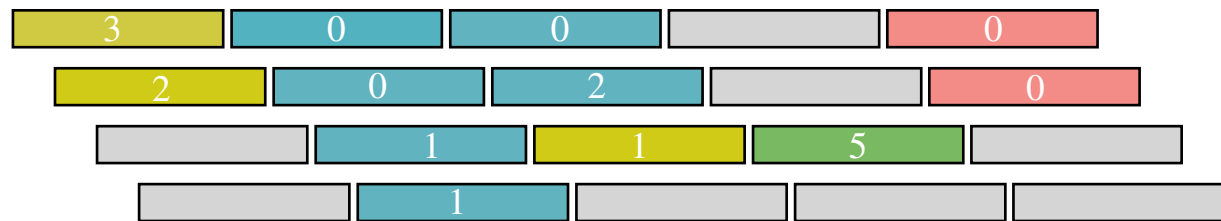


Query sequence



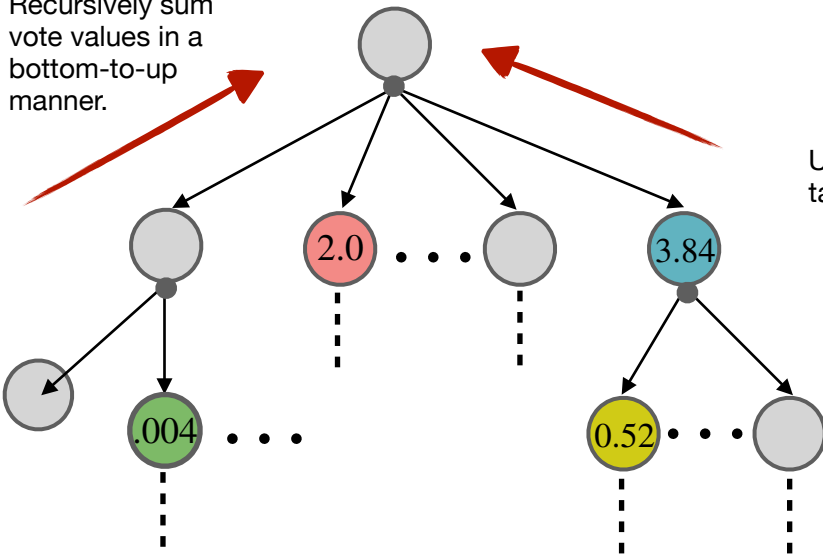
Query k -mers with match distances



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

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

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



Use total vote values for taxonomic identification.

