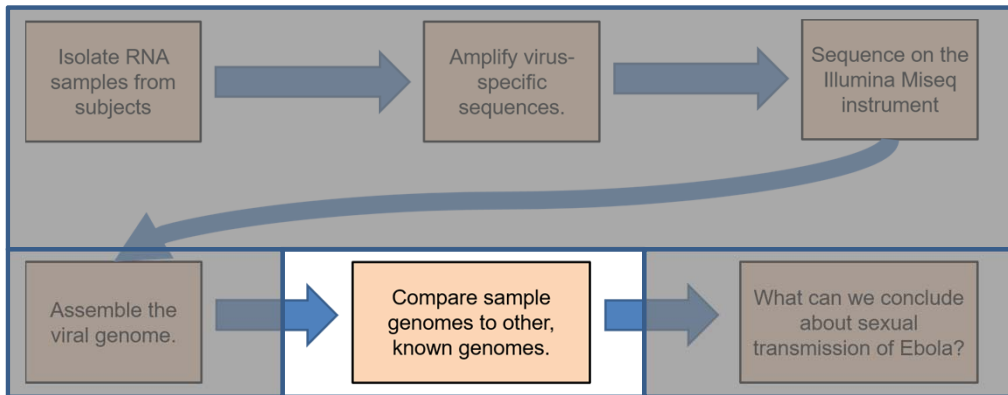
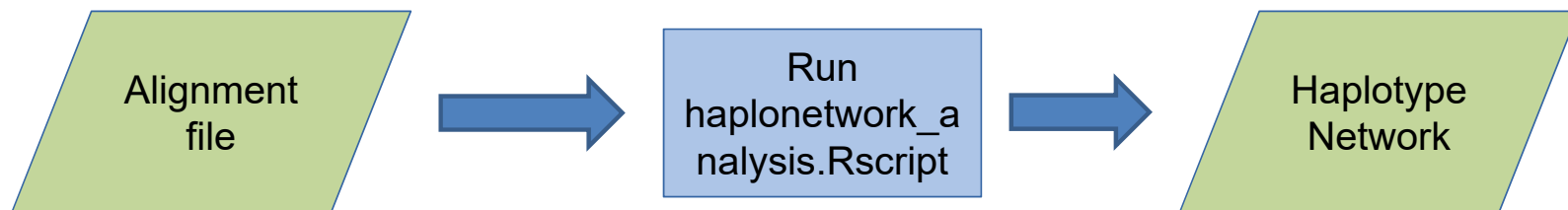


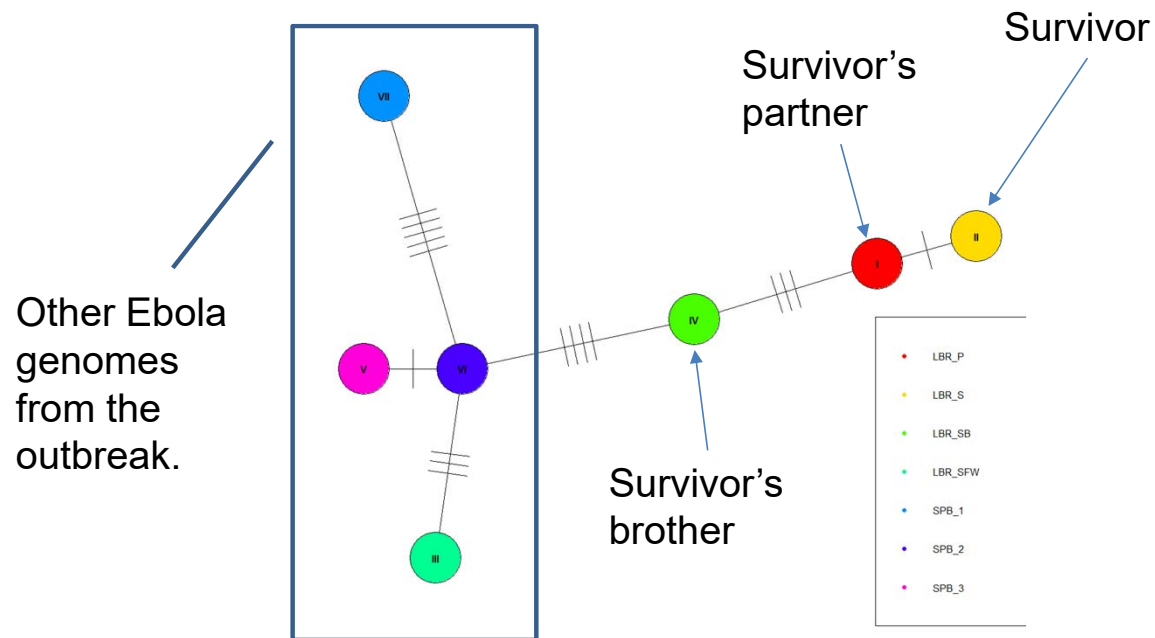
## Haplotype Network Analysis



- **Start with the alignment file made in the previous step.**
- **Arrange the genomes in a haplotype network: where each genome is connected by a line to the genomes it is most similar to.**

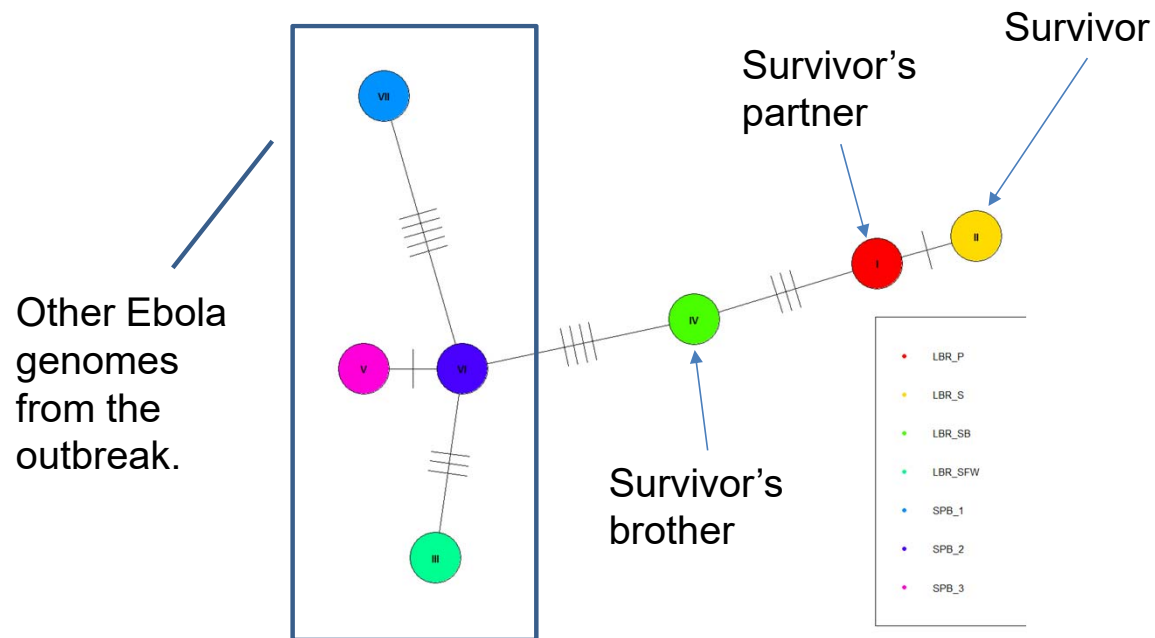


# Compare the genomes in the study and other Ebola genomes using a haplotype network



- A haplotype is a region of DNA inherited from the parent.
- NOTE: for viruses, the haplotype is the full genome.
- Each circle (node) represents a genome sequence.
- Hash marks on the lines show the number of differences between the genomes connected by the lines.
- Remember our original question: Is the partner sample more similar to the survivor sequence? Or to the other samples from this outbreak?

# Compare the genomes in the study and other Ebola genomes using a haplotype network



- The Survivor and Survivor's Partner have one difference between them.
- There are at least three differences between the Survivor's Partner and the next most similar genome.
- **This data is consistent with sexual transmission from the Survivor to the Survivor's Partner.**