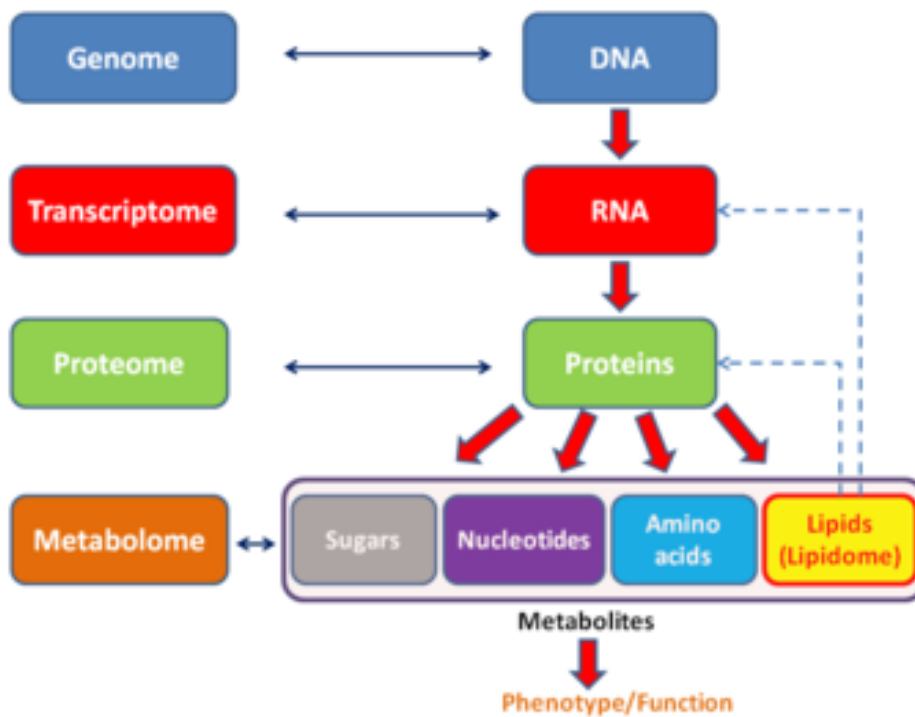# Pan-Transcriptome

Why in News?

Recently, researchers at the **University of California, Santa Cruz,** have proposed a **"Pan-transcriptome"** which combines a **transcriptome** and a **pan-genome.**

- Mapping transcriptome **(complete set of RNA molecules)** allows researchers to better understand an individual's gene expression.

What is a 'Pan-transcriptome'?

- Pan-transcriptome is a **reference that contains genetic material from a cohort of diverse individuals,** rather than just a single linear strand.
- The pan-transcriptome builds on the emerging concept of "pan-genomics" in the genomics field.
  - Typically, when evaluating an individual's genomic data for variation, scientists compare the individual's genome to that of a reference made up of a single linear strand of DNA bases.
- A **"pan-transcriptome"** is a combination of a **transcriptome** and a **pan-genome.**
  - **Transcriptome:**
    - A transcriptome is the **complete set of RNA molecules** in a cell or tissue including mRNA, rRNA, tRNA, and other **non-coding RNA**, that are produced by the genetic material of an organism.
    - It is the complement of the **genome**, which is the entire set of **genetic material** in an organism.
  - **Pan-genome:**
    - A **pan-genome** is a reference that contains **genetic material** from a diverse group of individuals, rather than just a **single linear strand.**
    - Using a pangenome allows researchers to **compare an individual's genome to that of a genetically diverse cohort of reference sequences** all at once, sourced from individuals representing a diversity of biogeographic ancestry.

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What is the Use of Pan-transcriptome?

- **Discovery of New Genes:** A **pan-transcriptome** can be used to identify **novel genes** that may not have been detected through traditional **genome sequencing methods.**
- **Regulating Gene Expression:** The **Pan-transcriptome** can change in response to **environmental** or **physiological conditions,** and it plays a **key role in regulating gene expression.**
- **Characterizing Genetic Diversity:** Pan-transcriptomes can be used to identify **genetic variations** within and between **different populations** of organisms.
  - This can provide insights into the evolution and adaptation of different species.

What is RNA Mapping?

- **About:**
  - **RNA mapping** is a technique used to **identify** and **map** the **location of RNA molecules** within a **cell** or **tissue.**
  - It is typically used to **study the expression** and **localization of different types of RNA**, including **messenger RNA (mRNA), ribosomal RNA (rRNA),** and **transfer RNA (tRNA).**
- **Method for RNA mapping:**
  - **In- situ hybridization (ISH):**
    - **In- situ hybridization (ISH)** allows researchers to see where a specific **RNA** is located within a cell or tissue, and can provide insights into the function of that **RNA.**
  - **RNA-seq (RNA sequencing):**
    - It allows for the **simultaneous analysis of thousands or even millions of RNA molecules** in a sample.
    - **RNA-seq** can be used to generate a detailed picture of the transcriptome, including the abundance and location of different **RNA molecules.**
- **Uses:** This information can be used to study-
  - Gene expression patterns
  - Identify novel transcripts
  - Detect genetic variations

Q. In the context of the developments in Bioinformatics, the term 'transcriptome', sometimes seen in the news, refers to (2016)

(a) a range of enzymes used in genome editing
(b) the full range of mRNA molecules expressed by an organism
(c) the description of the mechanism of gene expression
(d) a mechanism of genetic mutations taking place in cells

Ans: (b)

Source: TH

PDF Refernece URL: https://www.drishtiias.com/printpdf/pan-transcriptome