## XI International Conference on Computational Methods in Marine Engineering

## Computational modelling to predict flow induced marine biofilm deformation and detachment

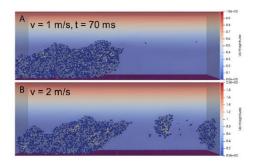
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## **ABSTRACT**

The Ships are fouled by marine biofilms, causing increased frictional drag and can lead to at least 20% additional fuel cost. Hydrodynamic stress can cause biofilm erosion and detachment, leading to lower profile, lower drag biofilms [1]. Therefore, understanding about hydrodynamics induced biofilm removal is essential for operators to manage fouling. However, the experimental procedure to detect and monitor the biofilm erosion and detachment is very time consuming. Therefore, it is essential and timely to develop a computational modelling to predict biofilm deformation and detachment. To fill this gap, we have developed a discrete element method (DEM) coupled with computational fluid dynamics (CFD). This modelling was built on our previous modelling framework [2-3]. Our modelling has predicted the temporal change of biofilm during flow induced deformation and detachment for marine biofilm at different flow velocities (e.g. Figure 1). The simulation results are consistent with relevant experimental measurements. We have also investigated how materials properties related adhesion could affect marine biofilm detachment. Our modelling results offer promising avenues for designing more effective antifouling coatings and treatments.



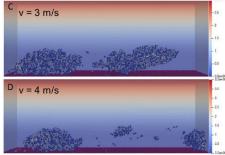


Figure 1: An example of modelling predicted marine biofilm deformation and detachment at varied flow velocity.

## References

- [1] Yebra et al, Antifouling technology-past, present and future steps towards efficient and environmentally friendly antifouling coatings Progress in Organic Coatings 50 (2004) 75-104
- [2] Xia et al, Coupled CFD-DEM modelling to predict how EPS affects bacterial biofilm deformation, recovery and detachment under flow conditions. Biotechnology and Bioengineering 119 (2022) 2551–2563
- [3] Jayathilake et al, A mechanistic Individual-based Model of microbial communities. PloS one 12 (2017) e0181965.