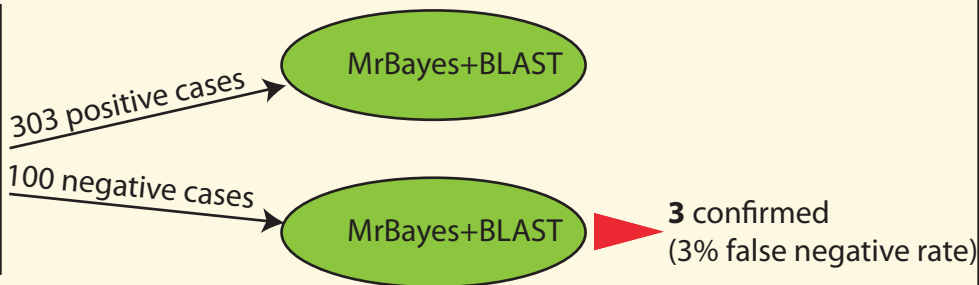


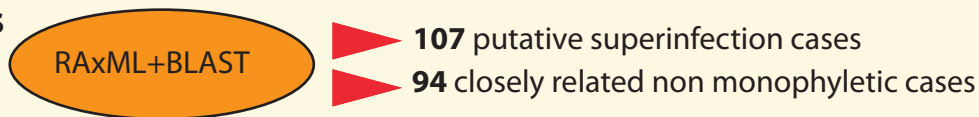
Preliminary analysis

4425 patients' routinely collected *pol* sequences analyzed with RAxML
100 randomly initialized ML tree built on 13816 sequences



Calibration to Final analysis Comparing RAxML+BLAST vs MrBayes+BLAST on **170** patients and calibrating size of background sequence set

Final analysis



Validation by sequencing

Fresh sample amplification and sequencing of *pol* and *env* genes in **14 putative superinfection** cases

