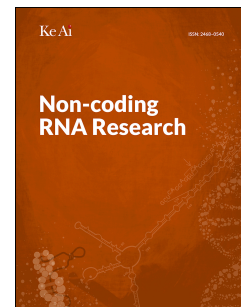


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Unraveling long non-coding RNAs through analysis of high-throughput RNA-sequencing data

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## Abstract

Extensive genome-wide transcriptome study mediated by high throughput sequencing technique has revolutionized the study of genetics and epigenetic at unprecedented resolution. The research has revealed that besides protein-coding RNAs, large proportions of mammalian transcriptome includes a heap of regulatory non protein-coding RNAs, the number encoded within human genome is enigmatic. Many taboos developed in the past categorized these non-coding RNAs as “dark matter” and “junks”. Breaking the myth, *RNA-seq*-- a recently developed experimental technique is widely being used for studying non-coding RNAs which has acquired the limelight due to their physiological and pathological significance. The longest member of the ncRNA family-- *long non-coding RNAs*, acts as stable and functional part of a genome, guiding towards the important clues about the varied biological events like cellular-, structural- processes governing the complexity of an organism. Here, we review the most recent and influential computational approach developed to identify and quantify the long non-coding RNAs serving as an assistant for the users to choose appropriate tools for their specific research.

**Keywords:** transcriptome; high throughput sequencing; genetic and epigenetic; long non-coding RNA; RNA-sequencing; RNA-seq

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