

## **Numerical Methods and Uniqueness for the Canham-Helfrich Model of Biomembranes**

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The classical Canham-Helfrich models of biomembranes consist of a family of geometric constrained variational problems. Their physical importance and mathematical challenge attract the attention of both biophysicists and geometric analysts. In this article, we develop a numerical method for these models. Our method uses a high-order approximation of surfaces with arbitrary topology based on subdivision methods. We also develop multiscale and parallel versions of our method which substantially speed up computations. We use our solver to explore a phenomenon known as conformal diffusion in the biophysical literature, which is also connected to the open uniqueness question for the Canham and Helfrich variation problems. We establish the uniqueness of solution of the Canham and Helfrich problem in a special case related to the Willmore conjecture (now the Marques-Neves theorem).

Joint work with Jingmin Chen, Rob Kusner and Andrew Zigerelli