

Bacterial Foraging Optimization –Genetic Algorithm for Multiple Sequence Alignment with Multi-Objectives

P.Manikandan¹, Dr. D. Ramyachitra²,

¹Research Scholar, ²Assistant Professor,

Department of Computer Science, Bharathiar University, Coimbatore-641 046, India.

manimkn89@gmail.com¹, jaichitra1@yahoo.co.in.

Performance Measures of Optimization Algorithms and Phylogenetic Tree Construction

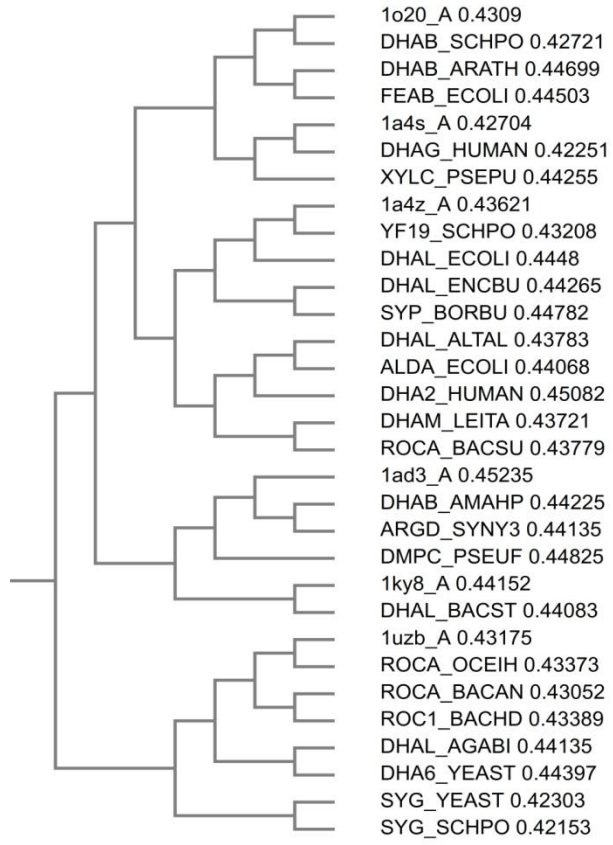
The Supplementary Table 1-2 shows the comparison of performance measures such as the Sum-of-Pairs (SP) and Total Column Score (TCS) for the proposed and existing algorithms (GA, ACO, ABC, PSO) and also with various online MSA tools such as T-Coffee, Muscle, K-Align, MAFFT and Clustal Omega. From these results, it is inferred that the proposed BFO-GA algorithm provides better results than the existing methods and tools. Also the Supplementary Fig. 1 shows the small tree containing a part of Operational Taxonomic Unit (OTUs) for the proposed and existing algorithms with respect to RV3 reference family in BaliBASE database.

Table.1 : Comparisons of Sum of Pairs (SP) scores for the existing and the proposed algorithm for the MSA datasets

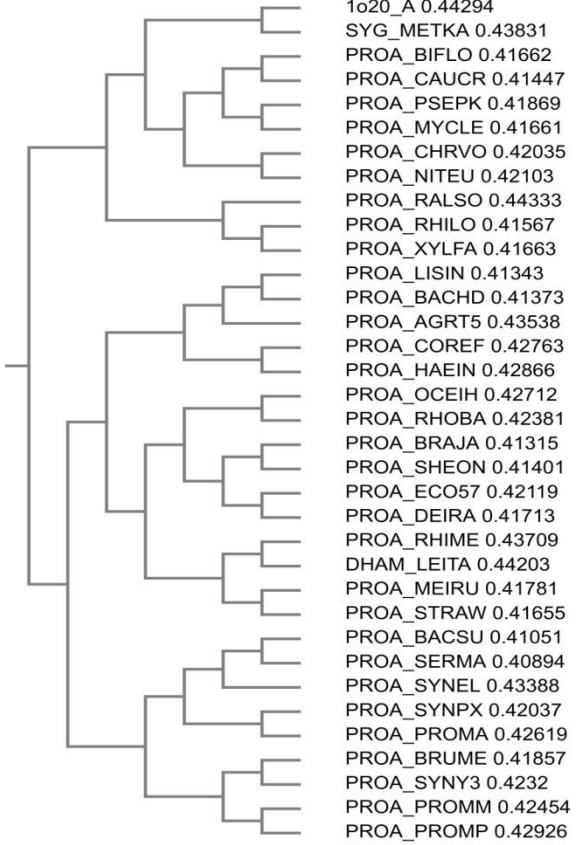
Database	T-Coffee	Clustal Omega	Kalign	MUSCLE	MAFFT	GA	ACO	ABC	PSO	BFO-GA
Balibase	54	55	55	59	61	63	70	80	83	90
Sabmark	57	58	59	61	62	64	74	82	82	90
Prefab	57	52	51	55	59	60	65	80	76	88
Oxbench	50	49	51	55	58	61	74	83	86	90

Table.2 : Comparisons of Total Column Score (TCS) scores for the existing and the proposed algorithm for the MSA datasets

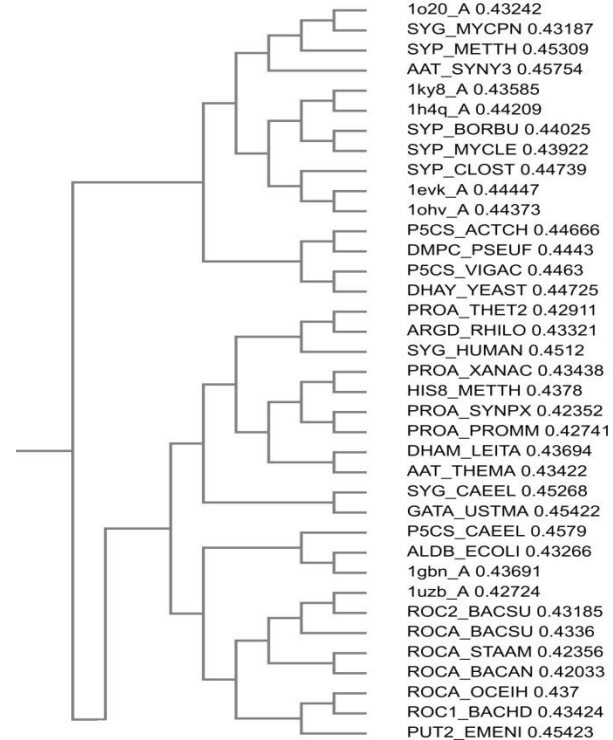
Database	T-Coffee	Clustal Omega	Kalign	MUSCLE	MAFFT	GA	ACO	ABC	PSO	BFO-GA
Balibase	42	43	45	49	53	58	58	56	67	77
Sabmark	43	48	52	53	55	57	56	61	55	79
Prefab	51	49	50	53	54	56	59	64	59	75
Oxbench	48	46	50	52	54	56	59	67	56	75



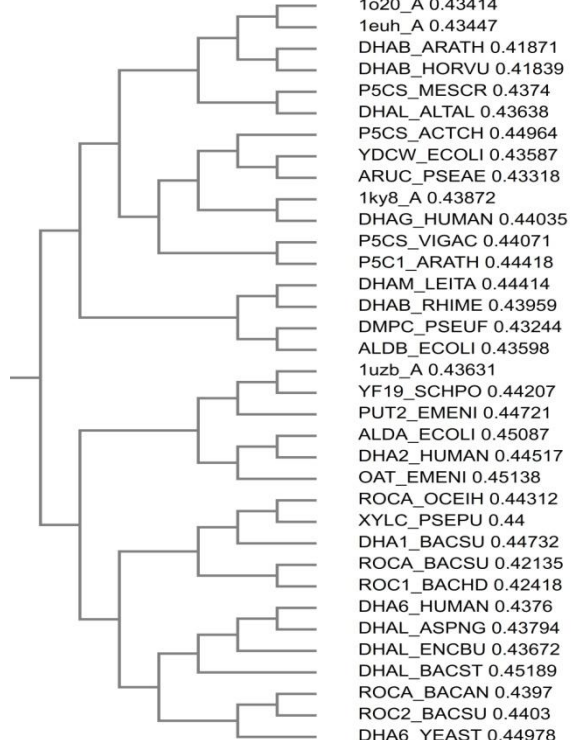
GA



ACO



ABC



PSO

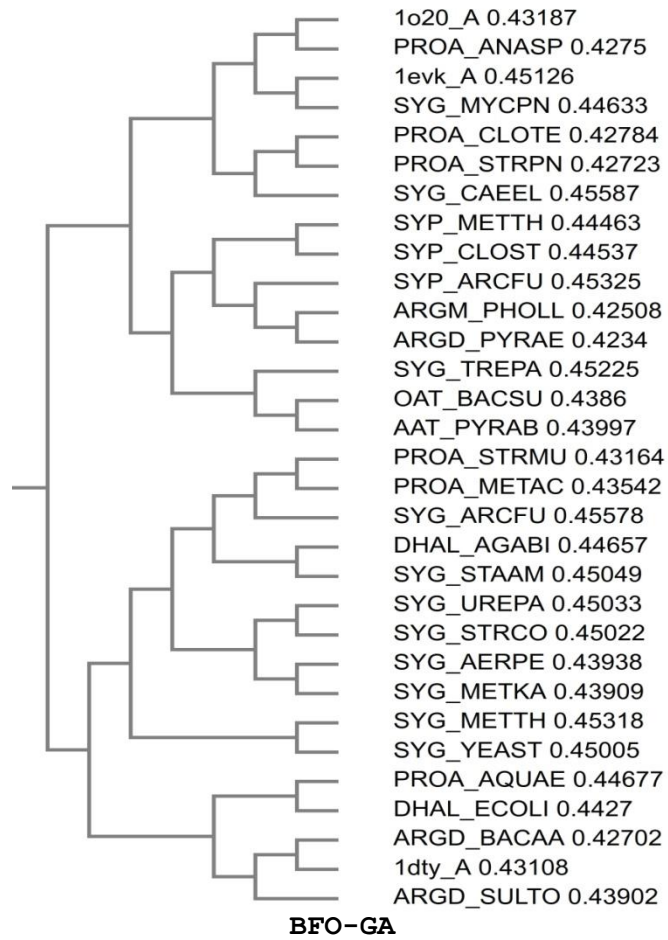


Fig. 1: Phylogenetic Trees of RV 3 reference family in BaliBASE 3.0 Dataset