Use of Fast Multipole to Accelerate Discrete Circulation-Preserving Vortex Sheets for Soap Films and Foams

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Abstract

We report the integration of a FMM (Fast Multipole Method) template library "FMMTL" into the discrete circulation-preserving vortex sheets method to accelerate the Biot-Savart integral. We measure the speed-up on a bubble oscillation test with varying mesh resolution. We also report a few examples with higher complexity than previously achieved.

Keywords: fluids, vortex sheet, fast multipole method

1 Introduction

[Da et al. 2015] proposed a discrete circulation-preserving vortex sheets method for simulating the dynamics of soap films and foams. The method is based on a vortex sheets representation which captures the velocity field by its vorticity concentrated on a 2D surface mesh. A key step in the approach is the computation of the velocity field from the vortex sheets, using the Biot-Savart integral:

$$\mathbf{u}(\mathbf{x}) = \frac{1}{4\pi} \int_S \frac{\gamma(\mathbf{x}') \times (\mathbf{x} - \mathbf{x}')}{\|\mathbf{x} - \mathbf{x}'\|^3} d\mathbf{x}'. \qquad (1)$$

Since this boundary integral needs to be evaluated at each vertex during mesh movement, a naive implementation that directly discretizes the integral through quadratures results in a quadratic time complexity in the mesh size. In general, fast summation techniques such as fast multipole method (FMM) have been developed to improve the scaling of such computation.

Fast Multipole Method Template Library (FMMTL) [Cecka and Layton 2015] is a generalized framework for FMM with various kernels. It is a versatile template library that accelerates matrix-vector multiplications where the matrix is a kernel matrix resulting from integrals like Biot-Savart, while encapsulating the implementation details of FMM from the client application. We employ this library to replace the original quadratic-time implementation of the Biot-Savart integral.

2 Time Complexity

The implementations with and without FMMTL integration are compared on a test where a single bubble with an ellipsoidal initial shape is allowed to relax towards and then oscillate around the spherical equilibrium configuration. The number of vertices in the mesh is varied roughly from 400 to 40,000. Each mesh resolution results in a series of frames, whose individual computation time and precise vertex counts are recorded, and plotted in log-log in Fig. 1 with respective linear fits.

Note that the computation time recorded above consists of only the time spent on Biot-Savart integral and excludes all other components of the simulation such as mean curvature computation. In this bubble oscillation example, the Biot-Savart integral is by far the performance bottleneck in the naive implementation, usually two orders of magnitude more expensive than the second component which is remeshing.
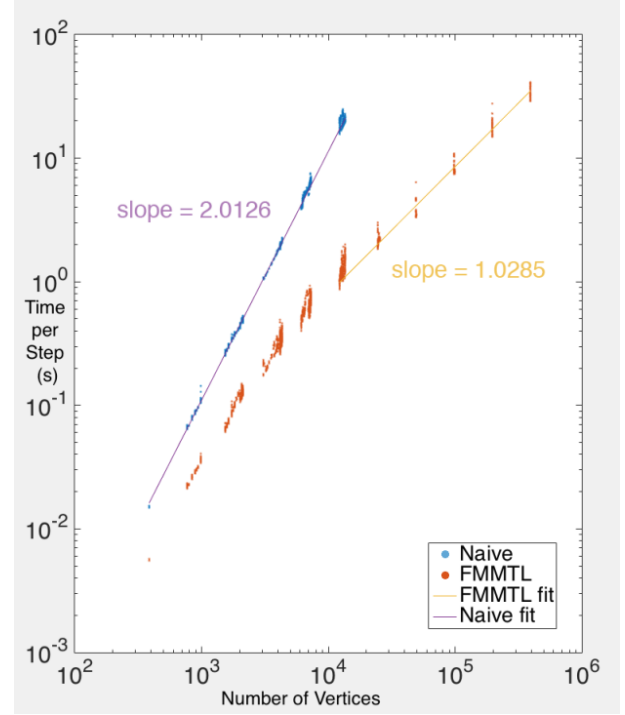

Figure 1: *The scaling of computation time with mesh size.*

The plot confirms the quadratic time complexity of the naive implementation, evident from the slope of 2. The timing for the FMMTL version shows a slope of 1 on the right part of the curve which dips down as the vertex number decreases, consistent with a nonlinear curve $\log T = \log N + \log \log N$ resulting from the expected time complexity of $T = O(N \log N)$. Around $N = 10^4$ vertices, the FMMTL version is more than 10 times faster than the naive version.

3 Large Foam Tests

The accelerated Biot-Savart integral allows for simulation of foams with more bubbles. Fig. 2 shows a bubble cluster rearrangement example similar to Figure 1 left in [Da et al. 2015], but with an order of magnitude more bubbles, starting from a regular 5 by 5 by 5 cubic grid. Fig. 3 shows an even bigger foam cluster with 512 bubbles. In both examples, the individual bubbles gradually slide past each other to seek a more energetically favorable arrangement, transforming the global shape of the whole cluster to a near spherical configuration in the process.

4 Conclusion

We have demonstrated the integration of FMMTL library into the discrete circulation-preserving vortex sheets method for soap film and bubble simulation. We have demonstrated significant speed-up during the Biot-Savart integral computation, which enabled simu-

Figure 2: *Bubble cluster rearrangement test with 125 bubbles. The bubbles start off from a regular grid and gradually rearrange into a near-spherical cluster.*

Figure 3: *Bubble cluster rearrangement test with 512 bubbles.*

lation of larger and more complex foam structures than before.

References

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DA, F., BATTY, C., WOJTAN, C., AND GRINSPUN, E. 2015. Double bubbles sans toil and trouble: discrete circulation-preserving vortex sheets for soap films and foams. *ACM Tra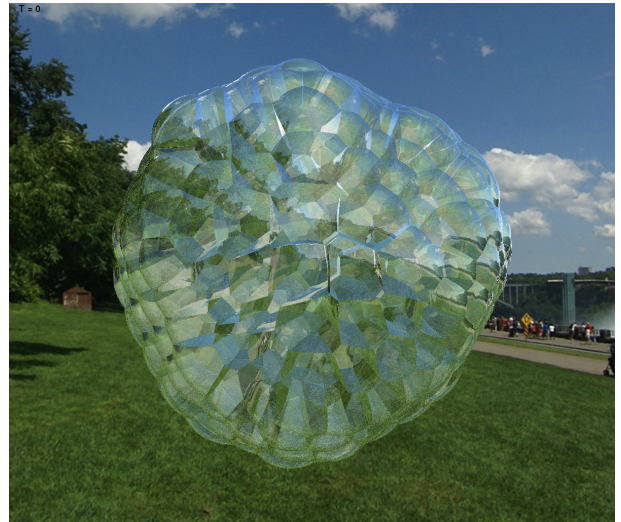nsactions on Graphics (TOG) 34*, 4, 149.