

Artificial Immune Recognition System*

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Abstract

The Clever Algorithms project aims to describe a large number of Artificial Intelligence algorithms in a complete, consistent, and centralized manner, to improve their general accessibility. The project makes use of a standardized algorithm description template that uses well-defined topics that motivate the collection of specific and useful information about each algorithm described. This report describes the Artificial Immune Recognition System using the standardized algorithm description template.

Keywords: Clever, Algorithms, Description, Optimization, Artificial, Immune, Recognition, System

1 Introduction

The Clever Algorithms project aims to describe a large number of algorithms from the fields of Computational Intelligence, Biologically Inspired Computation, and Metaheuristics in a complete, consistent and centralized manner [3]. The project requires all algorithms to be described using a standardized template that includes a fixed number of sections, each of which is motivated by the presentation of specific information about the technique [4]. This report describes the Artificial Immune Recognition System using the standardized algorithm description template.

2 Name

Artificial Immune Recognition System, AIRS

3 Taxonomy

The Artificial Immune Recognition System belongs to the field of Artificial Immune Systems, and more broadly to the field of Computational Intelligence. It is was extended early to the canonical version called the Artificial Immune Recognition System 2 (AIRS2) and provides the basis for extensions such as the Parallel Artificial Immune Recognition System [12]. It is related to other Artificial Immune System algorithms such as the Dendritic Cell Algorithm, the Clonal Selection Algorithm, and the Negative Selection Algorithm.

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4 Inspiration

The Artificial Immune Recognition System is inspired by the Clonal Selection theory of acquired immunity. The clonal selection theory credited to Burnet was proposed to account for the behavior and capabilities of antibodies in the acquired immune system [5, 6]. Inspired itself by the principles of Darwinian natural selection theory of evolution, the theory proposes that antigens select-for lymphocytes (both B and T-cells). When a lymphocyte is selected and binds to an antigenic determinant, the cell proliferates making many thousands more copies of itself and differentiates into different cell types (plasma and memory cells). Plasma cells have a short lifespan and produce vast quantities of antibody molecules, whereas memory cells live for an extended period in the host anticipating future recognition of the same determinant. The important feature of the theory is that when a cell is selected and proliferates, it is subjected to small copying errors (changes to the genome called somatic hypermutation) that change the shape of the expressed receptors. It also affects the subsequent determinant recognition capabilities of both the antibodies bound to the lymphocytes cells surface, and the antibodies that plasma cells produce.

5 Metaphor

The theory suggests that starting with an initial repertoire of general immune cells, the system is able to change itself (the compositions and densities of cells and their receptors) in response to experience with the environment. Through a blind process of selection and accumulated variation on the large scale of many billions of cells, the acquired immune system is capable of acquiring the necessary information to protect the host organism from the specific pathogenic dangers of the environment. It also suggests that the system must anticipate (guess) at the pathogen to which it will be exposed, and requires exposure to pathogen that may harm the host before it can acquire the necessary information to provide a defense.

6 Strategy

The information processing objective of the technique is to prepare a set of real-valued vectors to classify patterns. The Artificial Immune Recognition System maintains a pool of memory cells that are prepared by exposing the system to a single iteration of the training data. Candidate memory cells are prepared when the memory cells are insufficiently stimulated for a given input pattern. A process of cloning and mutation of cells occurs for the most stimulated memory cell. The clones compete with each other for entry into the memory pool based on stimulation and on the amount of resources each cell is using. This concept of resources comes from prior work on Artificial Immune Networks, where a single cell (an Artificial Recognition Ball or ARB) represents a set of similar cells. Here, a cell's resources are a function of its stimulation to a given input pattern and the number of clones it may create.

7 Procedure

Algorithm 1 provides a high-level pseudo-code for preparing memory cell vectors using the Artificial Immune Recognition System, specifically the canonical AIRS2. An affinity (distance) measure between input patterns must be defined. For real-valued vectors, this is commonly the Euclidean distance:

$$dist(x, c) = \sum_{i=1}^n (x_i - c_i)^2 \quad (1)$$

where n is the number of attributes, x is the input vector and c is a given cell vector. The variation of cells during cloning (somatic hypermutation) occurs inversely proportional to the stimulation of a given cell to an input pattern.

Algorithm 1: Pseudo Code for training the Artificial Immune Recognition System (AIRS2).

Input: InputPatterns, $clone_{rate}$, $mutate_{rate}$, $stim_{thresh}$, $resources_{max}$, $affinity_{thresh}$
Output: $Cells_{memory}$

```

1  $Cells_{memory} \leftarrow \text{InitializeMemoryPool}(\text{InputPatterns});$ 
2 foreach  $\text{InputPattern}_i \in \text{InputPatterns}$  do
3    $\text{Stimulate}(Cells_{memory}, \text{InputPatterns});$ 
4    $Cell_{best} \leftarrow \text{GetMostStimulated}(\text{InputPattern}_i, Cells_{memory});$ 
5   if  $Cell_{best}^{class} \neq \text{InputPattern}_i^{class}$  then
6      $Cells_{memory} \leftarrow \text{CreateNewMemoryCell}(\text{InputPattern}_i);$ 
7   else
8      $Clones_{num} \leftarrow Cell_{best}^{stim} \times clone_{rate} \times mutate_{rate};$ 
9      $Cells_{clones} \leftarrow Cell_{best};$ 
10    for  $i$  to  $Clones_{num}$  do
11       $Cells_{clones} \leftarrow \text{CloneAndMutate}(Cell_{best});$ 
12    end
13    while  $\text{AverageStimulation}(Cells_{clones}) \leq stim_{thresh}$  do
14      foreach  $Cell_i \in Cells_{clones}$  do
15         $Cells_{clones} \leftarrow \text{CloneAndMutate}(Cell_i);$ 
16      end
17       $\text{Stimulate}(Cells_{clones}, \text{InputPatterns});$ 
18       $\text{ReducePoolToMaximumResources}(Cells_{clones}, resources_{max});$ 
19    end
20     $Cell_c \leftarrow \text{GetMostStimulated}(\text{InputPattern}_i, Cells_{clones});$ 
21    if  $Cell_c^{stim} > Cell_{best}^{stim}$  then
22       $Cells_{memory} \leftarrow Cell_c;$ 
23      if  $\text{Affinity}(Cell_c, Cell_{best}) \leq affinity_{thresh}$  then
24         $\text{DeleteCell}(Cell_{best}, Cells_{memory});$ 
25      end
26    end
27  end
28 end
29 return  $Cells_{memory};$ 

```

8 Heuristics

- The AIRS was designed as a supervised algorithm for classification problem domains.
- The AIRS is non-parametric, meaning that it does not rely on assumptions about that structure of the function that is approximating.
- Real-values in input vectors should be normalized such that $x \in [0, 1)$.
- Euclidean distance is commonly used to measure the distance between real-valued vectors (affinity calculation), although other distance measures may be used (such as dot product), and data specific distance measures may be required for non-scalar attributes.

- Cells may be initialized with small random values or more commonly with values from instances in the training set.
- A cell's affinity is typically minimizing, where as a cells stimulation is maximizing and typically $\in [0, 1]$.

9 Code Listing

Listing 1 provides an example of the Artificial Immune Recognition System implemented in the Ruby Programming Language. The problem is a contrived classification problem in a 2-dimensional domain $x \in [0, 1], y \in [0, 1]$ with two classes: 'A' ($x \in [0, 0.4999999], y \in [0, 0.4999999]$) and 'B' ($x \in [0.5, 1], y \in [0.5, 1]$).

The algorithm is an implementation of the AIRS2 algorithm [11]. An initial pool of memory cells is created, one cell for each class. Euclidean distance divided by the maximum possible distance in the domain is taken as the affinity and stimulation is taken as $1.0 - affinity$. The meta-dynamics for memory cells (competition for input patterns) is not performed and may be added into the implementation as an extension.

```

1 def random_vector(minmax)
2   return Array.new(minmax.length) do |i|
3     minmax[i][0] + ((minmax[i][1] - minmax[i][0]) * rand())
4   end
5 end
6
7 def generate_random_pattern(domain)
8   class_label = domain.keys[rand(domain.keys.length)]
9   pattern = {:class_label=>class_label}
10  pattern[:vector] = random_vector(domain[class_label])
11  return pattern
12 end
13
14 def create_cell(vector, class_label)
15   return {:class_label=>class_label, :vector=>vector}
16 end
17
18 def initialize_cells(domain)
19   memory_cells = []
20   domain.keys.each do |key|
21     memory_cells << create_cell(random_vector([0,1],[0,1]), key)
22   end
23   return memory_cells
24 end
25
26 def euclidean_distance(v1, v2)
27   sum = 0.0
28   v1.each_with_index do |v, i|
29     sum += (v1[i]-v2[i])**2.0
30   end
31   return Math.sqrt(sum)
32 end
33
34 def stimulate(cells, pattern)
35   max_affinity = euclidean_distance([0.0,0.0], [1.0,1.0])
36   cells.each do |cell|
37     cell[:affinity] = euclidean_distance(cell[:vector], pattern[:vector]) / max_affinity
38     cell[:stimulation] = 1.0 - cell[:affinity]
39   end
40 end
41
42 def get_most_stimulated_cell(memory_cells, pattern)

```

```

43   stimulate(memory_cells, pattern)
44   return memory_cells.sort{|x,y| y[:stimulation] <=> x[:stimulation]}.first
45 end
46
47 def mutate_cell(cell, best_match)
48   range = 1.0 - best_match[:stimulation]
49   cell[:vector].each_with_index do |v,i|
50     min = [(v-(range/2.0)), 0.0].min
51     max = [(v+(range/2.0)), 1.0].max
52     cell[:vector][i] = min + (rand() * (max-min))
53   end
54   return cell
55 end
56
57 def create_arb_pool(pattern, best_match, clone_rate, mutate_rate)
58   pool = []
59   pool << create_cell(best_match[:vector], best_match[:class_label])
60   num_clones = (best_match[:stimulation] * clone_rate * mutate_rate).round
61   num_clones.times do
62     cell = create_cell(best_match[:vector], best_match[:class_label])
63     mutate_cell(cell, best_match)
64     pool << cell
65   end
66   return pool
67 end
68
69 def competition_for_resources(pool, clone_rate, max_resources)
70   pool.each {|cell| cell[:resources] = cell[:stimulation] * clone_rate}
71   pool.sort!{|x,y| x[:resources] <=> y[:resources]}
72   total_resources = pool.inject(0.0){|sum,cell| sum + cell[:resources]}
73   while total_resources > max_resources
74     cell = pool.delete_at(pool.length-1)
75     total_resources -= cell[:resources]
76   end
77 end
78
79 def refine_arb_pool(pool, pattern, stim_thresh, clone_rate, max_resources)
80   mean_stim, candidate = 0.0, nil
81   begin
82     stimulate(pool, pattern)
83     candidate = pool.sort{|x,y| y[:stimulation] <=> x[:stimulation]}.first
84     mean_stim = pool.inject(0.0){|sum,cell| sum + cell[:stimulation]} / pool.size.to_f
85     if mean_stim < stim_thresh
86       candidate = competition_for_resources(pool, clone_rate, max_resources)
87       pool.size.times do |i|
88         cell = create_cell(pool[i][:vector], pool[i][:class_label])
89         mutate_cell(cell, pool[i])
90         pool << cell
91       end
92     end
93   end until mean_stim >= stim_thresh
94   return candidate
95 end
96
97 def add_candidate_to_memory_pool(candidate, best_match, memory_cells)
98   if candidate[:stimulation] > best_match[:stimulation]
99     memory_cells << candidate
100   end
101 end
102
103 def train_system(memory_cells, domain, num_patterns, clone_rate, mutate_rate, stim_thresh,
104   max_resources)
105   num_patterns.times do |i|

```

```

105     pattern = generate_random_pattern(domain)
106     best_match = get_most_stimulated_cell(memory_cells, pattern)
107     if best_match[:class_label] != pattern[:class_label]
108         memory_cells << create_cell(pattern[:vector], pattern[:class_label])
109     elsif best_match[:stimulation] < 1.0
110         pool = create_arb_pool(pattern, best_match, clone_rate, mutate_rate)
111         candidate = refine_arb_pool(pool, pattern, stim_thresh, clone_rate, max_resources)
112         add_candidate_to_memory_pool(candidate, best_match, memory_cells)
113     end
114     puts " > iteration#{i+1} memory_cells=#{memory_cells.size}"
115 end
116 end
117
118 def classify_pattern(memory_cells, pattern)
119     stimulate(memory_cells, pattern)
120     return memory_cells.sort{|x,y| y[:stimulation] <=> x[:stimulation]}.first
121 end
122
123 def test_system(memory_cells, domain)
124     correct = 0
125     100.times do
126         pattern = generate_random_pattern(domain)
127         best = classify_pattern(memory_cells, pattern)
128         correct += 1 if best[:class_label] == pattern[:class_label]
129     end
130     puts "Finished test with a score of #{correct}/#{100} (#{correct}%)"
131 end
132
133 def run(domain, num_patterns, clone_rate, mutate_rate, stim_thresh, max_resources)
134     memory_cells = initialize_cells(domain)
135     train_system(memory_cells, domain, num_patterns, clone_rate, mutate_rate, stim_thresh,
136                 max_resources)
137     test_system(memory_cells, domain)
138 end
139
140 if __FILE__ == $0
141     domain = {"A"=>[[0,0.4999999],[0,0.4999999]], "B"=>[[0.5,1],[0.5,1]]}
142     num_patterns = 100
143     clone_rate = 10
144     mutate_rate = 2.0
145     stim_thresh = 0.9
146     max_resources = 150
147
148     run(domain, num_patterns, clone_rate, mutate_rate, stim_thresh, max_resources)
149 end

```

Listing 1: Artificial Immune Recognition System in the Ruby Programming Language

10 References

10.1 Primary Sources

The Artificial Immune Recognition System was proposed in the Masters work by Watkins [14], and later published [15]. Early works included the application the AIRS by Watkins and Boggess to a suite of benchmark classification problems [10], and a similar study by Goodman and Boggess comparing to a conceptually similar approach called Learning Vector Quantization [7].

10.2 Learn More

Marwah and Boggess investigated the algorithm seeking issues that affect the algorithms performance [9]. They compared various variations of the algorithm with modified resource allocation

schemes, tie-handling within the ARB pool, and ARB pool organization. Watkins and Timmis proposed a new version of the algorithm called AIRS2 which became the replacement for AIRS1 [11]. The updates reduced the complexity of the approach while maintaining the accuracy of the results. An investigation by Goodman, et al. into the so called ‘*source of power*’ in AIRS indicated that perhaps the memory cell maintenance procedures played an important role [8]. Watkins, et al. provide a detailed review of the technique and its application [13].

11 Conclusions

This report described the Artificial Immune Recognition System using the standardized algorithm description template. This report was based on prior work by the author investigating the algorithm [1, 2] and the implementation provided for the WEKA machine learning workbench <http://weka.classalgos.sourceforge.net/>.

12 Contribute

Found a typo in the content or a bug in the source code? Are you an expert in this technique and know some facts that could improve the algorithm description for all? Do you want to get that warm feeling from contributing to an open source project? Do you want to see your name as an acknowledgment in print?

Two pillars of this effort are i) that the best domain experts are people outside of the project, and ii) that this work is subjected to continuous improvement. Please help to make this work less wrong by emailing the author ‘Jason Brownlee’ at jasonb@CleverAlgorithms.com or visit the project website at <http://www.CleverAlgorithms.com>.

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