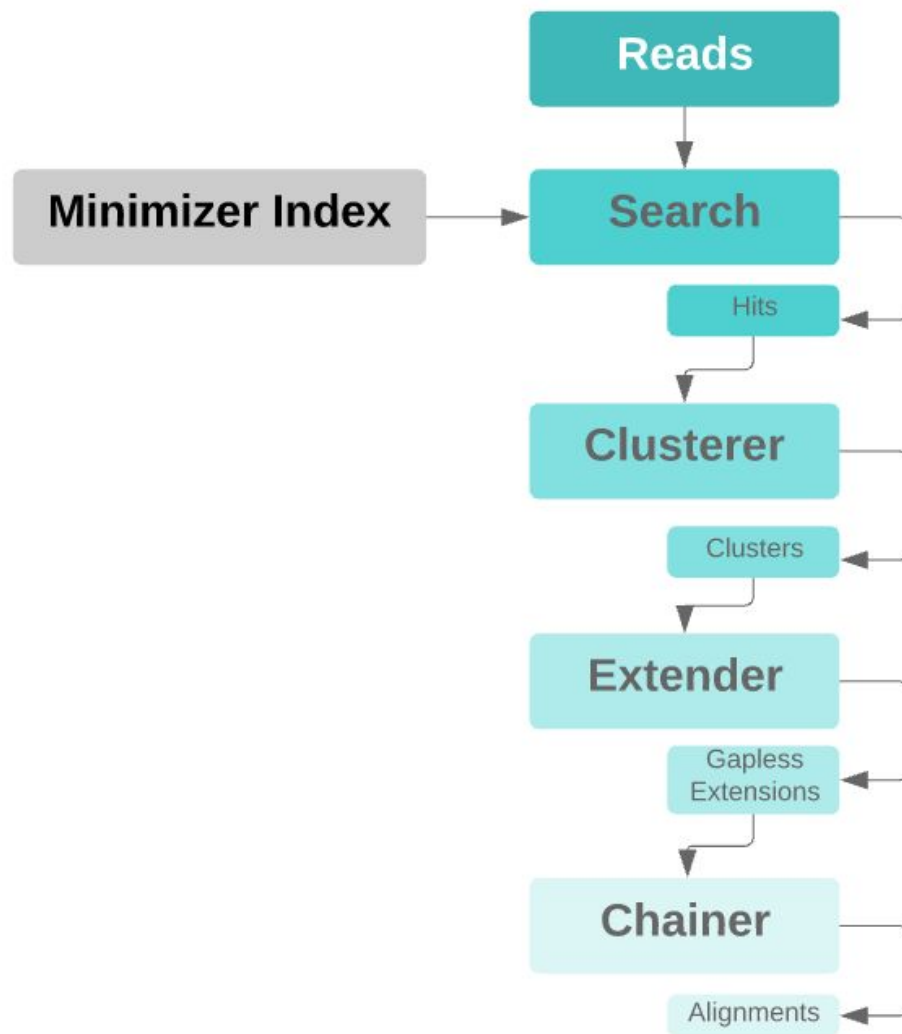
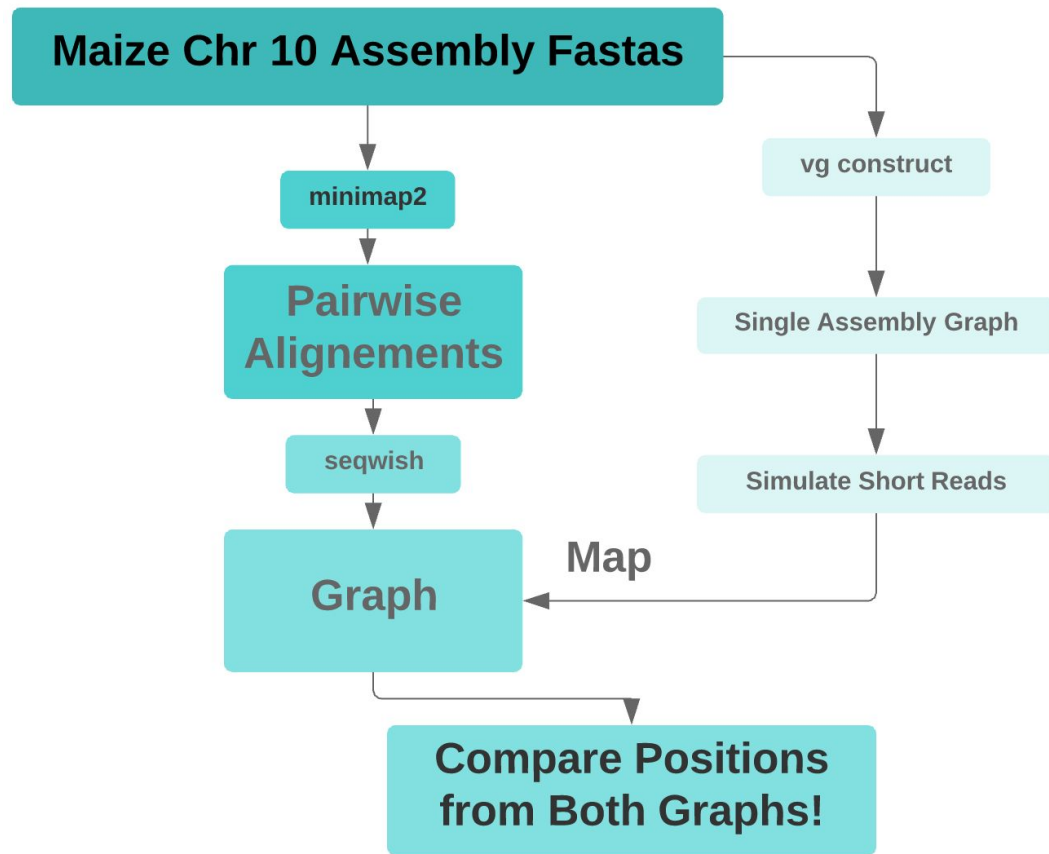


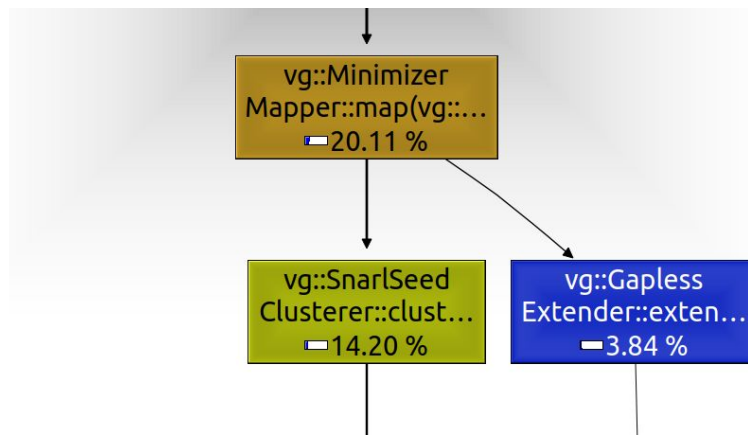
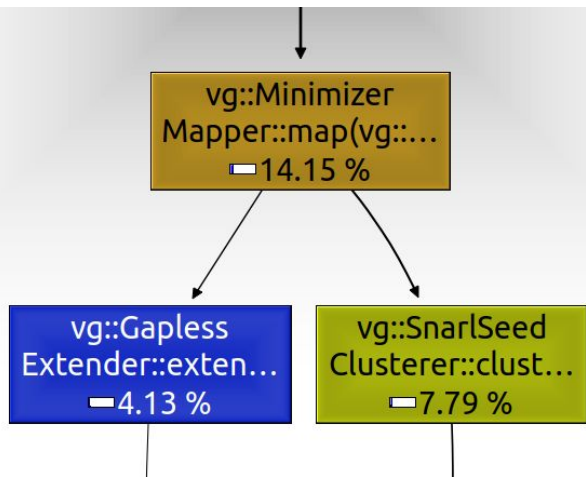
# Team Giraffe!





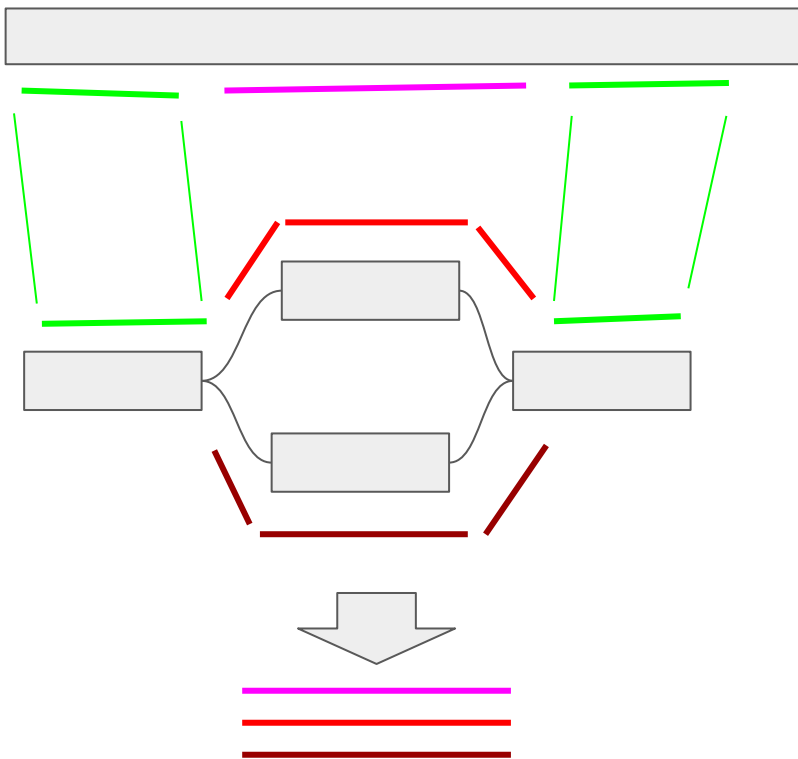


# Clustering Function Speed Test



**7.79% vs. 14.20%**  
**Preliminary Testing Suggests x2 as Fast!**

# Chainer



Find haplotype-consistent paths between seeds

Align intervening sequence to each

Find optimal linearization of the resulting multipath alignment