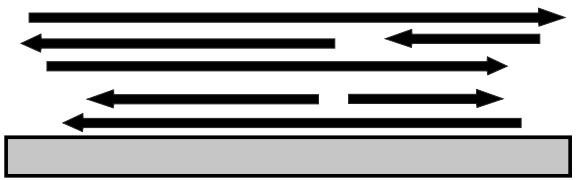
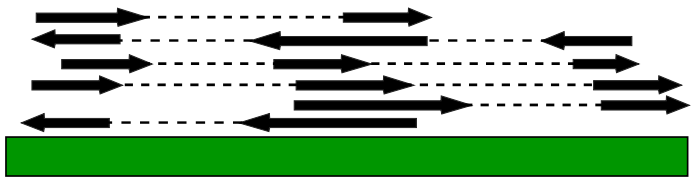
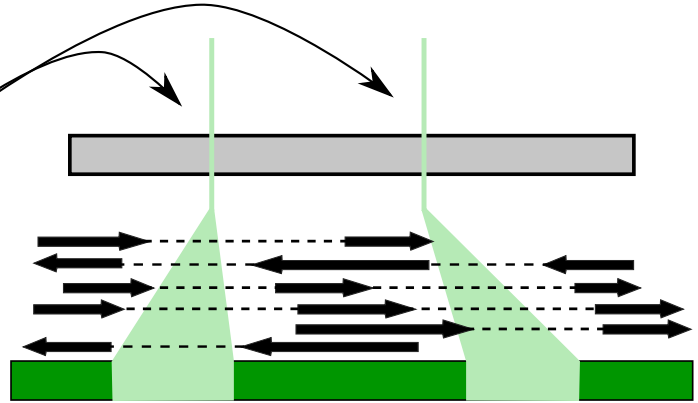
MultiBreak-SV



1. Sequence reads from individual genome using any sequencing platform



2. Align reads to reference genome; reads may map to different locations



3. Determine SVs from the alignments and compute novel adjacency probabilities