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

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## <u>Performance Measures of Optimization Algorithms and Phylogenetic Tree</u> <u>Construction</u>

The Supplementary Table 1-2 shows the comparison of performance measures such as the Sumof-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



1o20 A 0.4309 DHAB SCHPO 0.42721 DHAB ARATH 0.44699 FEAB\_ECOLI 0.44503 1a4s\_A 0.42704 DHAG\_HUMAN 0.42251 XYLC\_PSEPU 0.44255 1a4z A 0.43621 YF19 SCHPO 0.43208 DHAL\_ECOLI 0.4448 DHAL\_ENCBU 0.44265 SYP BORBU 0.44782 DHAL\_ALTAL 0.43783 ALDA ECOLI 0.44068 DHA2 HUMAN 0.45082 DHAM LEITA 0.43721 ROCA\_BACSU 0.43779 1ad3\_A 0.45235 DHAB\_AMAHP 0.44225 ARGD\_SYNY3 0.44135 DMPC\_PSEUF 0.44825 1ky8\_A 0.44152 DHAL\_BACST 0.44083 1uzb\_A 0.43175 ROCA OCEIH 0.43373 ROCA\_BACAN 0.43052 ROC1\_BACHD 0.43389 DHAL\_AGABI 0.44135 DHA6 YEAST 0.44397 SYG\_YEAST 0.42303 SYG\_SCHPO 0.42153



ABC

1o20\_A 0.43242 SYG MYCPN 0.43187 SYP\_METTH 0.45309 AAT\_SYNY3 0.45754 1ky8\_A 0.43585 1h4q\_A 0.44209 SYP\_BORBU 0.44025 **SYP MYCLE 0.43922** SYP\_CLOST 0 44739 1evk A 0.44447 1ohv\_A 0.44373 P5CS\_ACTCH 0.44666 DMPC\_PSEUF 0.4443 P5CS\_VIGAC 0.4463 DHAY\_YEAST 0.44725 PROA\_THET2 0.42911 ARGD RHILO 0.43321 SYG\_HUMAN 0.4512 PROA\_XANAC 0.43438 HIS8\_METTH 0.4378 PROA\_SYNPX 0.42352 PROA PROMM 0.42741 DHAM LEITA 0.43694 AAT THEMA 0.43422 SYG\_CAEEL 0.45268 GATA\_USTMA 0.45422 P5CS\_CAEEL 0.4579 ALDB ECOLI 0.43266 1gbn\_A 0.43691 1uzb A 0.42724 ROC2\_BACSU 0.43185 ROCA\_BACSU 0.4336 ROCA\_STAAM 0.42356 ROCA\_BACAN 0.42033 ROCA\_OCEIH 0.437 ROC1 BACHD 0.43424 PUT2\_EMENI 0.45423





1o20 A 0.44294 SYG\_METKA 0.43831 PROA\_BIFLO 0.41662 PROA\_CAUCR 0.41447 PROA\_PSEPK 0.41869 PROA MYCLE 0.41661 PROA\_CHRVO 0.42035 PROA NITEU 0.42103 PROA\_RALSO 0.44333 PROA\_RHILO 0.41567 PROA\_XYLFA 0.41663 PROA\_LISIN 0.41343 PROA\_BACHD 0.41373 PROA AGRT5 0.43538 PROA\_COREF 0.42763 PROA\_HAEIN 0.42866 PROA\_OCEIH 0.42712 PROA\_RHOBA 0.42381 PROA BRAJA 0.41315 PROA\_SHEON 0.41401 PROA ECO57 0.42119 PROA\_DEIRA 0.41713 PROA RHIME 0.43709 DHAM\_LEITA 0.44203 PROA\_MEIRU 0.41781 PROA STRAW 0.41655 PROA\_BACSU 0.41051 PROA\_SERMA 0.40894 PROA SYNEL 0.43388 PROA SYNPX 0.42037 PROA\_PROMA 0.42619 PROA\_BRUME 0.41857 PROA\_SYNY3 0.4232 PROA\_PROMM 0.42454 PROA\_PROMP 0.42926

1o20\_A 0.43414 1euh\_A 0.43447 DHAB\_ARATH 0.41871 DHAB\_HORVU 0.41839 P5CS\_MESCR 0.4374 DHAL ALTAL 0.43638 P5CS\_ACTCH 0.44964 YDCW\_ECOLI 0.43587 ARUC PSEAE 0.43318 1ky8\_A 0.43872 DHAG\_HUMAN 0.44035 P5CS\_VIGAC 0.44071 P5C1 ARATH 0.44418 DHAM\_LEITA 0.44414 DHAB\_RHIME 0.43959 DMPC\_PSEUF 0.43244 ALDB\_ECOLI 0.43598 1uzb\_A 0.43631 YF19\_SCHPO 0.44207 PUT2\_EMENI 0.44721 ALDA\_ECOLI 0.45087 DHA2\_HUMAN 0.44517 OAT\_EMENI 0.45138 ROCA\_OCEIH 0.44312 XYLC PSEPU 0.44 DHA1 BACSU 0.44732 ROCA BACSU 0.42135 ROC1 BACHD 0.42418 DHA6\_HUMAN 0.4376 DHAL\_ASPNG 0.43794 DHAL\_ENCBU 0.43672 DHAL BACST 0.45189 ROCA\_BACAN 0.4397 ROC2\_BACSU 0.4403 DHA6 YEAST 0.44978



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