RNA Sequencing-Based Immune Cell Deconvolution

Definition

RNA sequencing-based immune cell deconvolution is a computational method that estimates the proportion and types of immune cells present in bulk tissue RNA-seq data. It allows researchers to infer immune composition from gene expression profiles, without the need for single-cell or flow cytometry data.

Key Concepts

- Works on **bulk RNA-seq data**, which includes mixed cell populations
- Uses known **immune cell gene signatures** to deconvolute expression
- Output is typically a **cell type proportion matrix** (e.g. % CD8+ T cells, % macrophages)

Common Tools

- **CIBERSORT / CIBERSORTx** – Reference-based method using a leukocyte signature matrix (LM22)
- **xCell** – Uses gene set enrichment to score cell types
- **EPIC** – Designed for tumor environments
- **MCP-counter** – Estimates abundance of immune and stromal populations
- **TIMER** – Focused on tumor immune estimation across cancer types

Applications

- Characterize the **tumor immune microenvironment (TIME)**
- Predict response to **immunotherapy**
- Stratify patients based on immune infiltration patterns
- Complement histological or flow-based findings

Example Insight

In lung adenocarcinoma RNA-seq data, CIBERSORT may reveal elevated M2 macrophages and reduced CD8+ T cells in non-responders to PD-1 blockade therapy.

Limitations

- Accuracy depends on the quality of the reference signature
- Cannot capture spatial information
- Performance can vary with tumor heterogeneity or stromal contamination