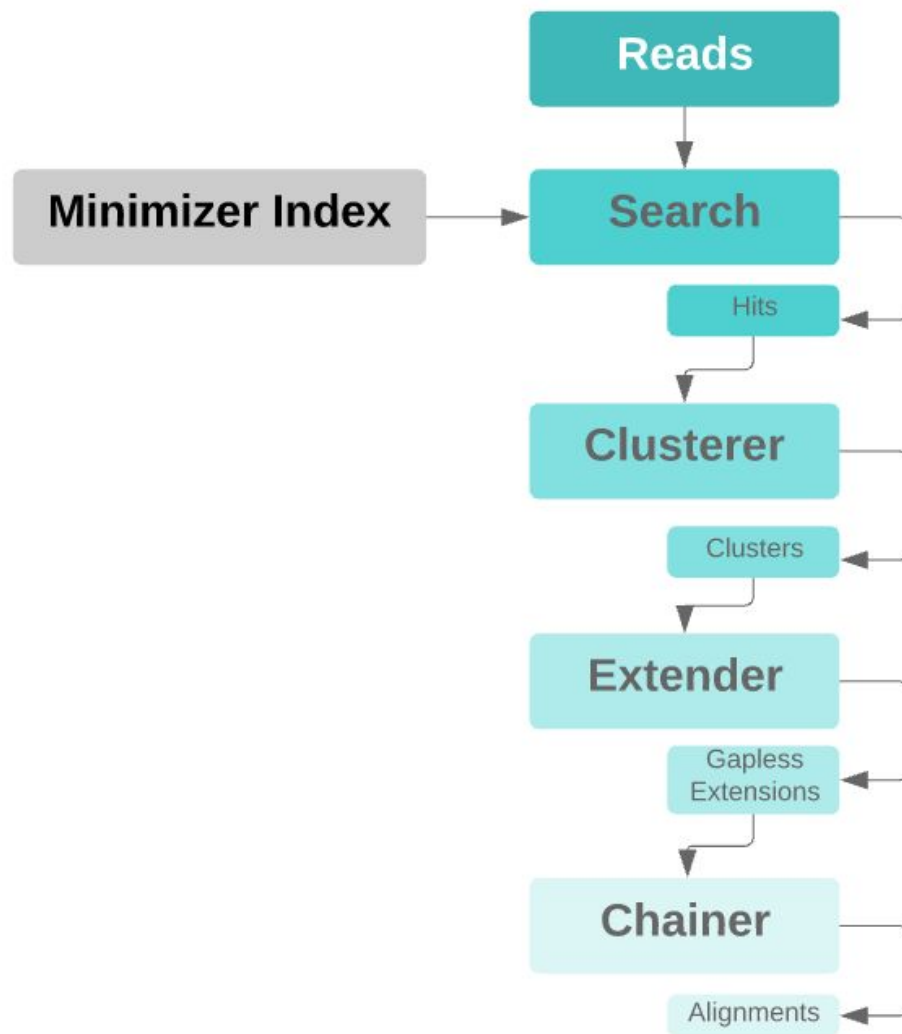
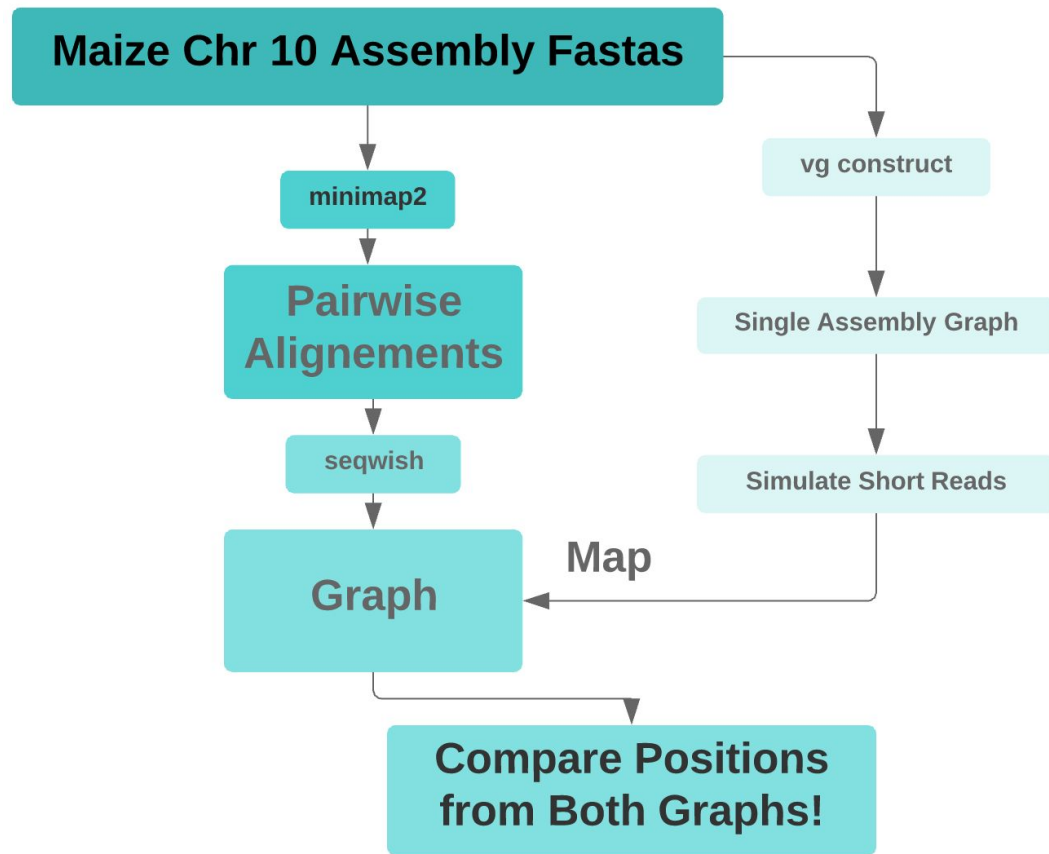


# Team Giraffe!





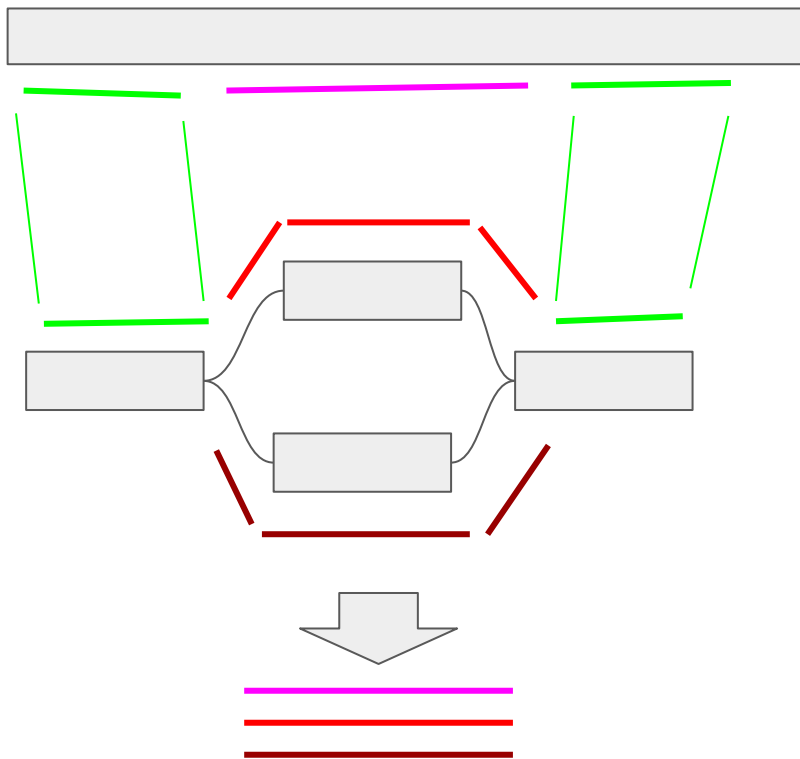


# Clusterer

Probably not slower!

TODO: profile new implementation and compare to original

# Chainer



Find haplotype-consistent paths  
between seeds

Align intervening sequence to  
each

Find optimal linearization of the  
resulting multipath alignment