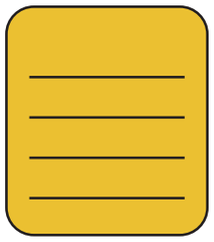
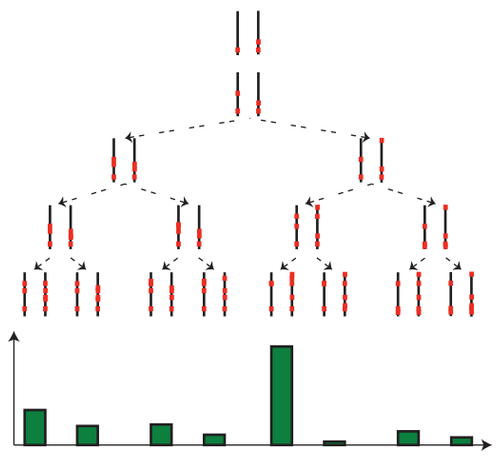
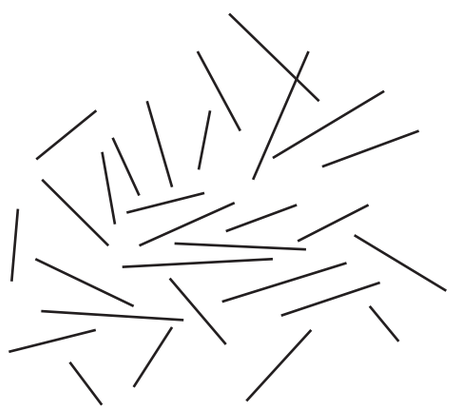
1. Generate list with ground truth variants



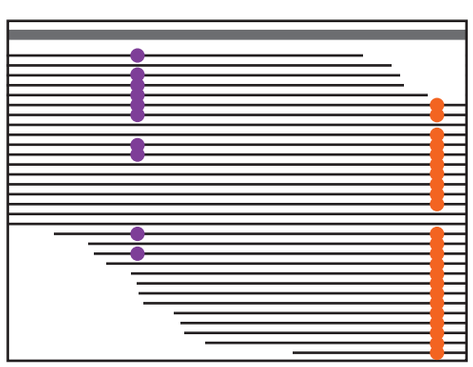
2. Place variants into the clonal ancestor tree and determine abundance of each cancer clone



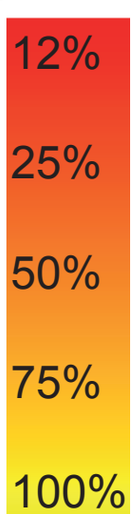
3. Generate reads from each cancer clone and the normal sample
(Exome capture)



4. Align reads to reference genome (default alignment + a more sensitive alignment)



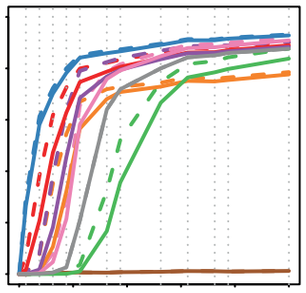
Coverage in percent from the complete alignment:

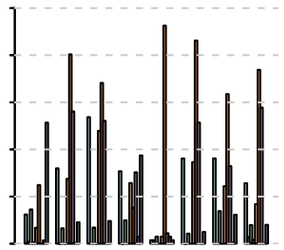


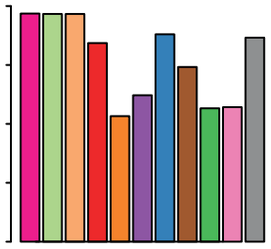
(complete bam file)

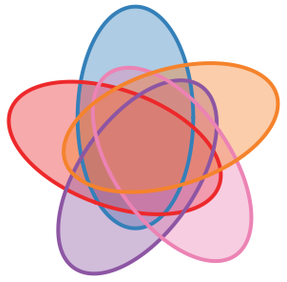
Normal contamination in percent:

5. For each of the two alignment settings, generate 8 different simulated cancer samples

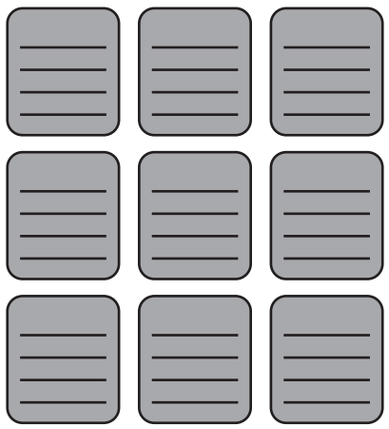








6. Run the nine variant callers; Redo with different parameters & pipeline modifications



7. Evaluate tools: compute sensitiviy & precision, analyze error sources etc.