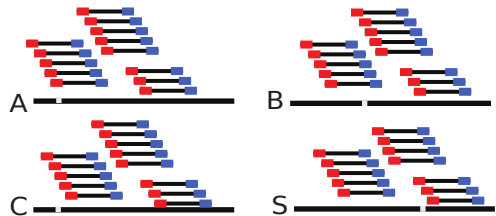
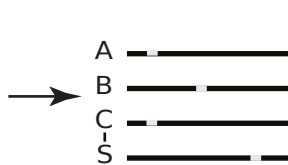
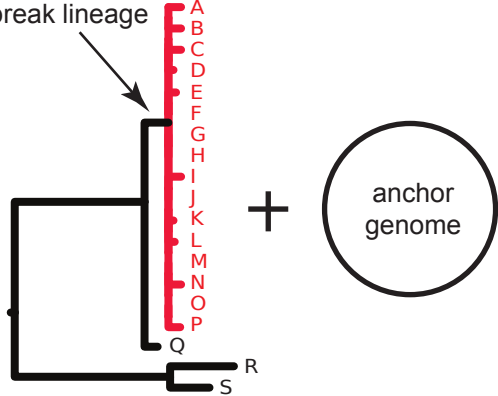


Outbreak lineage



a) Input: Newick tree file and background/anchor genome.

b) Simulate mutations across taxa according to defined set of parameters.

c) Simulate raw reads (fastq files)