The Application of Knowledge-Growing System to Multiagent Collaborative Computation for Inferring the Behavior of Genes Interaction

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Summary
Knowledge Growing System (KGS) is a novel perspective in Artificial Intelligence (AI) which is aimed to emulate how the human brain obtains new knowledge from information delivered by human sensory organs. The new knowledge is then used as the basis for making estimation in the future of the phenomenon being observed as the basis for the most appropriate decision or action that will be decided or taken. In this paper we address the application of KGS to infer the behavior of genes interaction in Genetic Regulatory System (GRS) in order to estimate their behavior in the subsequent interaction time. For this purpose we model the genes as multi-agent that performs collaborative computations in Multiagent Collaborative Computation (MCC) paradigm. The knowledge regarding the genes behavior is obtained by applying a novel information-inferencing fusion method called Observation Multi-time Arwin-Adang-Aciek-Sembiring (OMA3S). In order to show how KGS works in MCC framework, we use yeast genes-interaction values as the case study

Keywords:
AI, GRS, knowledge growing, KGS, MCC, OMA3S

1. Introduction

Humans since their born are already equipped with much grandeur that evolves as the time passes. The most ultimate humans' grandeur is the intelligence that is not possessed by other living things. This intelligence grows along with the accretion of information they perceive from the environment time-by-time. This is a humans' unique phenomenon that we call as knowledge-growing mechanism. Based on this observation followed with deep-investigation on this phenomenon we have developed a novel perspective in Artificial Intelligence (AI) called Knowledge Growing System (KGS) [1-4].

The research in AI field has also defined a new term called agent [5][6] which a representation of human agent in computing world. In its very simple definition agent is an entity that performs the work on behalf of another entity or a group of entities [7]. We also made some observations in the real-life that humans always work together to solve complex problems. They usually partition a complex problem into some sub-problems that will be solved by some groups of people. By doing in this way, they can work on the sub-problems in parallel manner to achieve sub-goals. In the end, all sub-goals will be fused or combined to become a single goal. This is the mechanism that we call as collaborative computation. Because we are doing it in multiagent framework, therefore we define a new term called Multiagent Collaborative Computation (MCC) [7-9].

It is not easy to find a case that can be used to present the mechanism occurred within KGS. From our other research we found that the evolution of humans' intelligence is connected very much to the internal process in humans' body called Genetic Regulatory System (GRS), i.e. a system that regulates when and in what form a gene or genes will be expressed [10]. Why? Humans' body is formed by millions of cells where their functions are performed by genes in sequences of well-coordinated activities. The function of a living cell is performed by a sequence of well-coordinated activities by a large number of genes. The gene itself is a sequence of Deoxyribonucleic Acid (DNA).

The expression of a gene is a biological process which a DNA sequence is translated to become a protein. The protein is an important molecule for determining the structure, mortality, metabolism, signaling, reproduction, etc. of a cell. Some genes influence how other gene or genes are expressed. Modifying genes may change the affect of other genes. The expression of a gene or genes is regulated by a mechanism called GRS. The GRS' task is to control whether genes are active or inhibit.

Of ways for understanding and analyzing the behavior of GRS is by using microarray data. Microarray is sets of miniaturized reaction areas that may also be used to test the binding of DNA fragments [11] and it exploits the preferential binding of complementary nucleic acid

Manuscript received November 5, 2009
Manuscript revised November 20, 2009

sequences to simultaneously measure expression levels of thousands of genes [12]. By having knowledge regarding the influence of a gene or genes to the others in microarray data, we can make estimations of the genes behavior in GRS in order to obtain better products in the future. According to [13], there are three basic questions that can be answered by using microarray data:

(1) What genes are expressed in a given sample?
(2) Which genes are differentially expressed between different samples?
(3) How can one find different classes, or clusters, of genes which are expressed in a correlated fashion across a set of samples? How can one find different classes of samples based on their gene expression behavior?

In this paper we address the application of KGS in MCC framework to model the genes' interactions in GRS to address question (1). Simply, each gene will be represented by an agent that performs internal activities and performs communications with other genes as occurred in biological genes. We use secondary data of yeast cycle database taken from [6] as the case study. The rest of the paper is structured as follows. The concept of MCC and a review of the state-of-the-art of GRS research will be delivered in Section 2. In this section we also explain the concept of KGS as well as MCC. In Section 3, we present the application of KGS to MCC for inferring the behavior of the genes in GRS. Finally, the paper is concluded in Section 4 with some concluding remarks and discussions.

2. State-of-the-Art of Genetic Regulatory System Research, the Concept of Knowledge-Growing System and Multiagent Collaborative Computation

2.1. What is GRS?

The expression of a gene is a biological process which a DNA sequence is translated to become a protein. The protein is an important molecule for determining the structure, mortality, metabolism, signaling, repro-duction, etc. of a cell. The expression of a gene may be controlled during Ribonucleic Acid (RNA) processing and transport (in eukaryotes), RNA translation, and the post-translational modification of proteins. The proteins fulfilling these regulatory functions are produced by other genes.

This gives rise to genetic regulatory systems structured by networks of regulatory interactions between DNA, RNA, proteins, and other molecules. Therefore, GRS is a mechanism for determining when, where, in what form and to which extent a gene or genes will be expressed. The mechanism occurs in the GRS is depicted in Fig. 1.

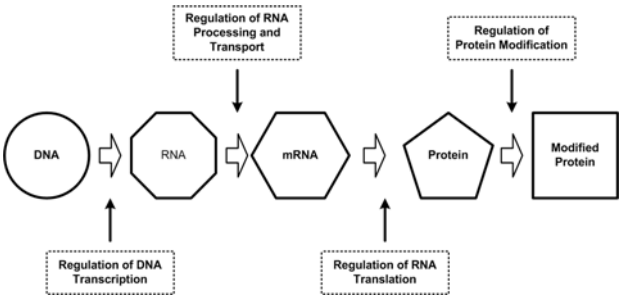

Fig. 1. Regulation of gene expression at different stages of protein synthesis [8] adapted from [14].

2.2. State-of-the-Art of Genetic Regulatory System Research

The research, studies, and experiments on GRS have been done widely all over the world. These efforts are aimed to one objective namely, how to obtain the most suitable model in order to present the mechanism occurs in GRS. In these endeavors, there are two approaches that have been carried out.

In the first approach the GRS mechanism is directly modeled by utilizing available methods such as Dynamic Bayesian Network (DBN) based on knowledge growing [15], weight matrices [16], petri nets [17], artificial gnome model [18], neural network (NN) [19] or its combination with fuzzy technique such as done by [20] with his Evolving Connectionist System (ECOS), piece-wise linear [21], Boolean [22], and power graph analysis [23].

The second one is to model the GRS by inferring its structure utilizing techniques such as best-fit extension problem [24], linear programming combined with supervised learning framework [25], DBN [26], evolutionary computation [27], graph and Linearized Additive Model (LAM) [28], steady-state gene expression [29], Dynamic Differential BN (DDBN) [30], combination of DBN with Reversible Jump Markov Chain Monte Carlo (RJMCC) [31] or with Greedy search algorithm and Markov Chain Monte Carlo (MCMC) [32], Bayesian and MCMC [33], iterative algorithm based on epistemic approach of conjecture and refutation [34], NN [35], and combination of clustering techniques with NNs [36].

On the writing of this paper, there is no literature that studies the analysis or inferring the behavior of genes in GRS in order to estimate their expression in the future especially that utilizes multiagent approach. There is also no method in AI that utilizes the concept we put into KGS namely the combination of information-inferencing fusion and intelligent programming [1-4]. These are the primary

matters that will be discussed in this paper. Our hypothesis is by utilizing KGS to MCC we can obtain knowledge regarding the genes behavior in GRS in order to estimate their behavior in the future for better life. Therefore, by having the knowledge of their behavior we can carry out anticipation actions in order to prevent the negative expression of genes that can cause negative effects to living organisms.

2.3. Knowledge-Growing System

Essentially, KGS is a system that is capable of growing its knowledge along with the accretion of information as the time passes [1-4]. The concept of KGS emerges from the observation of the mechanism occurs in human brain when performing information-inferencing fusion to obtain new knowledge. In order to have a more depth understanding on this mechanism, we developed a model of Human Inference System (HIS) [1] [2][37] as the basis for our model of KGS as depicted in Fig. 2.

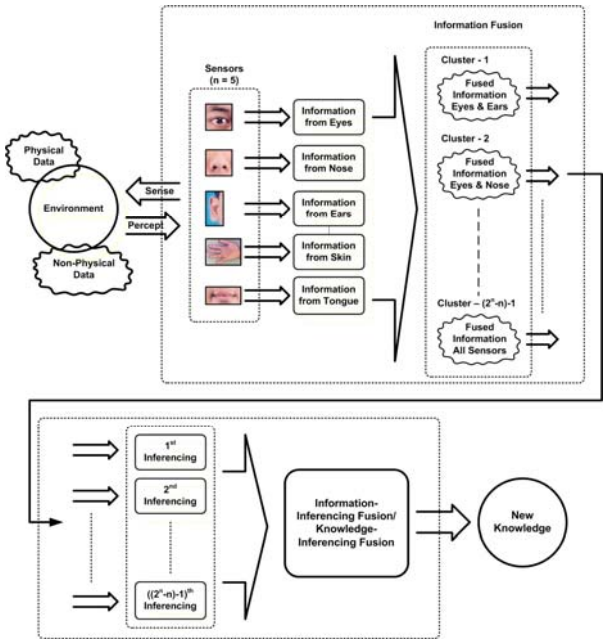

Fig. 2. A simplified illustration of human inference system [1] where n is the number of sensor.

As we can see in Fig.2, the process in obtaining new knowledge from information of a phenomenon observed by the sensory organs will have to get through three phases, i.e. information fusion, information inferencing, and information-inferencing fusion [1]. Based on the HIS model, we developed the mechanism that will be occurred in our model of KGS as depicted in Fig.3.

New knowledge in this scheme is called as comprehensive information with Degree of Certainty (DoC) or inferencing which means a value that determines the certainty of the new knowledge regarding the observed phenomenon is accurate. Term "T" is the representation of the time needed to obtain the new knowledge. The mechanism of knowledge-growing in KGS as illustrated in Figure 3 is performed by applying a novel information-inferencing fusion method called Observation Multi-time Arwin-Adang-Aciek-Sembiring (OMA3S) [1-4][38][39]. In general, the formula of OMA3S is presented in Equation (1) and Equation (2) as follows.

$$P(\Psi_i) = \frac{\sum_{j=1}^{m} P(\vartheta_i^j)}{m} \quad (1)$$

$$P(\Psi)_{estimate} = \max_{i=1,\ldots,n} \left[P(\Psi_i) \right] \quad (2)$$

with $P(\Psi_i)$ is New-Knowledge Probability Distribution (NKPD), $P(\vartheta_i^j)$ is knowledge regarding i in the existence of indication j, where $i = 1,\ldots,n$ is the number of hypothesis of the knowledge and $j = 1,\ldots,m$ is the number of indication. $P(\Psi)_{estimate}$ is the highest value of NKPD that is assigned as the information with the highest DoC that will be used as the basis for making estimation.

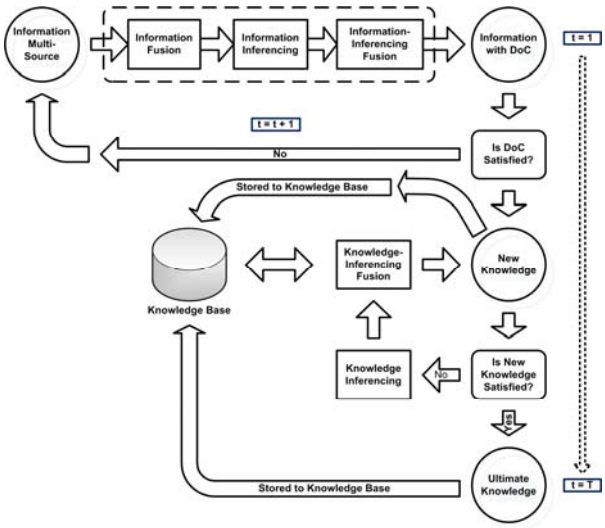

Fig. 3. The model of knowledge-growing mechanism in KGS [38].

In Equation (1), we focused on how to obtain inferencing by manipulating the Bayesian Inference Method (BIM) results which are its posteriors, with a mechanism what we call as Joint Probabilities. The best estimation regarding the phenomenon being observed is the maximum value of NKPD. Equation (1) presents the general form of OMA3S

information-inferencing fusion method while Equation (2) shows how to obtain the maximum value of NKPD.

2.4. Multiagent Collaborative Computation

The Concept of Agent [40]

In real life, agent is defined as a thing that causes a significant effect on a situation. In order to give this effect, agent must have capabilities. "Capability" in this circumstance is the ability to manage when the tasks will be carried out, knows where to move, knows how to do the tasks, knows the success level of the tasks being carried out, and the consequences of the tasks being done. The essential thing that enables the agent in performing its activities is the brain, a place where the information processing is carried out. This is the most grandeur that is not possessed by other living things.

In accomplishing the assigned tasks, the agent always senses its surrounding environment to get as much as information that can affect its activities. The gathered information is processed in its brain, combining it with the existing information, inferencing on the fused information, information inferencing fusion, and making the best decision for actions to be done in anticipating the environment dynamics. The relation of an agent with its surrounding environment as well as its information processing mechanism is simply depicted in Figure 1.

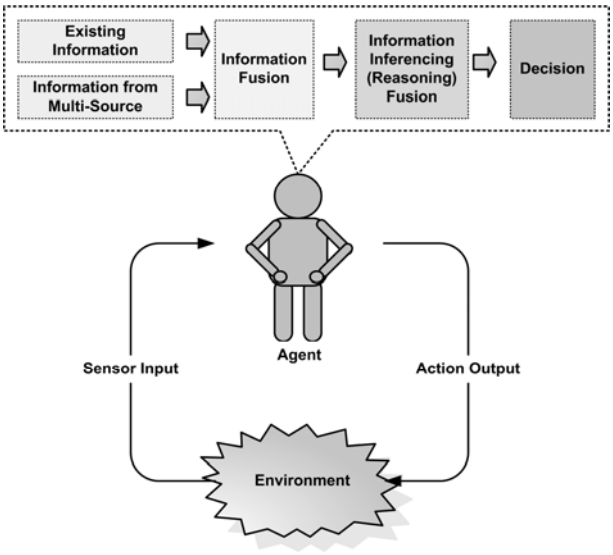

Fig. 4. The concept of agent [38].

In many literatures, agent is stated must have an intelligent characteristic. However, because there is no uniform definition of what agent is, one common consensus is taken that autonomy or we call this as self-governing, is the essential characteristic. Self-governing means the agent has capability to instruct itself to accomplish the tasks and do self-evaluation to value the success rate of the assigned tasks accomplishment for future enhancement. The essential thing of self-governing is inferencing capability.

The Concept of Collaborative Computation [7-9]

Collaboration is taken from the Latin word "collaborare" meaning "to work together", while "collaborative" is an adjective form of "collaboration". So, collaboration is defined as to work with another or others on a joint project or in deeper definition is a process in which entities share information, resources and responsibilities to jointly plan, implement, and evaluate a program of activities to achieve a common goal.

In collaborative scheme, a group of entities enhance the capabilities of each other that implies in sharing risks, resources, responsibilities, and reward. Collaboration involves mutual engagement of participants to solve a problem together, which implies mutual trust and thus takes time, effort, and dedication. On the other side, "computation" is defined as a calculation involving numbers or quantities. By employing computational approach, we can manipulate a large database to solve problems at hand very fast. The consequence is faster, more complete, and more accurate results than that can be achieved by conventional approach.

By combining the two definitions previously explained, we define "collaborative computation" as a calculation on quantities done by a group of agent or multiagent that works together to achieve common or joint goals as depicted in Figure 5.

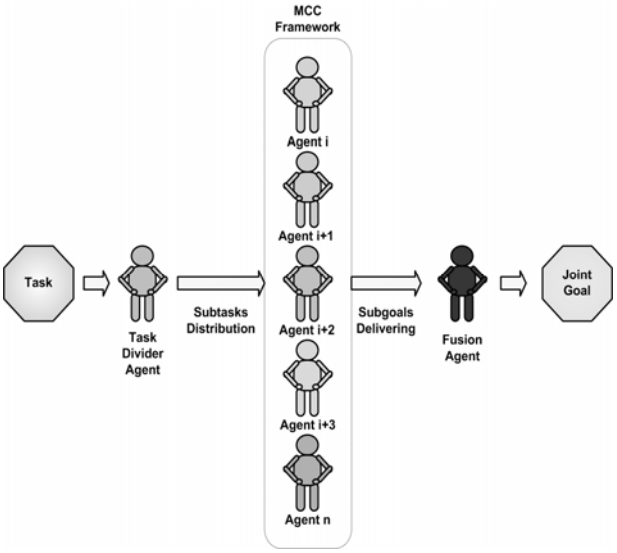

Fig. 5. The concept of MCC.

The Merits of Multiagent Collaborative Computation Approach

GRS is a very complex structure that regulates millions of genes in living organism's body. We believe that multiagent approach is suitable to model the genes' interactions in GRS with some strong reasons. The multiagent system is aimed to cope with large-scale, realistic, and complex problems that cannot be handled by single agent [41] in order to find a solution of global problems or to regulate or control complex systems [42]. In MCC framework, the given task will be divided into subtasks according to each agent specific task. By performing this, the information processing can be done in simultaneous manner by all agents so that the processing time can be reduced to minimum [7].

Assume that we have five agents in MCC framework. Given a task that a single agent can process it in t time. If the task is divided into n subtasks and distributed them to n agents, theoretically, the result of the process can be obtained in t/n time with total $t/n + \tau$ where τ is the time reserved for dividing the task and fusing or combining the subgoals into a joint goal or the ultimate result. Therefore, by utilizing MCC the information-processing time can be reduced from t to $t/n + \tau$, or $(t/n + \tau) < t$.

3. The Application of KGS in MCC Framework for Inferring the Genes Behavior in GRS

Table 1 : Genes' names and their interaction values over time for yeast25-cdc28 cycle

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1		t-1	t-2	t-3	t-4	t-5	t-6	t-7	t-8	t-9	t-10	t-11	t-12	t-13	t-14	t-15	t-16	t-17
2	ACE2	-0,22	0,07	-0,39	-0,31	-0,02	-1,31	-0,96	-0,42	0,19	0,36	0,63	0,55	0,72	0,51	-0,31	-0,58	0,21
3	ASH1	1,48	1,23	0,48	-0,23	-0,29	-0,86	-1,21	-0,86	-0,54	-0,51	-0,92	-0,34	0,78	2	1,35	0,46	0,23
4	FKH1	0,37	-0,63	0,09	-0,31	-1,41	-1,11	-1,04	0,28	1,26	1,34	0,72	0,36	0,28	-0,6	-0,9	-0,22	0,32
5	MBP1	1,27	-0,6	-1,12	-1,63	-0,16	-0,3	-0,33	0,08	0,32	0,27	0,27	0,03	-0,01	-0,54	-0,24	-0,15	0,33
6	MCM1	-0,8	0	-0,23	-0,23	-0,34	0,09	0,3	0,11	0,16	0,13	0,02	0,22	-0,24	0,38	0,19	0	-0,53
7	NDD1	0,89	0,12	-0,08	-0,24	-0,41	-0,9	0,18	0,55	0,49	0,36	0,2	0,06	-0,26	-0,5	-0,38	0,19	0,38
8	NTR1	-0,27	0,55	0,09	0,15	-0,11	0,54	1,42	0,78	-0,64	-0,67	-0,84	0	-0,17	0,91	0,73	0,61	0,22
9	SWI4	0,01	0,3	0,3	0,24	-0,21	0,18	0,86	0,04	-0,35	-0,38	-0,51	-0,2	0	0,92	0,77	0,41	0,14
10	SWI5	0,75	-0,1	-0,81	-0,58	-1,82	-1,35	-0,65	-0,67	-0,4	0,34	0,57	0,47	0,51	0,34	0,12	-0,25	0,08
11	SWI6	-0,31	0,26	0,17	0,12	-0,75	-0,42	0,01	0,28	0,32	0,29	0,09	0,05	-0,32	-0,1	0,12	-0,12	0,09
12	ALG7	-0,17	-0,65	-0,69	-0,41	-0,47	-0,94	0,22	0,32	0,19	0,03	0,29	-0,26	-0,11	-0,11	0,17	0,34	0,59
13	CDC20	0,77	-0,42	-1,09	-0,71	-0,71	0,62	1,09	0,45	-0,5	0,14	0,05	-0,3	-0,07	0,07	0,17	0,12	0,2
14	CDC21	0,73	0	-0,01	0,03	-0,49	0,51	1,41	1,23	0,28	-0,35	-1,16	-1,38	-1,16	-0,31	1,03	1,25	1,06
15	CDC5	-0,46	0,2	-0,37	-0,23	-1,59	-1,29	-1,54	-0,75	-0,24	0,5	1,08	1,22	0,89	-0,12	-0,24	-0,36	0,32
16	CDC6	-0,03	0,44	0,09	-0,03	-0,56	-0,79	0,25	0,19	0,2	0,11	-0,01	0,03	0,09	0,5	0,15	-0,24	0,08
17	CLB2	-0,07	-0,17	-0,91	-0,91	-1,35	-0,57	-0,95	-0,7	0,14	0,57	1,06	1,24	0,84	0,01	-0,35	-0,64	-0,11
18	CLB5	0,24	-0,11	-0,16	-0,34	-0,33	0,16	1,32	0,43	-0,1	-0,2	-0,59	-0,82	-0,63	0,78	0,91	-0,13	-0,12
19	CLN1	-0,28	-0,39	-0,31	-0,29	0	0,21	0,97	0,53	0,14	0,16	-0,34	-0,66	-1,49	0,35	1,05	0,62	0
20	CLN2	-0,25	0,13	0,13	0	0	0,85	1,47	0,54	0,03	-0,15	-0,28	-0,5	-1,57	-0,18	0,52	0,86	0
21	CTS1	1,8	1,8	2,32	2,24	-0,06	0,91	-0,37	-1,16	-1,01	-0,31	-0,41	-0,95	-1,41	1,01	1,67	1,03	0
22	EGT2	1,58	0,41	0,41	-0,35	-0,49	-0,15	-0,92	-0,82	-0,35	-0,11	-0,76	-1,03	-0,1	1,63	1,31	1,23	0
23	FAR1	0,83	0,94	0,59	0,01	-1,18	-1,02	-1,74	-1,69	-0,82	-0,19	-0,31	0,72	0,76	1,75	1,43	0,44	0
24	HTA1	-1,7	-0,72	-0,23	0,4	-0,99	-0,71	0,38	0,21	0,04	-0,34	-0,04	-0,58	-0,78	0,2	0,33	0	-0,17
25	PCL2	0,31	0,71	0,24	0,15	0	0,86	1,14	-0,11	-0,32	-0,26	-0,84	-1,11	-0,24	0,61	1,23	0,54	0,02
26	SIC1	-0,4	1,63	1	0,45	-0,3	-0,56	-0,29	-0,5	-0,27	-0,29	-0,56	-1,04	0,32	1,57	0,9	0,45	0,17

In this section we will present the application of KGS to obtain new knowledge as the basis for understanding the genes behavior from their interactions. As previously mentioned in earlier section, the genes regulated by GRS will be represented by agents that will be working together in MCC framework. For this purpose, we use secondary data from [15] in [4] namely yeast25-cdc28 database as presented in Table 1. In this database, there are 25 genes from ACE2 to SIC1 as listed in column A with a time interval from $t-1$ to $t-17$ or $17t$ times as shown in line 1.

3.1. Definition of MCC Task and Goal

The task of MCC is performing computation to obtain the values of genes behavior and their expressiveness during certain interval time of interaction. The goal is the values of DoC that show the genes behavior and the most expressive genes during the interaction time. To achieve these goals, we create a strategy as follows.

- First, represent the genes into agents in multiagent system and construct the MCC framework for it.
- Second, represent the genes' interaction values into two-value state namely active and inhibit.
- Third, (1) observe the genes' interaction state in time-by-time manner and put arcs on the genes which relate to each other. In this case only the active ones; (2) apply OMA3S method to obtain the interaction values of the active genes. The result is the knowledge of the KGS at certain t. Carry out this procedure until the last t in time series.
- Fourth, obtain the inferencing of the MCC behavior for the whole interaction time as the representation of genes behavior in biological GRS. This inferencing becomes the ultimate knowledge obtained by the KGS.

3.2. Representing the Genes into Multiagent Structure

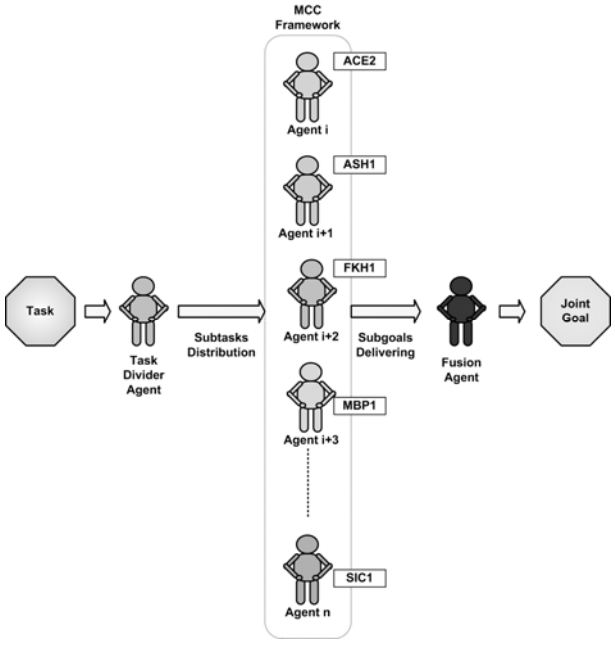

Fig. 6. The representation of genes by means agents in MCC.

We assume that the task divider agent is already done its task and produces Table 1. Refer to Figure 5 in Section 2

we can simply convert the genes into agents as follows. The first and the last genes in the list is gene ACE2 and gene SIC1 are represented by agent ***i*** and agent ***n*** where ***i = 1,…,n*** and ***n = 25***. The structure of the MCC is depicted in Figure 6.

3.3. Representing the Genes' Interaction Values into Two-State Value

The simplest means to represent the existence of the interaction among genes is by representing them with value '1' for 'active' interaction and '0' for 'inhibit" interaction. This is what is called as Boolean representation of genes interaction in GRS. We realize that each gene has its own highest and lowest value that cannot be treated the same one to another. In order to minimize the chances of error in collaborative computation process, we use the threshold-value equation in [34] as presented in Equation (3).

$$\phi_\tau^i = \begin{cases} 1, & \text{if } \psi_\tau^i < \dfrac{\sum_{i=1}^{\lambda} \psi_\tau^i}{\lambda} \\ 0, & \text{if } \psi_\tau^i \geq \dfrac{\sum_{i=1}^{\lambda} \psi_\tau^i}{\lambda} \end{cases} \qquad (3)$$

with $\phi_\tau^i \in \Pi$ is a binary-sequence that represents the set of interaction values at τ time, ψ_τ^i is the value of interaction for agent i at time τ and λ is the number of t where the observation is carried out.

3.4. Observing the Genes' Interaction State and Obtain the Knowledge of It

In this step we will create some graphs that explain the influences of genes to others. We also display the interaction values of the active genes according to each influence graph. Figure 7 to Figure 18 depicts the influence graph of MCC behavior at ***t-1***, ***t-2***, ***t-6***, ***t-11***, ***t-14***, and ***t-17***.

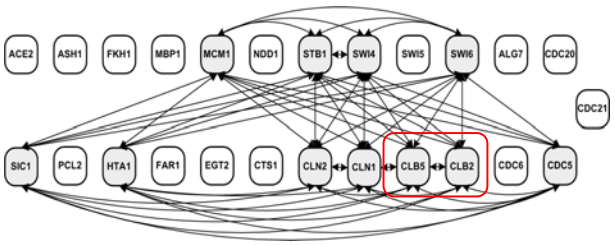

Fig. 7. The influence graph of MCC behavior at ***t-1***.

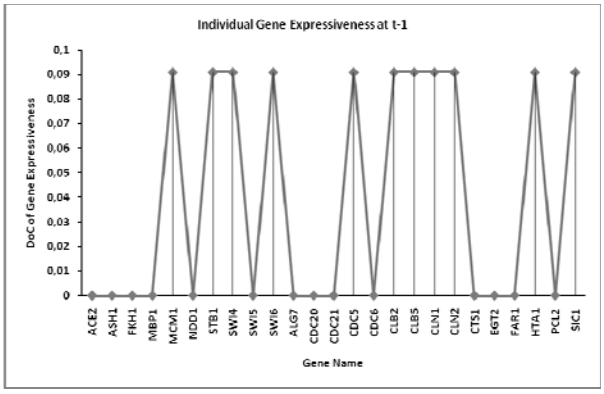

Fig. 8. The knowledge acquired by KGS regarding the MCC behavior at ***t-1***.

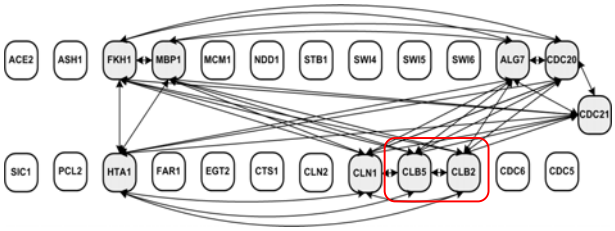

Fig. 9. The influence graph of MCC behavior at ***t-2***.

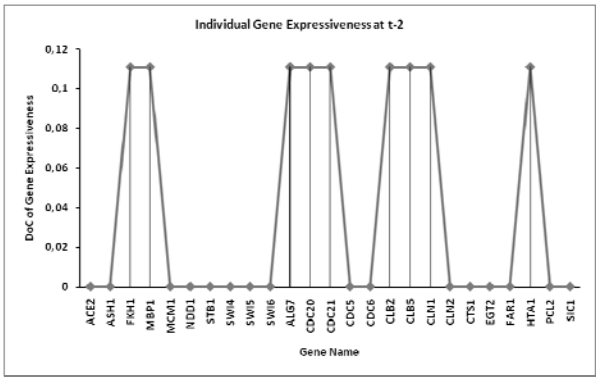

Fig. 10. The knowledge acquired by KGS regarding the MCC behavior at ***t-2***.

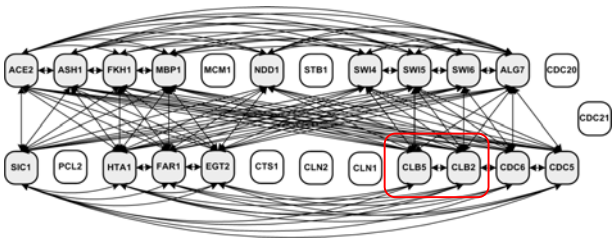

Fig. 11. The influence graph of MCC behavior at ***t-6***.

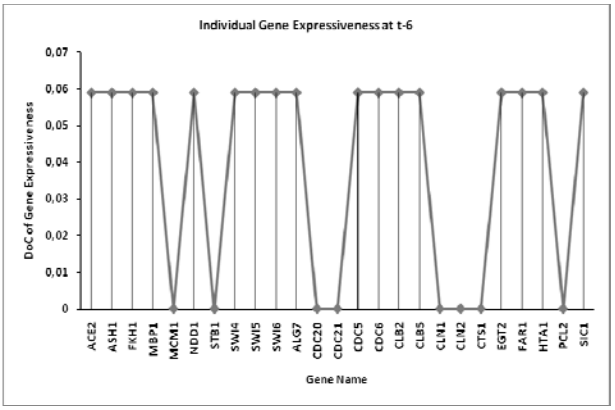

Fig. 12. The knowledge acquired by KGS regarding the MCC behavior at ***t-6***.

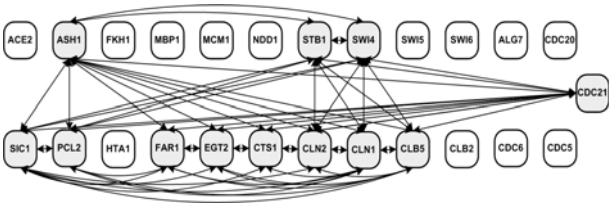

Fig. 13. The influence graph of MCC behavior at ***t-11***.

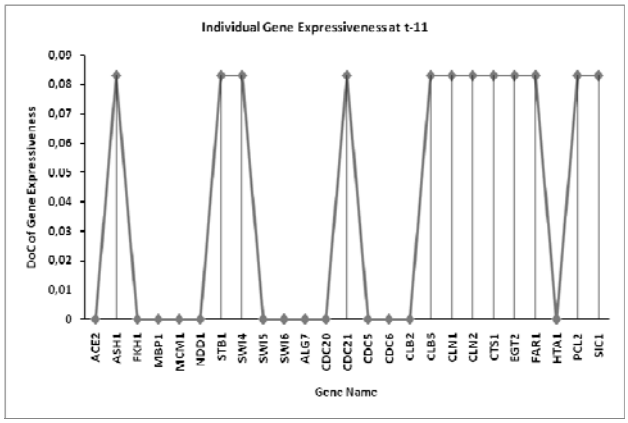

Fig. 14. The knowledge acquired by KGS regarding the MCC behavior at ***t-11***.

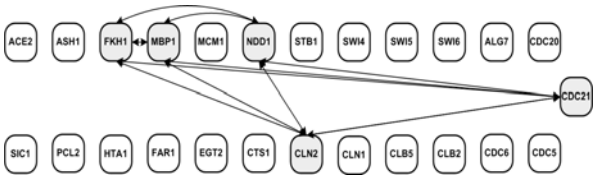

Fig. 15. The influence graph of MCC behavior at ***t-14***.

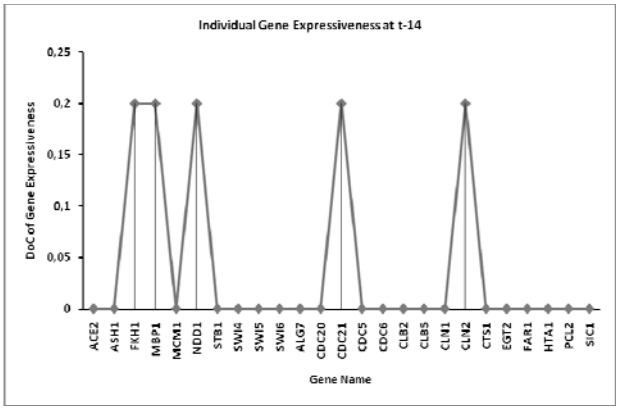

Fig. 16. The knowledge acquired by KGS regarding the MCC behavior at ***t-14***.

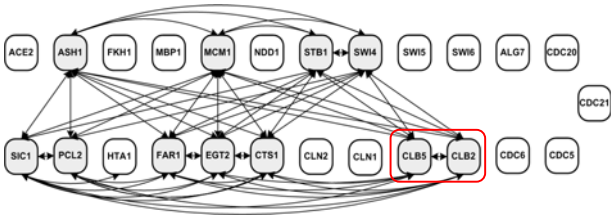

Fig. 17. The influence graph of MCC behavior at ***t-17***.

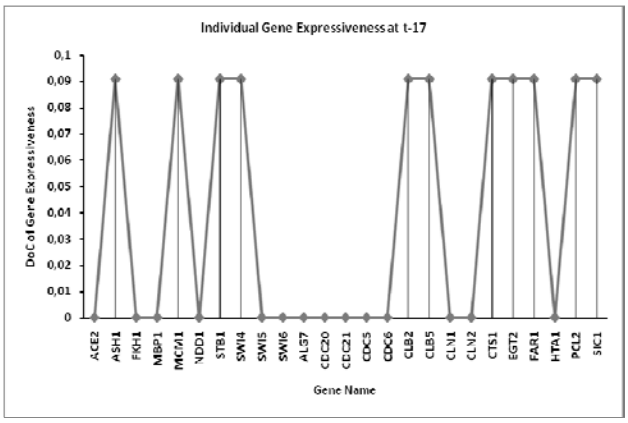

Fig. 18. The knowledge acquired by KGS regarding the MCC behavior at ***t-17***.

3.5. Inferencing regarding the MCC's behavior

We only take some samples at certain ***t*** just to show the influence of genes to others and vice versa in MCC structure. From those figures we can obtain inferencing as follows.

- At almost half of the observation time, between ***t-1*** to ***t-7***, genes CLB2 and CLB5 exhibit dominant role in the interactions. If we look at in online genes information [43], those two genes function as

promoters to begin transition in cell cycle progression and initiation of DNA replication. Based on this finding, the most expressive genes are CLB2 and CLB5.

- At ***t-11*** the interaction gets higher when almost three-fourth of genes involve in the interaction.
- The lowest interaction occurs at ***t-14***. We can compare this result with the genes' interaction values in Table 1.

To ensure that genes CLB2 and CLB5 have the most significant roles in yeast25-cdc28 cycle, we apply OMA3S method once more to obtain the holistic view of all genes behavior for 17t of interaction time as depicted in Figure 19. In this figure we can observe that the DoC of expressiveness of gene CLB2 is 0.062 while gene CLB5 is 0.066.

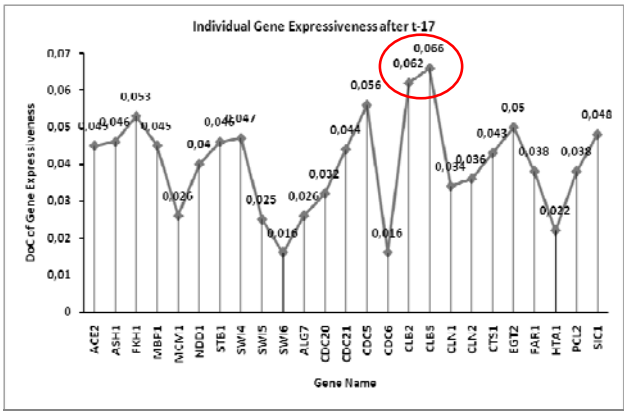

Fig. 19. The knowledge acquired by KGS regarding the MCC behavior after ***17t*** of interaction time.

After we collect the inferencing of the phenomena displayed by the MCC, we can make estimations as follows.

- The most probable genes that will be the most expressive ones between ***t-18*** and ***t-24*** are CLB2 and CLB5.
- The most probable time when the interaction gets higher is at ***t-28***.
- The most probable time when the interaction reaches its lowest state is at ***t-31***.

3.6. The Accuracy of OMA3S Method [9]

The estimation will not be worthy if the results of the application KGS to MCC cannot give good accuracy. To examine the accuracy of the application of KGS' method, that is OMA3S we compare the genes' DoC values presented in Figure 19 with the number of arcs in MCC structure obtained from the application of threshold-value method in Equation (3) to information in Table 1. Table 2 present this comparison as well as the comparison results. The numbers of arc given in Table 2 do not represent the arcs in MCC behavior given in Figure 7 to Figure 18, but they represent the number of each gene interaction to other genes during 17t of interaction time.

Table 2 : The comparison of genes behavior based on the similarity between the number of arc and the genes' DoC values after 17t of interaction time and the comparison result

Gene Name	DoC Value (KGS)	No. of Arc (MCC)	Behavior Match (1 for yes, 0 for no)
ACE2	0.053	8	1
ASH1	0.033	10	1
FKH1	0.035	8	0
MBP1	0.057	7	1
MCM1	0.045	6	1
NDD1	0.021	7	1
STB1	0.017	10	1
SWI4	0.023	10	1
SWI5	0.053	6	1
SWI6	0.035	4	1
ALG7	0.035	6	1
CDC20	0.058	7	1
CDC21	0.031	8	1
CDC5	0.065	10	1
CDC6	0.026	3	1
CLB2	0.073	11	1
CLB5	0.035	13	1
CLN1	0.034	7	1
CLN2	0.034	6	0
CTS1	0.037	9	1
EGT2	0.028	11	1
FAR1	0.037	8	1
HTA1	0.061	5	1
PCL2	0.026	8	1
SIC1	0.048	10	1
Number of match = 23 genes			

According to the finding presented in Table 2, the accuracy of the result after the application of OMA3S method is **23/25 * 100% = 92%,** a very accurate result. This accuracy also confirms that the representation of GRS by means of MCC equipped with KGS can be used to observe the behavior of the genes in GRS.

4. Concluding Remarks

As a novel perspective in AI, KGS has to be assessed to validate its feasibility in solving real-life problems. In this paper we have validated the KGS' knowledge-growing mechanism in order to obtain comprehensive information regarding the genes' behaviors in GRS by utilizing MCC framework. The application of MCC is to boost the computation process so that the comprehensive information can be obtained faster and the estimation can be done faster as well.

GRS is a very complex biological system that determines the traits of living organisms whether good or bad. Therefore, understanding and having knowledge of its behavior can be used to control its regulation in order to minimize the emergence of bad traits. The utilization of MCC is the most appropriate solution and approach to model the behavior of genes in GRS in order to obtain knowledge of their behavior in time-by-time manner and use the knowledge resulted to make estimations in the future.

Our model which is presented in form of influence graphs can give comprehensive views of the genes behavior in term of their influence ones to others. From the model we can have knowledge regarding what the most expressive genes in certain times, the time when the interaction gets higher, and the time when the interaction reaches its lowest state. By having the knowledge we can control the GRS for better generations. It means that the application of KGS to MCC has directly answered question (1) addressed in this paper.

The experiment results show that the knowledge gained by KGS with the accuracy of 92%, is very appropriate for making estimations regarding the multi-gene behavior and individual gene expressiveness in the next series of interaction time. The information delivered by KGS can be used by other fields such as medical, pharmacy, and biochemical, to make further investigation of this multi-gene behavior in the future for better life.

Acknowledgment

Authors would like to dedicate our great appreciation to **Chief of Staff of the Indonesian Air Force, Air Chief Marshal Subandrio** and **Governor of Indonesian Air Force Academy, Air Vice Marshal B.S. Silaen, S.IP** as well as their supporting staffs for their support to the first author's fast-track Doctorate program in School of Electrical Engineering and Informatics, Institut Teknologi Bandung, Bandung, Indonesia. Our great gratitude is also presented to **Rector of the Institut Teknologi Bandung, Prof.Dr.Ir. Djoko Santoso, MSc** for his continuous support in this research. This research is also supported by Incentive Program of Basic Research ITB year 2009 on Modeling and Simulation of Genetic Regulatory System on Mycobacterium Tuberculosis.

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