Single-End vs. Paired-End Sequencing in RNA-Seq

In RNA sequencing (RNA-seq), the terms single-end and paired-end refer to how the sequencing machine reads the fragments of RNA that have been converted into cDNA. Here's a clear breakdown:

Single-End Sequencing (SE)

➢ Reads only one end of each cDNA fragment.

➢ Produces one read per fragment.

➢ Faster and cheaper, but provides less information.

➢ Best for:

o Gene expression quantification

o Projects with limited budget or sample material

Paired-End Sequencing (PE)

➢ Reads both ends of each cDNA fragment.

➢ Produces two reads per fragment (forward and reverse).

➢ Offers more accurate mapping, especially in repetitive or complex regions.

➢ Best for:

o Transcriptome assembly
o Detecting splice variants
o Structure variant analysis

📊 Comparison Table

Feature	Single-End (SE)	Paired-End (PE)
Reads per fragment	1	2
Cost	Lower	Higher
Mapping accuracy	Moderate	High
Data volume	Less	More
Use cases	Expression quantification	Transcript discovery, variant detection