

Tentative Outline

Special Thematic Issue for the journal : Current Bioinformatics

Identification and functional prediction of lncRNAs using bioinformatic techniques Sectional Editor: Dr. Shizuka Uchida

- **Scope of the Thematic Issue:** With the increased usage of next generation sequencing technology [e.g., RNA sequencing (RNA-seq), including single-cell RNA-seq (scRNA-seq)], the number of long non-coding RNAs (lncRNAs) has increased dramatically compared to the decreasing number of protein-coding genes. Through gain- and loss-of-function studies, the functions of lncRNAs have been elucidated, which include transcriptional and translational regulations as well as functioning as decoys for other RNAs [e.g., microRNAs (miRNAs)] and proteins [e.g., RNA-binding proteins (RBPs)]. Yet, the functions of the majority of lncRNAs are still unknown, which poses a problem in understanding the cellular and molecular signaling that underly the homeostasis of cells and organisms as the dysregulation of lncRNAs has been linked various diseases, including cancer, autoimmune, cardiovascular, and neuromuscular diseases. Given that there are many high-throughput data available, bioinformatic approach to combine such data as well as further prediction of the potential lncRNA functions based on their sequence features and structures will benefit the research community greatly. In this thematic issue, we request authors to contribute their studies related to bioinformatic approaches to identify and to infer possible functions of lncRNAs.

Keywords: lncRNA, method, NGS, RNA-binding protein, RNA-seq, miRNA sponge, RBP sponge

Sub-topics:

The sub-topics to be covered within the issue should be provided:

- Screening methods
- Functional prediction of lncRNAs
- Interactions between lncRNA and miRNAs
- Interactions between lncRNA and RNA-binding proteins (RBP)

Tentative titles of the articles and list of contributors:

Tentative titles of the articles and list of contributors with their names, designations, addresses and email addresses should be provided.

1. Prof. Y-h. Taguchi

Chuo University (Tokyo, Japan)

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Tentative Title: Machine learning approach for lncRNA

2. Prof. Masanori

Brigham and Women's Hospital & Harvard Medical School (Massachusetts, USA)

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Tentative Title: Co-expression network driven functional annotation of long noncoding RNAs in cardiovascular diseases

3. Prof. Guowei Li

McMaster University (Ontario, Canada)

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Tentative Title: Non-coding RNA and Arrhythmias: Expression, Function and Molecular mechanism

4. Prof. Juw Won Park

University of Louisville (Kentucky, USA)

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Tentative Title: Translation of circular RNAs once known as non-coding

Schedule:

✧ Thematic issue submission deadline: December 31, 2022

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