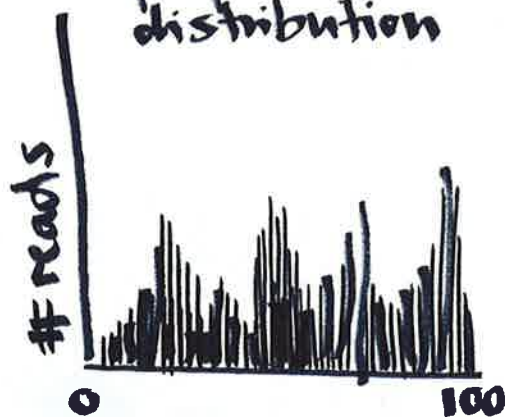


# STEP 1 Mutation Calling



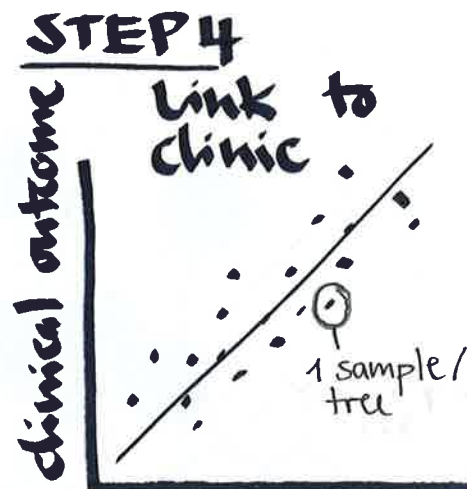
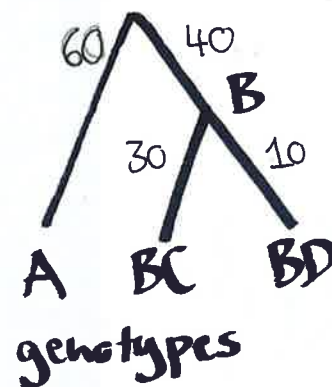
# STEP 2 frequency distribution



(i)

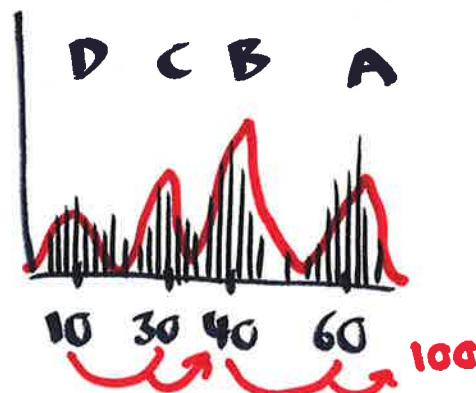
mutation freq  
corrected for CN, LOH

# STEP 3 tree reconstruction



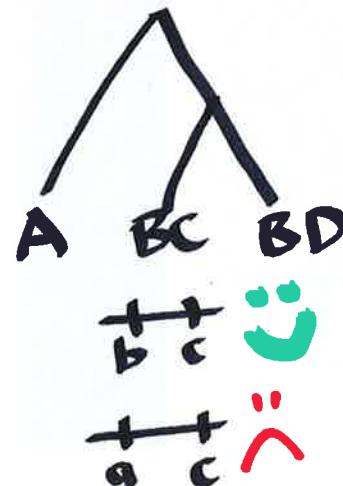
summary  
stat of  
heterogeneity/  
evolution (iv)

## Information for tree reconstruction



(ii)

tree prior  
Dirichlet mix



reads with  
multiple mutations

(iii)