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Loop Entropy

Guest Editor:

Prof. Dr. Gregory S. Chirikjian
Department of Mechanical Engineering, Johns Hopkins University, 223 Latrobe Hall, 3400 North Charles Street, Baltimore, MD 21218-2682, USA

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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

Prof. Dr. Kevin H. Knuth
Department of Physics, University at Albany, 1400 Washington Avenue, Albany, NY 12222, USA

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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Contact Us

Entropy Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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