BSRCA: Biological Sequence Analysis Approach to Robotic Soccer with Cellular Automata Classifier

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ABSTRACT

This paper reports on the application of sequence analysis algorithms for agents in robotic soccer and a suitable representation is proposed to achieve this mapping. The objective of this research is to generate novel better in-game strategies with the aim of faster adaptation to the changing environment. A homogeneous non-communicating multi-agent architecture using the representation is presented. To achieve real-time learning during a game, a bucket brigade algorithm is used to reinforce Cellular Automata Based Classifier. A technique for selecting strategies based on sequence analysis is adopted.

Keywords
Multi-agent architecture, bucket brigade algorithm, reinforce learning, Cellular Automata Classifer.

1. INTRODUCTION

Although each domain presents a variety of approaches, from a research perspective the ideal domain embodies as many issues as possible. Robotic soccer is a particularly good domain for studying multi-agent systems. Originated by Alan Mackworth **[1]**, it has been gaining popularity in recent years with several international competitions taking place **[2]**. Even though robotic soccer is a game, most real-world complexities are maintained. Some of the distinguishing characteristics of the domain include: real-time, noisy with hidden state, collaborative and adversarial goals. It is the ideal test bed for evaluating different machine learning techniques in a direct manner, as it provides for multiple levels of evaluation such as evaluation of low-level behavior e.g. maneuvering on the field as well as evaluation of strategic responses to changing scenarios.

Several Multi-agent system scenarios are possible:

- Homogeneous, on-communicating
- Homogeneous, communicating
- Heterogeneous, on-communicating
- Heterogeneous, communicating

Each of which have their own set of challenging research issues. In homogeneous, non-communicating multi-agent systems, all of the agents have the same internal structure including goals, domain knowledge, and possible actions. They also have the same procedure for selecting among their actions. The only differences among agents are their sensory inputs and the actual actions they take: they are situated differently in the world.

A DNA fragment is usually written as a sequence of letters A, C, T and G – representing the four nucleotides Adenine, Cytosine, Thymine and Guanine. DNA is the master behind all the activities in the cell and is responsible for the synthesis of proteins. Proteins are complex macromolecules having a highly complex 3D structure, but even they are represented in the form of a single dimensional sequence comprising of 20 different letters, each representing an amino acid. Hence the problem of studying DNA and proteins has been reduced to the problem of sequence analysis.

In this paper, Section-2 gives an overview of related work. A representation scheme for robotic soccer is presented in Section-3. An architecture depicting a homogeneous non-communicating agent utilizing the above representation is proposed in Section-4. Section-5 discusses experimental results and Section-6 deals with future directions and concludes the paper.

2. RELATED WORK

Balch and Arkin **[6]** use homogeneous, reactive, non-communicating agents to study formation maintenance in autonomous robots. The robots' goal is to move together in a military formation such as a diamond, column, or wedge. They periodically come across obstacles which prevent one or more of the robots from moving in a straight line. After passing the obstacle, all robots must adjust in order to regain their formation. The actual robot motion is a simple weighted sum of these vectors.

Levy and Rosenschein **[7]** create agents that each act in service of its own goals. They use game theoretic techniques to find equilibrium points and thus to decide how to act. These agents are clearly deliberative, as they search for actions rather than simply retrieving them.

There are also several existing systems and techniques that mix reactive and deliberative behaviors. One example is the OASIS system which reasons about when to be reactive and when to follow goal-directed plans **[8]**. Another example is reactive deliberation **[9]**. As the name implies, it mixes reactive and deliberative behavior: an agent reasons about which reactive behavior to follow under the constraint that it must choose actions at a rate of 60 Hz. Reactive deliberations was developed on the first robotic soccer platform.

3. SEQUENTIAL REPRESENTATION OF ROBOTIC SOCCER

The game of robotic soccer involves a vast amount of data with respect to both player and ball movement. The movement of the ball during the course of a match is tracked to obtain a game sequence. Also, each individual's contribution to the game can be assessed by focusing on player movements during the game, yielding a player sequence. This is instrumental in characterizing a player's contribution to the success or failure of the game.

Table 1: Task Table

Action	Base
Turn towards ball	A
Move towards ball	C
Kick towards goal	G
Pass to team-mate	T

For example, we consider a game played over a period of 60 minutes and represent this game as a sequence of length 60, where each letter represents the player who is in possession of the ball at that minute. Game 1: bcgad-bccc-g-aab—bbaggd..

and the Player sequence for player 'a' would be represented as –

Player a: ACTTGC-AG--TTCCCA-....

where '-' denotes an idle action or that the ball is in motion. A history of games played can be collected and analyzed using the sequence analysis algorithms employed frequently in bio-informatics. Similarly, a number of player sequences is obtained for analysis. These sequences can then be used to formulate appropriate conditions for classifiers to enable correct responses to environmental inputs. Table 1 shows the tasks of different DNA bases.

3.1 Algorithm for Finding Tandem Repeats

The concept of finding tandem repeats has been employed here to trace subsequences or regions that frequently repeat in the game and whether such repetition is ideal for the game.

Table 2: Distinct patterns and their occurrence in each player sequence

PATTERN	NO. OF OCCURENCES	PLAYER
CACC	4	player-a
ACCC	3	player-b
ACCC	3	player-d
ACCC	5	player-c
CCCC	5	player-a
CCCCB	2	player-b
CCCAGCC	2	player-a
CC-G	3	player-d

It involves two subtasks

- Finding all possible unique subsequences of a specified length.
- Finding the location and number of tandem repeats.

The input to the first subtask is the starting and ending lengths of the pattern and the result is the creation of a list of unique patterns that range from the specified lower to the upper range. This list becomes the input to the second stage which checks the provided input sequence against these patterns for matches. Table 2 gives the different patterns and occurrences of players.

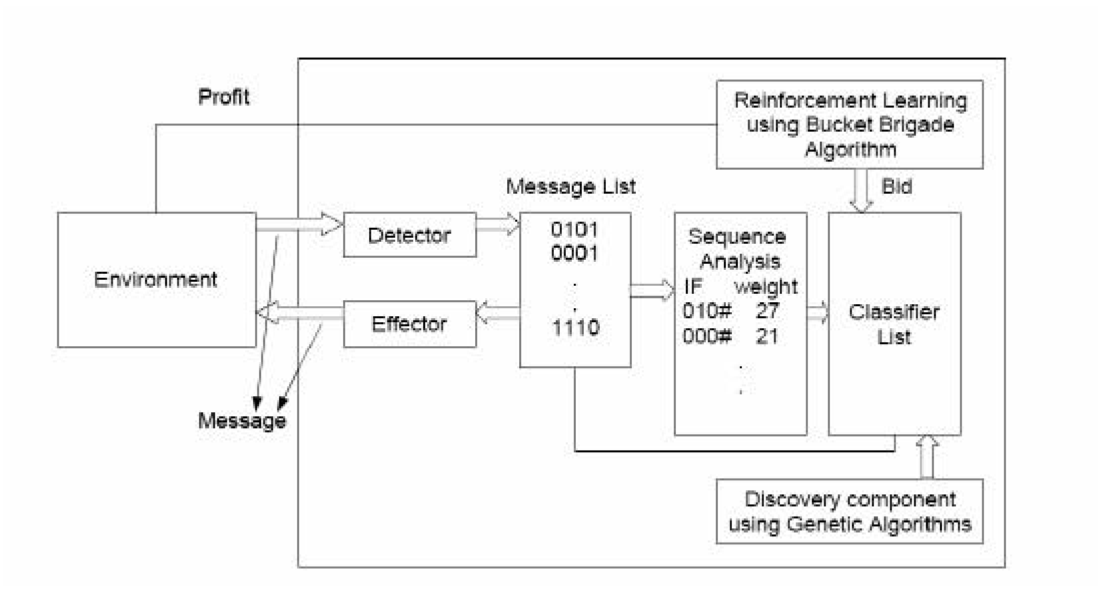


Fig. 1 : Sequence Driven Classifier System Architecture

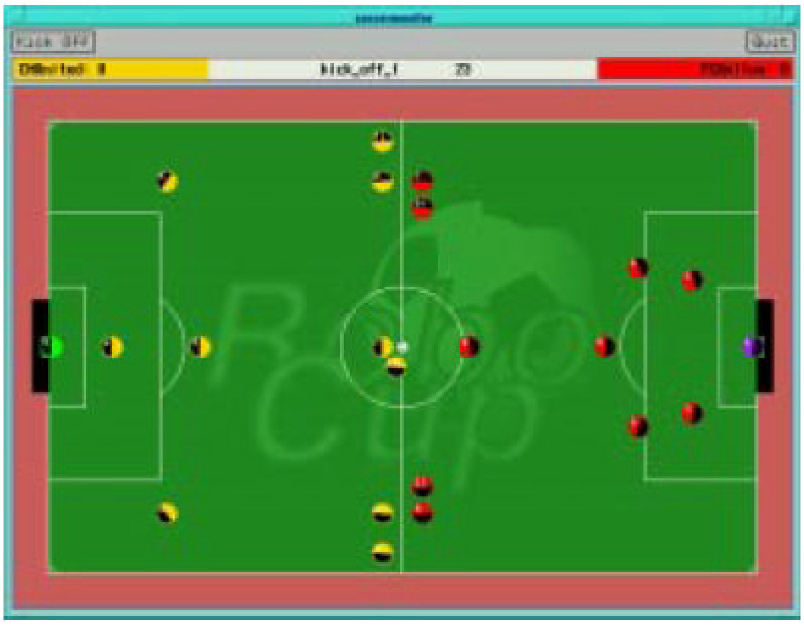
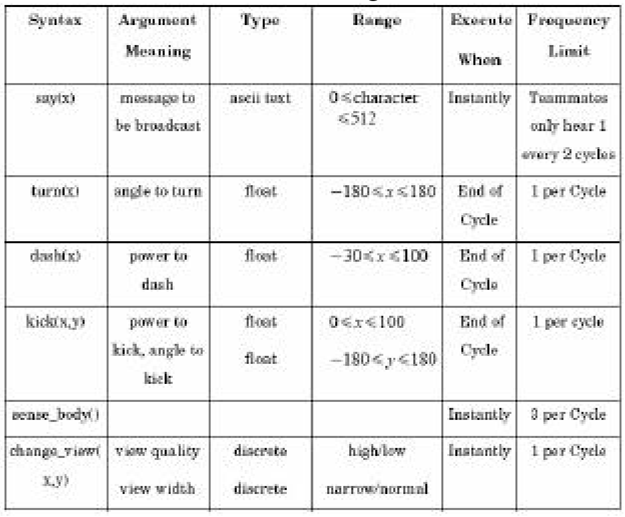


Fig 2: The soccer server display. Each player is represented as a two-halved circle. The light side is the side towards which the player is facing. All players are facing the ball, which is in the middle of the field. The black bars on the left and right sides of the field are the goals.

Table 3: The Soccer server agent's commands



Syntax	Argument Meaning	Type	Range	Execute When	Frequency Limit
say(x)	message to be broadcast	ascii text	$0 \leqslant$ character $\leqslant 512$	Instantly	Teammates only hear 1 every 2 cycles
turn(x)	angle to turn	float	$-180 \leqslant x \leqslant 180$	End of Cycle	1 per Cycle
dash(x)	power to dash	float	$-30 \leqslant x \leqslant 100$	End of Cycle	1 per Cycle
kick(x,y)	power to kick, angle to kick	float float	$0 \leqslant x \leqslant 100$ $-180 \leqslant y \leqslant 180$	End of Cycle	1 per cycle
sense_body()				Instantly	3 per Cycle
change_view(x,y)	view quality view width	discrete discrete	high/low narrow/normal	Instantly	1 per Cycle

The agent has just four actuators for physically manipulating the world: *turn*, *dash*, *kick* and *catch*. The server only executes one of these commands for each player at the end of each simulator cycle. If an agent sends more than one such command during the same cycle, only one is executed non-deterministically. Since the simulator runs asynchronously from the agents, there is no way to keep perfect time with the server's cycle. Therefore any given command could be missed by the server. It is up to the agent to determine whether a given command has been executed by observing the future state of the world.

4. PROPOSED WORK

We propose soccer-playing agent architecture with a sequential analysis component, utilizing the representation described in the previous section

Shooting Behavior

We make a simple strategy for shooting the ball into the goal. To shoot the ball to the goal, it is important that the robot can see both ball and goal. Therefore, the robot must round the ball until the robot can see both ball and goal with the camera toward the ball. Finally, the robot kicks the ball strongly. The concrete procedure of shooting behavior is follows:

```
1)Find the ball
2)Approach the ball
While approaching the ball
if the area of the ball > 20 then stop
3)Round the ball
d ←the direction of the goal
switch(d)
right: clockwise round the ball(AGGGT)
with the camera toward the ball(ACCCT)
left: counterclockwise round the ball(AAACT)
 with the camera toward the ball(TTTAC)
 if the robot can see both ball and goal then stop
 4)Turn the body of the robot towards the ball(ATACT)
 5)Kick the ball strongly(AATAA)
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4.1. Cellular Automata (CA) and Fuzzy Cellular Automata (FCA)

A CA [4], [5], [6], consists of a number of cells organized in the form of a lattice. It evolves in discrete space and time. The next state of a cell depends on its own state and the states of its neighboring cells. In a 3-neighborhood dependency, the next state *qi* (*t* + 1) of a cell is assumed to be dependent only on itself and on its two neighbors (left and right), and is denoted as

$$qi(t+1) = f(qi\text{-}1(t), qi(t), qi+1(t)) \qquad (1)$$

where *qi* (*t*) represents the state of the i^{th} cell at t^{th} instant of time, *f* is the next state function and referred to as the rule of the automata. The decimal equivalent of the next state function, as introduced by Wolfram, is the rule number of the CA cell. In a 2-state 3-neighborhood CA, there are total 256 distinct next state functions.

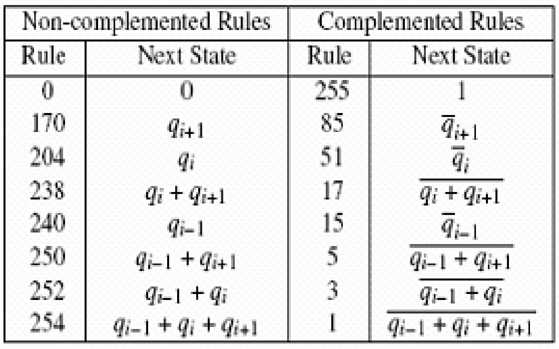
4.1.1 FCA Fundamentals

FCA [2], [6] is a linear array of cells which evolves in time. Each cell of the array assumes a state *qi*, a rational value in the interval [0, 1] (fuzzy states) and changes its state according to a local evolution function on its own state and the states of its two neighbors. The degree to which a cell is in fuzzy states 1 and 0 can be calculated with the membership functions. This gives more accuracy in finding the coding regions.In a FCA, the conventional Boolean functions are AND , OR, NOT.

4.1.2 Dependency Matrix for FCA

Rules defined in equations 1, 2 should be represented as a local transition function of FCA cell. That rules are converted into matrix form for easier representation of chromosomes [16].

Table 4. Rules



Non-complemented Rules		Complemented Rules	
Rule	Next State	Rule	Next State
0	0	255	1
170	q_{i+1}	85	$\overline{q}_{i+1}$
204	q_i	51	$\overline{q}_i$
238	$q_i + q_{i+1}$	17	$\overline{q_i + q_{i+1}}$
240	q_{i-1}	15	$\overline{q}_{i-1}$
250	$q_{i-1} + q_{i+1}$	5	$\overline{q_{i-1} + q_{i+1}}$
252	$q_{i-1} + q_i$	3	$\overline{q_{i-1} + q_i}$
254	$q_{i-1} + q_i + q_{i+1}$	1	$\overline{q_{i-1} + q_i + q_{i+1}}$

Example 1: A 4-cell null boundary hybrid FCA with the following rule
< 238, 254, 238, 252 > (that is, < (*qi*+*qi*+1), (*qi*-1+*qi*+*qi*+1), (*qi* + *qi*+1), (*qi*- 1 + *qi*) >) applied from

left to right, may be characterized by the following dependency matrix

While moving from one state to other, the dependency matrix indicates on which neighboring cells the state should depend. So cell 254 depends on its state, left neighbor, and right neighbor fig (1). Now we represented the transition function in the form of matrix. In the case of complement FMACA we use another vector for representation of chromosome.

$$T = \begin{bmatrix} 1 & 1 & 0 & 0 \\ 1 & 1 & 1 & 0 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 1 & 1 \end{bmatrix}$$

Fig 3: Matrix Representation

Once we formulated the transition function, we can move form one state to other. For the example 1 if initial state is P (0) = (0.80, 0.20, 0.20, 0.00) then the next states will be

P (1) = (1.00 1.00, 0.20, 0.20),
P (2) = (1.00 1.00, 0.40, 0.40),
P (3) = (1.00 1.00, 0.80, 0.80),
P (4) = (1.00 1.00, 1.00, 1.00).

We just introduced the concept of Cellular Automata in this section. CA is a linear array of cells which evolves in time. Each cell of the array assumes a state *qi*, a rational value in the interval [0, 1] (fuzzy states) and changes its state according to a local evolution function on its own state and the states of its two neighbors. The degree to which a cell is in fuzzy states 1 and 0 can be calculated with the membership functions. This gives more accuracy in finding the coding regions. In a FCA, the conventional Boolean functions are AND , OR, NOT.

Figure 1,2 shows the architecture of the proposed sequence-driven classifier system. This system differs from standard classifier systems **[5]** in two main ways

4.1.4 FMACA Based Tree-Structured Classifier

Cellular Automata choose the rules carefully after trying many other possibilities, some of which caused the cells to die too fast and others which caused too many cells to be born. Life balances these tendencies, making it hard to tell whether a pattern will die out completely, form a stable population, or grow forever. Life is just one example of a **cellular automaton**, which is any system in which rules are applied to cells and their neighbors in a regular grid.

A good way to get started in Life is to try out different patterns and see what happens. Even completely random starting patterns rapidly turn into Life objects recognizable to anyone with a little experience. In this section, we follow a simple-looking pattern called the R-pantomime. I starts out with just five cells, but gets complicated very fast. We can see many of the early discoveries in Life just by running this one pattern in the applet

Like decision tree classifiers, FMACA based tree structured classifier uses the distinct k-means algorithm recursively partitions the training set to get nodes (attractors of a FMACA) belonging to a single class. Each node (attractor basin) of the tree is either a leaf indicating a class; or a decision (intermediate) node which specifies a test on a single FMACA, according to equations 1,2.

Suppose, we want to design a FMACA based pattern classifier to classify a training set $S = \{S1, S2, \cdot, SK\}$ into K classes. First, a FMACA with k-attractor basins is generated. The training set S is then distributed into k attractor basins (nodes). Let, S' be the set of elements in an attractor basin. If S' belongs to only one class, then label that attractor basin for that class. Otherwise, this process is repeated recursively for each attractor basin (node) until all the examples in each attractor basin belong to one class. Tree construction is reported in [7]. The above discussions have been formalized in the following algorithm. We are using genetic algorithm classify the training set.

***Algorithm 1*: FMACA Tree Building (using distinct K means algorithms)**

```
Input  :   Training set $S = \{S1, S2, \cdot\cdot, SK\}$
Output:    FMACA Tree.

Partition($S, K$)
Step 1: Generate a FMACA with $k$ number of attractor basins.
Step 2: Distribute $S$ into $k$ attractor basins (nodes).
Step 3: Evaluate the distribution of examples in each attractor basin (node).
Step 4: If all the examples (S') of an attractor basin (node) belong to only one class, then label the attractor basin (leaf node) for that class.
Step 5: If examples (S') of an attractor basin belong to $K'$ number of classes, then Partition (S', $K'$).
Step 6: Stop.
```

First, the proposed system adds an event-analysis section and prepares a record of past game sequences/player sequences that are analyzed using sequence analysis.

Second, the classifier discovery section using genetic algorithms targets only actions while the conditions are generated using information provided by sequence analysis. The systems also provides for different types of reward – a large reward for winning matches and smaller rewards that can be obtained from succeeding in a single play, such as passing the ball

5. EXPERIMENTAL RESULTS

The Sequence Analysis algorithms were tested on player and game sequences of varying lengths and distinct sub sequences yielded the following results from which various inferences for improving the next match were made. Client 1 sends movement commands after every perception it receives. This strategy works out fine in cycle t-1; but in cycle t it misses the opportunity to act because it receives no perceptions; and in cycle t+1 it sends two movement commands, only one of which will be executed. Client 2, on the other hand, successfully sends one movement command every cycle. Note that in cycle t it must act with no new perceptual information, while in cycle t+1, it receives two perceptions prior to acting and one afterwards. Ideally, it would act after receiving and taking into account all three perceptions. However, it does not know precisely when the simulator cycle will change internally in the soccer server and it cannot know ahead of time when it will receive perceptions. Thus, in exchange for the ability to act every simulator cycle, it sometimes acts with less than the maximal amount of information about the world. However, as each simulator cycle represents only a short amount of real time (*simulator_step* msec), the world does not change very much from cycle to cycle, and the client can act accurately even if it takes some of its perceptions into account only before its subsequent action.

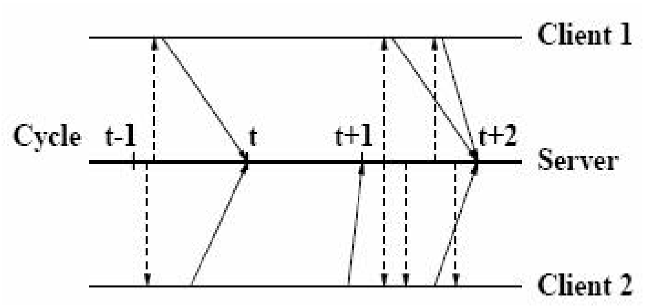


Figure 4: A sample period of the server-client interface over the course of 3 simulator cycles at times t-1, t, and t+1. The thick central horizontal line represents the real time as kept by the server. The top and bottom horizontal lines represent the time-lines of two separate clients. The dashed arrows from the server towards a client represent perceptions for that client. The solid arrows from a client towards the server represent movement commands sent by that client. These arrows end at the point in time at which the server executes the movement commands, namely the end of the simulator cycle during which they are sent.

Asynchronous sensing and acting, especially when the sensing can happen at unpredictable intervals, is a very challenging paradigm for agents to handle. Agents must balance the need to act regularly and as quickly as possible with the need to gather information about the environment. Along with asynchronous sensing and action, the soccer server captures several other real-world complexities, as will become evident throughout the remainder of this section.

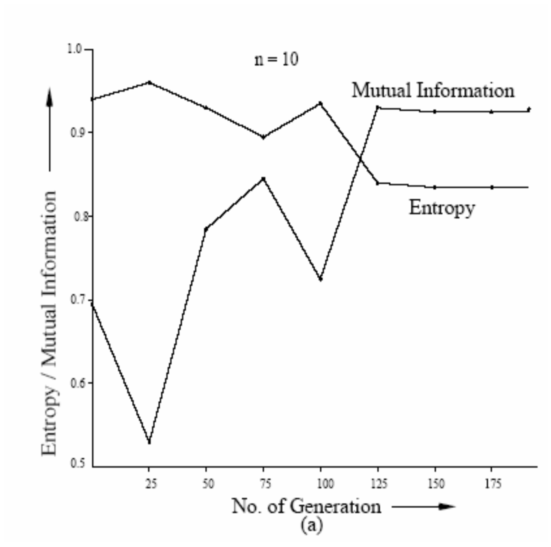


Fig 5: Entropy & Mutation information for n=10

These results were translated into strength values and directly modified within the LCS. In order to justify that this proposed architecture is indeed faster at learning targeted behavior at a much faster pace, “Clean Slate” experimental conditions were maintained. The Classifier rule set initially is completely randomly generated – to simulate a blank knowledge base. The rule set is then generated prior to the first iteration and the LCS was run for up to 200,000 iterations. Initialization parameters for the Genetic Algorithm specify the algorithm to run every 4000 iterations – this interval is necessary so that the strengths of the rule sets are given time to stabilize after credit apportionment.

The figure shows the application of the algorithm for a single game which when applied to hundreds of games, useful inferences could be made. The patterns thus identified through the application of tandem repeats algorithm served to identify the risk of threats and goals thereby enabling dynamic decision making in future games with reference to past history of games played. The goal sequences identified were xxCCT, where x represents any of the 4 characters. The following is a table showing the sequences that are likely to occur in the case of a goal or threat and their percentage of occurrences.

Table 4: Distinct patterns and their number of occurrences in each player sequence

PATTERN	NO. OF OCCURENCES	PLAYER
CACC	4	player-a
ACCC	3	player-b
ACCC	3	player-d
ACCC	5	player-c
CCCC	5	player-a
CCCCB	2	player-b
CCCAGCC	2	player-a
CC-G	3	player-d

The motion of CA rule space in successive generations is characterized by evaluating the entropy and mutual information of CA rule vectors of a population. The rule vectors for study are sampled out at a gap of 5 generations. The top most fit rule vectors of the selected population is subjected to closer scrutiny.

The entropy and mutual information of the CA in successive generations of GA are reported in Fig 5,6 ,7,8 for four different CA size (*n*= 10, 15, 20, 30). For each of the cases, the values of entropy and mutual information reach their steady state once the AIS FMACA for a given pattern set gets evolved. For understanding the motion, the initial population (IP) is randomly generated. All these figures points to the fact that as the CA evolve towards the desired goal of maximum pattern recognizing capability, the entropy values fluctuate in the intermediate generations, but saturate to a particular value (close to the critical value 0·84 [245]) when fit rule is obtained. Simultaneously, the values of mutual information fluctuate at the intermediate points prior to reaching maximum value that remains stable in subsequent generations. All these figures indicate that the CA move from chaotic region to the edge of chaos to perform complex computation associated with pattern recognition.

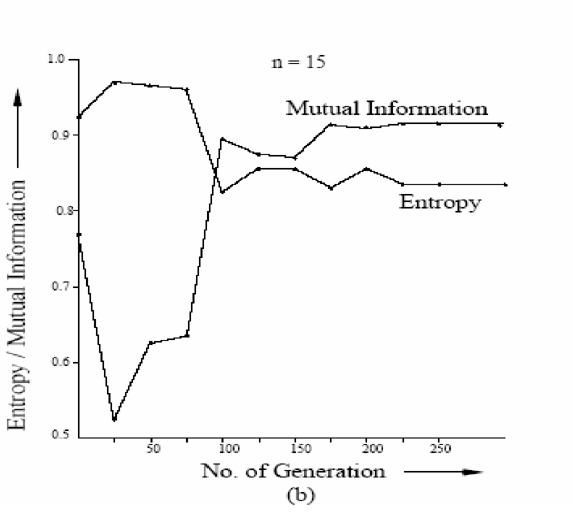


Fig 6: Entropy & Mutation information for n=15

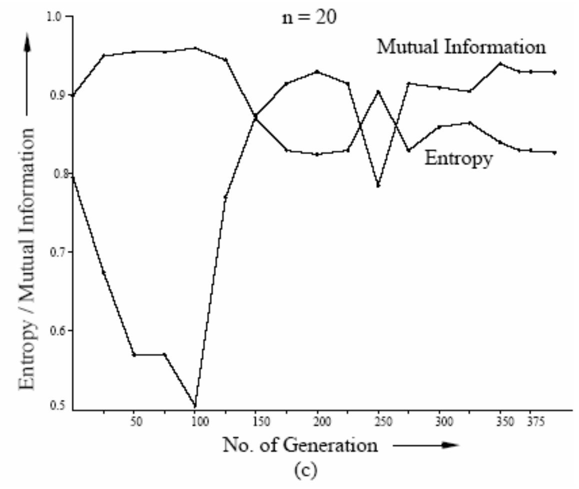


Fig 7: Entropy & Mutation information for n=20

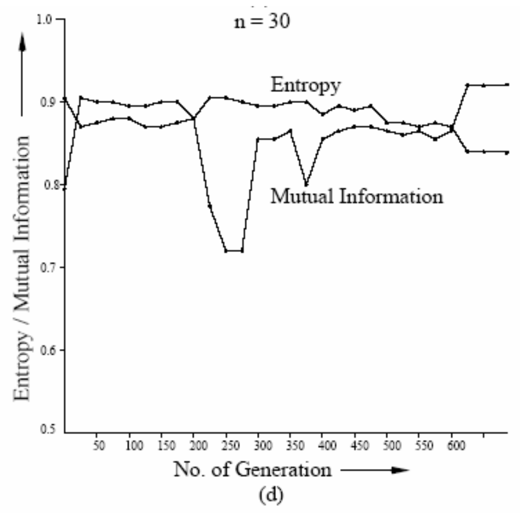


Fig 8: Entropy & Mutation information for n=30

Table 3 shows the application of the algorithm for a single game which when applied to hundreds of games, useful inferences could be made. The patterns thus identified through the application of tandem repeats algorithm served to identify the risk of threats and goals thereby enabling dynamic decision making in future games with reference to past history of games played. The goal sequences identified were xxCCT, where x represents any of the 4 characters. The following is a table showing the sequences that are likely to occur in the case of a goal or threat and their percentage of occurrences.

The goal sequences were identified by application of the algorithm for finding tandem repeats. These sequences were in turn checked using the algorithm for Trans-membrane region to find the percentage of occurrences of these patterns in multiple numbers of games.

Table 3: Percentage of occurrence of Goal and Threat sequences

SEQUENCES	95%	75%	50%	< 50%
Goal (xxCCT)	TCCCT	CACCT	CxCCT	CCAT
Threat	CTCCC	CCACC	CCxCC	GCAC

The Learning classifier system was first tested by first evolving completely random classifier rules and then placed in the environment to gage the learning rate. Figure 2 shows the proportion of correct actions proposed by the learning classifier system versus the time epochs taken. Subsequent experiments were conducted by constructing a history of 10,000 games – and the performance of the classifier system was observed.

Fig 7. shows the performance of LCS, an accuracy rate of nearly 75% was obtained after merely 100,000 iterations. This is observed to be far less when compared to other agent learning mechanisms based on reinforcement learning. Given a good balance between desired accuracy and training time, this technique will yield a good “knowledge base” of conditions and actions upon which the agent will base all its responses.

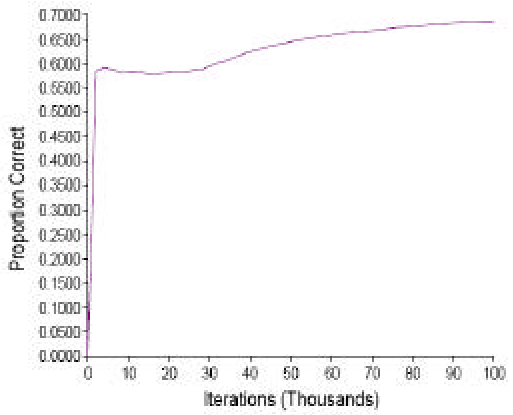


Fig 9. Graph (Proportion Correct VS Iterations)

6. CONCLUSION

The advantage of adopting sequence analysis for evaluating strategy is that the analysis is capable of distinguishing individual strategy of an agent as well the overall strategic play of the team as such. This approach could easily be adapted towards developing squad-based tactics of team behavior evolution, by evolving specific strategies for specific groups - for example, creating a group of defenders whose overall goal is to defend their goal, and a squad of offensive players whose only aim is to target the opposing team's goal. Furthermore, use of advanced genetic operations during the discovery stages could enable the classifier system to discover better actions within a smaller time-bound and improve the real-time response of the system.

A representation scheme for robotic soccer in the form of biological sequence has been presented. Two new algorithms to find repeating patterns and ideal game strategies similar to biological problems have been developed and tried on the sequences generated. A number of sequences has been generated from various games played and the algorithms proved effective in analysing various repeating patterns before a goal and finding faulty moves. Interesting sub-problems, such as stamina conservation of players have been identified and solutions have been proposed using the above representation scheme and associated algorithms – Moves that result in increased stamina expenditure have been identified and removed from player sequences. An agent learning Architecture has been proposed using the above representation scheme. Enhancements to the Rule discovery components and the Credit apportionment schemes have been shown to yield positive results and improvements in agent learning times.

The current drawbacks of the presented scheme is the added overhead of human intervention and the resulting loss of automation. The immediate area for improvement would be to have some sort of database that include some predetermined knowledge about the desired actions and enabling automated lookup by the sequence analysis algorithms to best select sub-sequences based on the data stored in the database. Further enhancements to the Genetic algorithm would also be possible with regards to selection criteria.

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