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Investigating the Properties of Bio-Chemical Networks of Artificial Organisms with Opposing Behaviours

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Abstract

Organisms, be it singled-celled organisms or multi-cellular organisms, are constantly faced with opposing objectives requiring different sets of behaviours. These behaviours can be classified into two, *predatory* behaviours or *anti-prey* behaviours, with one set of behaviours causing an opposite effect to the other. A healthy organism aims to achieve its equilibrium state or to be in homeostasis. Homeostasis is achieve when a balance between the two opposing behaviours is created and maintained. This raises some questions: is there an innate mechanism that encodes for these categories of behaviours? Is there also an innate mechanism(s) that resolves conflicts and allows switching between these two opposing behaviours? If we consider artificial organisms as single-celled organisms, how do the organisms' gene regulatory network, metabolic network and/or signalling network (their biochemical networks) maintain homeostasis of the organisms? This paper investigates the properties of the networks of best evolved artificial organisms, in order to help answer these questions, and guide the evolutionary development of controllers for artificial systems.

Keywords: artificial bio-chemical network, artificial genetic regulatory network, artificial organism, evolutionary algorithm

1. Introduction

An organism is constantly faced with the dilemma of balancing varying and opposing behaviours. This paper investigates the properties of bio-chemical networks of various artificial organisms, to investigate how their behaviours are encoded in the networks. Analysis of these properties may help us understand how a biological organism coordinates the switching of opposing behaviours. This understanding can also help us in the evolution of the bio-chemical networks for the artificial organisms.

The paper is divided into seven sections. Section 2 provides a brief understanding on how the opposing behaviours of the biological organisms are organised. In Sec. 3, a number of questions that will be used to help guide the analysis to understand how the evolved bio-chemical networks of (artificial) organisms produced their behaviours are categorised. Section 4 describes what is the artificial bio-chemical network. Section 5 revisits the proposition that was made in the previous analysis of bio-chemical networks of artificial organisms (Mokhtar, 2012). Section 6 presents the results of analysis of other varying artificial organisms and network characteristics. Section 7 summarises and concludes this paper.

2. Opposing *predatory* and *anti-prey* behaviours

An organism's behaviours can be categorised into two distinct categories of behaviours, defined as either *preda-*

tory or *anti-prey* behaviours.

2.1. Multi-cellular organisms

In multi-cellular organisms, *predatory* behaviours are to forage, fight and/or kill other animals in order to obtain food for the body. This category of behaviours typically requires high energy consumption and is considered high risk behaviours; but, to become a predator, one can lead to greater reward for the organism. For example, a carnivore (lion or tiger) would require high amount of energy to chase and capture a fast escaping deer (prey). This can cause exhaustion; but, the killed deer can provide greater reward in a form of extra food for the body. This will be different to when the carnivore choose to forage for carcases (dead animals) for food (this type of behaviour can be considered as *anti-prey* behaviour). This type of behaviour requires less energy (no chasing of prey is required) but only provides small reward to the animal.

A herbivore, for example, is performing *predatory* behaviour when it forages further from its nest in order to gather more food. The animal is considered as the predator and the environment is its prey. The animal may risk becoming prey to carnivores when foraging, but the reward is higher; in comparison to just staying to where the nest is at (this we considered as *anti-prey* behaviour[1]).

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[1]We consider anti-predatory behaviour or behaviour in response

A balance between the two opposing behaviours ensures that the organism is in homeostasis, a state important for the organism's survivability. If the animal is constantly favouring one behaviour in comparison to the other, this can significantly affect its survivability. If the carnivore favours (and unsuccessfully) capturing and killing its prey, the animal may exhaust its energy, leading to death[2]. At time of low energy, the organism may wish to forage for carcases in oder to preserve its energy. Similarly, if a herbivore choses to stay close to its nest, this can result in the significant drop in food availability near its nest. The animal may have insufficient food at times of high demand (for example, when there is significant change in environmental conditions that can reduce the animal's foraging capabilities).

Even in humans, these two categories of behaviours can be seen. *Predatory* behaviours are behaviours performed when we are at work and *anti-prey* behaviours are when we are at rest. We must perform both these categories of behaviour in moderation and in balance, because if we only concentrate on work, we will become exhausted and can damage our mental and physical health. But, if we only choose to rest, we will become obese and be affected by diseases caused by obesity.

We can further summarise that *predatory* behaviours are (pro-)active behaviours, with *anti-prey* behaviours as resistive, dormant and reactive behaviours.

2.2. Single-celled organisms

The categorisation of behaviours are not only limited to multi-cellular organisms. Single-celled organisms' behaviours can also be categorised into the two. We have indicated in (Mokhtar, 2012) that bacteriophage lambda[3] can survive in two phages: either lysic, which we have considered as a *predatory* phage, or lysogenic, classified as the *anti-prey* phase. We have categorised the Bacteriophage lambda's behaviours as such because lysogenic is when the bacteriophage incorporates its DNA into the *E. Coli*'s genome (its host) to ensure the survival of its species (*anti-prey*). Lysic is considered as *predatory* phage, because when the bacteriophage senses that its host (*E. Coli*) is weak, it will cause the destruction of its host in order for the bacteriophage to create new offsprings (Hasty et. al., 2001). If the bacteriophage remains lysogenic, the bacteriophage will die with its host. If the bacteriophage remains constantly lysic, this may reduce the availability of hosts, which in turn can affect the survival of its progeny.

Another example provided in (Mokhtar, 2012), is the flora bacteria residing in the gut. The flora bacteria survive in the hostile environment of the human gut by maintaining a symbiotic relationship with the gut. We have categorised the symbiotic relationship as an *anti-prey* behaviour and the high rate reproduction as the *predatory* behaviour. If the bacteria choses to predominantly perform one type of behaviours, the human immune system may produce a response that results in the destruction of its species (Rey et. al., 2006).

The two categories of behaviour can also be found in *Dictyostelium discoideum*, an example of an early multi-cellular organism[4]. As indicated in (Mokhtar, 2012), the collective (singular) behaviour of the *Dictyostelium discoideum*, for example, are to forage, fight and/or kill for food, in order to have sufficient food to form a collective morphology, move and reproduce in its environment. The former is considered as *predatory* behaviour and the later is *anti-prey*. If there are no balance between these two categories of behaviour, this may affect the survivability of the organism.

3. Regulation of Behaviours

The brain is responsible for the coordination of the two opposing categories of behaviour in multi-cellular organisms. In single-celled organisms, such coordination is provided directly by its gene regulatory network, or GRN, (de Jong, 2002), (Wolf and Eeckman, 1998). If we consider our artificial organism as a single-celled organism, we will be looking into how the GRN of the artificial organisms describe their behaviours. This will help us answer the following questions:

1. What encodes the organism's two different categories of behaviours? Can the behaviour be divided into *predatory* and *anti-prey* behaviours?

2. Is there an innate mechanism(s) that switches and resolves conflicts between the two opposing behaviours?

3. How do the organism's GRNs maintain homeostasis of the organism?

Lones et. al. (2011) have pointed out that in biological cells, the most significant interaction within the cells that underlies its behaviour is the interaction between its bio-chemical networks: *"how the GRN indicates when and where proteins are expressed, which thereby determines which enzymes are present in the metabolic network and hence which reactions can take place within the cell"*. Essentially, the GRN is responsible in determining the cell's behaviour.

Therefore, we also ask:

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to the presence of predation (Hegner, 1985), (Riechert and Hedrick, 1990), (Lima and Bednekoff, 1999) as *predatory* behaviour. This is because more energy is required when there is an increase in the awareness of the organism, since the organism must be well prepared to respond to an attack by the predator (Hegner, 1985), (Riechert and Hedrick, 1990).

[2]Chasing prey causes acid build up in the muscle (anaerobic). Excess acid build up can result in death for the animal.

[3]Bacteriophage lambda is not a single-celled organism but a virus; although its behaviours (be it simple behaviours) can be categorised into two: *predatory* or *anti-prey*.

[4]The *Dictyostelium discoideum* is considered as early multi-cellular organism because the *Dictyostelium discoideum* are a collection of individual single-celled organisms working collectively as one.

1. How does an organism's GRN affect the metabolic network and/or signalling network of the organism in order to maintain homeostasis?

4. Artificial Bio-chemical Network

Lones et. al. (2011) proposed an artificial bio-chemical network architecture that couples an artificial genetic regulatory network to an artificial metabolic network.

4.1. Artificial Genetic Regulatory Network

The AGRN was formally defined by (Lones et. al., 2010) as $< G, L_G, I_G, O_G >$ and is presented in Algorithm 1.

Algorithm 1: Artificial Genetic Regulatory Network.

Constant: y time steps in an experiment run.
Constant: $i_t = 10$ no. of network iterations per time step t.
Constant: $a =$ No. of genes in the AGRN.
1   $G =$ An index set of genes, with g_x, $x = \{0, ..., a\}$.
2   $\lambda_x =$ The gene expression level for g_x.
3   $R_x \subseteq G =$ The regulatory inputs (λ) used by the gene g_x.
4   $f =$ The gene regulation function.
5   $L_G =$ An indexed set of initial expression levels, with $|L_G| = |G|$
6   $I_G \subset G =$ The external inputs applied to the network.
7   $O_G \subset G =$ The outputs of the network.

8   **begin**
9   **for** $t = 1 : y$ **do**
10       $\lambda_{I_G} \leftarrow I_G$;
11   **for** $x = 1 : (a - I_G)$ **do**
12         $\lambda_x \leftarrow L_x$;
13   **end**
14   **for** $n = 1 : i_t$ **do**
15   **for** $x = 1 : a$ **do**
16           $\lambda_x \leftarrow f(R_x)$;
17   **end**
18   **end**
19   O_G are presented as the outputs to the system;
20   **end**
21 **end**

4.2. Artificial Metabolic Network

The AMN is formally described by (Lones et. al., 2011) as $AMN = < C, E, I_E, O_E >$ and is formulated using Algorithm 2.

4.3. Coupled Artificial Bio-chemical Network or CABN

The AGRN couples to the AMN using an injective coupling function $\chi : G_C \rightarrow E$. $G_C \subseteq G$ is the set of enzyme coding genes.

The AGRN is coupled to the AMN because in the biological coupled bio-chemical network, the GRN controls the expression of the metabolic network (Lones et. al., 2011). The coupling of the AGN to the AMN is illustrated in Fig. 1.

Algorithm 2: Artificial Metabolic Network.

Constant: y time steps in an experiment run.
Constant: $i_t = 10$ no. of network iterations per time step t.
Constant: $s =$ No. of chemical expressions in the AMN.
Constant: $a =$ No. of enzymes in the AMN.
1   $C =$ The indexed set of random chemical concentrations $\{c_0, c_1, ..., c_s\}$.
2   $E =$ The indexed set of enzymes $\{e_0, e_1, ..., e_a : e_i = < S_i, P_i, m_i >\}$
3   $S_i \subset C =$ The concentration of the substrates used by the enzyme.
4   $P_i \subset C =$ The concentration of products generated by the enzyme.
5   $m_i =$ The enzymes' substrate-product mapping function.
6   $I_E \subset E =$ The set of enzymes used as inputs.
7   $O_E \subset E =$ The set of enzymes used as outputs.

8   **begin**
9   **for** $t = 1 : y$ **do**
10       $S_{I_E} \leftarrow I_E$;
11   **for** $i = 1 : (a - I_E)$ **do**
12   S_i is randomly initialised;
13   **end**
14   **for** $i = 1 : a$ **do**
15   P_i is randomly initialised;
16   **end**
17   **for** $n = 1 : i_t$ **do**
18   **for** $i = 1 : a$ **do**
19           $P_i \leftarrow m(\frac{\sum_{j=1}^{J} S_j}{J})$, $S_j \subset S_i$;
20   **end**
21   **end**
22   O_E are presented as the outputs to the system;
23   **end**
24 **end**

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5. Energy Management of an Artificial Organism using the ABN (Mokhtar, 2012)

To help answer the questions posed in Sec. 3, a population of artificial bio-chemical networks (ABN) were evolved, with the aim to manage the energy usage for an artificial organism. The objectives of the organism are:

1. to make use of the available energy resources (E_R) to meet with their required energy demand (E_D): $U_E = E_R.C_{O2}$
2. to save energy (E_S) in storage S_E at times when $E_R > E_D$: $E_S = E_R.(1 - C_{O2})$ and $S_E = S_E + E_S$.
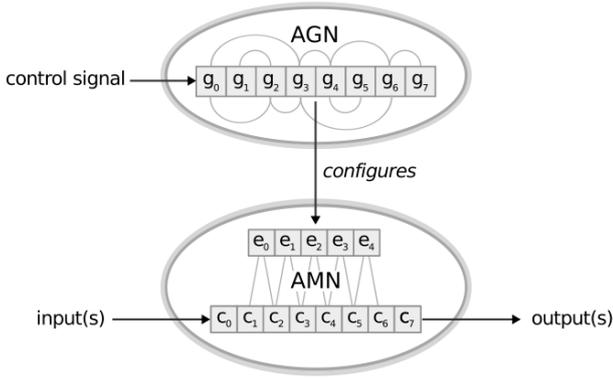
3

Figure 1: The coupled artificial bio-chemical network. Figure taken from (Lones et. al., 2011).

3. to use energy in S_E to help meet with the demand E_D when $E_R < E_D$: $U_S = S_E.C_{O1}$ and $S_E = S_E - U_S$.

The ABN consists of 6 genes in its AGRN, comprising of 54 weights (w) and 6 slopes (s). The 6 genes codes for 6 gene expression levels that lead to the production of 2 chemical outputs C_{O1} and C_{O2} ($6w$ and $2s$ in its AMN). The chemical outputs govern the three listed behaviours: U_E, E_S and U_S. $w \in [-1, 1]$, $s \in [-1, 1]$ and $C_{Oy} \in [0, 1]$.

The values of w and s are evolved so that the best evolved ABNs achieved the fitness objectives of:

1. $E_D \approx (U_E + U_S)$
2. $S_E > 0$

A population of 1000 ABN were evolved using SPEA2 (Strength Pareto Evolutionary Algorithm 2) developed by Popov (2005). The mutation rate = 0.0143 and crossover rate = 0.5. Network iteration $i_t = 1$.

The evolved ABNs utilise the sigmoid function (1) for f in the AGRN and m in the AMN, respectively.

$$f = (1 + exp^{(-b-s\sum wz)})^{-1} \qquad (1)$$

$z \subset \lambda$ for the AGRN and $z \subset S_i$ for the AMN.

The results of evolution were presented in (Mokhtar, 2012). Results indicated that in the evolved solutions, a balance or homeostasis between the two opposing behaviours can be achieved when the following characteristics within its ABN are observed (the output is $C_{Ox} \in [0, 1]$):

1. to make use of the available energy in S_E to meet with the required E_D (U_S) is considered as *anti-prey* behaviour. A behaviour is considered as *anti-prey* behaviour when its chemical output C_{Ox} is constantly < 0.5.
2. to use E_R to meet with the required E_D (U_E) is considered as *predatory* behaviour. A behaviour is considered as *predatory* behaviour when its chemical output C_{Ox} is constantly > 0.5.

3. 50% of the genes are *predatory* genes or are genes that are constantly producing $g_x > 0.5$.
4. 25% of the genes are *anti-prey* genes or are genes that are constantly producing $g_x < 0.5$.
5. 25% of the genes oscillate with g_x mean of 0.5.

Furthermore, Mokhtar (2012) indicated that:

1. The more positive weights w within a gene/enzyme, the higher the likelihood for the gene/enzyme to be switched off ($C_{Ox}/g_x = 0$).
2. The more negative weights w within a gene/enzyme, the higher the likelihood for the gene/enzyme to be switched on ($C_{Ox}/g_x = 1$).
3. The more varied its weights w, the higher the likelihood that the gene/enzyme will become an oscillator.

These heuristics, as pointed out in (Mokhtar, 2012), indicate that the organism's behaviours can be described by the properties of its genes and chemicals produced by its ABN.

6. Observations From ABNs Evolved to Solve Other Tasks

To test if the heuristics presented in Sec. 5 and (Mokhtar, 2012) are also observed in other AGRNs and ABNs, the properties of ABNs evolved to solve other tasks were analysed.

6.1. Controlling Legged Robot Locomotion

Lones et. al. (2011) presented the use of AGRNs (Sec. 6.1.1) and coupled ABNs (Sec. 6.1.2) for the purpose of controlling quadrupedal robot locomotion. The quadrupedal robot used by the authors is a simple robot design, comprising of a square top section with four legs connected by actuators at each corner. The actuators are limited to movement in the x-axis plane, with a maximum elevation of 60° from vertical.

6.1.1. Artificial Genetic Regulatory Network

The inputs to the AGRN are the four actuator angles of the robot, each presented to a gene $I_G \subset G$ at $n = 0$. The outputs ($O_G \subset G$) are used to set the torques of the actuators at every $n = i_t = 10$ network iterations. The inputs are delivered via the initial gene expressions levels of g_0, g_1, g_2 and g_3, whilst the outputs are produced by g_6, g_7, g_8 and g_9.

The fitness value used in the evolution of the controller is the Euclidean distance of the robot from its start location (at $y = 0$) to the location at $y = 500$ time steps. Therefore, the higher the fitness value, the further the distance, the better the AGRN controller.

To help answer the questions presented in Sec. 3, the best populations evolved by (Lones et. al., 2011) were analysed[5]. We analysed the populations by calculating

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[5]50 populations, each evolved for 100 generations.

4

the values of λ for G with $i_t = 1$ and $L_G = 1$ ($\rho = \lambda$ when $f(1)$). $L_G = 1$ was chosen because of the limited experiment data and information provided for the analysis, data and information which was used in the evolution of the controllers. $L_G = 1$ was also chosen because this is the maximum input value that can be provided to the AGRN, therefore forcing the AGRN to operate at its most extreme conditions.

Because of this, a new definition of *predatory* and *anti-prey* genes are also required. If $\rho_x = f_{g_x}(1)$ and $f_{g_x}(x)$ utilises the sigmoid function (1), *predatory* and *anti-prey* genes are defined as:

1. *Predatory* genes are genes with $\rho_x \geq 0.6$
2. *Anti-prey* genes are genes with $\rho_x \leq 0.4$
3. *Neutral* genes are genes with $0.4 < \rho_x < 0.6$

Figure 2 shows the attributes of the best evolved AGRN controllers. It shows that the best evolved controllers have equal numbers of *predatory* and *anti-prey* genes within the AGRN. Further investigation of the best evolved AGRN show similar symmetry in its AGRN. This is indicated in Fig. 3 to Fig. 5.
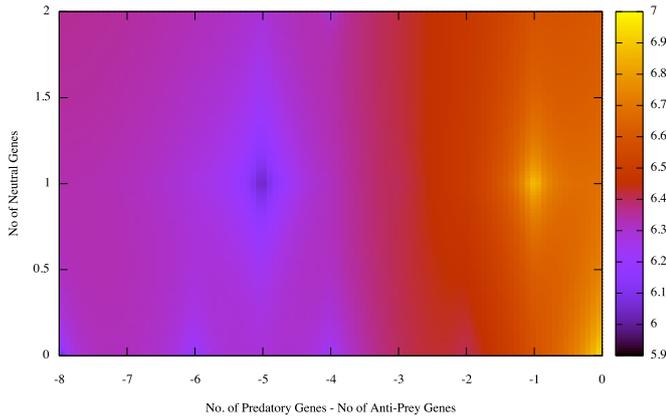

Figure 2: The attributes of the best evolved population of AGRN controllers. Symmetry is observed by the best evolved AGRNs, whereby the best evolved AGRNs have almost equal number of *predatory* and *anti-prey* genes. *Predatory* genes are genes with $\rho \geq 0.6$. *Anti-prey* genes are genes with $\rho \leq 0.4$. The colour values indicate the fitness value for a particular AGRN in the population (ignoring the 0.5 values in the y-axis). The higher the fitness value, the lighter the colour, the better the controller.

6.1.2. Coupled Artificial Bio-Chemical Network or CABN

The objectives of the Coupled Artificial Bio-Chemical Network (CABN), different from the AGRN, is to walk as far as possible from the start location (similar to Sec. 6.1.1), and to return back to its start location when an external control signal is presented to the robot's CABN. The authors indicated that the best evolved controllers are coupled AGRNs with the sigmoid function (1) for f and the Chirikov's Standard Map (2) for m in the AMN.

$$
\begin{aligned}
p_{n+1} &= (p_n + K \sin \theta_n) \mod 2\pi \\
\theta_{n+1} &= (\theta_n + p_{n+1}) \mod 2\pi
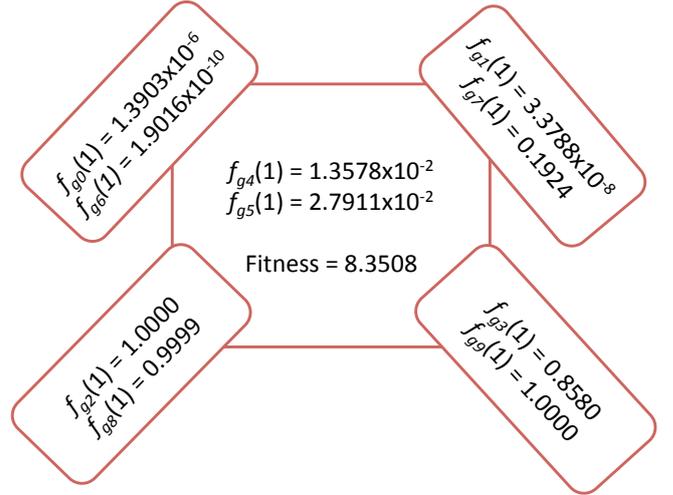\end{aligned}
\tag{2}
$$

Figure 3: The values of $f_{g_x}(1)$ of the robot incorporated with the third best evolved solution. The values showed that symmetry is observed by the O_G and I_G in the (artificial) organism's AGRN.
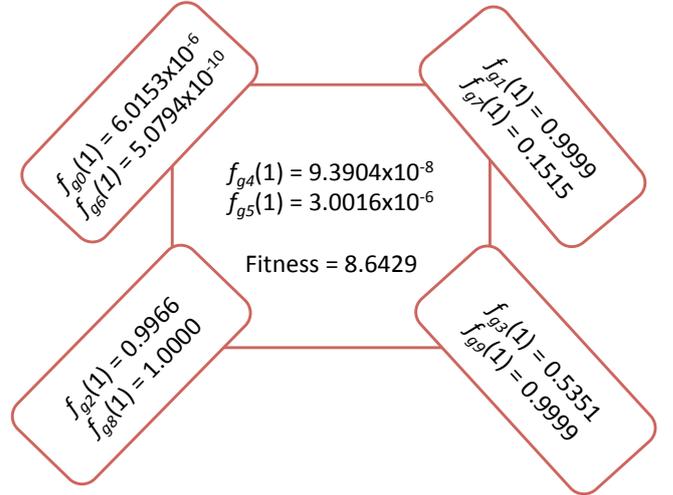

Figure 4: The values of $f_{g_x}(1)$ of the robot incorporated with the second best evolved solution. Symmetry is too observed by the O_G and I_G in the (artificial) organism's AGRN.

To investigate if the properties listed in Sec. 5 were observed in their best evolved controllers, their evolved CABNs' properties were analysed. We perform similar analysis techniques that were described in the previous section. We first observed the properties of the AGRN before looking at how the coupling between the two networks affects the robot's locomotion.

6.1.3. CABN's Artificial Genetic Regulatory Network

The Sigmoid AGRN properties are those described in Sec. 6.1.1. Section 5 described that in order for the artificial organism to provide for the required behaviours, its AGRN should consist of (i) 50% *predatory* genes, (ii) 25% *anti-prey* genes, and (iii) 25% *neutral* genes. There are 10 genes in each AGRN; therefore, the best evolved solutions should have 5 *predatory* genes, and 2 to 3 *anti-prey* and
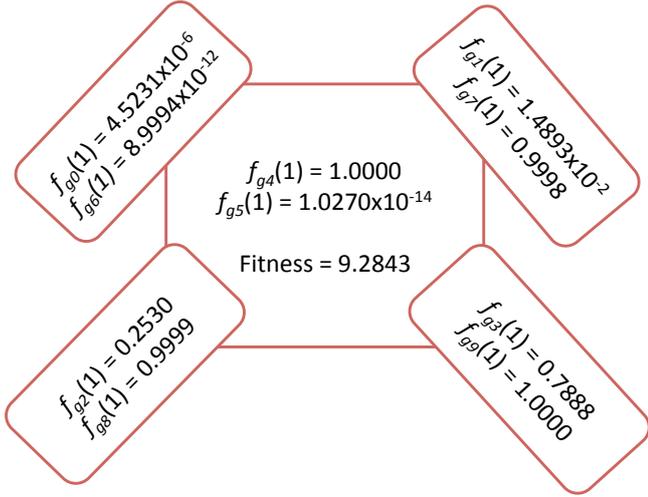
Figure 5: The values of $f_{g_x}(1)$ of the robot incorporated with the best evolved solution. Symmetry is too observed by the genes of the AGRN. This is because there is an almost equal number of *predatory* genes to *anti-prey* genes in the AGRN, with zero *neutral* gene in the AGRN.

neutral genes in their AGRN. There are also 10 chemical outputs produced by the AMN.

Figure 6 illustrates the properties of the best evolved population. This shows that best evolved CABNs have similar attributes to those listed in Sec. 5; with the best evolved controllers having $\sim 25\%$ *neutral* genes (2-4 genes) and $\sim 50\%$ to 70% *predatory* genes. We defined AGRNs with higher number of *predatory* genes as AGRNs that are prone towards *predatory* behaviours.
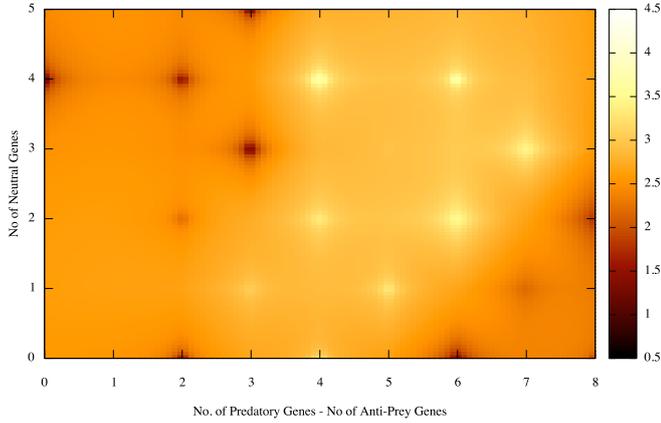

Figure 6: The properties of AGRNs from the best evolved populations. The higher the fitness value, the better the controller. There are 10 genes in the AGRN. The best evolved controllers have $\sim 25\%$ *neutral* genes (2-4 genes) and $\sim 50\%$ to 70% *predatory* genes. The colour values (see legend) indicate the fitness value attributed to a particular AGRN of the CABN.

6.1.4. CABN's Artificial Metabolic Network

The AGRN is coupled with a Chirikov's Standard Map AMN in order to provide for the required robot locomotion. To help us with our analysis, we will restrict our

analysis to only the best evolved controllers. We will be analysing the chemical concentrations generated by the enzymes ($P_i \subset C$) with:

1. The gene expression levels of the genes when $z = 1$ (1)
2. The enzymes' initial conditions $S_i = 1$
3. After network iteration $n = i_t = 10$ ($c_i(10)$).

We define a *predatory* chemical as when $c_i \geq 0.6$, and an *anti-prey* chemical when $c_i \leq 0.4$. A *neutral* chemical has $0.4 < c_i < 0.6$.

Figures 7 - 10 illustrates the values produced by g_i and c_i after $n = i_t = 10$. $c_0 - c_3$, each is presented with the actuator angle at its respective gait (I_E) and $c_6 - c_7$, each is its torque value (O_E). Figures 7 - 10 indicated that, when $z = 1$ (1) for each gene and the enzymes' initial conditions $S_i = 1$, there are a total of $\approx 50\%$ *predatory* genes + *predatory* chemicals in the CABN. The figures, therefore, show that the CABN has produced similar attributes to that of the previous system (Sec. 6.1.1 and in (Mokhtar, 2012)); whereby in the best evolved controllers, with 50% of the genes and chemicals produced by the CABN are categorised as *predatory*.

The *predatory* prone AGRN (due to the high number of *predatory* genes in the AGRN) is balanced by the AMN that produced $> 50\%$ *anti-prey* or *neutral* chemicals; hence symmetry within the network is observed.
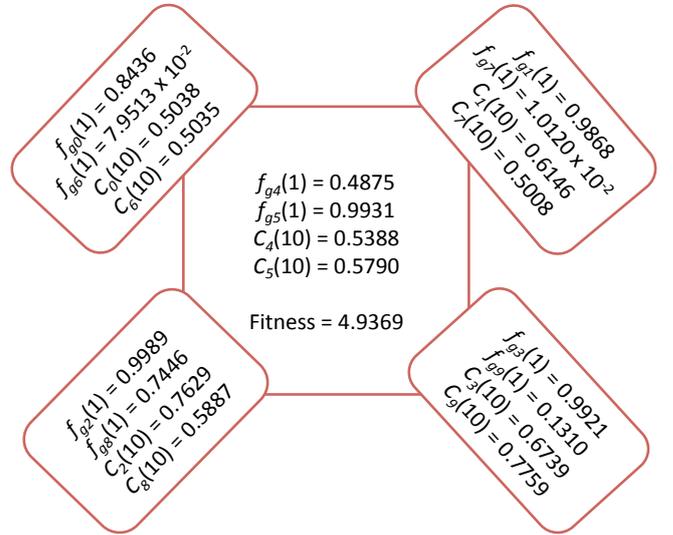

Figure 7: How symmetry is observed by the genes and enzymes in the (artificial) organism's CABN of the fourth best evolved solution. In its AGRN, there are 6 *predatory* genes, 3 *anti-prey* genes and 1 *neutral* gene. In its AMN, there are 4 *predatory* chemicals and 6 *neutral* chemicals produced. This suggests that the higher number of *neutral* chemicals in the AMN helps to balance the *predatory* bias found in the AGRN.

6.1.5. Summary of Analysis

Results of analysis on the AGRN and CABN evolved by (Lones et. al., 2011) indicated that the best AGRN and
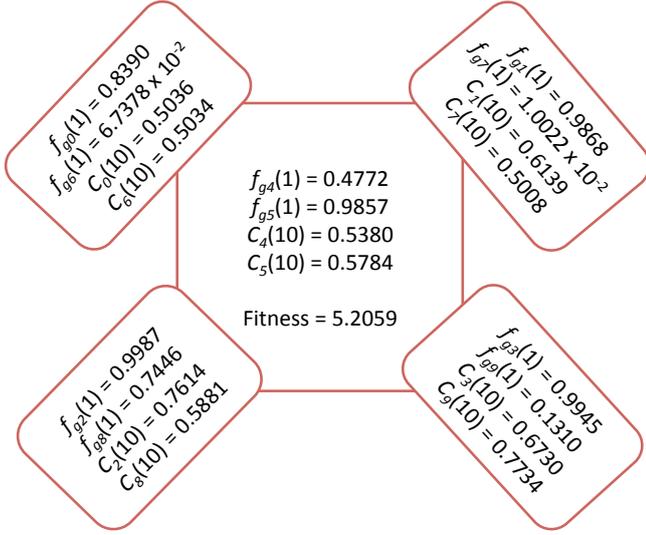
Figure 8 (top-left node):

$f_{g1}(1) = 0.8390$
$f_{g0}(1) = 6.7378 \times 10^{-2}$
$f_{g6}(1) = 0.5036$
$C_0(10) = 0.5034$

(top-right node):

$f_{g1}(1) = 0.9868$
$f_{g7}(1) = 1.0022 \times 10^{-2}$
$C_1(10) = 0.6139$
$C_7(10) = 0.5008$

(centre):

$f_{g4}(1) = 0.4772$
$f_{g5}(1) = 0.9857$
$C_4(10) = 0.5380$
$C_5(10) = 0.5784$

Fitness = 5.2059

(bottom-left node):

$f_{g2}(1) = 0.9987$
$f_{g8}(1) = 0.7446$
$C_2(10) = 0.7614$
$C_8(10) = 0.5881$

(bottom-right node):

$f_{g3}(1) = 0.9945$
$f_{g9}(1) = 0.1310$
$C_3(10) = 0.6730$
$C_9(10) = 0.7734$

Figure 8: How the symmetry is observed by the genes and enzymes in the (artificial) organism's CABN of the third best evolved solution. There are 6 *predatory* genes, 3 *anti-prey* genes and 1 *neutral* gene, and there are 4 *predatory* chemicals and 6 *neutral* chemicals produced. The high number of *neutral* chemicals produced has help balanced the *predatory* tendencies provided by the *predatory* prone AGRN (that has higher number of *predatory* genes in comparison).

Figure 9 (top-left node):

$f_{g1}(1) = 0.8902$
$f_{g0}(1) = 1.0000$
$f_{g6}(1) = 0.2738$
$C_0(10) = 0.4692$

(top-right node):

$f_{g1}(1) = 1.0000$
$f_{g7}(1) = 1.4690 \times 10^{-3}$
$C_1(10) = 0.3836$
$C_7(10) = 0.5001$

(centre):

$f_{g4}(1) = 0.8887$
$f_{g5}(1) = 0.9931$
$C_4(10) = 0.5707$
$C_5(10) = 0.5790$

Fitness = 5.2075

(bottom-left node):

$f_{g2}(1) = 0.9980$
$f_{g8}(1) = 0.7446$
$C_2(10) = 0.2332$
$C_8(10) = 0.2231$

(bottom-right node):

$f_{g3}(1) = 0.9949$
$f_{g9}(1) = 7.2297 \times 10^{-2}$
$C_3(10) = 0.3238$
$C_9(10) = 0.4507$

Figure 9: How the symmetry is observed by the genes and enzymes in the (artificial) organism's CABN of the second best evolved solution. There are 8 *predatory* genes and 2 *anti-prey* genes. There are 5 *anti-prey* chemicals and 5 *neutral* chemicals produced, to help balance the *predatory* tendencies described by the *predatory* prone AGRN (higher number of *predatory* genes in comparison).

CABN controllers (controllers with the best fitness values) have:

1. Symmetry within its network; whereby the best evolved AGRN controllers have equal number of *predatory* and *anti-prey* genes in its AGRN and small number of *neutral* genes.
2. Similar to (Mokhtar, 2012), the best evolved CABN controllers' $\approx 50\%$ *predatory* genes + chemicals are

Figure 10 (top-left node):

$f_{g1}(1) = 0.9463$
$f_{g0}(1) = 0.5720$
$f_{g6}(1) = 0.5931$
$C_0(10) = 0.4692$

(top-right node):

$f_{g1}(1) = 0.9945$
$f_{g7}(1) = 0.5789$
$C_1(10) = 0.8323$
$C_7(10) = 0.5001$

(centre):

$f_{g4}(1) = 0.9051$
$f_{g5}(1) = 0.9912$
$C_4(10) = 0.2994$
$C_5(10) = 0.5000$

Fitness = 5.5849

(bottom-left node):

$f_{g2}(1) = 0.9945$
$f_{g8}(1) = 0.7446$
$C_2(10) = 0.5080$
$C_8(10) = 0.2231$

(bottom-right node):

$f_{g3}(1) = 0.9831$
$f_{g9}(1) = 0.1457$
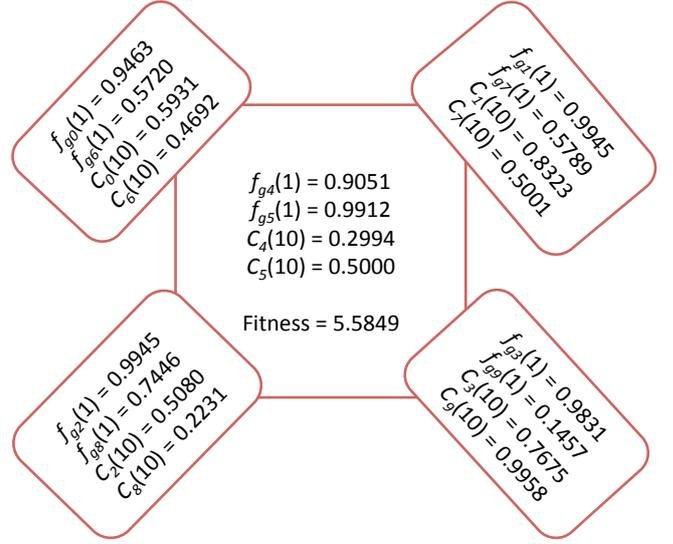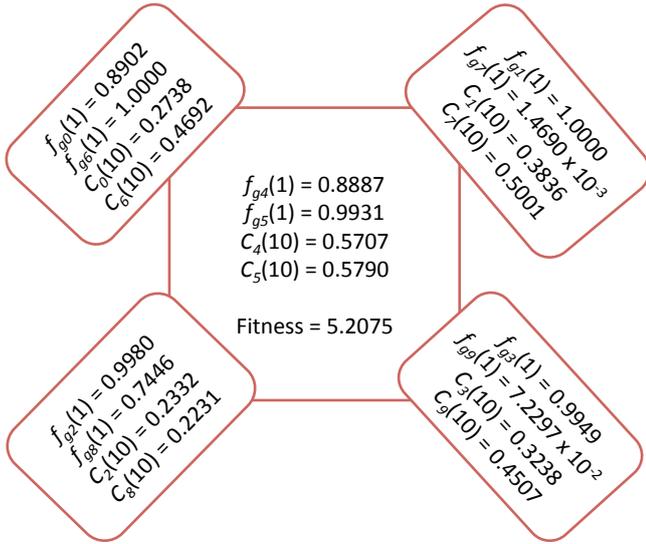$C_3(10) = 0.7675$
$C_9(10) = 0.9958$

Figure 10: How the symmetry is observed by the genes and enzymes in the (artificial) organism's CABN of the best evolved solution. There are 7 *predatory* genes, 1 *anti-prey* genes and 2 *neutral* genes. There are 3 *predatory* chemicals, 2 *anti-prey* chemicals and 5 *neutral* chemicals produced. The *predatory* tendencies that is provided by the *predatory* prone AGRN is balanced by the high number of *neutral* chemical produced by the AMN.

balanced by the $\approx 50\%$ *anti-prey* and *neutral* genes + chemicals.

6.2. Similar Objectives to (Mokhtar, 2012)

We revisited the system that was described in Sec. 5 and its objectives. We (re-)evolved the ABN and the AGRN-only controllers in order to investigate if the attributes listed are also observed in these systems, or whether they are similar to those described in Sec. 6.1. We will first discuss the attributes of the AGRN (Sec. 6.2.1) with $i_t = 1$ and $i_t = 10$, followed by the ABN (Sec. 6.2.2). The new evolved ABN has $i_t = 10$.

6.2.1. Artificial Genetic Regulatory Network

We re-run the experiment described in (Mokhtar, 2012), but with only the AGRN (Sec. 4.1) providing the required controls. The population of 1000 AGRN was evolved using SPEA2 (Popov, 2005), with the mutation rate = 0.0143 and crossover rate = 0.5. The inputs E_D, E_R and S_E are presented to all genes, and g_x to $g_{x-(d-1)}$ are the output genes with d is the number of output and x is the number of genes in the AGRN.

For $n = 1$, we first evolved using the same fitness objectives listed in (Mokhtar, 2012). The AGRNs are first evolved so that the best evolved AGRNs achieved the fitness objectives of (Algorithm 3):

1. $E_D \approx (U_E + U_S)$ (F_1)
2. $S_E > 0$ (F_2)

The population is evolved for 1000 generations. The AGRN differs from the previous, whereby each AGRN has

Algorithm 3: Calculating fitness objectives F_1 and F_2. SPEA2 evolves the solutions towards minimising the fitness values.

Constant: $y = 100$. There are 100 time steps for in the simulation.

```
1  begin
2  |    F₁(0) = y;
3  |    F₂(0) = y;
4  |    for t = 1 : y do
5  |    |    if E_D(t) ≤ U_E(t) + U_S(t) and
   |    |       E_D(t) + 0.25 > U_E(t) + U_S(t) then
6  |    |    |    F₁(t) = F₁(t − 1) − 1;
7  |    |    end
8  |    |    if S_E(t) > 0 then
9  |    |    |    F₂(t) = F₂(t − 1) − 1;
10 |    |    end
11 |    end
12 end
```

$d = 3$ output genes instead of 2. Each of the output genes is responsible for:

1. to make use of the available E_R to meet with the required E_D: $U_E = E_R . g_x$. x is the number of genes in the AGRN.

2. to save energy (E_S) in S_E: $E_S = E_R . g_{x-1}$ (instead of $E_S = E_R . (1 - g_x)$, if $d = 2$).

3. to use energy in S_E to help meet with E_D: $U_S = S_E . g_{x-2}$ (instead of $U_S = S_E . g_{x-1}$, if $d = 2$).

Mokhtar (2012) indicated that:

1. U_E provided by g_x is considered as *predatory* behaviour.

2. U_S provided by g_{x-2} if $d = 3$ or g_{x-1} if $d = 2$ is considered as *anti-prey* behaviour.

Because of the third output gene, another fitness objective is added, which states the population is to evolve so that:

1. $g_{x-1} + g_x \leq E_R$ (F_0).

Two definitions of *predatory* and *anti-prey* genes are presented:

1. Mokhtar (2012) states that:
   (a) *Predatory* genes are genes that are constantly producing the output ≈ 1
   (b) *Anti-prey* genes are genes that are constantly producing the output ≈ 0
   (lines 3 - 21 in Algorithm 4)

2. In Sec. 6.1, we stated that if $\rho_x = f(1)$ and $f_x(1)$ utilises the sigmoid function (1):
   (a) *Predatory* genes are genes with $\rho_x \geq 0.6$
   (b) *Anti-prey* genes are genes with $\rho_x \leq 0.4$
   (lines 3 - 11 in Algorithm 5)

Algorithm 4: Calculating fitness objectives F_3 to f_6. SPEA2 evolves the solutions towards the minimised fitness values.

Constant: $y = 100$. There are 100 time steps for in the simulation.
Constant: $x = $ Number of genes (g) in the AGRN.
Input: $\lambda_i = $ The gene expression level for g_i; $i \in x$.
Output: $g_x \subset G = $ Output gene responsible for U_E.
Output: $g_{(x-1)} \subset G = $ Output gene responsible for U_S.

```
1  begin
2  |    P_{g_x} = y;
3  |    for t = 1 : y do
4  |    |    for z = 1 : x do
5  |    |    |    if λ_z(t) ≥ 0.6 then
6  |    |    |    |    P_{g_z}(t) = P_{g_z}(t) + 1;
7  |    |    |    else if λ_z(t) ≤ 0.4 then
8  |    |    |    |    P_{g_z}(t) = P_{g_z}(t) − 1;
9  |    |    |    end
10 |    |    end
11 |    end
12 |    P = 0; A_P = 0; N = 0;
13 |    for z = 1 : x do
14 |    |    if P_{g_z}(y) ≥ 5 then
15 |    |    |    P = P + 1;
16 |    |    else if P_{g_z}(y) ≤ −5 then
17 |    |    |    A_P = A_P + 1;
18 |    |    else
19 |    |    |    N = N + 1;
20 |    |    end
21 |    end
22 |    F₃ = |P − A_P| × 10;
23 |    F₄ = |A_P − N| × 10;
24 |    if P_{g(x−1)} ≥ 5 then
25 |    |    F₅ = 100;
26 |    else if P_{g(x−1)} ≤ −5 then
27 |    |    F₅ = 0;
28 |    else
29 |    |    F₅ = 50;
30 |    end
31 |    if P_{g_x} ≥ 5 then
32 |    |    F₆ = 0;
33 |    else if P_{g_x} ≤ −5 then
34 |    |    F₆ = 100;
35 |    else
36 |    |    F₆ = 50;
37 |    end
38 end
```

The best evolved solution have the fitness values of $F_1 = 30$, $F_2 = 0$ and $F_0 = 57$.

1. If based on the definition of *predatory* and *anti-prey* genes described in (Mokhtar, 2012), the best evolved

Algorithm 5: Calculating fitness objectives F_7 to F_{10}. SPEA2 evolves the solutions towards the minimised fitness values.

Constant: $x = $ Number of genes (g) in the AGRN.

Input : $\rho_i = $ The gene expression level for g_i when $\lambda_i = f(1)$; $i \in x$ and $f(1)$ is calculated using (1)

Output : $g_x = $ Output gene responsible for U_E.

Output : $g_{(x-1)} = $ Output gene responsible for U_S.

```
 1 begin
 2 │   P = 0; A_P = 0; N = 0;
 3 │   for z = 1 : x do
 4 │   │   if ρ_z ≥ 0.6 then
 5 │   │   │   P = P + 1;
 6 │   │   else if ρ_z ≤ 0.4 then
 7 │   │   │   A_P = A_P + 1;
 8 │   │   else
 9 │   │   │   N = N + 1;
10 │   │   end
11 │   end
12 │   F_7 = |P − A_P| × 10;
13 │   F_8 = |A_P − N| × 10;
14 │   if ρ_(x−1) ≥ 0.6 then
15 │   │   F_9 = 100;
16 │   else if ρ_(x−1) ≤ 0.4 then
17 │   │   F_9 = 0;
18 │   else
19 │   │   F_9 = 50;
20 │   end
21 │   if ρ_x ≥ 0.6 then
22 │   │   F_10 = 0;
23 │   else if ρ_x ≤ 0.4 then
24 │   │   F_10 = 100;
25 │   else
26 │   │   F_10 = 50;
27 │   end
28 end
```


Figure 11: The U_E, U_S, E_S, g_x, g_{x-1} and g_{x-2} for the best evolved AGRN from Set 1. This best evolved AGRN has the fitness values of $F_1 = 30$, $F_2 = 0$ and $F_0 = 57$. The top figure shows the outputs of the AGRN aiming to meet E_D. The bottom figure, however, shows the AGRN violates the rule $g_{x-1} + g_x \leq E_R$, whilst doing so.

AGRN has 6 *predatory* genes, 5 *anti-prey* genes and 1 *neutral* genes[6]. Results also show that in the best evolved AGRN:

(a) g_x is categorised as a *predatory* gene,

(b) g_{x-1} is categorised as a *neutral* gene, and

(c) g_{x-2} is categorised as an *anti-prey* gene.

These categorisation of behaviours are similar to the observation made by (Mokhtar, 2012).

2. If based on the definition of *predatory* and *anti-prey* genes described in Sec. 6.1, this best evolved AGRN instead has 1 *predatory* genes, 4 *anti-prey* genes and 8 *neutral* genes. Results also show that in the best evolved AGRN:

(a) g_x is categorised as a *predatory* gene,

(b) g_{x-1} is categorised as a *neutral* gene, and

(c) g_{x-2} is categorised as an *anti-prey* gene;

Similar observations are also described in (Mokhtar, 2012).

The best evolved AGRN, however, violates the rule $g_x + g_{x-1} \leq E_R$. This is as shown in Fig. 11.

To help improve the outcome of the evolution, a second population of AGRNs are evolved using the fitness objectives F_1 and F_2, as well as new fitness objectives derived based on the analysis presented in (Mokhtar, 2012) (F_3 and F_4). The new fitness objectives state that there should be almost equal number of *neutral* and *anti-prey* genes in the AGRN (lines 22 - 23 in Algorithm 4)[7]. Similar to (Mokhtar, 2012), the AGRN has $d = 2$ output genes.

The population was also evolved for 1000 generations. The best fitness values produced after the 1000th generation are $F_1 = 37$ and $F_2 = 1$.

1. If based on (Mokhtar, 2012), the best evolved AGRN has 4 *predatory* genes, 5 *anti-prey* genes and 3 *neutral* genes. g_x and g_{x-1} are both categorised as *predatory* genes.

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[6]These characteristics are similar to the systems discussed in Sec. 6.1 (the characteristics of the best evolved AGRNs and CABNs used to control the legged robot).

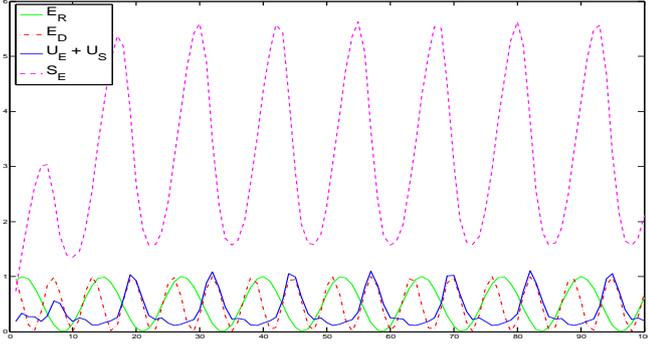[7]The population was evolved with F_3 because of the contradicting observation presented in Sec. 6.1.1

Figure 12: The U_E and U_S (g_x and g_{x-1}) for the best evolved AGRN from Set 2. This best evolved AGRN has the fitness values of $F_1 = 37$ and $F_2 = 1$.

2. If based on Sec. 6.1, this best evolved AGRN has 3 *predatory* genes, 5 *anti-prey* genes and 4 *neutral* genes. g_x is categorised as a *predatory* gene and g_{x-1} is categorised as an *anti-prey* gene.

The best evolved AGRN has more *anti-prey* genes than *predatory* genes. This causes the organism to save as much energy as possible ($U_S \rightarrow S_E$), to use at time when the energy resources (E_R) is low. This is as shown in Fig. 12. These characteristics were too observed by Mokhtar (2012).

A third population was evolved using the fitness objectives F_1 to F_4, as well as a new set of fitness objectives derived based on the analysis of the best evolved AGRNs and ABNs described in Sec. 6.1 (F_5 to F_{10}). The fitness objectives state that:

1. g_{x-1} is considered as *anti-prey* (F_5), lines 24 - 30 in Algorithm 4.
2. g_x is considered as *predatory* genes (F_6), lines 31 - 37 in Algorithm 4.
3. Almost equal number of *predatory* and *anti-prey* genes in the AGRN given $\rho = f(1)$ (F_7 and F_8), lines 3 - 13 in Algorithm 5.
4. ρ_{x-1} is considered as *anti-prey* genes (F_9), lines 14 - 20 in Algorithm 5.
5. ρ_x is considered as *predatory* genes (F_{10}), lines 21 - 27 in Algorithm 5.

The population is evolved for 1000 generations[8], and there are two output genes in the AGRN similar to (Mokhtar, 2012).

The best evolved solution has the fitness values $F_1 = 23$ and $F_2 = 0$. The AGRN:

1. if based on (Mokhtar, 2012), the best evolved AGRN has 6 *predatory* genes, 6 *anti-prey* genes and 0 *neutral* genes. g_x is categorised as a *predatory* gene and g_{x-1} as an *anti-prey* gene.

---

2. if based on Sec. 6.1, this best evolved AGRN has 6 *predatory* genes, 6 *anti-prey* genes and 0 *neutral* genes. g_x is categorised as a *predatory* gene and g_{x-1} is categorised as an *anti-prey* gene.

The symmetry in this best evolved AGRN is similar to that of the best evolved AGRNs and CABNs used to control the legged robots (Sec. 6.1). The characteristics of the last evolved population for the third set, illustrated in Fig. 14, indicate the similarity and symmetry. This best evolved AGRN is also best among the three sets because its $U_E + U_S$ values match closer to its E_D (Fig. 11 to Fig. 13)

The results also show that, with the introduction of the proposed fitness objectives F_3 - F_{10}, better evolved solutions can be produced. This combination of fitness objectives are used from this point forth.
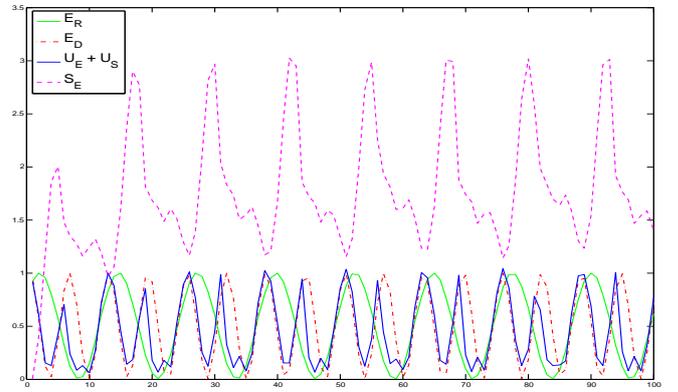

Figure 13: The U_E and U_S (g_x and g_{x-1}) for the best evolved AGRN from Set 3. This best evolved AGRN has the fitness values of $F_1 = 23$ and $F_2 = 0$.

For the AGRN with $i_t = 10$, the population were evolved using the fitness objectives presented in Algorithms 4 and 5 (F_3 - F_{10}). After 1000 generation, the best evolved AGRN has the fitness value of $F_1 = 41$ and $F_2 = 0$.
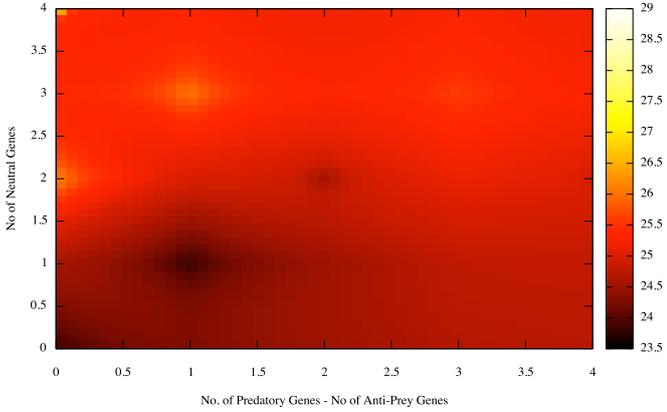
1. If based on (Mokhtar, 2012), the best evolved AGRN has 4 *predatory* genes, 4 *anti-prey* genes and 4 *neutral* genes. g_x is categorised as a *predatory* gene and g_{x-1} as an *anti-prey* gene.
2. If based on Sec. 6.1, this best evolved AGRN has 4 *predatory* genes, 6 *anti-prey* genes and 2 *neutral* genes. g_x is categorised as a *predatory* gene and g_{x-1} is categorised as an *anti-prey* gene.

Figure 16 illustrates how well this best evolved AGRN's $U_E + U_S$ aims to meet its E_D given the E_R. The figure shows that the best evolved organism is unable to meet E_D most effectively. This is because it refuses to use its energy in S_E when $E_D > E_R$ most appropriately. If based on the observation made by (Mokhtar, 2012), these behavioural tendencies are the result of the inequality in the AGRN due to the higher number of *anti-prey* + *neutral* genes.

The characteristics of the last evolved population is shown in Fig. 15. The figure does however show similar
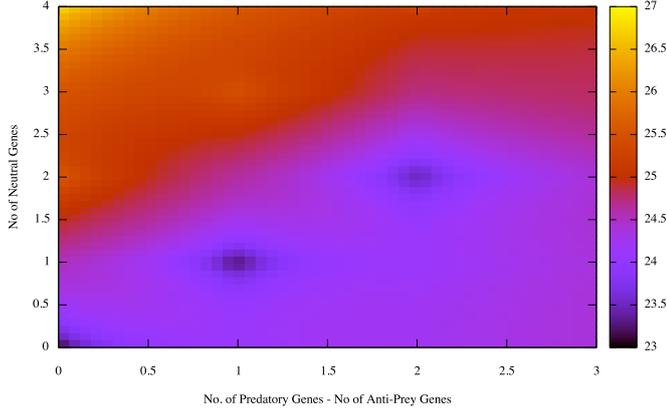
(a) Derived based on the method of analysis described in Sec. 6.1 (Algorithm 5)

(b) Derived based on the method of analysis described in (Mokhtar, 2012)

Figure 14: The properties of AGRNs from the best (and last) evolved population of the third set. The colour values (legend) indicate the fitness value F_1 for a particular AGRN ($F_2 < 5$). The lower the fitness value, the better the (artificial) organism. Figures show that the best evolved organism has symmetrical property in its AGRN, with an almost equal number of *predatory* and *anti-prey* genes, and low number of *neutral* genes (ignoring the 0.5 values in the y-axis). This observation is similar to the results of analysis described in Sec. 6.1.

characteristics to that described in Sec. 6.1, which shows that good solutions (solutions with low fitness values) have an almost equal number of *predatory* and *anti-prey* genes and low number of *neutral* genes in its AGRN (Fig. 17).

6.2.2. Artificial Bio-chemical Network

We re-run the experiment described in (Mokhtar, 2012), but with $i_t = 10$ and the fitness objectives F_1 to F_{10}. A population of 750 ABN was evolved using SPEA2 (Popov, 2005), with the mutation rate = 0.0143 and crossover rate = 0.5, for 1000 generations.

The evolutionary process has produced the best evolved ABN with similar characteristics to that of the previous systems. The best evolved solution with fitness values of $F_1 = 32$ and $F_2 = 0$ has:

1. If based on the categorisation of behaviours described
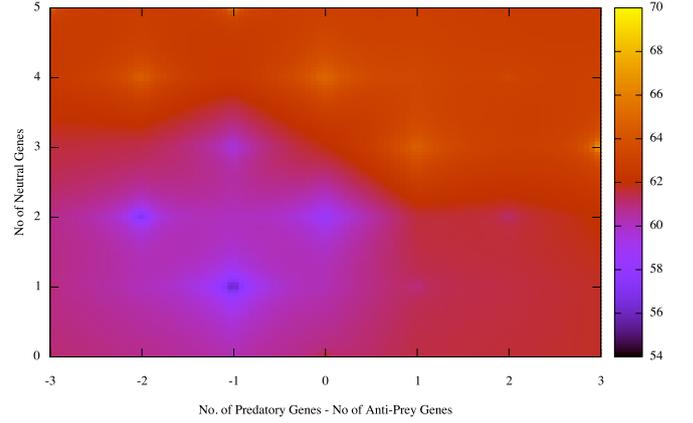
(a) Derived based on the method of analysis described in Sec. 6.1 (Algorithm 5)
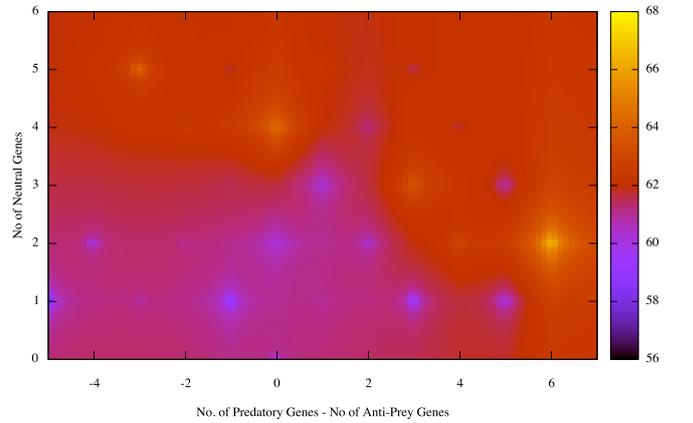
(b) Derived based on the method of analysis described in (Mokhtar, 2012)

Figure 15: The properties the best evolved population of the AGRNs with $i_t = 10$. The colour values (legend) indicate the fitness value F_1 for a particular AGRN ($F_2 < 5$). The lower the fitness value, the better the (artificial) organism. Figures show that the best evolved organism has more *anti-prey* genes in comparison to the *predatory*. genes. This has resulted in the best evolved solution having greater tendencies to store energy at time when $E_D < E_R$, and not to use the energy when $E_D > E_R$ (Fig. 16). Figures also show that when there is an almost equal number of *predatory* and *anti-prey* genes and low number of *neutral* genes, the fitness value is low, which indicates for a good solution (Fig. 17).

by (Mokhtar, 2012), there are 3 *predatory* genes, 3 *anti-prey* genes and 0 *neutral* genes, with

   (a) C_{O1} used to decide on the U_S (which indicates how to utilise the available energy in S_E to meet with the required E_D) is categorised as *neutral*.

   (b) C_{O2} that decides on the U_E (how to use E_R to meet with the required E_D) is considered as *neutral*

2. If is based on Sec. 6.1, there are 3 *predatory* genes, 3 *anti-prey* genes and 0 *neutral* genes, with

   (a) C_{O1} is categorised as an *anti-prey* behaviour,

   (b) C_{O2} is considered as *predatory* behaviour,
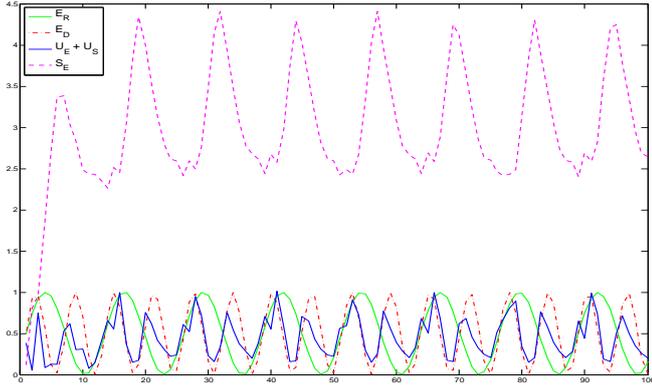
   similar to that described in Mokhtar (2012).

Figure 16: The U_E and U_S (g_x and g_{x-1}) for the best evolved AGRN with $i_t = 10$. This best evolved AGRN has the fitness values of $F_1 = 41$ and $F_2 = 0$. If based on Sec. 6.1, the AGRN consists of 4 *predatory* genes, 6 *anti-prey* genes and 2 *neutral* genes. This has resulted in the best evolved solution having greater tendencies to store energy at time when $E_D < E_R$, and not to use the energy to meet E_D when $E_D > E_R$.
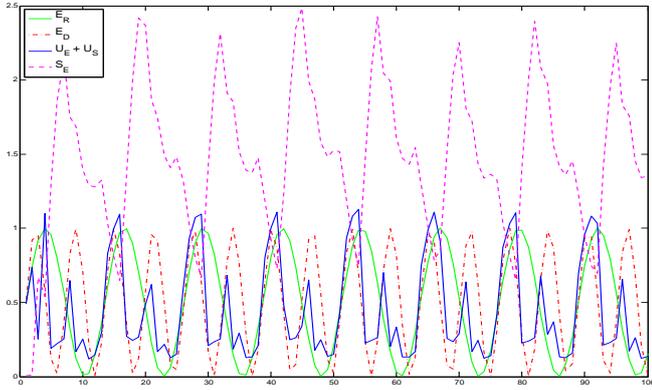

Figure 17: The U_E and U_S (g_x and g_{x-1}) for the evolved AGRN with $i_t = 10$, fitness values of $F_1 = 47$ and $F_2 = 0$, and an almost equal number of *predatory* and *anti-prey* genes and low number of *neutral* genes in its AGRN (if based on Sec. 6.1).

Figure 18 illustrates the properties of the evolved population. Figure shows that there is symmetry (equal number of *predatory* and *anti-prey* genes, with low number of *neutral* genes) in the best evolved AGRN. This observation is similar to other best evolved solutions. Figure 19 illustrates how well the best evolved ABN's $U_E + U_S$ meets its E_D given the E_R.

6.2.3. Summary of Results

Results show that the (artificial) organisms with the best fitness values are the organisms that are in homeostasis. The organisms are in homeostasis when they have an almost equal number of *predatory* and *anti-prey* genes/chemicals in its (artificial) bio-chemical network, and with low (or zero) number of *neutral* genes. This observation differs from the initial heuristics made in (Mokhtar, 2012), which states that the AGRN should consist of (i) 50% *predatory* genes, (ii) 25% *anti-prey* genes,
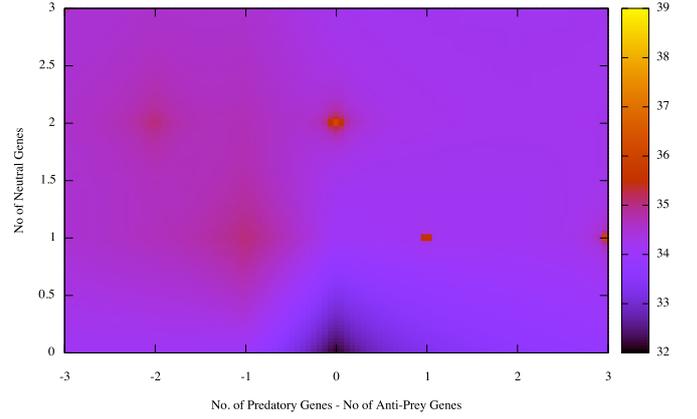
(a) Derived based on the method of analysis described in Sec. 6.1 (Algorithm 5)
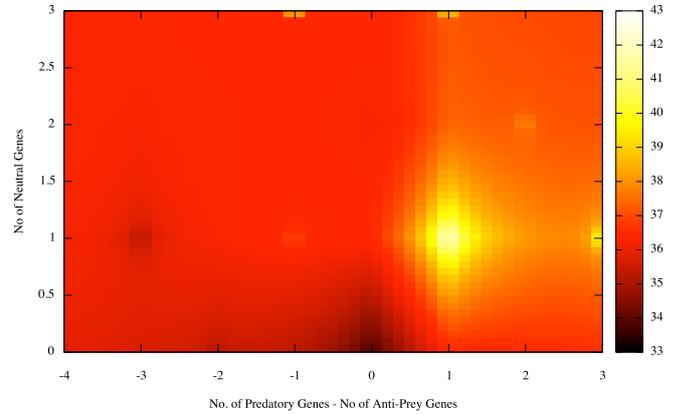
(b) Derived based on the method of analysis described in (Mokhtar, 2012) (Algorithm 4)

Figure 18: The properties of the AGRNs of the evolved ABNs. The colour values (legend) indicate the fitness value F_1 for a particular AGRN ($F_2 < 5$). The lower the fitness value, the better the (artificial) organism. Figure shows that the best evolved organism has symmetrical property in its AGRN, with an almost equal number of *predatory* and *anti-prey* genes, and zero *neutral* genes (ignoring the 0.5 values in the y-axis). The best evolved ABN's C_{O1} is categorised as *anti-prey* behaviour, and C_{O2} as *predatory* behaviour; therefore symmetry is preserved in the organism.

and (iii) 25% *neutral* genes.

The new heuristics are also useful in guiding the evolution of the artificial organism. This is because better AGRNs and ABNs were found when using the fitness objectives derived from these new heuristics ($F_1 - F_{10}$). Further analysis of the results indicate that the fitness objectives F_4 (in Algorithm 4) and F_8 (in Algorithm 5) are no longer ideal for use in the evolution of the ABNs and AGRNs for the artificial organisms. This is because when two separate populations of ABN were evolved, the results of these evolution (Fig. 21 - 22) indicate that F_4 and F_8 can delineate from finding the best solutions.
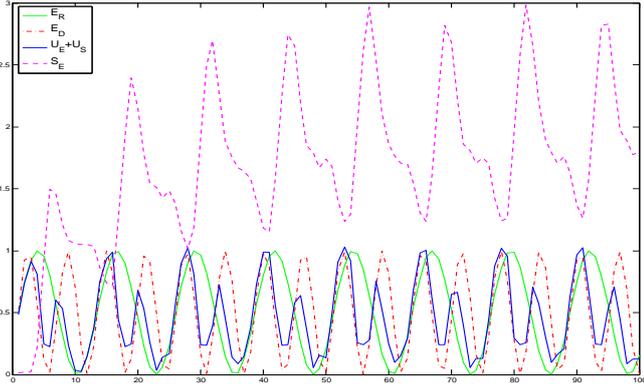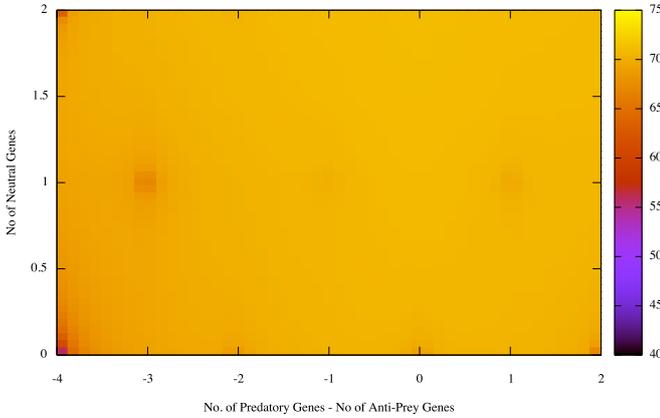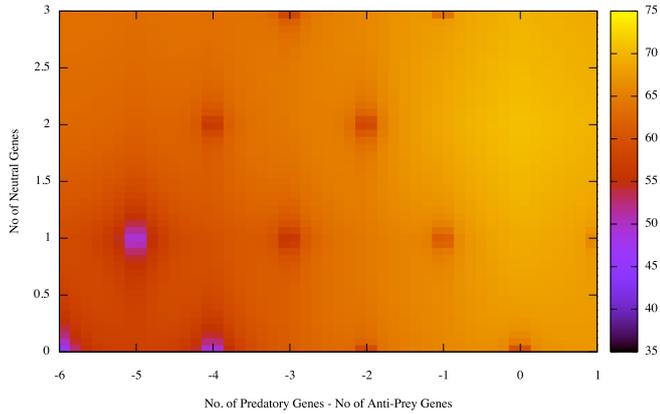
Figure 19: The U_E and U_S (C_{O1} and C_{O2}) for the best evolved ABN. This best evolved ABN has the fitness values of $F_1 = 32$ and $F_2 = 0$.
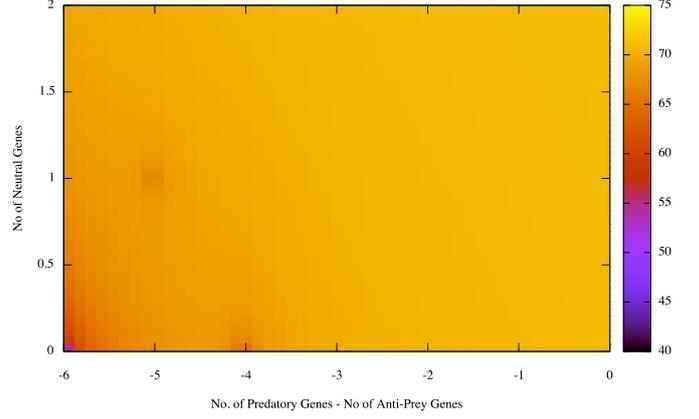

(a) Population no. 2

(b) Population no. 3

Figure 20: The properties of the AGRNs of a second and third separate populations of the evolved ABNs, derived based on the method of analysis described in (Mokhtar, 2012). (Algorithm 4)
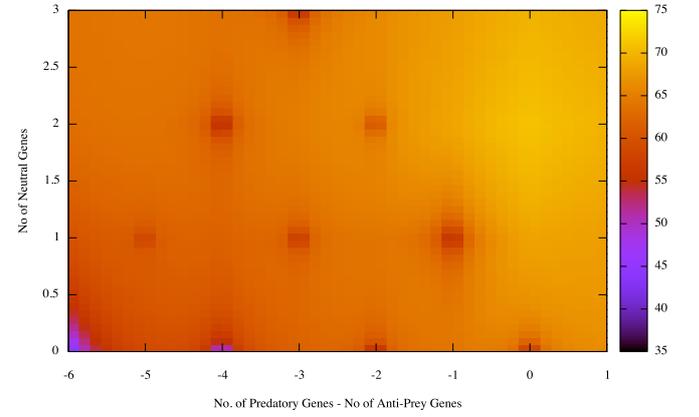
7. Conclusions

The results of analysis have provided useful information that can help us answer the following questions:

1. What encodes the organism's two different categories

(a) Population no. 2

(b) Population no. 3

Figure 21: The properties of the AGRNs of a second and third separate populations of the evolved ABNs, derived based on the method of analysis described in Sec. 6.1 (Algorithm 5). The populations were evolved for up to 1000 generations with fitness objectives F_1 to F_{10}. The colour values (legend) indicate the fitness value F_1 for a particular AGRN ($F_2 < 5$). The lower the fitness value, the better the (artificial) organism. Figures show that the best evolved organism has low number of (or zero) *neutral* genes in its AGRN (ignoring the 0.5 values in the y-axis). Figures therefore indicate that F_4 and F_8 can delineate from finding the best solutions.

of behaviours?

   (a) Can the behaviour be divided into *predatory* and *anti-prey* behaviours?

2. Is there an innate mechanism(s) that switches and resolves conflicts between the two opposing behaviours?

3. How are the organism's GRN maintains homeostasis of the organism?

4. How the organism's GRN affects the metabolic network and/or signalling network (the bio-chemical network) of the organisms in order to maintain homeostasis?

The results of analysis show that there are innate properties and mechanisms that describe and govern the switching of two opposing behaviours in an (artificial) organisms, whereby:
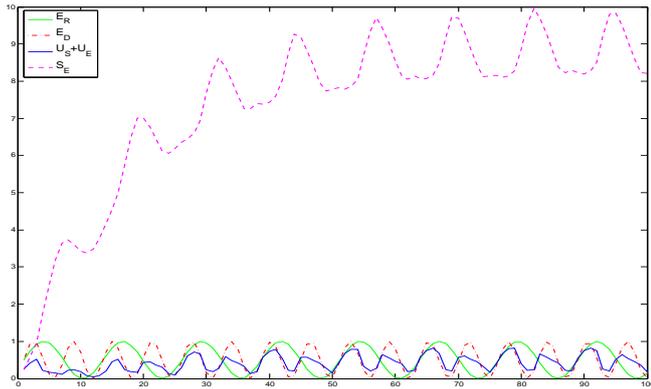
13

Figure 22: The U_E and U_S (C_{O1} and C_{O2}) for the evolved ABN of population no. 3 (Fig. 20 and Fig 21), with equal number of *predatory* and *anti-prey* genes and chemicals in the AGRN and ABN, and zero *neutral* genes. This best evolved ABN has the fitness values of $F_1 = 50$ and $F_2 = 3$.

1. *Predatory* behaviours are behaviours provided by the genes or chemical outputs within its ABN with:
   (a) $f(1)/m(1) \geq 0.6$, and
   (b) g_x/C_{Ox} are constantly producing $\lambda_x \approx 1$.
2. *Anti-prey* behaviours are behaviours provided by the genes or chemical outputs with:
   (a) $f(1)/m(1) \leq 0.4$, and
   (b) g_x/C_{Ox} are constantly producing $\lambda_x \approx 0$

Results also show that the (artificial) organisms are in homeostasis when they have an almost equal number of *predatory* and *anti-prey* genes/chemicals in its (artificial) bio-chemical network, and with low number of (or zero) *neutral* genes/chemicals in its AGRN/ABN. This indicates that the organisms are in equilibrium.

These heuristics can and had helped in the evolution of the bio-chemical networks for the artificial organisms.

Acknowledgement

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