CUDA Acceleration of MG-FEM-BEM Methods for Dielectric Interfaces

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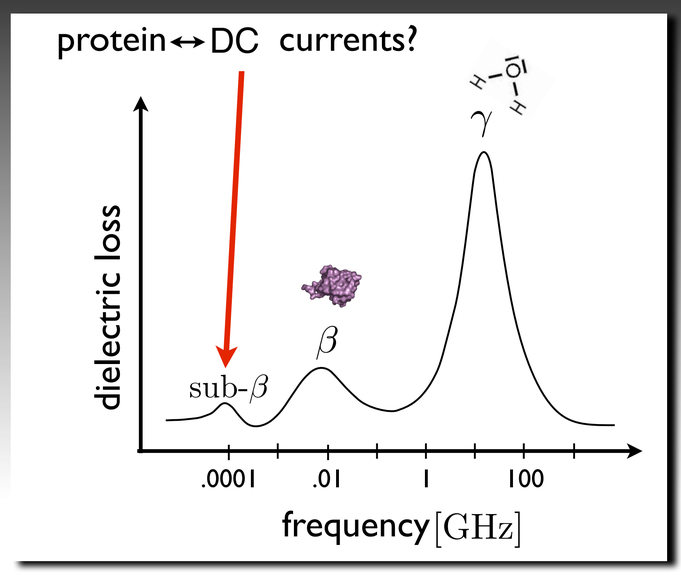
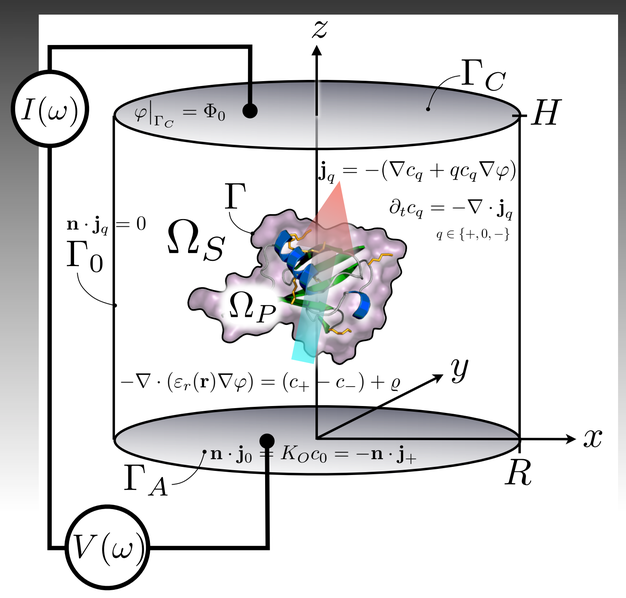
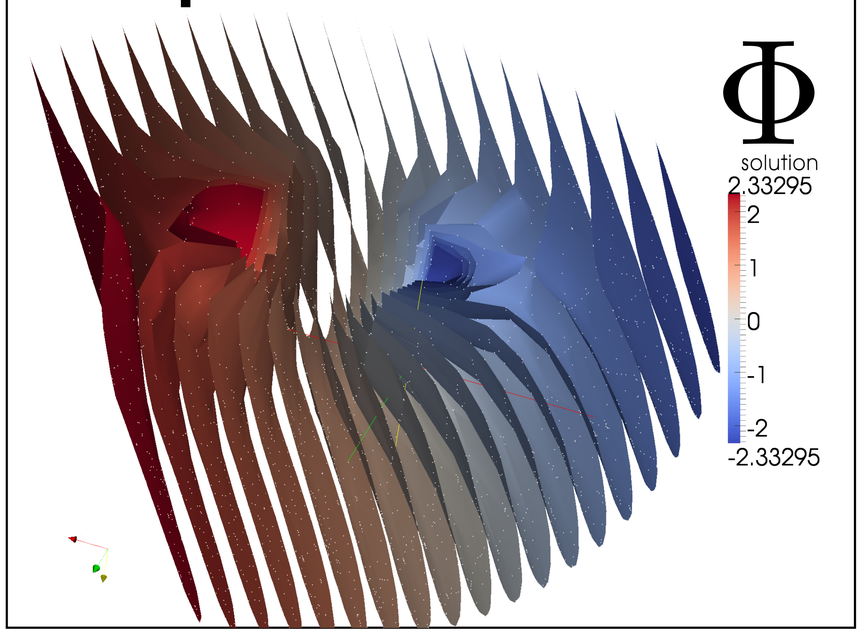
Dielectric Relaxation of Proteins





Dipole Isosurfaces



FEM-BEM Assembly Parallelization

(A) FEM : 12 QThreads + CUDA for BEM

(B) FEM : 1 QThread + CUDA for BEM

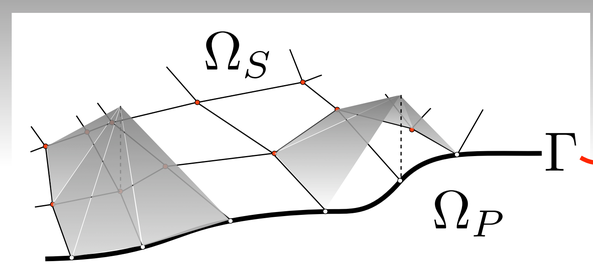
(C) FEM+BEM : 12 QThreads

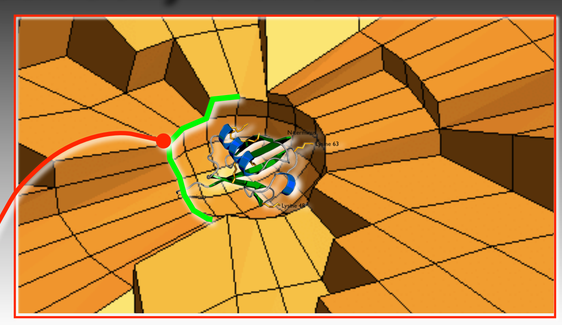
(D) FEM+BEM : 1 QThread

Protein as Non-local Boundary Condition

FEM

$$-\nabla \cdot (\varepsilon_S \nabla \Phi) = 0 \; + \; BC$$



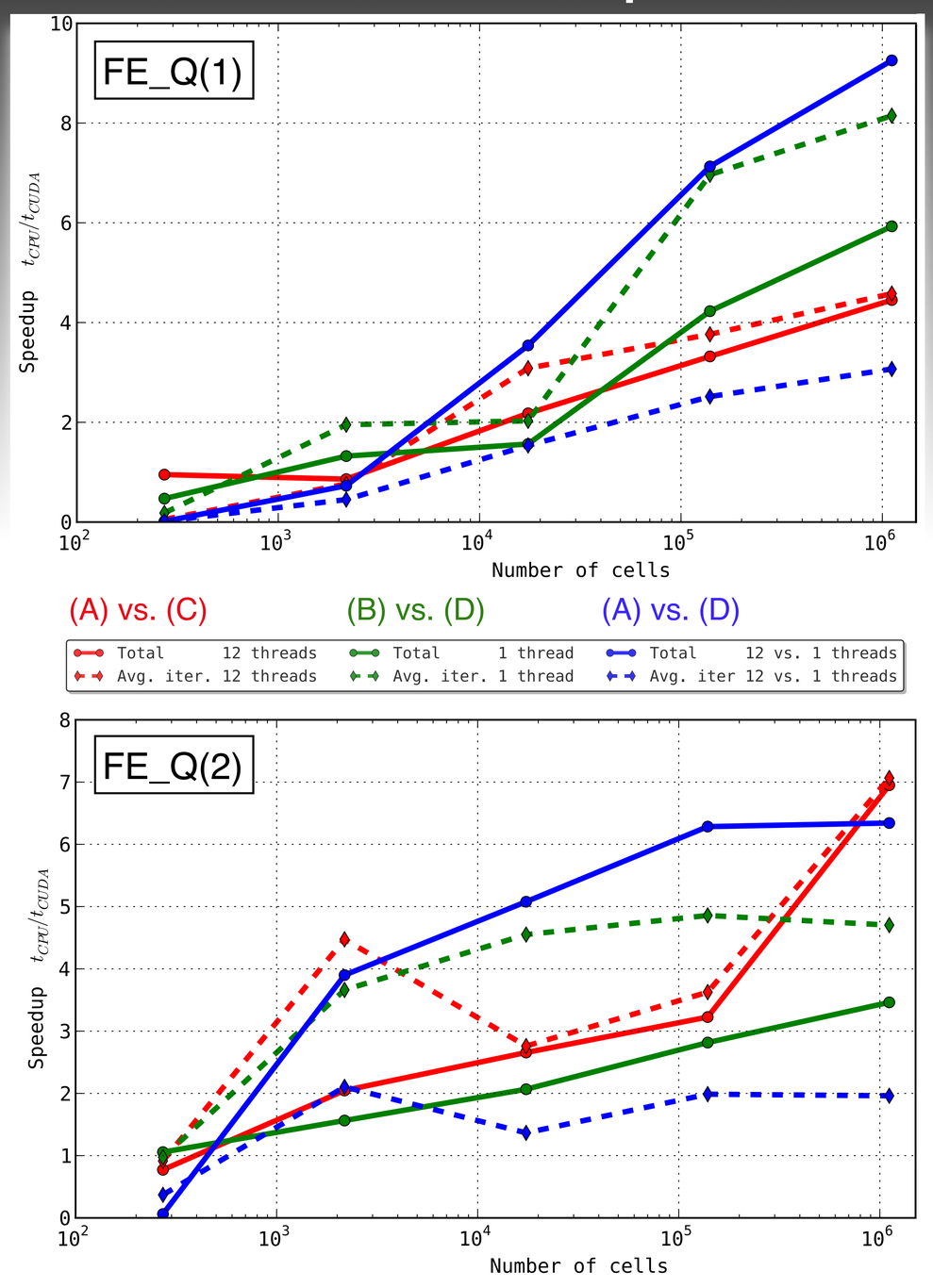


BEM

$$\frac{1}{2}\Phi(\mathbf{x}) + \oint_\Gamma \left[\Phi(\mathbf{x}')\frac{\partial G_\mathbf{x}}{\partial \mathbf{n}'}(\mathbf{x}') - G_\mathbf{x}(\mathbf{x}')\frac{\varepsilon_S}{\varepsilon_P}\frac{\partial \Phi}{\partial \mathbf{n}'}\right] = \phi^C(\mathbf{x})$$

Speedup

4th order surface & BEM quad. order 8

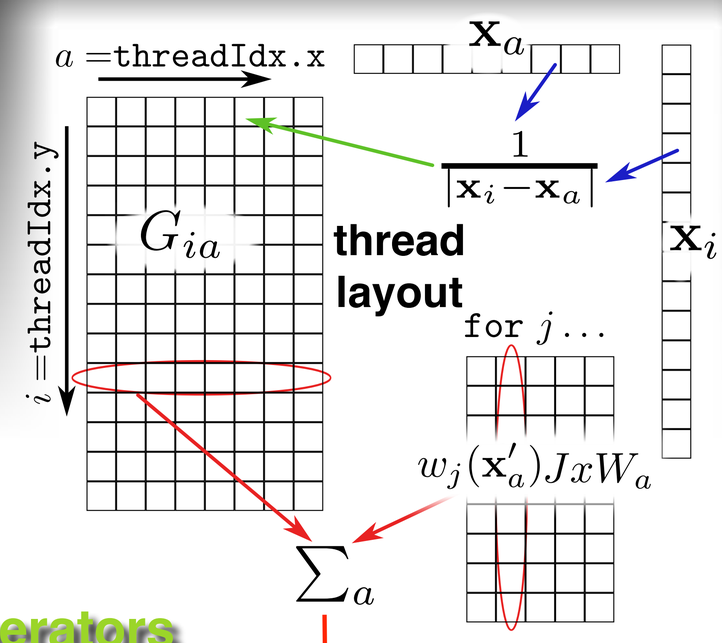


BEM Matrix Assembly with CUDA

Ansatz

$$\Phi = \sum_j \Phi_j w_j$$

$$\frac{\partial \Phi}{\partial \mathbf{n}'} = \sum_j t_j \psi_j$$



Discretized BEM Operators

single-layer $$V_{h,ij} = \sum_{E \subset S_j} \sum_{a \in E} G_{ia} \psi_{aj} JxW_a \,,$$

double-layer $$K_{h,ij} = \frac{1}{2}\delta_{ij} - \sum_{E \subset S_j} \sum_{a \in E} H_{ia} w_{aj} JxW_a$$

References

[1] D. Ban et al., 2011. *Kinetics of Conformational Sampling in Ubiquitin.* Angewandte Chemie Int Ed. 2011, 50, 11437 - 11440

[2] S. Kramer, R. Kree, *Single Molecule Impedance Spectroscopy of Proteins by Numerical Simulation,* (in preparation)

[3] S. Kramer PhD Thesis, *CUDA-based Scientific Computing - Tools and Applications,* Universität Göttingen, 2012

[4] C. Holme, *step-28*, CUDA Lab Course 2013

Conclusions

- Assembly of boundary element part implemented with CUDA
- Assembly of finite element part parallelized with QThreads
- CUDA acceleration carries over to individual host thread
- Speedup of **5-8** of hybrid CUDA+QThread implementation (A) over QThread-only (C)