

Special Issue

Complexity, Information and Quantitative Modelling in Single Cell Multiomics

Message from the Guest Editor

Single-cell omics technologies are now ubiquitous and provide high resolution in time and space on complex biological processes at the level of individual cells. Yet, this poses novel theoretical and computational challenges in translating high-throughput multimodal data into intelligible biological mechanisms and quantitative, falsifiable predictions. In this Special Issue, we encourage the submission of novel theoretical and computational approaches to advance the interpretability and model-generating potential of single-cell data. The proposed approaches can focus on any biological process (i.e., transcription, gene regulation, cell–cell interactions, cell lineage, etc.) and can be based on any modeling framework (i.e., information theory, stochastic modeling, machine learning, etc.) as long as the connection with single-cell methodologies is clear and justified.

Guest Editor

Dr. Federico Bocci

Radboud Institute for Molecular Life Science, Radboud University, 6525 XZ Nijmegen, The Netherlands

Deadline for manuscript submissions

15 July 2025



Entropy

an Open Access Journal
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Impact Factor 2.0
CiteScore 5.2
Indexed in PubMed



mdpi.com/si/212265

Entropy
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
entropy@mdpi.com

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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.

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.

Editor-in-Chief

Prof. Dr. Kevin H. Knuth

Department of Physics, University at Albany, 1400 Washington Avenue,
Albany, NY 12222, USA

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