

Abstract Submitted
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Simulations of bacterial chemotaxis in the turbulent ocean RO-MAIN WATTEAUX, JOHN TAYLOR, Department of Applied Mathematics and Theoretical Physics, University of Cambridge — Nearly half of the global primary production occurs in the oceans. Between 30 and 50% of the newly generated carbon is released into the surrounding water as dissolved organic matter (DOM), and is almost exclusively accessible to bacteria. By consuming DOM and returning the carbon to the marine food web, bacteria act as recyclers. Some bacteria are motile and have the ability to modify their otherwise random motility in response to a chemical cue, a process known as chemotaxis. It has been recently shown that motile bacteria can benefit from turbulence by clustering around thin DOM filaments, thereby increasing their uptake (Taylor and Stocker, *Science*, *accepted*). Here, we extend the previous analysis by considering weakly diffusive DOM patches (with a Schmidt number, $Sc = \nu/\kappa_C$ up to 1000), and examine the counteracting effects of chemotaxis and random motility. Using direct numerical simulations (DNS), we find that the uptake enhancement depends on characteristic length scales of DOM and bacteria filaments, which in turn depend on three parameters: the turbulent dissipation rate, the bacteria swimming speed, and the DOM diffusivity. By exploring a range of realistic parameter values, we are able to characterize the advantage afforded by motility.

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