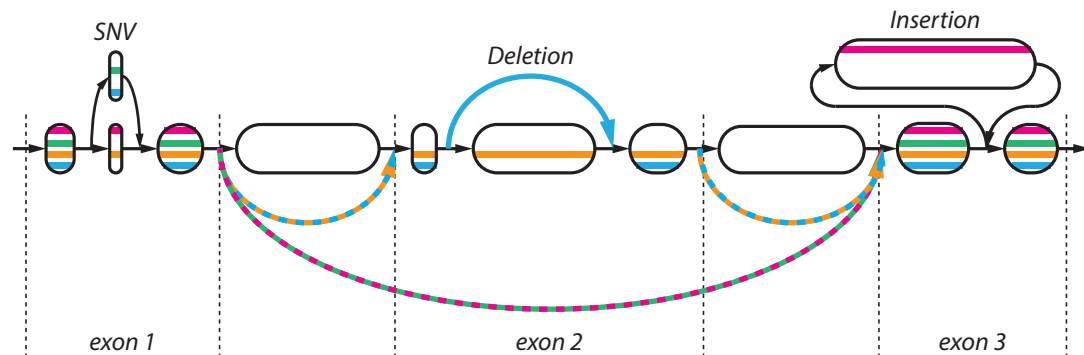
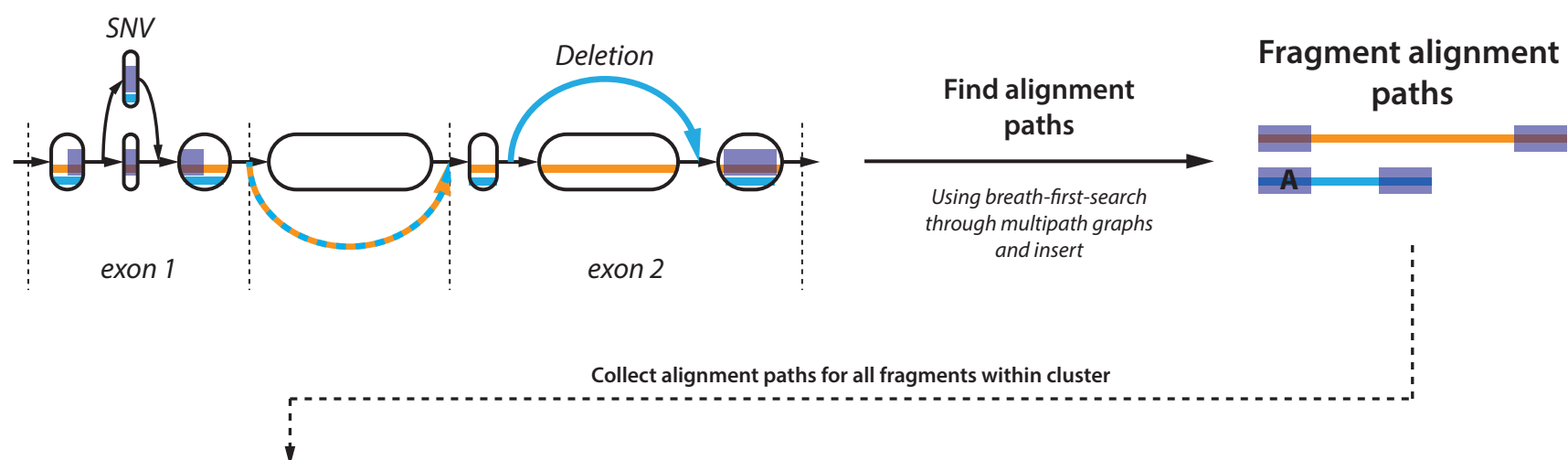
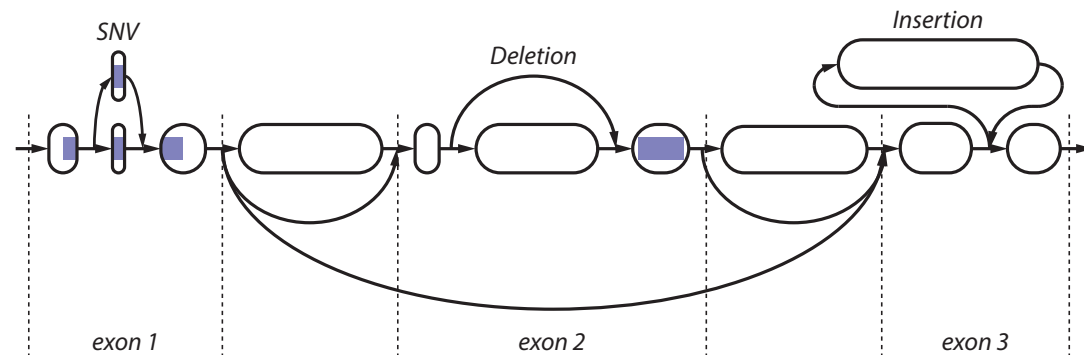


a**Pantranscriptome****Paired multipath alignment****b****Fragment alignment path sets****Calculate fragment-HST probabilities**

Using alignment scores,
fragment lengths and
mapping qualities

Probability matrix

	HST 1	HST 2	HST 3	HST 4
Fragment 1	0	0	0.7	0.3
⋮				

Use probability matrix for expression inference

c**Haplotype-specific transcripts****Infer diplotypes**

Sampling from
posterior assuming
uniform expression

**Infer expression**

Using expectation-
maximization

