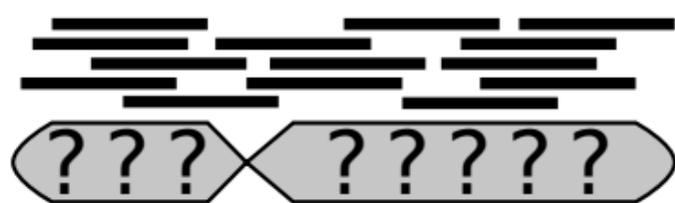


Paired Reads
Multi-Linked Reads
Long Reads
Combination of Data

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

