

Tentative Outline

Special Thematic Issue for Combinatorial Chemistry & High Throughput Screening

Machine learning techniques for high-throughput structure and function analysis for proteomics and genomics

Guest Editors: Dr. Quan Zou

Aims & Scope:

With the development of high-throughput sequencing techniques, more and more sequencing data is available, such as genomics reads, transcriptomes data, and proteomics sequences. It is critical to use these data to uncover their structure and functions. Genomics function can also be identified from the classification results, such as motif identification, regulatory regions detection, and even epigenomics and disease relationship prediction.

Machine learning methods are important techniques for this task, especially for the ensemble learning, large scale data process, various kernel design, and imbalanced classification methods.

We invite authors to contribute original research manuscripts to this special session, focusing on the advanced machine learning algorithms and their applications in proteomics or genomics sequences analysis.

Keywords: High Throughput Screening, Machine Learning, genomics, epigenetics.

Subtopics:

Potential topics include, but are not limited to:

1. Protein structure prediction with machine learning methods
2. Special protein identification methods
3. Epigenomics and disease relationship prediction
4. Motif and regulatory elements identification from high-throughput data
5. Advanced machine learning methods with the application to bioinformatics
6. Cloud computing and parallel machine learning techniques for protein structure and genomics function analysis

Schedule:

- ◇ Manuscript submission deadline: 30th Sep, 2019
- ◇ Peer Review Due: 31st Oct, 2019
- ◇ Revision Due: 30th Nov, 2019
- ◇ Announcement of acceptance by the Guest Editors: 31st Dec, 2019
- ◇ Final manuscripts due: 31st Jan, 2020

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