



Symbiotic Artificial Immune Systems: A Novel Bio-inspired Search Optimization Algorithm

Author: Junhao Song Email: js2001@hw.ac.uk

Supervisors: Dr. Wei Pang and Dr. James McKinna

School of Mathematical and Computer Sciences, Heriot-Watt University, Edinburgh, UK



Introduction

Artificial Immune System (AIS) refers to algorithms built to solve a variety of complex problems by simulating the behaviour in the biological immune system [1]. The Symbiotic Artificial Immune System (SAIS), inspired by symbiotic interactions (mutualism) between different species in biology. An example is the flower and bee in Figure 1.



Figure 1: Mutualism between flower and bee (CC BY-ND 2.0 Licenses)

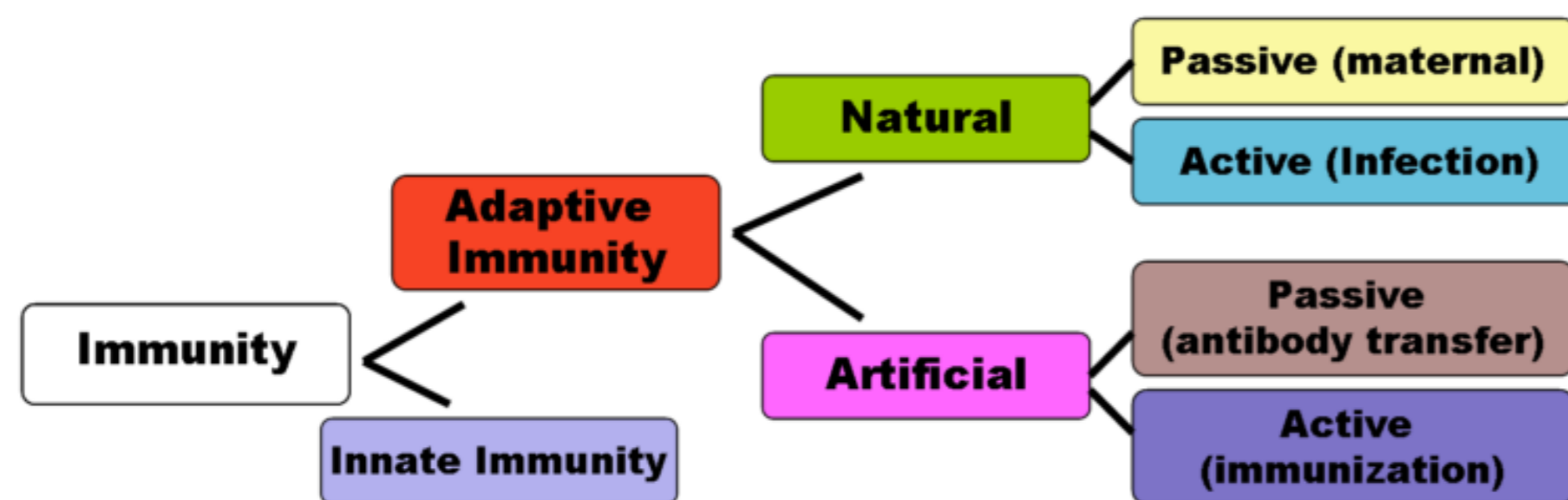


Figure 2: Hierarchical diagram of the AIS inspired by the immune system [2]

The design of SAIS, like all AIS, contains two main components, innate and adaptive immunity. This is shown in Figure 2.

Motivations and Objectives

1. Motivation:

- Generality of AIS.
- Complexity of use.
- Accurate simulation of the biological immune system.

2. Objectives:

- Develop mathematical formulation of SAIS and validate the performance of SAIS on benchmark problems.
- SAIS is analysed in comparison with other well-known AIS algorithms.
- SAIS performance is assessed in terms of speed of convergence, quality of solution and robustness of the algorithm.

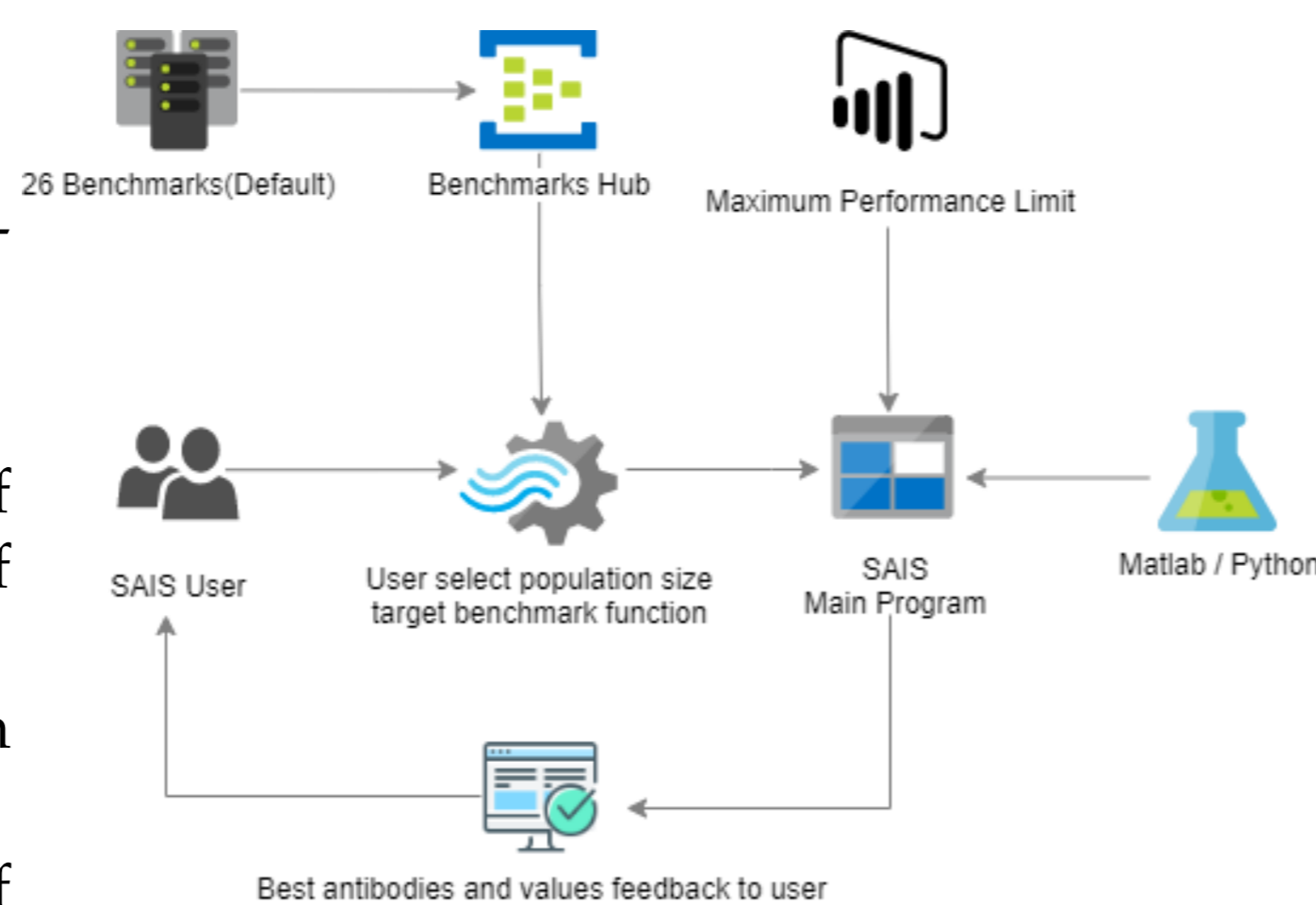
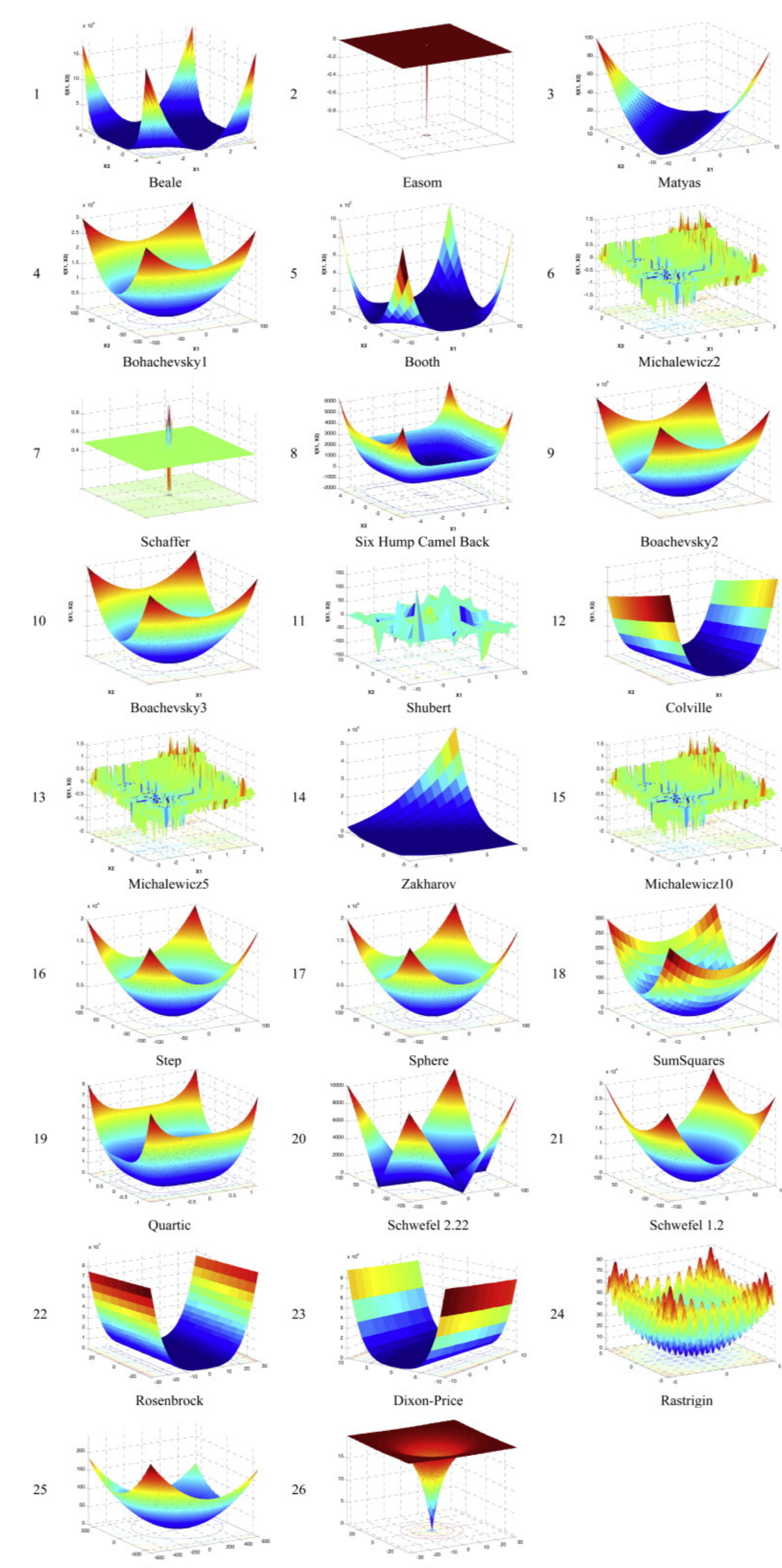
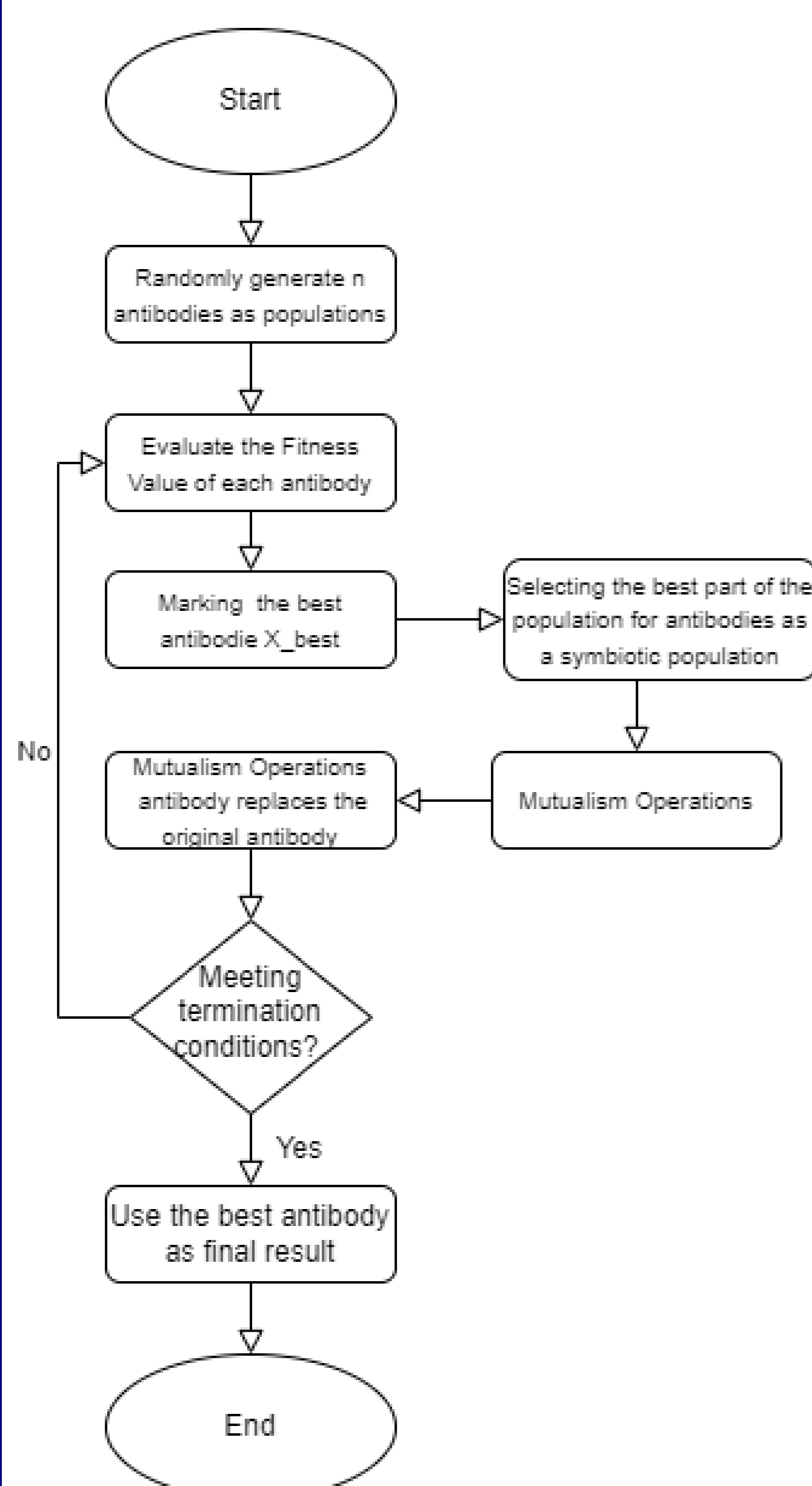


Figure 3: Diagram of the SAIS Usage Process

Methods for Symbiotic Artificial Immune Systems



The flow chart on the left shows the entire SAIS process in action, while the one on the right shows the benchmark functions for testing SAIS, of which there are 26 in total. In the mutualism operations, an antibody x_n is considered to be the n -th antibody of the population. In the symbiotic population, every antibodies maintain an interaction. In equations, R_m (mutualism relationship) shows the interaction between each antibody. $rand(0, 1)$ is a random number between $[0, 1]$; x_{best} is the optimal antibody. bf is benefit factors which can be the integer from 1 to n , represents the level of benefit that an antibody receives from the mutualism relationship indicates the possibility of n times benefit.

$$x_n^{new} = x_n + rand(0, 1) * (x_{best} - R_m * bf) \quad (1)$$

$$R_m = \frac{\sum_{i=1}^n x_i}{n} \quad (2)$$

In Figure 4. n represents the population size, m represents the mutation rate, p the clone rate [1], and t represents the NSA threshold [3]. Here the parameters were set to half the maximum value for control purposes. c denotes the crossover probability of GA [1]. g represents the generation gap. w represents the inertia weights [3]. v indicates the velocity of the particle [1]. β denotes the reciprocity parameter between antibodies. u denotes the immune computing unit/node [2]. i denotes the inter-antibody gain coefficient. d is the Deletion Percentage in SymbAIS (another AIS), which is used to eliminate ineligible antibodies.

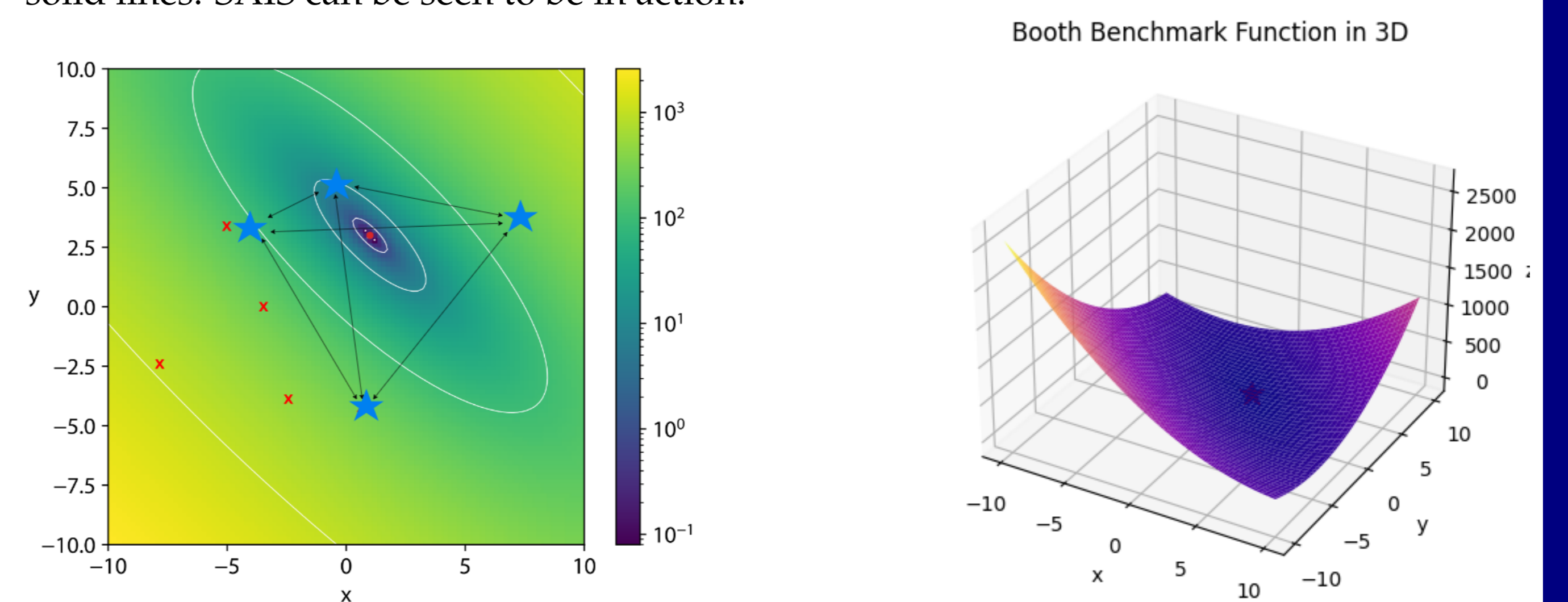
NSA	CLONALG	GA	PSO	SOS	aiNet	SymbAIS	SAIS
$n = 100$							
$m = 0.01$	$m = 0.01$	$m = 0.01$	$w = 0.2$		$\beta = 2$	$\beta = 2$	
$p = 0.1$	$p = 0.1$	$c = 0.8$	$v = 0.1$		$p = 0.1$	$p = 0.1$	
$t = x_{max}/2$		$g = 0.9$			$i = 2$	$d = 2$	
					$u = 100$		

Figure 4: Parameter Settings of the Algorithms

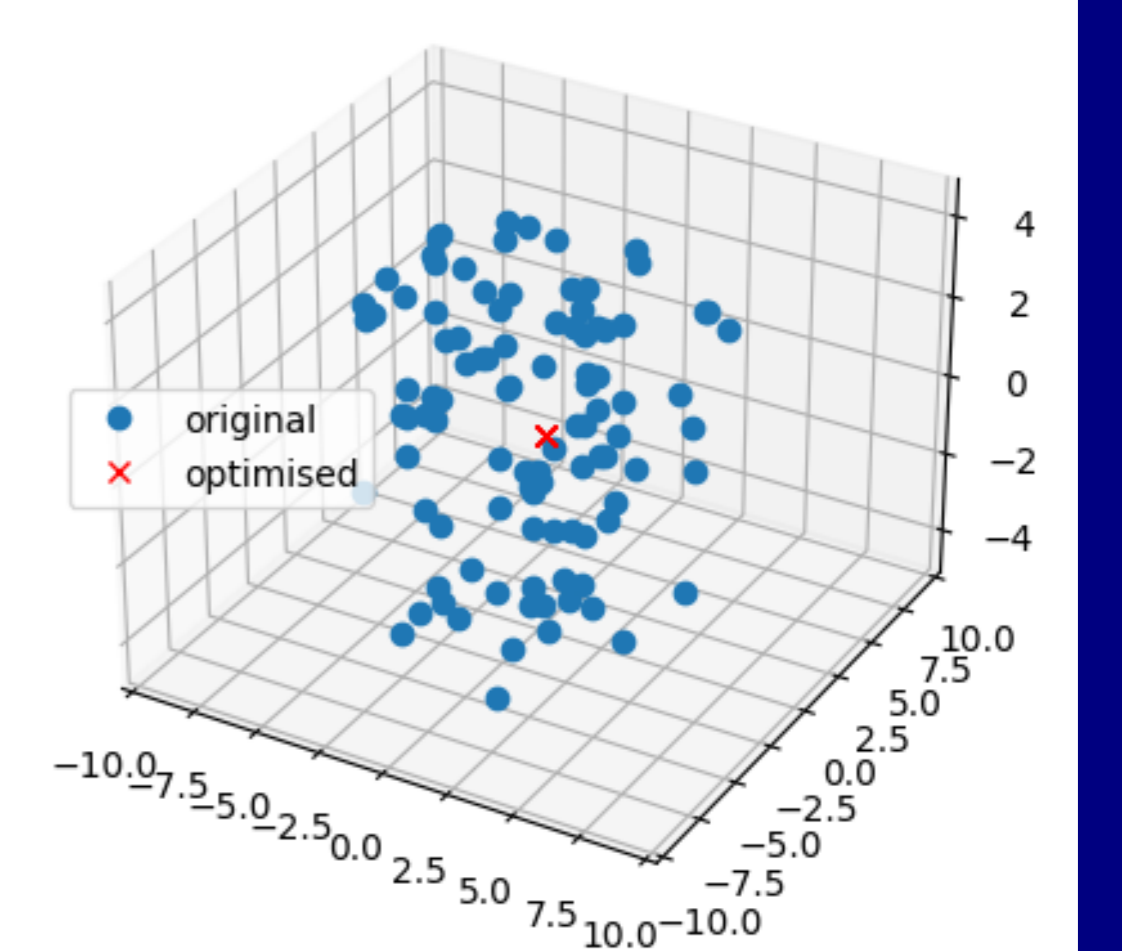
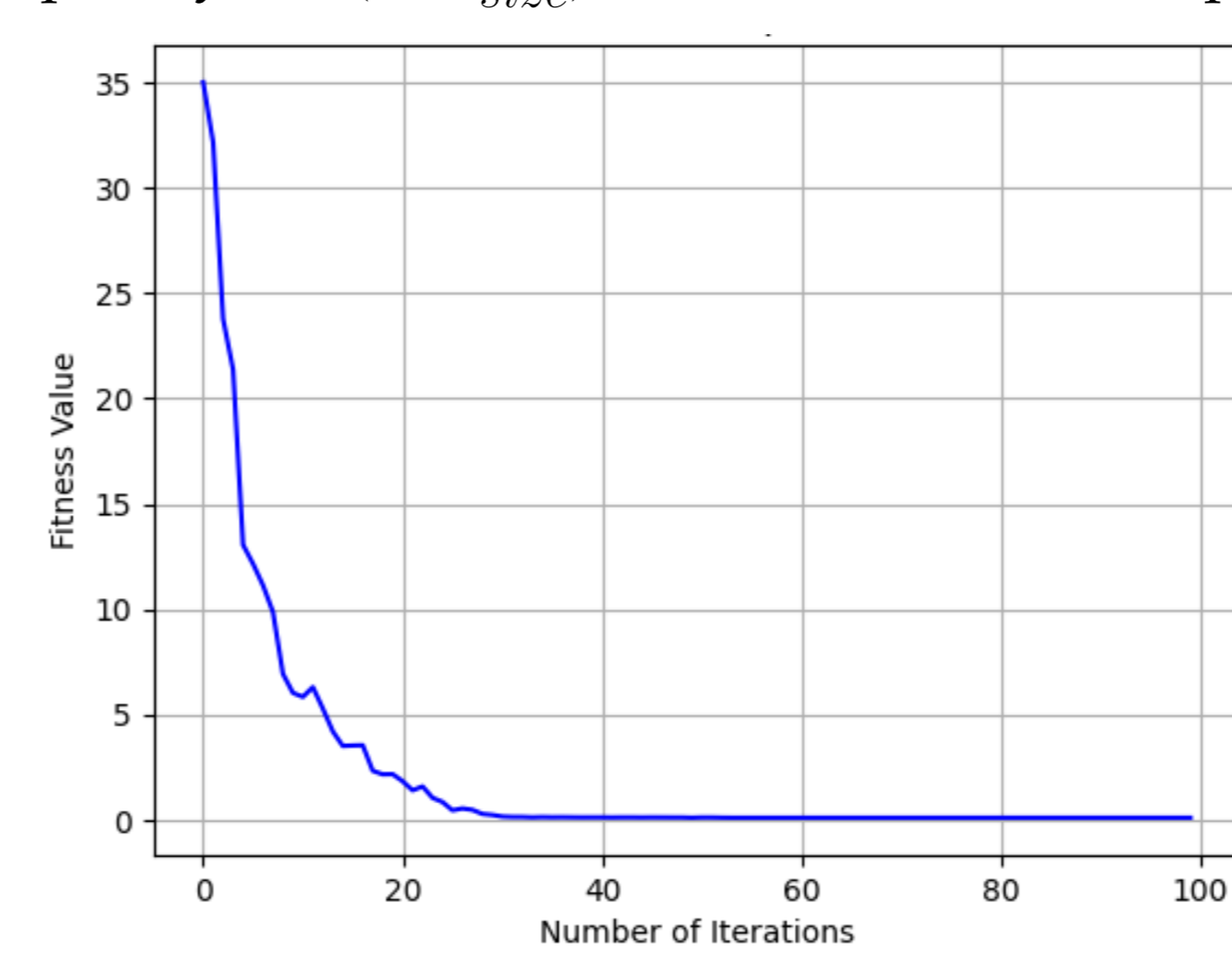
The experiment was evaluated by comparing SAIS with other algorithms. We control for parameters by way of the literature and we choose GA, SymbAIS and SOS as the comparison algorithms and run them 100 times on each of the first 12 benchmark functions [2]. Finally a non-parametric statistical experiment (Wilcoxon Signed-Ranks Test) was used to compare the results of all the algorithms after running benchmarks [4].

Experimental Results

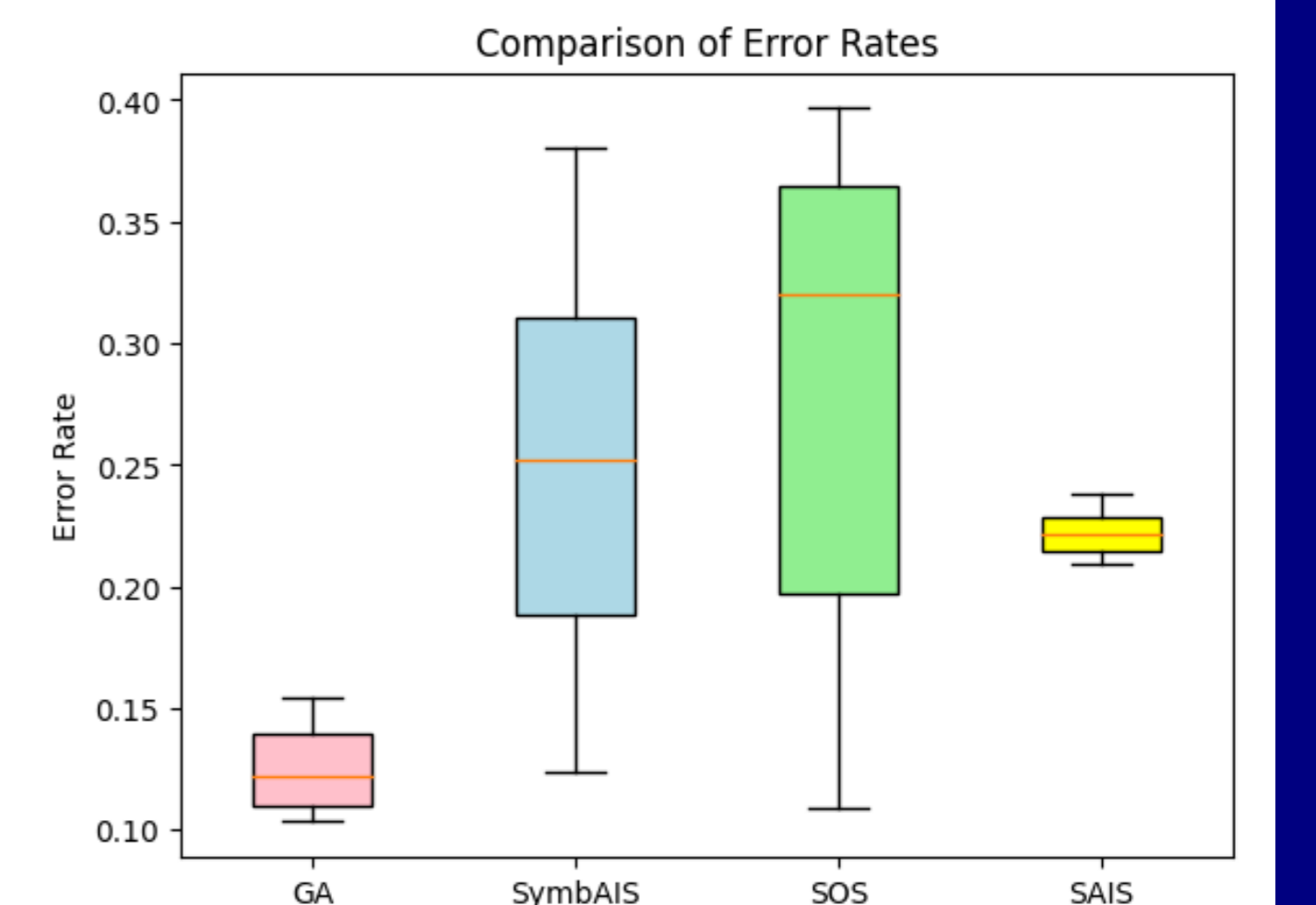
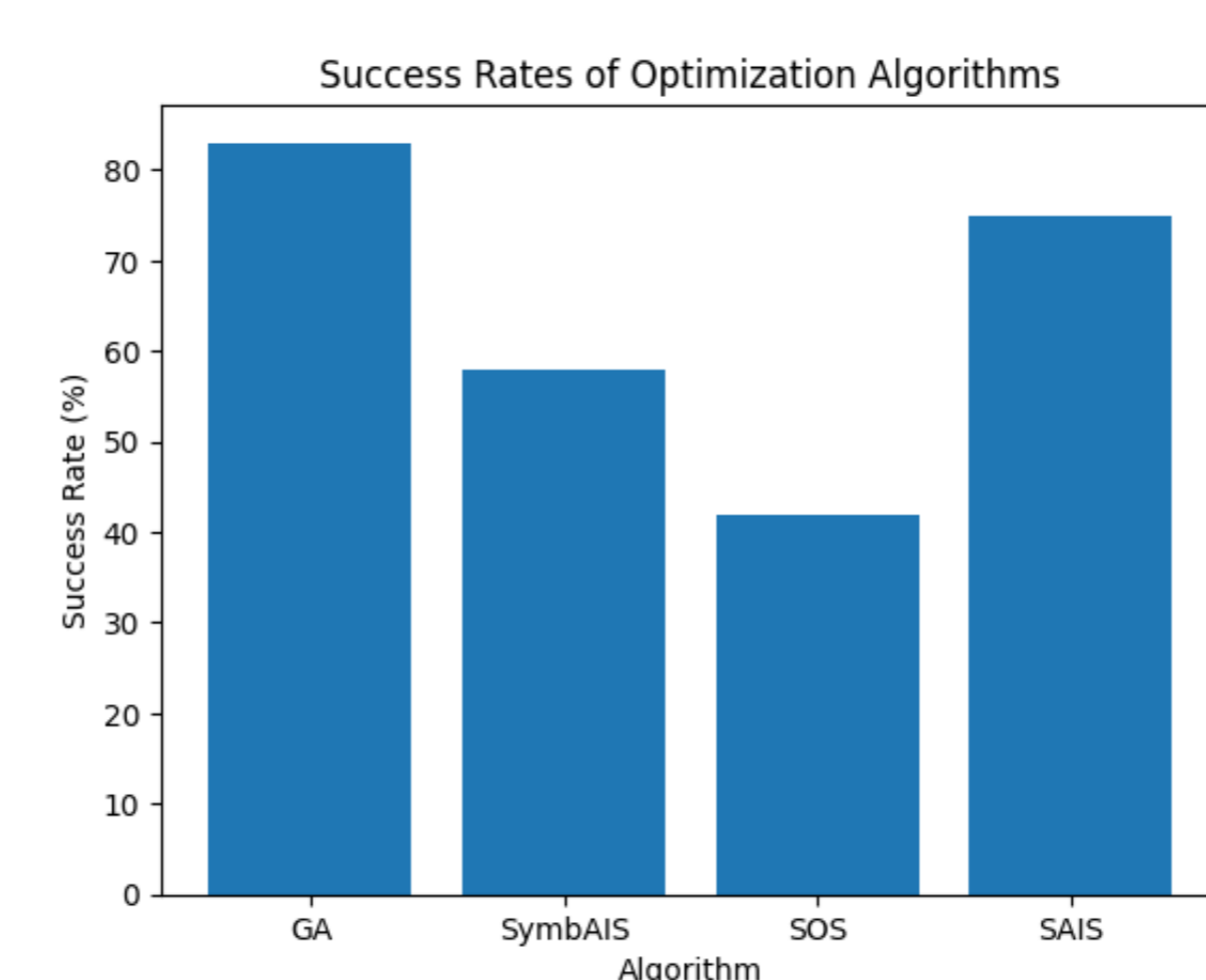
This poster takes the Booth benchmark function as an example. The red crosses in the legend are the SAIS antibodies in the randomly generated initialisation population. The blue stars are the top antibodies in the populations selected by SAIS (symbiotic populations). These antibodies are interacting with each other, so they are connected by bidirectional solid lines. SAIS can be seen to be in action.



SAIS for each solution's fitness value is calculated with a time complexity of $O(1)$. Finding the best solution requires traversing the fitness score with time complexity $O(s_{size})$. In the most adapted solution, the operations performed have time complexity $O(s_{size})$, where R_m and $local_{best}$ are constants. Since the SAIS contains two nested loops, the total time complexity is $O(n \cdot s_{size}^2)$. SAIS was able to complete convergence quickly in each benchmark.



Conclusion



Advantages of SAIS: few parameters, fast convergence and high accuracy in low latitude problems.

Limitations of SAIS: premature convergence in high latitude problems, low accuracy in high latitude environments, weak directionality of the algorithm.

Future work: Explore the accuracy of SAIS in relation to diversity and complete testing of the high-latitude function.

References

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