Convergence and Dominance in the Minimal Clonal Selection Algorithm

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***Abstract*-The minimal clonal selection provides a reduced realisation of the principles of the clonal selection theory, embodying the information processing properties of a parallel mutation-based hill climber and the winner-take-all competitive learning policy. In the work proposing the approach, a set of performance expectations were proposed regarding convergence and resource utilisation of the approach. This work investigates these expectations of the minimal clonal selection algorithm in a equally minimal random antigenic determinant problem domain. The resource utilisation behaviour is demonstrated to occur as expected, although the number of determinants is show to linearly increase the number of exposures the system requires to acquire the full set of patterns from the domain. This variation on the expected consistent convergence behaviour is speculated to be caused by the interactive competition effects of the winner-take-all principle applied across the population of cells.**

Keywords-Clonal Selection Algorithm, Experimentation, Evaluation, Antigenic Determinants, Convergence, Clonal Dominance

I. INTRODUCTION

The clonal selection theory describes the diversity of antibodies and the acquired immune response [1,2]. In considering the principle information processing properties of the immunological theory, a minimal clonal selection algorithm was proposed [5]. The minimal approach provides a realisation of the information processing properties of the theory, considering the procedure as a general adaptive plan (much like the adaptive and reproductive plans of Holland [9]). The algorithm employs a set of adaptive units (cells) in the context of a pathogenic environment consisting of antigenic determinants, as defined in the hierarchical framework for modelling the acquired immune system [7]. The algorithm is minimal with regard to other clonal selection algorithms (for example [4]) in that the selective-adaptive principles of the adaptive plan have been reduced to a simple winner-take-all competitive learning system [6]. This work considers the basic phenomenology of the proposed system with regard to system stabilisation (convergence) and clonal dominance (resource utilisation) in the context of a simple, yet suitable random-pattern antigenic determinant problem.

Section I introduces the objectives of the experimentation and a summary of the expected outcomes (hypotheses) of the experimentation. Section II considers the methodology of the experimentation, summarising the algorithm, the problem, and the specific algorithm-configuration and problem instance pairs to be considered, as well as the measures that will be used to assess the expectations of the systems. Section III provides a summary of the results and section IV provides some analysis of the results as they pertain to the expected behaviour. Finally, the work is concluded in considering the outcomes in the context of the objectives of the work in section V, and some extensions are considered in section VI.

A. *Aim*

The objective of this work is to verify some principle expectations of the minimal clonal selection algorithm with regard to its realisation of the winner-take-all (WTA) principle. The verification of the results in this work will provide a basis for comparison for the series of extensions proposed to the minimal algorithm in the elaborated clonal selection algorithm [5].

***Objective**: The objective of this work is to verify some fundamental expectations of the minimal clonal selection algorithm with regard to its realisation of the winner take all principle*

The objective will be achieved through empirical experimentation on an indicative and suitable problem domain that matches the antigenic-determinant pattern of the hierarchical framework.

B. *Expectations*

Two principle expectations of the minimal algorithm were proposed in the previous work [5]. The first is that the system will rapidly stabilise, converging on cells that sufficiently acquire the information the system is exposed to by the environment. The second is that specific cells will dominant the selection and adaptive response of the system.

***Expectation-1**: Given sufficient resources, the convergence behaviour of the system is relatively impervious to variations in the number of antigenic determinants that must be learned concurrently*

***Expectation-2**: Given sufficient or an overestimation of resources, the number of cells used by the system will be approximately equal to the number of different determinates to which the system is exposed*

In verifying both of the proposed expectations, various configurations of the system will be exposed to various instances of an antigenic determinant domain. The adaptive behaviour of the system (ability to acquire information) will be evaluated and compared to a theoretical expectation. The second expectation will be verified by evaluating the resources allocated by the system during the adaptive process.

***Factor-1**: The system is impervious to the number of determinants because the algorithm (with the WTA principle) is (in effect) a parallel hill-climber.*

Both of the proposed expectations are suggested to be caused by the winner-take-all principle. The convergence behaviour is expected to be relatively impervious to the number of determinant it must learn (assuming an overestimation of resources) because the system is expected to perform a parallel-hill climbing operation. The clonal dominance effect (dominant adaptive cells) is expected to occur because the WTA selection-adaptive strategy will cause each determinant to select and adapt the same respective cells on each exposure, which is also an artefact of the parallel hill-climbing behaviour.

The algorithm employs the winner-take-all principle, the principle results in clonal dominance, and dominance results in rapid and consistent convergence

The important assumption for the proposed expectations is that the allocated adaptive resources (units of selection, cells) are equal or overestimated regarding the number of different determinants in the environment. This is a reasonable assumption, as not only are the patterns themselves withheld from the system (interaction is indirect via a mapping function), but the extent of the environment that the system is exposed to is also unknown. Thus, the clonal selection principle overestimates the required resources. Overestimation has an important implication (that will subsequently provide the basis for the elaborations): *clonal dominance in the minimal clonal selection algorithm results in the underutilisation of allocated resources*. Thus, the minimal clonal selection algorithm represents a departure from the clonal selection principles with this regard. An effective utilisation of resources by the clonal selection principles includes at least (1) redundancy of acquired information, (2) multiple varied perspectives of acquired information. These two limitations of the minimal clonal selection will be verified through the verification of the singular clonal dominance effect of the algorithm.

II. METHOD

This section is concerned with the methodology used to address the objectives and verify the expectations of this work. The minimal clonal selection algorithm is described, highlighting system parameters and default configuration values. The general random antigenic determinant domain is defined, highlighting its suitability for investigations at the cellular level of the hierarchical framework. Finally, the experimental scenarios are described as consisting of algorithm configurations, problem instance configurations, and specific system measurements.

A. *Minimal Clonal Selection Algorithm*

The *minimal clonal selection algorithm* (MCSA) is a parallel realisation of the ES(1+1) algorithm [3,11] (mutation hill climber, see [8] for a summary), where each adaptive unit (cell) in the population is independent. Thus, there is no interaction between adaptive units, other than competition for selection by antigenic determinants and resultant adaptation. Further, the selective-adaptive properties of the algorithm resemble and embody the winner-take-all principles of competitive learning, specifically because of the multiple-pattern (multiple landscapes) characteristic of the learning (see [6] for a summary).

Step1: *Initialise* the repertoire with a set of randomly generated bit strings
Step2: *Expose* the system to an randomly selected antigen
Step3: *Select* the highest affinity bit string from the evaluated repertoire
Step4: *Clone* the best matching cell with genetic copying errors
Step5: *Replace* the best matching cell with the clone if >= antigen match
Step6: *Repeat* steps 2-5 until a stopping condition is triggered

Figure 1 - Minimal Clonal Selection Algorithm Listing

In the original proposal of the algorithm, Step5 always accepted the single clone, irrespective of the affinity of the clone with respect to the triggering antigen. In this implementation of the algorithm, Step5 of the algorithm is adjusted such that a clone is only accepted if it has equal or improved affinity for the triggering antigen. This change was made for two reasons: (1) the motivating biological system is proposed to release (accept) high-affinity B-cell clones from the germinal centre, and (2) the 'accept if-equal-or-better' principle is employed in the ES(1+1) mutation hill climber, which provides benefits for theoretical comparison (used later in this work).

Parameter Name	Summary	Default and Constraints
String Length (L)	The fixed number of bits in each bitstring in the population	Defined by the problem domain $L \in [1,\infty)$
Repertoire Size (S)	The total number of bitstrings in the population	PN, where P is a multiplication factor (default to a small number: 1), and N is the number (or estimate) of different antigenic patterns (defined by the domain) $S \in [1,\infty], P \in [1,\infty)$
Mutation Rate (M)	The independent probability of a given bit position being mutated	$\frac{1}{L}, M \in [0,1]$

Table 1 - Minimal Clonal Selection Algorithm Parameters

A final note regarding the implementation of the algorithm is that of the unit of information considered as the results for a given exposure. A naïve implementation of the algorithm considers whatever is selected by the exposure event as the response. The mutation hill climber algorithm, which this algorithm is derived, evaluates the mutated information before deciding whether to store or discard it. At the end of the time of exposure (before the next exposure), the systems response is the best possible information it has available. Thus, the minimal clonal selection algorithm returns the mutated clone as the response if it is better than the triggered cell, otherwise it returns the triggered cell as

the response.

B. ***Random Antigenic Determinant Problem***

Algorithms of the cellular level (multiple cells within a tissue) are concerned with the information processing of multiple determinants (for example see [7]). Thus, an antigenic determinant based problem domain is used to evaluate the algorithm. In this domain, a given system configuration is successively exposed to a set of bitstring patterns that are drawn randomly from a possibility space before the beginning of a run. Thus, the problem domain is called the *random antigenic determinant problem* (RADP). Patterns are selected randomly, although without duplication, such that each pattern in the antigenic set is distinct. Thus, a given pattern in the antigenic set must be a minimum distance (*D*) from all other patterns in the set, with the default being a one-bit difference to ensure the distinctness requirement (*D=1*). A Hamming distance mapping function is used to indirectly provide information about an antigenic pattern to an exposed system. The affinity assigned to the matched adaptive units (cell) in the system is a Hamming distance from the exposed pattern. In a simple one-pattern, one-cell scenario, the problem represents a simple linear optimisation problem.

$$\sum_{i=1}^{L} X_i \oplus Y_i \ , \ X,Y \in \{0,1\}^L$$

Equation 1 - Hamming Distance, where X is a cell and Y is a determinant

From a problem perspective, one may be interested in the amount of time (exposures) it takes for a given system to acquire a given antigen or antigenic set, as well as the systems behaviour with regard to the quality of the information acquired over time.

Parameter Name	Summary	Default and Constraints
String Length (L)	The length of bitstrings in the domain	32, thus there are 2^L (4,294,967,296) possible patterns
Antigen Patterns (N)	The number of antigenic patterns selected at random and exposed to the system	Defined by the specific problem (experiment) instance $N \in [1,2^L]$
Minimum Distance (D)	The minimum Hamming distance between all patterns in the antigenic set	Defaults to 1 (no duplicates) $D \in [1, L]$

Table 2 - Parameters for the Random Antigenic Determinant Problem

C. ***Experiments***

This section defines the specific algorithm configuration, problem instance configurations, and measures collected which collectively define a series of experiments. The premise of these experiments is to evaluate the time-until-convergence and resource-utilisation of various overestimations of required resources in the minimal clonal selection algorithm on a small set of different random antigenic determinant problem instances.

Premise*: Observe the effect of the overestimation of resources in the minimum clonal selection algorithm in the random antigenic determinant problem domain*

The experiments employ three different instances of the problem domain, the first (RADP-0) is indicative of the previous layer in the hierarchical framework (1-cell and 1-determinant), provided as the basis for comparison. The remaining instances (RADP-1 and RADP-2) provide relatively small antigenic sets (*N*). The motivation for the selected problem instances is to investigate whether the expected algorithm effects hold over varied antigenic set sizes.

Problem Instances*: Expect the general algorithm effects to hold over some different problem configurations*

Instance	Configuration Summary
RADP-0	One-Determinant (L=32, N=1, D=8)
RADP-1	Small (*L=32, N=10, D=8*)
RADP-2	Medium (*L=32, N=100, D=8*)

Table 3 - Summary of experimental problem configurations

The experiments employ four different configurations of the minimal clonal selection algorithm, the first of which (MCSA-0) provides a complement configuration for (RADP-0). The remaining algorithm configurations provide a variety of antigenic-set overestimation sizes (*P*) which ultimately vary the cell-repertoire size of the algorithm (*S*). The motivation for the variation in repertoire size is to investigate whether the expected algorithm effects hold for various degrees of over estimation.

Algorithm Configurations*: Expect the general algorithm effects to hold over some different degrees of overestimation*

Configuration	Summary
MCSA-0	Accurate (*L=32, S=PN, P=1, M=0.03125*)
MCSA-1	Overestimate 1 (*L=32, S=PN, P=2, M=0.03125*)
MCSA-2	Overestimate 2 (*L=32, S=PN, P=5, M=0.03125*)
MCSA-3	Overestimate 3 (*L=32, S=PN, P=10, M=0.03125*)

Table 4 - Summary of experimental algorithm configurations

The stop condition used for the algorithm is the number of exposures to the antigenic set (epochs). An upper-limit on the number of epochs is set such that it is expected that the system is able to acquire the information from the domain before the stop condition is triggered. Given that the algorithm is proposed to be a parallel variation of the ES(1+1) algorithm, and that the Hamming-distance based objective function provides a linear optimisation problem, the theoretical expected time until algorithm convergence (for 1-cell, 1-determinant) is defined by $O(L\ lnL)$ [3,10] (~111 epochs). Thus, a maximum epochs is configured to be ten times as large for all experimental runs (1111). Another important experimental configuration is the number of repeats of a given experiment (algorithm-problem combination). The results of a set of experimental runs are then summarised (such as the central tendency), and compared to other experimental runs. It is important to highlight that for each experimental run, the results will be different. For a given experimental run different randomly drawn set of antigenic patterns will be drawn and exposed to the system, and the system itself will be initialised with a different random set of adaptive units (cells).

Parameter Name	Summary	Default and Constraints
Maximum Epochs (E)	The maximum number of exposures to a given system of the antigenic set	Theoretical=O(L lnL), given L=32, a factor-ten of the theoretical expectation is used as the default $E \in [1, \infty]$
Total Repeats (R)	The total number of experimental runs for a given algorithm configuration	Theoretically R>=30 according to central limit theorem, use 100 as a default $R \in [30, \infty]$

Table 5 - Summary of the experimental configuration parameters

The following table lists the combinations of algorithm configurations and problem instances that make up the set of four experiments.

Experiment	Summary
E0	MSCA-0 to MSCA-3 on RADP-0, E=1111, R=100
E1	MSCA-0 to MSCA-3 on RADP-1, E=1111, R=100
E2	MSCA-0 to MSCA-3 on RADP-2, E=1111, R=100

Table 6 - Summary of experiment configurations

A final important aspect of the experimental regime is the measurements collected during the experimental runs. As highlighted, from a problem perspective, the system should acquire the environmental information quickly (efficiency) and accurately (efficacy). The theoretical expectation suggests an average case for the system, which will be tested in the generalised case (parallel, independent version of the ES(1+1)). From a system perspective, the experiments are also concerned with the timely acquisition of the information in the environment (efficiency/efficacy), and with the systems utilisation of resources, especially overestimated resources.

***Measurements**: Interested in measuring the systems performance on the problem instance with regard to efficacy and efficiency, as well as the resource utilisation*

Measurement	Summary
Evaluations (efficiency) (EVA)	Total number of epochs (complete environment exposures), where a single epoch consists of a system being exposed to all antigenic patterns once, measured up until the stop condition (*algorithm stop condition: EVA=1000*)
OfflineError (efficacy) (OFF)	The average of the Hamming distance between each antigenic pattern in the set with the best matching unit in the system, after the stop condition (*ideally: OFF=0*)
OnlineError (efficiency) (ONL)	The epoch number when the system first (during a single run) perfectly acquires all of the antigenic patterns (first epoch when ONL=0)
CellLines (utility) (UTL)	The total number of different cell lines used (winners) over all epochs, until the stop condition is triggered. (*efficient usage: UTL=N*)

Table 7 - Summary of the measurements taken for each experimental run

Thus, considering the system measures in the context of the experimental scenarios, the expectations of the system may be rephrased.

#	Summary	Reduced
1	The number of best-matching-cells (winners) in the final population should equal the number of patterns in the antigenic set	WTA distinct cells over an epoch = N, UTL~N
2	Alternatively, the number of unused cells in the final population should be equal to the size of the population minus the number of antigenic patterns	Unused ~ (S-N)
3	The number of epochs for the system to acquire the information from the domain should be approximately equal to the theoretical expectation	ONL~111 epochs

Table 8 - Summary of experimental expectations in the context of the experimental scenarios

III. RESULTS

This section provides summaries of results, including the central tendency and variation from the central tendency for each experiment (set of *R* experimental runs). Results are presented as offline error concerning whether the information was acquired, online error concerning the stability expectation, and cell lines concerning the resource utilisation expectation.

A. *Offline Error*

The offline error provides an indication of whether the system was able to acquire the information to which it was exposed. The offline error (OFF) is presented as the average error, taken over a single epoch (all patterns in a single run) against the system. The unit of measure for the error is the number of mismatching bits (Hamming distance).

Problem (N)	Algorithm (S)	OFF Mean	OFF Stdev
RADP-0	*MCSA-0*	0.00	0.00
	MCSA-1	0.00	0.00
	MCSA-2	0.00	0.00
	MCSA-3	0.00	0.00
RADP-1	*MCSA-0*	2.64	0.94
	MCSA-1	1.00	0.76
	MCSA-2	0.24	0.40
	MCSA-3	0.31	0.31
RADP-2	*MCSA-0*	2.22	0.22
	MCSA-1	0.82	0.21
	MCSA-2	0.14	0.10
	MCSA-3	0.16	0.16

Table 9 - Summary of offline error (OFF) results

B. *Online Error*

The online error provides an indication of how quickly a given system is capable of acquiring the information it is exposed to in the domain. The results are presented as a summary of the number of runs where the domain was acquired. The unit of measure for the online error (ONL) is the number of epochs.

Problem (N)	Algorithm (S)	Found (n/100)	ONL Mean	ONL Stdev
RADP-0	*MCSA-0*	100	256.93	109.20
	MCSA-1	100	251.22	97.49
	MCSA-2	100	221.98	87.18
	MCSA-3	100	225.89	98.57
RADP-1	*MCSA-0*	0	-	-
	MCSA-1	22	489.77	166.14
	MCSA-2	71	458.48	177.08
	MCSA-3	68	472.12	0.63
RADP-2	*MCSA-0*	0	-	-
	MCSA-1	0	-	-
	MCSA-2	17	817.94	202.99
	MCSA-3	15	779.27	1.68

Table 10 - Summary of online error (ONL) results

C. ***Cell Lines***

The cell lines provides an indication of the internal utilisation of resources of a system over the course of its run. The unit of measure for cell lines (UTL) is the number of different units of adaptation (cells) selected and adapted over the course of a run.

Problem (N)	Algorithm (S)	UTL Mean	UTL Stdev
RADP-0	*MCSA-0*	1	0
	MCSA-1	1	0
	MCSA-2	1	0
	MCSA-3	1	0
RADP-1	*MCSA-0*	7.87	0.80
	MCSA-1	9.39	0.80
	MCSA-2	9.89	0.57
	MCSA-3	9.85	0.63
RADP-2	*MCSA-0*	80.77	2.42
	MCSA-1	95.95	2.36
	MCSA-2	101.27	1.72
	MCSA-3	101.03	1.68

Table 11 - Summary of cell lines (UTL) results

IV. ANALYSIS

This section is concerned with the analysis and interpretation of the results of the previous section in the context of the expectations of the algorithm. Specifically, results are considered in the context of the systems expected convergence behaviour, and the systems expected resources utilisation behaviour.

A. ***Concerning Convergence***

The expectation is that if the system is allocated sufficient results for a problem domain ($S>=N$), then the convergence behaviour of the system should be generally impervious to the number of patterns in the domain, and the amount of overestimation ($S>N$). Further, given the proposed system represents a parallel variation on the ES(1+1) algorithm, the system should stabilise, and potentially acquire all the information from the domain in approximately the order of O(L nlL) (about ONL ~111 epochs for the 32-bit strings).

1) Regarding offline error, the system acquired the majority of the information from the domain by the end of the allotted epochs. The error (average mismatching bits for an epoch) was slightly higher when S=N, than when S>N. For all N=1, the system always acquired the pattern irrespective of S.
2) Regarding online error, the system acquired the single pattern (N=1) consistently at about 240 epochs on average, although with a wide variance of about 100 epochs. Thus, for this domain, the system is about 100 epochs above the theoretical expectation, based on the approximately optimal mutation rate.
3) Although the final result (offline error) was good across the board, the system configurations found it difficult to acquire the domain within in the allotted epochs (ONL<E). The system acquired the domain more often with the smaller antigenic set (N=10) than the larger antigenic set (N=100). For both of these cases, when the system did acquire the domain, it did so in a consistent way, irrespective of allocated resources.

The consistency of the convergence behaviour both in the offline and in the online result (when acquired) demonstrate that that as long as sufficient resources are allocated (S>=N), the system will acquire the information relatively impervious to the increases in overestimation (S-N) for each domain instance (N). What the experiments demonstrated is that although the system is relatively impervious to changes in S for a given N, it is effected by changes in N, even when N is overestimated by factors of P=(2, 5 and 10). Finally, the results demonstrate that the theoretical expectation for the algorithm on a single pattern is achievable, although it is not the central tendency.

If the online error is taken as an approximate time until stabilisation, and given its consistency for each domain (N), why is there an approximately linear increase in the number of epochs with factors of ten increases in N for over-estimated (S>N) systems? This future study firstly requires verification of the assumptions (1) the effective identification of system stabilisation for different N's of factors of ten and (2) the demonstration that it is overestimation impervious. It is speculated that the decrease in performance (increase in epochs) is related to (1) the closeness of patterns in the antigenic set (D), and (2) the use (dominance) of single resources (at least initially in the run) by multiple 'close distance' antigenic patterns. This dominance-based hypothesis may be tested by evaluating a variation of the algorithm in which there is no competition between cells for selection, rather a one-to-one relationship that removes the interaction, and its speculated effects (a set of N independent ES(1+1) algorithms).

B. ***Concerning Resource Utilisation***

The expectation of the system if allocated sufficient resources for the problem domain (S>=N), then the resources utilised by the system should approximately equal the number of patterns the system is exposed to (UTL~N). Thus, the amount of system allocated resources (cell) not contributing to the solution should be in the order of S-N.

1) Regarding the one-pattern domain (N=1), the system utilised a single cell as expected, a behaviour that is impervious to the overestimation (S-N) of resources S=(2, 5, 10)
2) In those problem instances with N>1 and a system configured with sufficient resources (S=N), the system utilised approximately 80% of those resources with a low variance. This is different from the expected one-to-one mapping that was expected to emerge.
3) For those remaining algorithm configuration that overestimate (S>N) for problem instances with more than one pattern N>1, the system consistently (for different overestimations and different problem instances) conformed to the UTL=N expectation with a low variance. Although, this relationship is closer when the overestimation is more than a factor of two P>2 (S=5, 10).

As expected, the system did not use more resources than the number of patterns, although not a direct one-to-one relationship (as demonstrated in S=N), the system

approximated (with regard to resource utilisation) a parallel N independent ES(1+1), the approximation of which improved with the factor of overestimation of N. Further, the improved utilisation by the larger P's correlated with slightly improved online and offline error (less error). If the system is approximating a set of N-independent ES(1+1) (one for each pattern N), then why does the system underutilise resources (UTL<N) when allocated with N (S=N) resources?

It is speculated that the above interaction/dominance hypotheses forces the system to generalise input patterns (one resource generalizing the information of multiple patterns), via dominance in the run away winner-take-all competition. This hypotheses presumes that WTA results in a run-away dominance effect (winners keep winning) which holds from early in a run. Thus, this may be investigated by considering the generalisation of resource utilisation of an ideal and underestimated system (S=N and S<N). Further, the dominance effect should also occur in the overestimated case (S>N), although, without generalisation.

V. Conclusion

The minimal clonal selection algorithm uses the winner-take-all principle and a population of adaptive units that may or may not be equal to the number of patterns to approximate a parallel-independent mutation hill climber. The resource utilisation when the number of determents is overestimated is equal to the number of determinants (for practical purposes), although the system is sensitive to the number of patterns in the environment (relatively) irrespective of the factor of estimation. The relationship between the epochs needed to acquire a domain (close to ideally) appears to increase linearly with the number of determinants in the environment. This deviation from the expected behaviour, which is quite pronounced with the factor-ten increase in the number of determinants tested, is speculated to be caused by the interaction between competing cells in the winner-take-all selection-adaptation process. This speculation may be supported by the underutilisation of resources when the system is allocated the same amount of resources as there are determinants in the domain. The results from this scenario suggests that intra-repertoire competition for selection results in a generalisation effect (one cell for multiple patterns), which correlates with a slight decrease in performance.

***Principle**: The more determinant patterns, the more WTA-based competition interaction between cells*

The result, is that overestimation may relax this competition, although the system requires a linear increase in the number of epochs (exposure to all information in the domain) to acquire the domain information with the increase in the information to be acquired, which is relatively impervious to the overestimation of resources.

VI. Extensions

The most important extension is the confirmation that interactions that result from the winner-take-all principles cause the increased number of epochs (exposures to the entire domain) the system needs to acquire the information from the environment, and that the interaction effect scales linearly with the increase in determinants. The overestimation expectations of the system hold, the WTA system uses the bare minimum resources to address exposures, thus paving the way for extensions that attempt to consider a given determinant from multiple perspectives exploiting the underutilised resources (elaborations to the algorithm [5]). An area not taken into account by the elaborations of the algorithm is that of under-estimation of resources and generalisation. The clonal selection algorithm is recognised to facilitate generalisation in the cross-reactive response, although this concept applies to higher-order structures (same or similar determinant on multiple pathogen). The MCSA is expected to facilitate this type of generalisation, although it is considered not appropriate for the selected problem domain, in fact it is considered an undesirable behaviour at this low-level (results in errors).

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