Special Issue on
Statistical and Machine Learning Modeling in Computational Epigenetics

CALL FOR PAPERS

Epigenetics has recently emerged as one of the hottest fields in life sciences for studying heritable change in phenotype, gene function, or gene expression that are not directly encoded in the DNA itself. Up-to-date studies have shown that epigenetic modulations are fundamental in many developmental processes, from tissue and organ formation to allele-specific gene expression. When these normal epigenetic patterns modify, pattern of gene expression can be deregulated, and it has been proven that such mechanisms are central in several disorders and diseases, among which are psychiatric disorders, obesity, and etiology of a number of diseases such as cancer, schizophrenia, and Alzheimer, just to name a few. Today, thanks also to several large human epigenome projects, scientists have a better understanding of the basic principles of epigenetic mechanisms as well as their relevance to health disorders and disease. At the heart of this fascinating research field are computational tools that, by analyzing complex genomic information, play an essential role in discovering evidences to define new assessable hypotheses. In particular, the literature at a glance shows the effectiveness of a combination of statistical and machine learning techniques in several epigenetic analyses. This special issue aims to host original papers and reviews on recent research advances and the state-of-the-art methods in the fields of statistical and machine learning methodologies and algorithm design for the study of epigenetic mechanisms. Especially welcome are also software systems with a special emphasis on tools developed with the help of big data distributed processing framework like Hadoop and Spark to properly manage the huge amount of data coming from epigenome-scale experiments.

Potential topics include but are not limited to the following:

- Machine learning
- Statistical learning theory
- Fuzzy logic and systems
- Neuro-fuzzy systems
- Granular computing
- Data mining
- Probabilistic and statistical modelling
- Algorithms designed for epigenomic big data
- High-throughput data in the broad context of epigenomics
- Analysis, modeling, and prediction of DNA methylation patterns
- Analysis, modeling, and prediction of histone modifications in DNA sequences
- Identification of abnormal DNA methylation within CpG islands in different diseases
- Analysis of epigenetic marks in stem cells
- Analysis of miRNA changes in cancer and other diseases
- Simultaneous analysis of methylome and transcriptome
- Analysis of reciprocal regulation of noncoding RNA and methylation
- Study of the epigenetic role in metabolomics
- Analysis of microbiome role in epigenetic regulation of gene expression

Authors can submit their manuscripts through the Manuscript Tracking System at https://mts.hindawi.com/submit/journals/bmri/computational.biology/acim/.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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