

Information Theory in Computational Biology, Physiology and Health

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Abstract

Information theoretical concepts and tools will be discussed in relation to their applications in computational biology and physiology, such as sequencing and error correction, protein sequence, brain and heart signals, physiological networks, structure and interaction analysis gene expression and transcriptomics, alignment-free sequence comparison, genome-wide disease-gene association mapping, metabolic networks and metabolomics. The workshop aims at bringing together the state-of-the-art frameworks and solutions focused on interpreting biological data by means of entropy derived concepts.

CCS Concepts

• **Theory of computation** → **Randomness, geometry and discrete structures**; • **Mathematics of computing** → **Information theory**; • **Applied computing** → **Life and medical sciences**.

ACM Reference Format:

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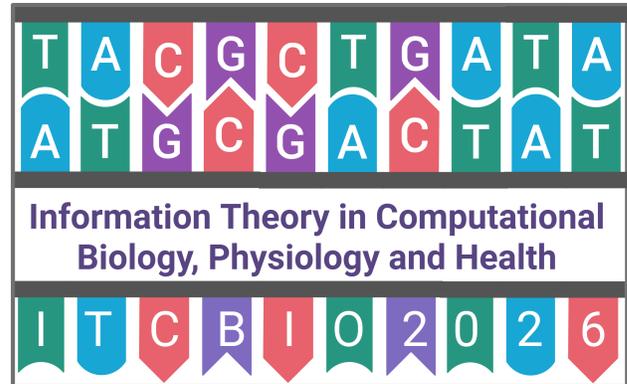
1 Motivation and rationale

Information theory is increasingly adopted in many areas of computational biology and biomedical research. The concepts and ideas pioneered in Shannon's work "A Mathematical Theory of Communication" are the basis of information theory, a cornerstone of statistical learning and inference, and has been playing a key role in disciplines such as physics and thermodynamics, probability and statistics, computational sciences and biological sciences. Thanks to the availability of increasingly enriched datasets and the development of domain-specific expertise, the information theory has increasingly proven useful in particular as a component of machine learning and deep learning techniques, to mine information obtained from different modalities for enhancing data understanding and perception, realizing cross-domain applications. As more and more data are collected and made publicly available, information theoretical tools will be instrumental to model and understand

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multi-source data, including but not limited to sequencing, 3D structure, brain-computer interfaces and many others.

2 Abstract Submission

Submissions at the intersection of information theory, statistical learning and biomedical research are encouraged. Topics include but are not limited to the following: (i) Omics & Systems Biology (Sequence Analysis, Single-cell Sequencing, Omics Data Integration and Analysis, Genomic Variation and Disease, Haplotypes and Population Genomics, Phylogenetics, Protein and RNA Analysis, Structure, and Dynamics, Metagenomics and Algorithms for Microbiomes) (ii) Clinical & Healthcare Informatics (Imaging Informatics, Imaging Genomics and Radiation Genomics, Computational Phenotyping, Automated Diagnosis and Prediction, Clinical Databases and Information Systems) (iii) AI & Data Science (AI and Machine Learning in Medicine and Healthcare, Multimodality Modeling, Natural Language Processing (NLP) and Text Mining.

A one-page summary complying with the required ACM format (ACM Proceedings Template: <https://www.acm.org/publications/proceedings-template>) should be submitted.

3 Important Dates

- Call For Paper: 1 March, 2026
- Abstract submission deadline: 30 April 2026
- Author Notification: 15 May 2026
- Workshop date: June 30, 2026

Updated details about programme, deadlines and logistics can be found at the ITCBIO 2026 <https://dasc.polito.it/ICTBIO2026.html> and ACM-BCB 2026 <https://acm-bcb.org/> websites.