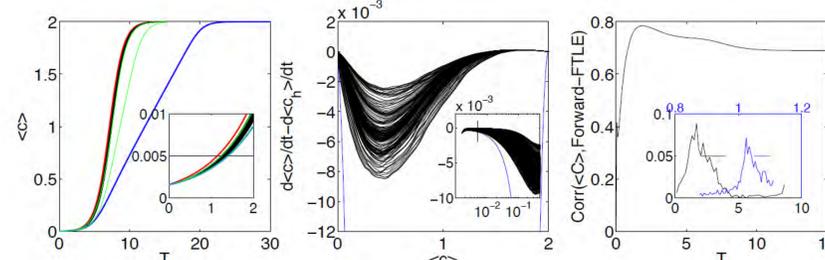

Figure 2: (Left) Time history of <c> and their variability subject to initial locations and flow types. (Center) The difference of the bulk reaction speed and a perfect logistic growth speed. (Right) Time history of correlation between <c> and FTLE and their PDF.

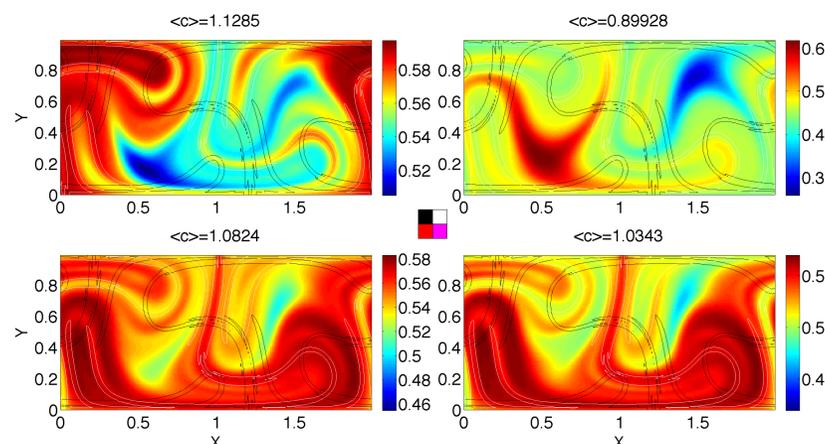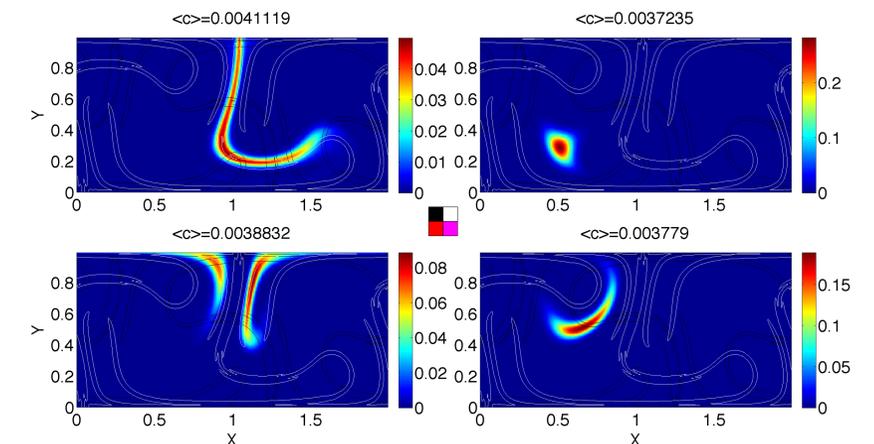Figure 3: c at T=7.5 for the highlighting cases.

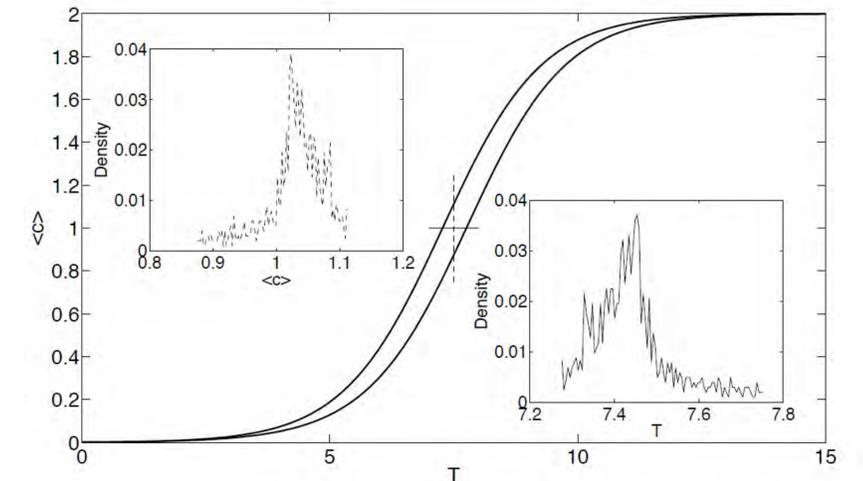Figure 4: c at T=1 for the highlighting cases, showing the early-time stretching.

Figure 5: Time history of reaction. (Left-inset) Variability of <c> at T=7.5. (Right-inset) Variability of T to reach <c>=1.

Conclusions

It was observed that the biological reaction processes are heavily modulated by the LCS present in the flow. With initial placement in repelling structures, the biological species is helped to spread out much faster, hence allowing biochemical reactions to take place more quickly. With initial placement in attracting structures, the biological species is brought to be highly concentrated, hence suppressing the overall growth of the biomass. With respect to initial placement in eddies, since trajectories are not separated so much, the biological reaction processes are more regular as if there were no stirring introduced.

The more interesting aspect of our results is that the variability of these processes is not Gaussian, and cannot simply be characterized by a mean and a variance. However, correlation with the LCS indicates that an LCS based parameterization could shed new light on the modeling of the advection-diffusion reaction processes.

Acknowledgements