Aims & Scope:
Since the first modified RNA ribonucleic acid was found 60 years ago, more than 100 kinds of known RNA modifications have been reported. Although they have been shown to be associated with a broad set of fundamental cellular processes, the mechanisms are still unclear. In order to rapidly and effectively revealing their biological functions, it is highly desirable to develop computational methods which are good complements to experimental techniques. In recent years, a series of computational methods have been developed to identify RNA modification sites and infer their regulatory functions. Therefore, this special issue aims to collect a diverse and complementary set of articles that demonstrate new developments and applications of machine learning methods in computational RNA epigenetics. Both original research papers and review articles related to computational RNA epigenetics will be considered for publication.

Keywords: RNA modification, Machine learning, Noncoding RNA, RNA epigenetics

Subtopics:
Specific topics of particular interest include, but are not limited to:
- Computational methods on RNA modification sites prediction;
- Reviews or surveys on the function of RNA modifications;
- RNA modification functional computational analysis.
- RNA modification and Diseases

Schedule:
- Manuscript submission deadline: 31 May 2019
- Peer Review Due: 31 July 2019
- Revision Due: 30 September 2019
- Announcement of acceptance by the Guest Editors: 1 November 2019
- Final manuscripts due: 31 December 2019

Contacts:
Guest Editor: Dr. Wei Chen
Affiliation: Center for Genomics and Computational Biology, North China University of Science and Technology, Tangshan 063210, China.
Email: chenweiimu@gmail.com