



Loop Entropy

Guest Editor:

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Deadline for manuscript
submissions:

closed (20 December 2012)

Message from the Guest Editor

Dear Colleagues,

Macromolecules such as polypeptides and nucleic acids form the basis for all living things. These molecules typically fold into tertiary structures that have highly ordered regions. However, it is often the case that some aspects of these tertiary structures remain underdetermined when viewed as a static object. This underdetermination manifests itself in the form of hinge and breathing motions, allosteric reorganization, intrinsically disordered regions, and loop motions. In this special issue of Entropy, models of the various aspects of conformational variability in biological macromolecules are examined. Concepts from polymer theory, statistical thermodynamics, computer science, molecular dynamics simulation, stochastic modeling, and information theory will be used to model the conformational disorder of biomolecules both in their denatured and folded states.

Gregory S. Chirikjian

Guest Editor





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Editor-in-Chief

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Message from the Editor-in-Chief

The concept of entropy is traditionally a quantity in physics that has to do with temperature. However, it is now clear that entropy is deeply related to information theory and the process of inference. As such, entropic techniques have found broad application in the sciences.

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