

Phylogenetics is a central discipline in the modern life sciences aimed at describing sequences similarity through evolutionary relationships among organisms. Although it may seem that the graphical representation of phylogenetic connection between organism is a mastered problem, the results always depend on correct choice of method of computation, especially for diverse data as sequences of bacterial metallothioneins. We shown how our used methods and algorithms in a suitable form gives a good results, which corresponds to affinity of bacterial metallothioneins.