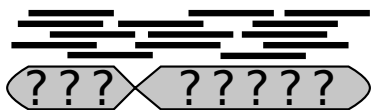


Paired Reads  
Multi-Linked Reads  
Long Reads  
Combination of Data

Multiple Alignments of Reads  
Many Adjacencies in Same Read

Computes Alignment & Adjacency Probabilities



*Individual*

**1. Sequence Reads from Individual**

**2. Align Reads to Reference**



*Reference*

**3. Determine SVs From Alignments**



*Deletion in Individual*

