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

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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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Editor-in-Chief

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