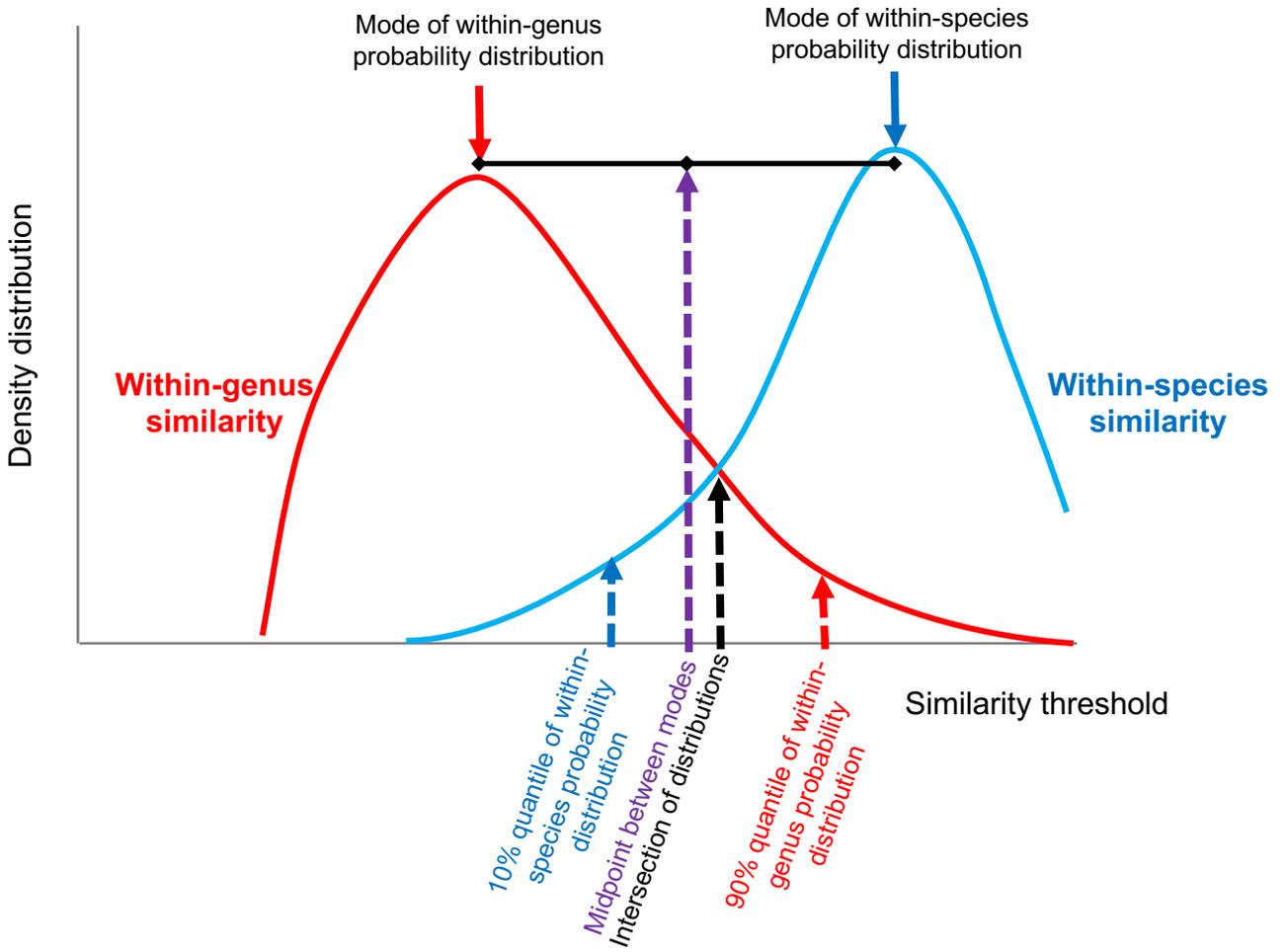


A) Approaches based on within-species and within-genus sequence similarities



B) Approaches based on over-splitting and over-merging rates

