MAR05-2004-002701

Abstract for an Invited Paper for the MAR05 Meeting of the American Physical Society

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Is biology renormalizable and amenable to multiscale simulation methods? Multiscale simulations provide a comprehensive computational model, spanning many length and time scales, starting with the characteristic molecular assemblies, and connecting them to meso scale and finally macro scale material properties. A hierarchy of overlapping calculations in space and time are performed. Parameters are input to each calculation based on the calculations from a smaller length and time scale and checked with calculations at a larger length scale. In this lecture examples will include the properties of proteins in an ultracentrifuge and the elastic properties of DNA from the atomic to the material length scales. These problems have an explicit coupling of length-scales from the microscopic correlations between molecules in the assembly to the shape of the resulting assembly to the continuum elastic properties. The results are tested against experiments and checked for consistency with known thermodynamic and structural data. The question of the renormalizablility of biology is shown to be linked to intrinsic complexity in space and time.