

EDITORIAL

Computational RNA Epigenetics

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Except for mRNA that encodes proteins, there is another kind of RNA, known as non-coding RNA (ncRNAs), that does not encode proteins. ncRNAs control various levels of gene expression in physiology and development, such as RNA splicing, RNA translation, cell proliferation and apoptosis. Accumulated evidence have demonstrated that ncRNAs are correlated with the progression of a series of diseases.

Besides ncRNAs, RNA modification is another layer of epigenetic regulation of gene expression. Since the first modified RNA ribonucleic acid was found in 1957, more than 150 kinds of known RNA modifications have been reported. RNA modifications play critical roles in a series of biological processes, such as RNA degradation, localization and degradation, and even circadian rhythm. Recent studies revealed that RNA modifications are also associated with metabolic diseases, cancer, neurological disorders and cardiovascular diseases.

Due to their important roles, more researchers have devoted to the researches on ncRNAs and RNA modification. However, the biological functions and mechanisms of ncRNAs and RNA modification are still unclear. Since experimental methods are cost-ineffective to rapidly and effectively reveal their biological functions, it is highly desirable to develop computational methods which are good complements to experimental techniques for this aim. In recent years, a series of computational methods have been developed to infer the regulatory functions of RNA modification and ncRNA. Therefore, the thematic issue was proposed with the aim to collect a diverse and complementary set of articles that demonstrate new developments and applications of machine learning methods in computational RNA epigenetics.

This thematic issue has attracted 6 papers from highly regarded researchers around the world. After the rigorous peer review, 3 of them were accepted for publication.

Guan *et al.* [1] contributed a review article, where they summarized the recent advances in pre-miRNA recognition from the following aspects, namely the benchmark dataset, feature extraction, prediction algorithms, and the evaluation of existing models. The challenges and future perspectives are also discussed. It is believed that this review will provide novel insights into researches on computational identification of miRNA precursors.

In a mini review paper contributed by Li *et al.* [2], the authors reviewed available machine learning based methods for identifying RNA 5-methylcytosine (m⁵C) sites. Three essential elements, namely dataset, sequence encoding scheme, and machine-learning algorithms, required to constitute a predictor for identifying m⁵C sites were firstly discussed. More importantly, the bottleneck of those predictors was also pointed out, which should be considered when developing predictors for identifying m⁵C and even the other kinds of RNA modifications.

Govindaraj *et al.* [3] proposed a novel computational predictor termed as ERT-m6Apred based on extremely randomized tree to identify N⁶-methyladenosine (m⁶A), in which a two-step feature selection technique was used to obtain the optimal feature set.

Finally, the guest editor would like to thank all the authors who contributed their original works to the thematic issue and to the reviewers for their valuable comments on those works. The guest editor would also like to express sincere gratitude to the Editor in Chief, Dr. Christian Néri, of Current Genomics and the Assistant Manager Publications, Ms. Iqra Shafi for their excellent supports and providing the opportunity to organize the thematic issue.

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