

## Variational multiscale models for ion channel transport

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A major feature of biological sciences in the 21st Century will be their transition from phenomenological and descriptive disciplines to quantitative and predictive ones. Revolutionary opportunities have emerged for mathematically driven advances in biological research. However, the emergence of complexity in self-organizing biological systems poses fabulous challenges to their quantitative description because of the excessively high dimensionality. A crucial question is how to reduce the number of degrees of freedom, while preserving the fundamental physics in complex biological systems. This work focuses on a new variational multiscale paradigm for biomolecular systems. Under the physiological condition, most biological processes, such as protein folding, ion channel transport and signal transduction, occur in water, which consists of 65-90 percent of human cell mass. Therefore, it is desirable to describe membrane protein by discrete atomic and/or quantum mechanical variables; while treating the aqueous environment as a dielectric or hydrodynamic continuum. I will discuss the use of differential geometry for coupling microscopic and macroscopic scales on an equal footing. Based on the variational principle, we derive the coupled Poisson-Boltzmann, Nernst-Planck (or Kohn-Sham), Laplace-Beltrami and Navier-Stokes equations for the structure, dynamics and transport of ion-channel systems. As a consistency check, our models reproduce appropriate solvation models at equilibrium. Moreover, our model predictions are intensively validated by experimental data. Mathematical challenges include the well-posedness and numerical analysis of coupled partial differential equations (PDEs) under physical and biological constraints, lack of maximum-minimum principle, effectiveness of the multiscale approximation, and the modeling of more complex biomolecular phenomena.

### References

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