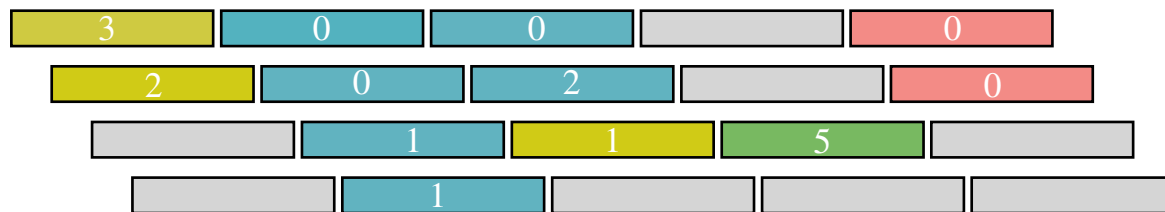


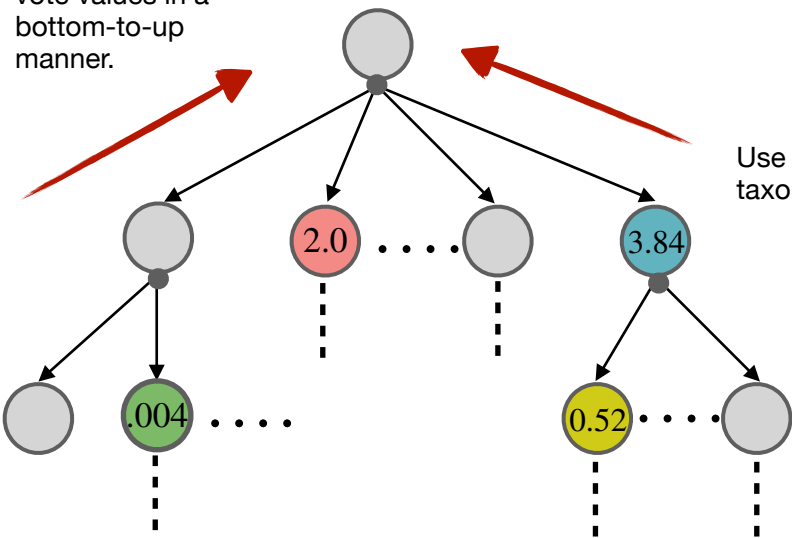
Query sequence



Query k -mers with match distances

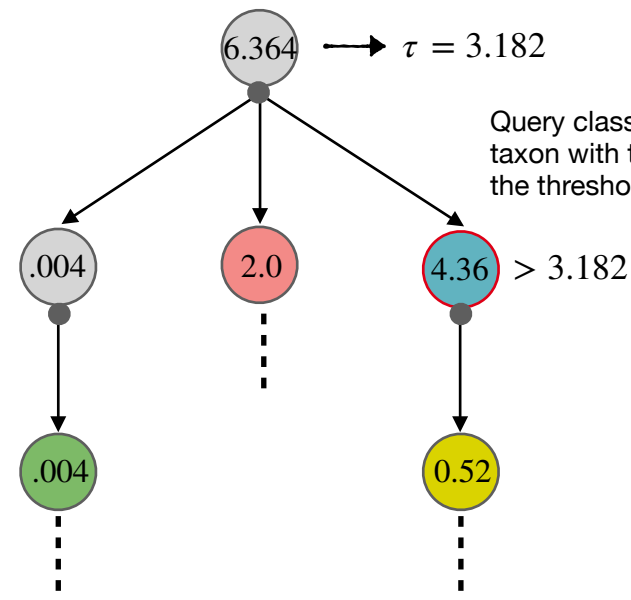
Compute vote values of taxa based on the Hamming distances of k -mer matches.

Recursively sum vote values in a bottom-to-up manner.



Use total vote values for taxonomic identification.

Threshold τ is equal to maximum total vote divided by 2.



Query classified as the lowest taxon with total vote greater than the threshold.