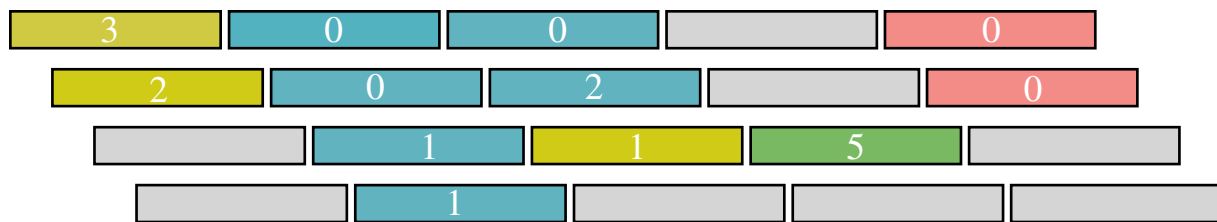


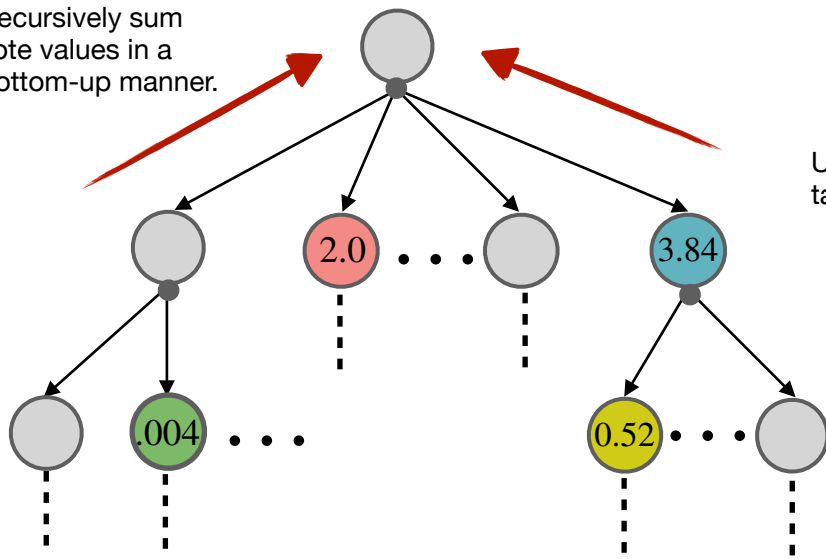
Query sequence



Query k -mers with match distances to the closest reference k -mer and colors stands for LCA taxa.

Compute votes of taxa based on the Hamming distances of k -mer

Recursively sum vote values in a bottom-up manner.



Use total votes for taxonomic identification.

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

