Paired-end vs Single-end Sequencing

Single-end (SE)

Method: Sequence from one end only
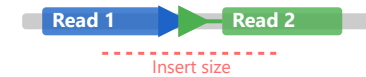
Read Length: 50-150 bp

Cost: Lower ($)

Time: Faster

Use Case: Gene expression, small RNA-seq

Paired-end (PE)

Insert size

Method: Sequence from both ends

Read Length: 2 × (75-300) bp

Cost: Higher ($$)

Time: Longer

Use Case: Variant calling, de novo assembly, structural variants

Paired-end Advantages

✓ Better alignment accuracy - confirms read location

✓ Detect structural variants and rearrangements

✓ Improved de novo assembly quality

✓ Span repetitive regions more effectively