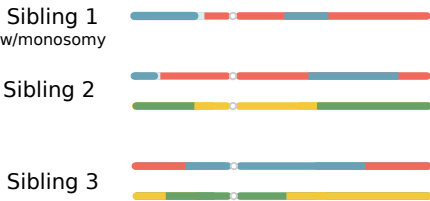


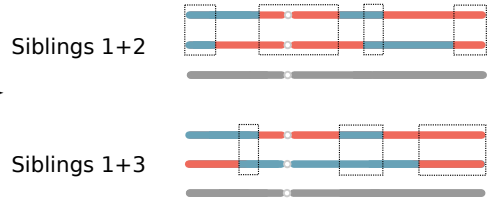
Chromosome 16



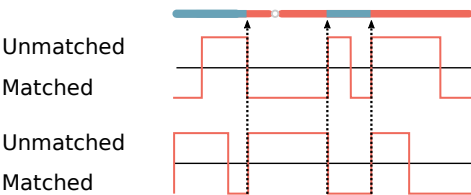
Initially we have no knowledge about the haplotypes composition



Our method identifies regions with matched haplotypes



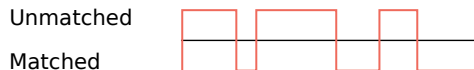
Common crossover positions are traced to the monosomy



The output for siblings 1+2



The output for siblings 1+3



The output signal of our method

