We aim to identify recombinants in multiple-source alignment, what we did is to employ the divison method in algorithm. The following plot is the example of three-source alignment, where two recombinants are involved in these four sequences. In fact, the identified recombinants from every two adjacent partitions are the same with true recombinants in each possible phylogenetic network.

Following tables illustrate the identification results from network in Figure 1.

partition 1 and partition 2	
triple	identified recombinant
abc	a
acd	a
abd	a
bcd	b, c or d

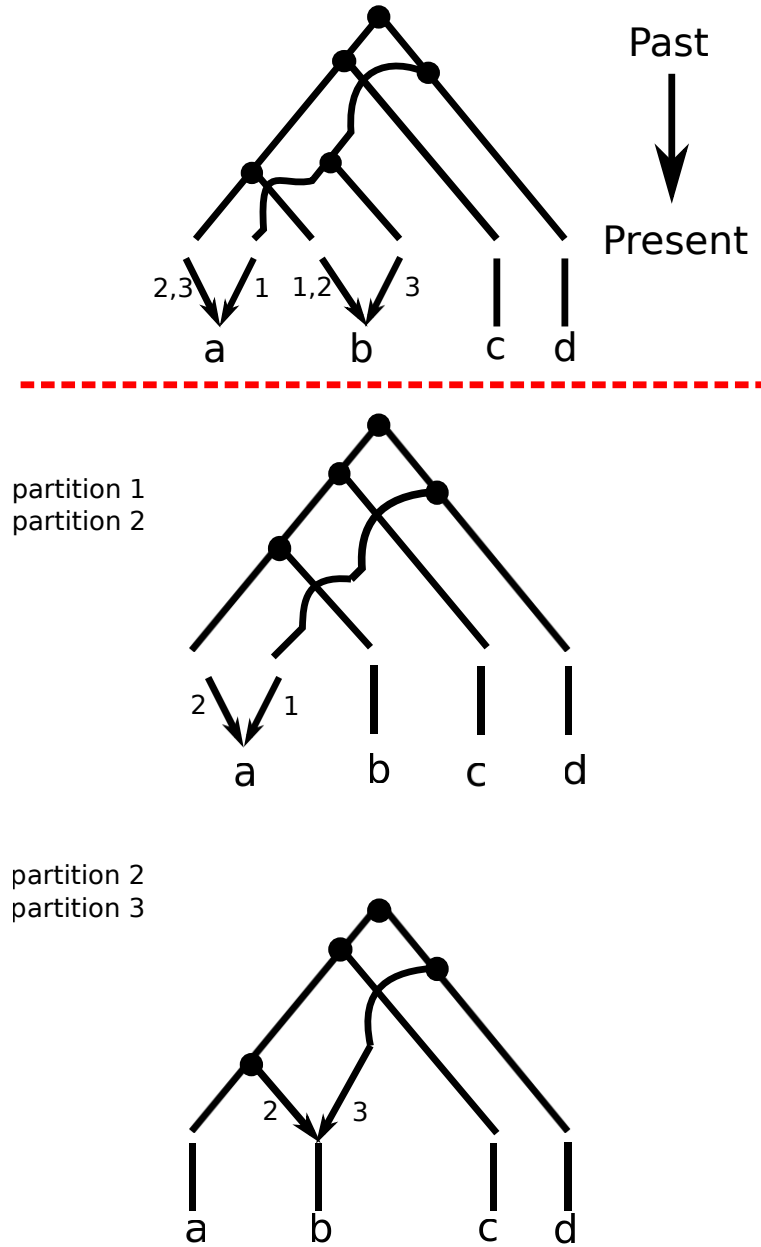| partition 2 and partition 3	
triple	identified recombinant
abc	b
bcd	b
abd	b
acd	a, c or d

Figure 1: Three-source alignment example. Numbers beside the line represent the alignment partition. Below two networks are the sub-networks, each is related with one of the two-source alignments. Based on sub-networks and recombinant identification technique in two-source alignment, we get all identified recombinants.