

Evolutionary profiles from the QR factorization of multiple sequence alignments

Anurag Sethi, Patrick O'Donoghue, and Zaida Luthey-Schulten*

Department of Chemistry, University of Illinois at Urbana-Champaign, Urbana, IL 61801

Communicated by Carl R. Woese, University of Illinois at Urbana-Champaign, Urbana, IL, January 10, 2005 (received for review December 2, 2004)

We present an algorithm to generate complete evolutionary profiles that represent the topology of the molecular phylogenetic tree of the homologous group. The method, based on the multi-

yet the problem of redundancy has not been addressed in an evolutionary context.

Here we present an algorithm based on the multidimensional QR