## Abstract Submitted for the APR13 Meeting of The American Physical Society

Direct Numerical Simulations of Phytoplankton Blooms CHRISTOPHER LUNA, Undergraduate Physics Student, Arizona State University, WENBO TANG, School of Mathematical and Statistical Sciences, Arizona State University, MIXING AT ARIZONA STATE UNIVERSITY TEAM — Motivated by observations of phytoplankton blooms in the North Atlantic obtained through satellite imaging, and by 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. The Lagrangian topologies are extracted as the extrema of the Finite-Time Lyapunov Exponent (FTLE) field for the flow, and the natural coordinate system used is based on the extracted invariant barriers. We found the dependence of reaction rates on the hyperbolic finite time invariant manifolds highlighting the largest stretching of scalars as well as the reaction rates in the transversal direction from eddy centers to their edges. It was observed that the biological reaction processes are heavily modulated by Coherent Structures 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.

> Christopher Luna Undergraduate Physics Student, Arizona State University

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