Special Issue

Information Theory in Computational Biology

Message from the Guest Editors

We are pleased to invite submissions to this Special Issue of *Entropy*, with the theme "Information Theory in Computational Biology". Submissions can include, but are not limited to, the following research areas: sequencing, sequence comparison, and error correction; gene expression and transcriptomics; biological networks; omics analyses; genome-wide disease-gene association mapping; and protein sequence, structure, and interaction analysis. Topics that are particularly welcome include analyses, and/or development of application tools, involving single-cell data; multi-omics integration; biological networks; human health; high-dimensional statistical theory for biological applications; unifying definitions and interpretations of statistical interactions; adaptation of existing information theoretic test statistics and estimators for cases involving missing, erroneous, or heterogeneous data; analyses when distributions of the test statistics under the null and the alternative hypotheses are unknown; biologically inspired information storage; and efficient analysis of very large datasets.

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Deadline for manuscript submissions

closed (31 July 2023)

Entropy

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About the Journal

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.
Entropy is an online open access journal providing an advanced forum for the development and/or application of entropic and information-theoretic studies in a wide variety of applications. *Entropy* is inviting innovative and insightful contributions. Please consider *Entropy* as an exceptional home for your manuscript.

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