

Guest Lecture on “Alternative splicing in cancer: Learning from human organogenesis” by Dr. Arashdeep Singh, Post-doctoral Researcher, Cancer Data Science Laboratory, NIH-National Cancer Institute, USA

Identification of cancer specific splicing events

RNA-seq data for cancer patients: *The Cancer Genome Atlas*

RNA-seq data for healthy tissues: *Genotype-Tissue Expression*

Cancer specific splicing events:
Differential splicing between TCGA - GTEx

The slide displays two screenshots of bioinformatics tools. The top screenshot shows a web interface for analyzing RNA-seq data from The Cancer Genome Atlas (TCGA), with a human figure overlaid. The bottom screenshot shows a 'Dataset Summary of Analysis Samples' from Genotype-Tissue Expression (GTEx), including a table with columns for 'Sample ID', 'Tissue', 'Cell Type', 'Sex', and 'Age'. A human figure is also overlaid on this screenshot.

Quantification of splicing

pre-mRNA

splicing

alternatively spliced mRNAs

translation

protein isoforms

The diagram illustrates the process of alternative splicing. It starts with a pre-mRNA molecule represented as a sequence of colored blocks (red, yellow, green, blue). An arrow labeled 'splicing' points to two different 'alternatively spliced mRNAs' molecules, each missing a different colored block. An arrow labeled 'translation' points from these mRNAs to two distinct 'protein isoforms', represented as 3D star-like structures.

Quantification of splicing

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This slide is identical to the one in the previous block, showing the flow from pre-mRNA to alternatively spliced mRNAs and then to protein isoforms through the processes of splicing and translation.