

Supplementary Materials:

Table S1. List of papers included in the SLR study.

#	Paper	Source
1	MSA-GA: multiple sequence alignment tool based on genetic approach.	[21]
2	Performance improvement of genetic algorithm for multiple sequence alignment.	[50]
3	Improvements in the sensibility of MSA-GA tool using COFFEE objective function.	[52]
4	A hybrid genetic algorithm with chemical reaction optimization for multiple sequence alignment.	[33]
5	Genetic algorithms and dynamic weighted sum method for RNA alignment.	[48]
6	Multiple sequence alignment with affine gap by using multi-objective genetic algorithm.	[49]
7	An enhanced algorithm for multiple sequence alignment of protein sequences using genetic algorithm.	[47]
8	Application of genetic algorithm by influencing the crossover parameters for multiple sequence alignment.	[53]
9	Multi-objective formulation of multiple sequence alignment for phylogeny inference.	[54]
10	A Hybrid Approach using Progressive and Genetic Algorithms for Improvements in Multiple Sequence Alignments.	[22]
11	Parallel multiple DNA sequence alignment using genetic algorithm and asynchronous advantage actor critic model.	[55]
12	A hybrid genetic algorithm with chemical reaction optimization for multiple sequence alignment.	[56]
13	A bi-objective function optimization approach for multiple sequence alignment using genetic algorithm.	[57]
14	Parallel niche pareto AlineaGA—an evolutionary multi-objective approach on multiple sequence alignment.	[58]
15	Optimizing multiple sequence alignments using a genetic algorithm based on three objectives: structural information, non-gaps percentage and totally conserved columns.	[59]
16	Cyclic genetic algorithm for multiple sequence alignment.	[60]
17	Progressive alignment method using genetic algorithm for multiple sequence alignment.	[51]
18	Vertical decomposition with genetic algorithm for multiple sequence alignment.	[61]
19	A genetic algorithm based approach for the optimization of multiple sequence alignment.	[12]
20	A multigroup parallel genetic algorithm for multiple sequence alignment.	[62]
21	A new genetic algorithm for multiple sequence alignment.	[63]
22	Multiple sequence alignment with multi-objective metaheuristics. a comparative study.	[64]
23	Multi-objective two-level swarm intelligence approach for multiple RNA sequence-structure alignment.	[66]

24	A novel two-level particle swarm optimization approach for efficient multiple sequence alignment.	[20]
25	NestMSA: a new multiple sequence alignment algorithm.	[65]
26	Particle swarm optimization with tabu search algorithm (PSO-TS) applied to multiple sequence alignment problem.	[10]
27	ProbPFP: a multiple sequence alignment algorithm combining hidden Markov model optimized by particle swarm optimization with partition function.	[67]
28	DNA sequence compression using adaptive particle swarm optimization-based memetic algorithm.	[90]
29	A characteristic-based framework for multiple sequence aligners.	[89]
30	Parallel H4MSA for multiple sequence alignment.	[88]
31	A hybrid multi-objective memetic metaheuristic for multiple sequence alignment.	[13]
32	A Comparison between Memetic algorithm and Genetic algorithm for the cryptanalysis of Simplified Data Encryption Standard algorithm.	[87]
33	A Memetic Cellular Genetic Algorithm for Multiple Sequence Alignment.	[86]
34	An algorithm of multiple sequence alignment based on consensus sequence searched by simulated annealing and star alignment.	[91]
35	Protein multiple sequence alignment by basic flower pollination algorithm.	[92]
36	Flower pollination algorithm with profile technique for multiple sequence alignment.	[93]
37	Multiple sequence alignment using a multi-objective artificial bee colony algorithm.	[94]
38	A Multi-objective Artificial Bee Colony Algorithm for Multiple Sequence Alignment.	[14]
39	A Decomposition and Dominance-Based Multi-objective Artificial Bee Colony Algorithm for Multiple Sequence Alignment.	[95]
40	Hybrid multiobjective artificial bee colony for multiple sequence alignment.	[96]
41	Artificial bee colony algorithm for solving multiple sequence alignment.	[97]
42	IBBOMSA: An improved biogeography-based approach for multiple sequence alignment.	[102]
43	A new hybrid bio-inspired approach to resolve the multiple sequence alignment problem.	[98]
44	Multiple sequence alignment using multi-objective based bacterial foraging optimization algorithm.	[74]
45	Bacterial foraging optimization–genetic algorithm for multiple sequence alignment with multi-objectives.	[99]

Table S2. Overview of the relevant MSA review publications.

Reference	Year	Scope and content	SLR	Benchmarks dataset	Evaluation Measures	Open Issues
[26]	2014	survey of benchmarks for MSA.	-	-	-	-
[24]	2016	Metaheuristics for bioinformatics.	-	-	-	-
[6]	2016	MSA modeling.	-	-	-	-

[8]	2017	Comparison of the metaheuristic quality measures.	-	-	✓	-
[40]	2017	Review Genetic algorithm for MSA.	-	-	-	-
[69]	2021	Metaheuristic-based review for MSA.	✓	-	-	-
[31]	2022	Nature Inspired Algorithms MSA Problem.	-	-	-	-
[36]	2022	Algorithms for Sequence Alignment.	-	-	-	-
[41]	2022	Parallel protein multiple sequence alignment approaches.	-	-	-	-
Proposed	2024	Bioinspired Algorithms for MSA.	✓	✓	✓	✓

Table S3. Quality Checklist.

NO.	Question
SQ1	Is the report coherent and clear?
SQ2	Is the method used for the data collection clearly explained?
SQ3	Is the primary research objective clearly mentioned?
SQ4	Are the main study findings credible?
SQ5	Are the diversity contexts been clearly investigated?
SQ6	Is there a clear link between the data, conclusion, and interpretations?
SQ7	Are the research procedures adequately documented?
SQ8	Are the methodology and experimentations clearly stated?
SQ9	Is it possible to replicate the research findings?