Computational Molecular Biology and Bioinformatics

Transcriptome Analysis

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1. What is a transcriptome?
2. Transcriptome analysis
3. Hands-on

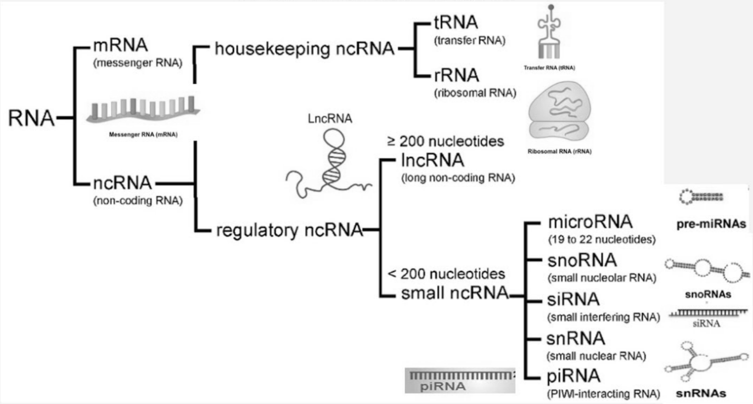
Basics

A transcriptome is a collection of all the gene readouts present in a cell.

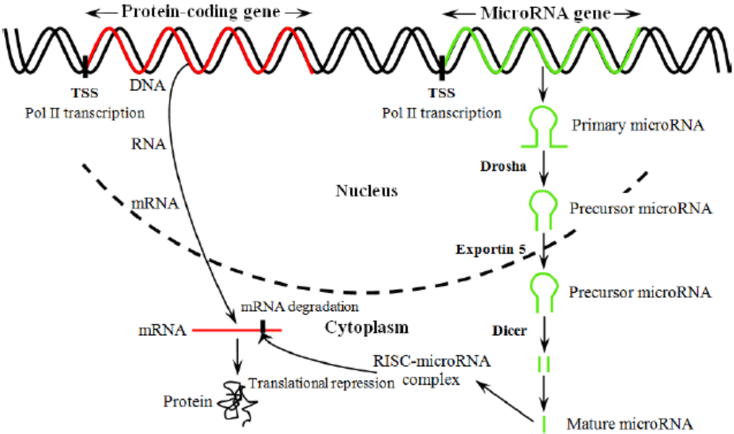
DNA must be *read* and transcribed (i.e., copied) into RNA during the transcription process. These gene readouts are called transcripts.

Note: Unlike mRNAs, DNA can also be transcribed into other types of RNAs that do not code for proteins. Such transcripts may serve to influence cell structure and to regulate genes.

The various types of RNAs



Biogenesis of protein-coding genes and microRNAs



Transcriptome analysis

Transcriptome analysis encompasses the study of the complete set of RNA transcripts that are produced by the genome, under specific circumstances or in a specific cell, using high-throughput methods.

Transcriptome analysis

Biological experiments

- Microarray analysis
    1. Expression analysis
- High–throughput RNA sequencing (RNA-seq)
    1. Expression analysis
    2. Mutation analysis
    3. Isoform analysis

Hands-on

1. Explore the UCSC Genome Browser through the following steps.
    i) Open the UCSC Genome Browser, select “Genome Browser” and enter. Select the human assembly “Dec. 2013 (GRCh 38/hg38)”.
    ii) Enter a position, say “chrX:1-810,000”. Note the genes present there.
    iii) Reopen the UCSC Genome Browser, select “Table Browser” and enter. Select the following options: clade - “Mammal”, genome - “Human”, assembly - “Dec. 2013 (GRCh 38/hg38)”.
    iv) Explore the different tables present and try to download some data.