



## Computational Models in Non-Coding RNA and Human Disease

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### Message from the Guest Editor

Dear Colleagues,

Recent transcriptomic and bioinformatics studies suggest that ncRNAs appear to comprise a hidden layer of internal signals that control various levels of gene expression in physiology and development. Furthermore, ncRNAs have also been revealed to contribute to diseases, including cancer, autism, Alzheimer's, and so on. However, little efforts have been made to understand and predict ncRNA–disease associations on a large scale until now. In contrast to the traditional experimental approaches, the aim of us is to assess these ncRNA–disease associations on a large-scale, in humans, with computational methods based on big data accumulated by previous experimental methods. To find associations between ncRNAs and their corresponding diseases, various statistical and computational techniques could be employed. Similar to the research on the ncRNA–disease association, research on ncRNA–protein interaction, function, and the structure of ncRNAs, and even drug effects associated with ncRNAs, are all fields that we will devote ourselves to.





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