

## Direct numerical simulation of algae migration in a lake

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**Direct Numerical Simulation of algae migration in a lake**Evelyn Aparicio Medrano<sup>1,2</sup>, Bas van de Wiel<sup>1</sup>, Rob Uittenbogaard<sup>2</sup> & Herman Clercx<sup>1</sup><sup>1</sup>Fluid Dynamics Laboratory and J. M. Burgers Center for Fluid Dynamics, Department of Physics, Eindhoven University of Technology, P.O. Box 513, 5600 MB Eindhoven, The Netherlands<sup>2</sup>Deltares, P.O. Box 177, 2600 MH Delft, The Netherlands**Abstract**

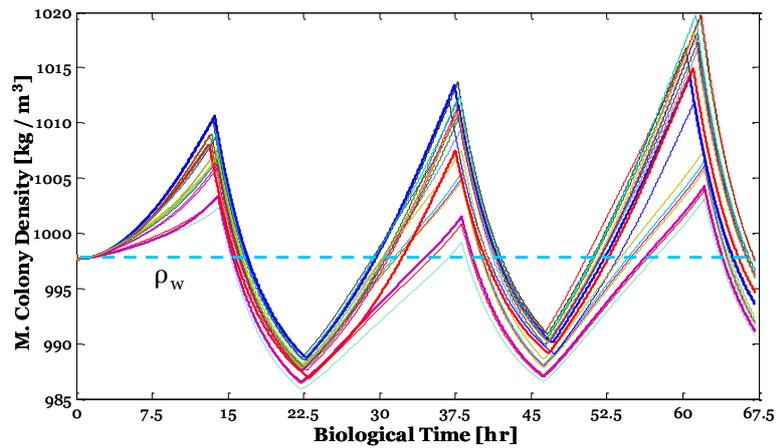
The spatial distribution of algae in lakes inter alia depends on ambient mixing conditions in the water, which, in turn, are driven by atmospheric conditions at the boundary. Also, their density can be actively regulated by a physiological response to light, as such to adjust their buoyancy. The aim of the present study is to investigate the combined effect of turbulent mixing and buoyancy regulation on the vertical migration of algae under natural conditions. Given the typical size of algae, small scale turbulence will play an important role in this migration. Therefore, in this research we propose coupling Direct Numerical Simulations of turbulent flow with particle tracking of biologically active organisms. The intrinsic gap between biological and flow time-scales makes such an endeavor a non-trivial exercise. Therefore, in order to conceal time scales of flow and biology we propose a scaling procedure. The proposed methodology is applied to study the vertical migration of a particular cyanobacteria species: *Microcystis Aeruginosa*. Our results show that our model is effective in representing the vertical daily migration of *Microcystis Aeruginosa*, in a sense that realistic characteristics are simulated as compared to nature.

**The Model**

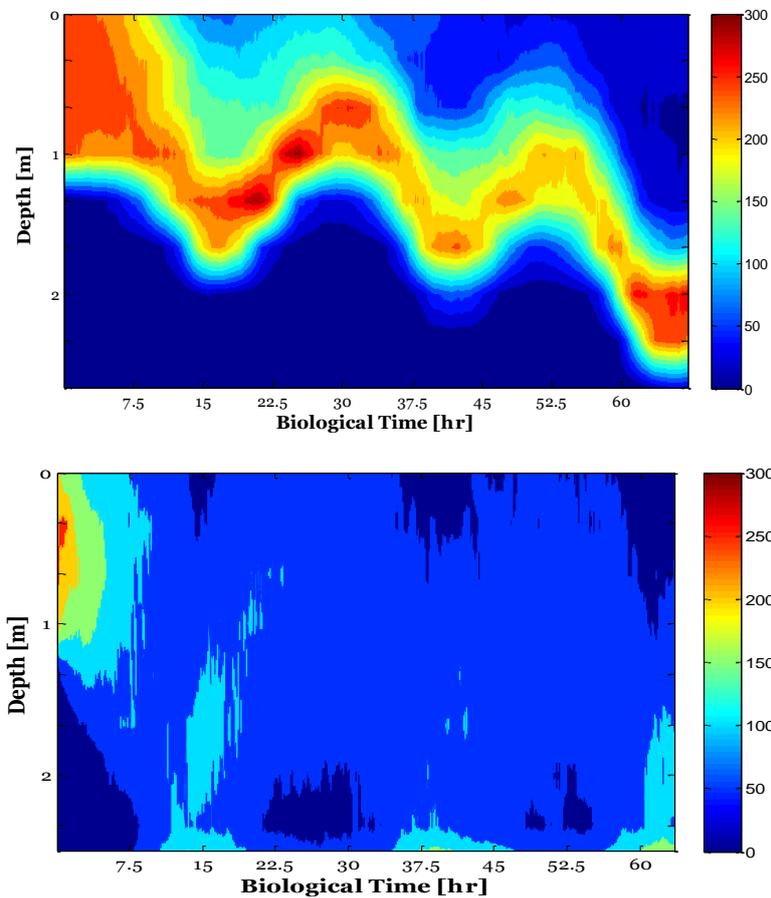
The flow is solved by using a Direct Numerical Simulation of the Navier-Stokes equations [1]. The particle dynamics are simulated using a reduced Maxey-Riley equation [2]. Here, the particles (*Microcystis* colonies) are approximated as rigid spheres and their trajectories are calculated using individual particle tracking. The particle component includes the active physiological changes in cell-tissue density that occurs depending on the light environment perceived by the algae [3]. Light extinction along the depth of the lake is modeled following Lambert Beer's law. Here, we speed up the physiological processes in order to make the biological-hydrodynamical coupling feasible within the computational limitations. This is done by using a formal scaling/normalization procedure. The scaling procedure follows from the nondimensionalization of the system core equations. The obtained non-dimensional parameters include among others: flow Reynolds number, particle Stokes number and flow-biological time scales ratio. The latter is the essential ratio of our speeding up procedure.

**Results**

Our methodology allows us to simulate three full daily cycles within one DNS simulation. Figure 1 shows the colony density changes of 20 particles. Under low turbulent conditions (turbulent energy dissipation  $\varepsilon = O(10^{-8} \text{ m}^2 \text{ s}^{-3})$ ), the vertical migration of *Microcystis* depends mainly on its buoyant status (see Figure 2a). Higher turbulent environments, ( $\varepsilon = O(10^{-5} \text{ m}^2 \text{ s}^{-3})$ ), supersede the buoyant ability of the algae and distribute them more uniformly within the domain (Figure 2b). We also performed a sensitivity analysis in order to analyze the effects of changes in particle size and light extinction (results not shown here). The present results seem to be in qualitative agreement with a more practical study. The latter couples a k-epsilon model with a Fokker-Planck approach to simulate particle migration dynamics [4].



**Fig 1.** Colony density changes in response to light and turbulence. The dashed line shows the density of water.



**Fig 2.** Colony concentration. a) Low turbulence intensity, b) High turbulence intensity.

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