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AN IMMERSED BOUNDARY METHOD FOR DIATOM SEDIMENTATION

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Abstract. We propose a mathematical model and immersed boundary method for the growth and breakup of diatom chains. Diatom chains are treated as zero thickness open curves thanks to their small aspect ratio. The growth of the chain is modelled by adding small pieces of diatoms at the two end points while the breakup is done by removing a small piece in the middle of the chain. Numerical experiments are carried out to investigate the effects of growth and breakup on the sedimentation rate of diatom chains. Simulations of multiple diatom chains show that sedimentation rate is highly dependent on diatoms' spatial distribution. The results can be used to explain the observations that diatoms often form chain-like structures in natural habitats.

Key words. Diatom sedimentation, hydrodynamic interaction, immersed boundary method.

1. Introduction

In many taxonomic groups, colony formation among planktonic organisms suspended in water is very common. The colonial structures are formed in many ways and many colonies take the form of chains [14]. Diatom is one of the most important species among those phytoplankton [1]-[3]. It is found that diatoms are capable of existing as independent units and also join together to form long chains as well [3]. Since diatoms are denser than water and they normally sink under gravity, any strategy that helps to create a condition to reduce the sedimentation speed will be evolutionary advantageous.

In [9], diatom chains are modelled as nearly inextensible two-dimensional fibres with large bending resistance. Sedimentation of diatoms are studied using the immersed boundary method. It was found that the speed of sedimentation is affected by the length as well as the orientation [8] for an isolated fibre or a group of fibres with relative large separation distance. On the other hand, when the separation distance is small, sedimentation speed is greatly enhanced, due to hydrodynamic interaction. It was also found that orientation of these fibres becomes less a factor under a shear flow. While these findings are informative, it is not clear what determines the separation distance among diatoms in an environment where planktons could grow. In this paper, we develop an immersed boundary method to investigate the dynamical process of diatom growth and sedimentation, where the separation distance among diatoms is a not a pre-determined parameter.

The main feature of our immersed boundary method is that the length of the immersed structure is under active control. First of all, the diatom chain element is nearly inextensible without growth, which is approximated by a nonlinear strain-hardening spring. Secondly, the growth of diatoms is modelled by adding extra element to the diatom chain. Finally, when the chain breaks, a repulsive force among diatom chains is imposed to modelled the thick setae structures found in

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some diatom species [13]. Otherwise, diatoms are allowed to move freely under gravity and the surrounding flow fields.

In Section 2, an immersed boundary formulation of Navier-Stokes equations and interfacial forces are described. A model for diatom growth and breakup is proposed in Section 3. In Section 4, we present simulations to demonstrate the effectiveness of our method. We finish our paper by a short conclusion in Section 5.

2. Mathematical model

A simple mathematical model of diatom sedimentation consists of dynamics of fluid, gravitational force, and deformation of diatoms. The corresponding immersed boundary formulation [10, 12, 16] is shown as follows.

$$\frac{\partial \boldsymbol{u}}{\partial t} + (\boldsymbol{u}\cdot\nabla)\,\boldsymbol{u} + \frac{1}{Re}\nabla p = \frac{1}{Re}\Delta\boldsymbol{u} + \frac{1}{ReCa}\boldsymbol{f}_s + \frac{1}{ReBn}\boldsymbol{f}_b + \frac{\beta}{Fr^2}\boldsymbol{f}_g, \tag{1}$$

$$\nabla\cdot\boldsymbol{u} = 0, \tag{2}$$

$$\boldsymbol{f}_s = \int_\Sigma \frac{\partial}{\partial s}\left(\sigma\boldsymbol{\tau}\right)\delta\left(\boldsymbol{x}-\boldsymbol{X}\right)\,ds, \tag{3}$$

$$\boldsymbol{f}_b = \int_\Sigma \frac{\partial^2}{\partial s^2}\left(b\frac{\partial\boldsymbol{\tau}}{\partial s}\right)\delta\left(\boldsymbol{x}-\boldsymbol{X}\right)\,ds, \tag{4}$$

$$\boldsymbol{f}_g = \int_\Sigma \begin{pmatrix} 0 \\ -1 \end{pmatrix}\delta\left(\boldsymbol{x}-\boldsymbol{X}\right)\,ds, \tag{5}$$

$$\frac{\partial \boldsymbol{X}}{\partial t} = \boldsymbol{U}(s,t) = \int_\Omega \boldsymbol{u}(\boldsymbol{x},t)\delta\left(\boldsymbol{x}-\boldsymbol{X}\right)\,d\boldsymbol{x}, \tag{6}$$

where Reynolds number Re represents the ratio of fluid inertia to viscous stress, capillary number Ca and Bn respectively describe the strength of interfacial tension and bending stiffness. The bending stiffness is simply a constant during diatoms sedimentation, while the interfacial tension is described as a nonlinear strain-hardening spring of the form $\sigma = \left(\sigma_l + \sigma_n {\Delta S_\alpha}^2\right)\Delta S_\alpha$, where σ_l and σ_n are respectively linear and nonlinear constants controlling inextensible strength, and ΔS_α is the difference of stretching factor. The Froude number Fr is the ratio of fluid inertia to gravitational force, and dimensionless number $\beta = \Delta\rho D$ is the relative density difference scaled by the diatom diameter (relative to its length). The diatom chain is parameterized as a function $\boldsymbol{X}(t,\alpha)$. Equations (3)-(5) distribute interfacial forces (on Σ) to body forces (on Ω) through Dirac delta function, while Equation (6) shows that the interfaces are carried by the fluid flow with interfacial velocity $\boldsymbol{U}$ which is interpolated using bulk fluid velocity $\boldsymbol{u}$.

3. Growth and breakup

Growth and breakup mechanisms play essential roles in life cycle of diatoms [5, 7]. Both affect the sedimentation speed such that diatoms can adapt the change of environments [2, 4]. Physically, growth mainly involves in the distribution of nutrition in sea water [2, 6, 15], which can be represented by the concept of concentration (weight per volume). Mathematically, the nutrition concentration can be simplified as $c(t,\boldsymbol{x})$, a function of time and space. The corresponding numerical methods to handle concentration issues can be found in [10, 11].

With the definition of concentration, the growth rate is intuitively a concentration dependent function, $v_g(c(t,\boldsymbol{X}))$. Here, an interpolation process to obtain the effective concentration $c(t,\boldsymbol{X})$ on interfaces is essential. Moreover, the average growth rate of a single diatom and corresponding growth of a diatom chain $L(t)$ in