

# Neural Network Estimation of LAL/VPC Resions of Silkmoth using Genetic Algorithm

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**Abstract**—When a male silk moth senses sexual pheromone of a female partner by using its antenna, it repeats certain series of walking pattern and arrives to the partner. This walking pattern is generated in Lateral Accessory Lobe (LAL) and the ventral protocerebrum (VPC) domain which controls physical exercise. Therefore, in this study, we elucidate the process of this behavior by constructing a neural network model of the LAL domain. Concretely, we build a model that treats some numbers of neurons as one neuron and estimate strength of each connection between 10 neuron representatives of neuron groups with Genetic Algorithm. The estimated network is verified and consided from engineering and biology.

## I. INTRODUCTION

Male silkmoths make a certain walking pattern when they sense sexual pheromone from females. The walking pattern is a sequence of actions which are straight forward, zig-zag turning and looping as shown in Fig.1. They take this sequential actions in every sensing of sexual pheromone and finally reach to the female in every time .

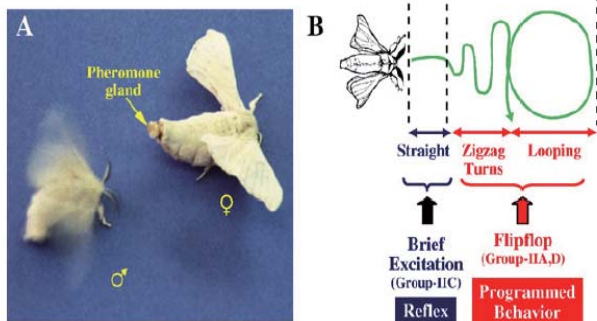


Fig. 1. A certain walking pattern with sexual pheromone[1]

This walking pattern is generated in small brain with stimulation from antennas. The brain of silkmoth can be easier to be analyzed than that of human brain, because

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the number of neurons of silkmoth brain is very few (about  $10^5$ ) compared with human brain (about  $10^{10}$ ). Therefore, biologists analyze relations between the neuron responses and stimulations and between actions and stimulations[2][3]. Especially, the neuron responses are very well analyzed in LAL-VPC regions where this sequential actions are considered to be related very much.

However, the neurons network analysis is not enough to explain how to generate the actions by the stimulations. Not only the neuron responses but network structure is very important to analyze the brain. The brain is too small to observe all neuron network. Therefore, our objective of this research is to estimate silkmoth neural network corresponding to the flip-flop actions.

The research [4] has the same objective with the same background using integrate-and-fire model. The research has made important results. However, the results is not enough to explain all silkmoth motion. We try to estimate the network in another approach.

For the estimation of the neural network in the brain of silkmoth, we apply engineering approach which includes modeling, equation and optimization. In the modeling, network model is constructed based on biological knowledge. Recently, robotics and system engineering is attracted considerable attention from biology as strong methodology for hypothesis and verifications.

Here, the neuron response is represented in equations. And network connection is estimated using Genetic Algorithm to fit the silkmoths' actions. According to the proposed method, we can obtain a hypothesis and consider the hypothesis.

## II. SILKMOTH IN BIOLOGY

In this research, the model of neural network structure and estimation of network connections are proposed. As inputs of the modeling, the silkmoth motion and the biological knowledge are considered.

The motion of silkmoth is generated by motor neurons of legs. The motor neurons of legs connect with the descending interneurons (DNs) from the lateral accessory lobe (LAL) and the ventral protocerebrum (VPC) in brain (Fig.2). The LAL and VPC regions exist at both left side and right side in the brain.

The DN's show a characteristic state-dependent activity "flip-flop circuit" shown in Fig.3[5]. There is strong relationship between the motion (zigzag turn) and this response. Therefore, we consider that the motion can be seemed to equal the DN's activity.

And, the stimulation of pheromone is brought from the antennas to LAL-VPC regions with some delay. The stimulation from antenna which touches pheromone is delayed 320 [msec] to the opposite side of LAL-VPC region compared with the same side LAL-VPC region[1]. It is considered that this delay is based on the length of transmission of the stimulation.

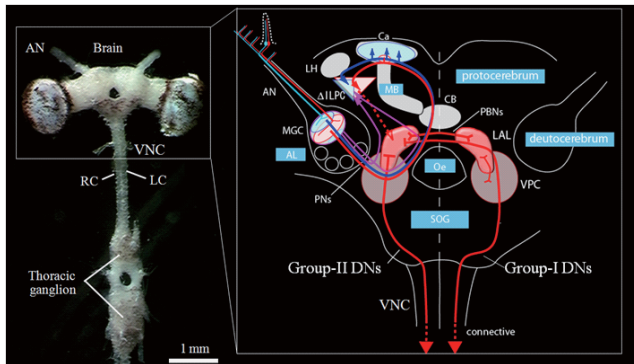


Fig. 2. Brain of silkmoth[1]

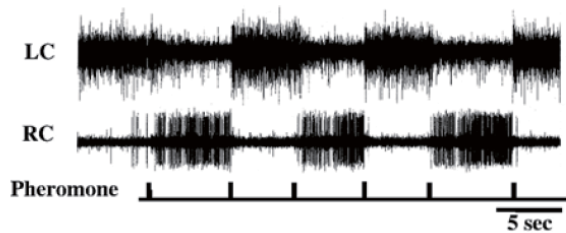


Fig. 3. Flip-flop output of DNns[1]

### III. ESTIMATION OF LAL-VPC NETWORK

#### A. 10 regions model

It seems that the motion of silkmoth is generated at both sides of the LAL-VPC region in brain [1]. For the analysis of the silkmoth brain, the neural connections in LAL-VPC regions wish to know. However, estimation of the all connections is very difficult because there are about 400 neurons and the connections are very large and complicated.

Then the model of LAL-VPC region is proposed based on the knowledge of biology. The neurons exist in biased 5 regions in LAL-VPC region on both sides, in total 10 regions [6][7], and the biased neurons are connected each other. The image is shown in Fig.4 from [6].

Therefore, we proposed 10 regions model of LAL-VPC region. The LAL-VPC region is divided to oLAL, iLAL, oVPC, iVPC and aiVPC. From the observation in biology, stimulation from antenna is brought to oLAL regions and DNns connect to aiVPC regions in both sides. The proposed 10 regions model is illustrated in Fig.5.

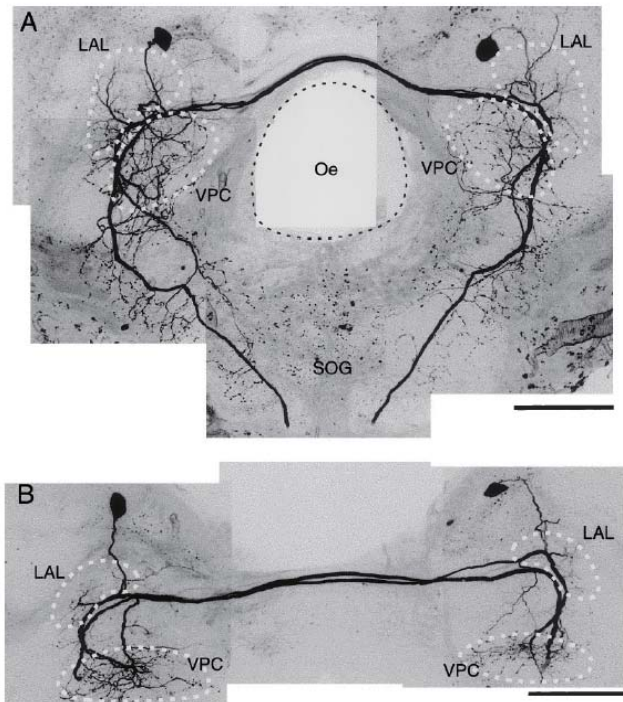


Fig. 4. LAL-VPC image : scale bars are 100μm[6]

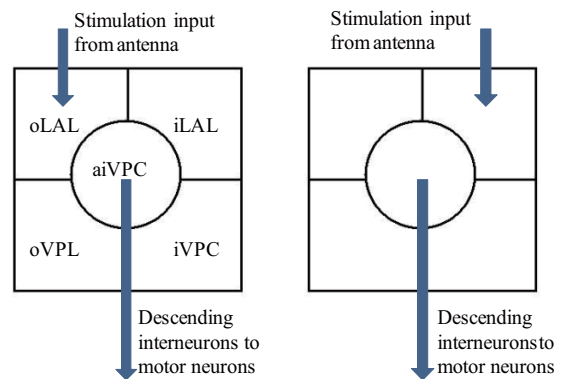


Fig. 5. 10 regions model

#### B. Model of neural response

Based on the proposed model, the each region has one neuron to connect to the others. The connections are various corresponding to the excitation or inhibition and the strength. Figure 6 shows an example. In this example, the left oLAL neuron connects to all the other neurons with several properties. The connection to the opposite side oVPC is very strong inhibition and that of the opposite side iVPC is very strong excitation.

With this model, the various representations can be obtained and the estimation of the connection is described in later.

The neural response is described with some mathematical equations based on the equations in [1]. In the research model, the number of neurons is just two and the variety of the connections is not considered. Therefore, we extend

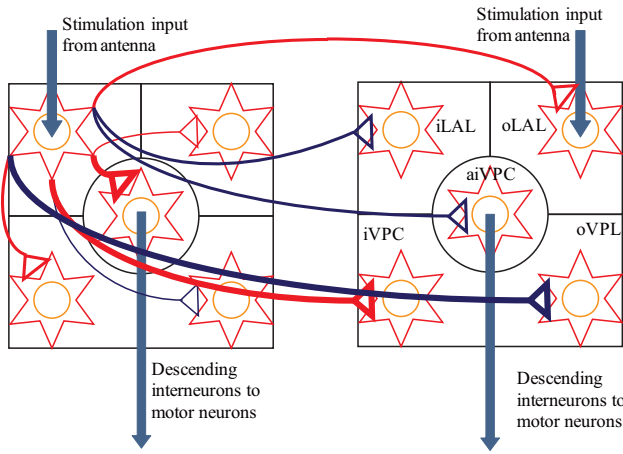


Fig. 6. Proposed network model: red connections represent excitation ones and blue connections represent inhibition ones. And the bold lines represent the strength of the connection. Each region is connected to the other regions with a certain kind and strength.

the neural response model with the consideration of the connections.

At the extended neural model, the neuron response at each region is represented with  $U_i$  which is the average membrane potential of the region,  $X_i$  which is the activity ratio of the region,  $s_i$  which is dynamics of the concentration of serotonin, and  $h_i$  which has the fatigue effect. The membrane potential  $U_i(t)$  of the 10 regions neuron in our model is shown in the equation (1) and the equation (2).

$$\tau \frac{dU_i}{dt} = -U_i(t) + \sum_{j=1}^{10} c_{ji} X_j(t) + s_i(t) \quad (1)$$

$$X_i(t) = \text{sigm}(U_i(t), h_i(t)) \quad (2)$$

Where  $i$  indicates the region number. And the function  $\text{sigm}(U_i, h_i)$  depends on the membrane potential  $U_i$  and the threshold level  $h_i$  and  $c_{ij}$  is connections between neurons with the variety and strength ( $-1 \leq c_{ij} \leq 1$ ). The  $\text{sigm}(U_i, h_i)$  is 1, if  $U_i \geq h_i$ , otherwise the function is 0.

It is well known that the neuron is fatigued with the excitation. For this property,  $h_i(t)$  increase when the neuron is excited. This is represented in the equation (3).

$$\tau_h(U_i) \frac{dh_i}{dt} = -h_i(t) + c_i X_i(t) + h_{i0} \quad (3)$$

$$\tau_{ph} = \frac{ds_i(t)}{dt} = -s_i(t) \quad (4)$$

The time constant  $\tau_h$  is a variable dependent on the membrane potential  $U_i(t)$ , so that as the membrane potential  $U_i$  becomes higher, the cell fatigues more quickly. Since  $\tau_h(U_i)$  has a low value under conditions where the  $U_i$  is less than the static level of the threshold  $h_{i0}$ , the threshold  $h_i(t)$  recovers to the initial static level  $h_{i0}$ , which is constant, quickly when the neuron becomes inactive.  $s_i(t)$  is damped slowly and the time constant  $\tau_{ph}$  determines this long-lasting response. In this research, we set  $\tau_{ph} = 10$ .

In this model, when a neuron is excited from antenna or the other neurons, the membrane potential increases. Or, when a neuron is inhibited from the other neurons, the membrane potential decreases. When the membrane potential increases and is higher than the threshold, the neuron fires and transmits the stimulation. When the membrane potential has been high, the threshold increases as fatigue. When the threshold is higher than the membrane potential, the neuron stops firing.

Only one region in each side of brain has been proposed in [1] with the above equations. The responses are shown in Fig.7. Right side region and left side region are activated like a flip-flop circuit. The detailed explanation of this figure is in [1].

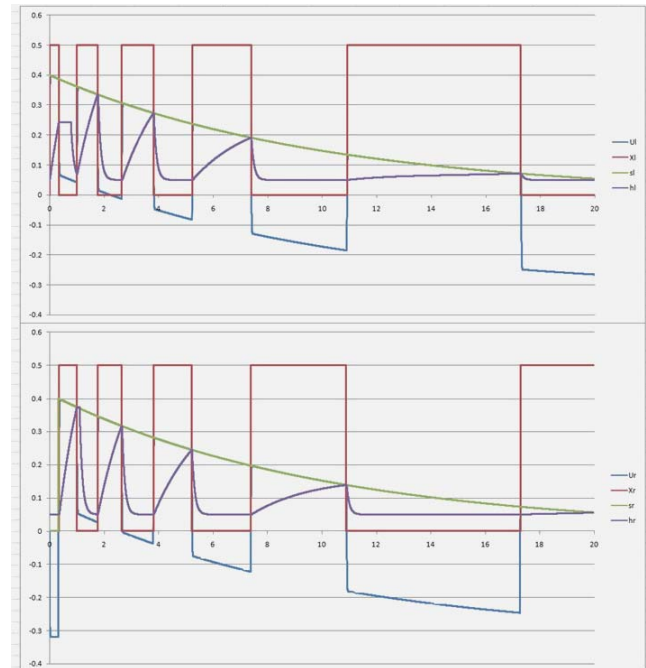


Fig. 7. Neuron response in 2 regions model

### C. Estimation of neural network connection using GA

For estimation of neural network, the connections is designed using Genetic Algorithm (GA), where fitness function is defined based on turn duration of the zigzag turn (describe in later) and we assume that the connections are symmetrical with respect to the right and left LAL-VPC regions. Therefore, the number of the connections is  $5 * 9 = 45$ . In our method, each connection is represented as 6 bit in GA, including variety and strength. Therefore, the length of gene is 270. Figure 8 shows the representation of the connections, where the first bit of each segment indicate excitation or inhibition and after 5 bit representation the strength.

The reason why GA is applied is that the relation between connections(input) and silkmoth actions(output) is obviously complicated and non-linear. GA is one of the strong optimization methods to such a problem.

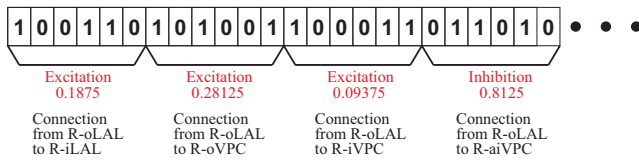


Fig. 8. Decoding to connections using GA: e.g.) first 6 bits segment represents the connection from the right oLAL to the right iLAL. This connection must be excitation one because first bit is 1. And the strength of this connection must be 0.1875 because of the after 5 bit.

TABLE I

TURN DURATION TIME(AVERAGE AND STANDARD DEVIATION)[8]

1 stimulation	1st turn	2nd turn	3rd turn
Turn duration time[sec]	1.2±0.1	1.9±0.3	2.1±0.4
number	16	16	8
Every 4 sec	1st turn	2nd turn	3rd turn
Turn duration time[sec]	1.1±0.1	1.6±0.1	1.7±0.1
number	48	48	29

#### D. Evaluation of estimated network

For the design using GA mentioned above, the fitness function should be defined.

Our objective is to estimate LAL-VPC region structure which makes the zigzag turn which is the character of silkworm motion. The zigzag turn motion is observed and measured in [8]. The result is shown in Table I. Here, there is 2 experimental conditions which are one pheromone stimulation and 0.25 [Hz] stimulation. "1 stimulation"(upper table) indicates former one and "Every 4 sec" indicates later one.

From the result, the turn duration time in "Every 4 sec" is shorter than those in "1 stimulation".

From these experiments, the fitness function of this method is formulated.

The formulation of fitness function is as follows:

$$fitness_i = \sum_{j=1}^3 \exp\left(\frac{(x_j - \mu_j)^2}{2\sigma_j^2}\right) \quad (5)$$

where  $x_j$  is turn duration time of  $j_{th}$  turn.

As the turn duration time of the model are close to this experimental result, the fitness value is high and the individual is easy to survive. The fitness of each turn is shown in Fig.9.

The output of the proposed model is the neuron activity of aiVPC regions in both sides, because the DN's from aiVPC regions are connected to the motor neurons of legs.

In the both conditions, the fitness values are calculated using the same models and networks and minimum one is to be a fitness value of the individual in GA.

## IV. EXPERIMENT

### A. settings

With simulations, we verify that your proposed model and method can be obtained a proper estimation.

As mentioned above, the fitness values are calculated based on the comparing with aiVPC activities and turn

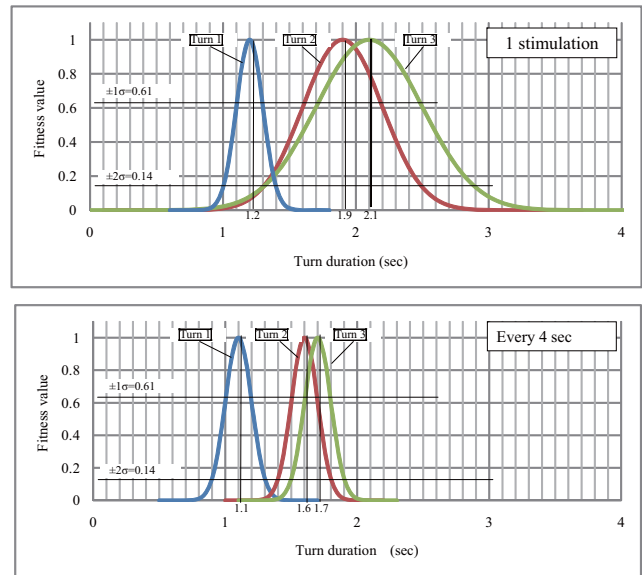


Fig. 9. Fitness value of turn duration time

TABLE II  
SIMULATION MACHINE

CPU	Core2 Duo 2.00GHz
RAM	2046MB
OS	Windows Vista
Programming	Java

duration time. Therefore, the experimental conditions are as blow.

- 1) 1 stimulation at init state
- 2) 4 stimulations from init state in every 4 second

In this simulation, the right side oLAL gets the stimulation from the antenna at first and the left oLAL region get the stimulation with 320 [ms] delay.

The sampling time is 10 [ms] in the simulations. The stimulations between neurons are not transmitted in 1 sampling time, but with 50 [ms] delay in the same side and 150 [ms] delay to the opposite side. This is also based on the biological experiments.

Settings of GA are shown in below.

- The number of individuals is 300
- The number of generations is 100
- The possibility of cross over is 0.7. The cross over is occurred at one point.
- The possibility of mutation is 0.05.
- The selection is based on the roulette selection.

And the computational conditions are shown in Table II.

### B. result

The simulation results are shown in this subsection. Figure 10 shows the activity of aiVPC regions in both sides. In each graph, right region activity is upper and left is lower. If both regions are active or non-active, the output is middle one. In



both conditions, which are one stimulation and every 4 sec stimulations, flip-flop output can be obtained.

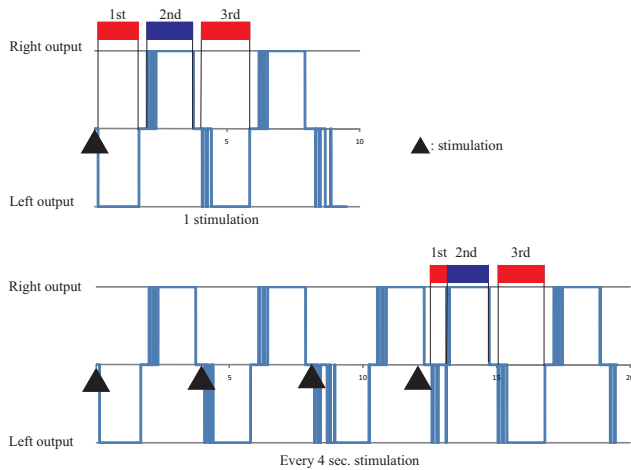


Fig. 10. Obtained outputs of both conditions (1 stimulation and every 4 sec stimulations) :black triangles indicate the stimulation time.

Figure 11 shows the turn duration time in each condition and each turn comparing with experimental results. With our modeling methodology, the turn duration time in every 4 sec stimulations are shorter that those in 1 stimulation on all turns. This inclination is the same in the experimental results.

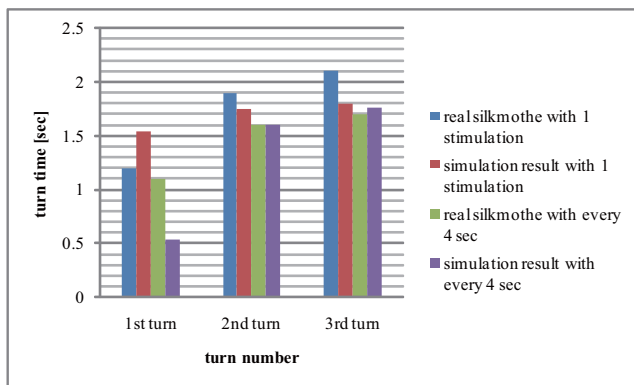


Fig. 11. The turn duration time comparing experimants and models in each turn

The obtained network is shown in Table III. In this table, the positive values mean excitation connections and the negative values mean inhibition connections. The gray cells mean that the connections do not make sense because neurons do not fire in these regions.

The red cells indicate that the connections are excitation ones. With these connections, the neurons fire with the stimulations from the other neurons. Of cause, oLAL regions get the stimulations from antenna and the neurons are excited.

Here, in our model, iLAL, oVPC and iVPC regions have no different meaning. Therefore, oVPC regions (active regions) can be alternative to iLAL or iVPC.

Figure 12 shows the transition of fitness value. It can be seen that the fitness value is larger, as generation become

TABLE III

OBTAINED NETWORK CONNECTIONS: "-" INDICATES INHIBITION.

to \ from	L-oLAL	L-iLAL	L-iVPC	L-oVPC	L-aiVPC
L-oLAL	0	-0.875	-0.625	-0.75	-1
L-iLAL	-1	0	0.875	0.125	-0.625
L-iVPC	-0.625	-0.75	0	-0.25	-0.375
L-oVPC	-0.375	-0.25	0	0	-0.375
L-aiVPC	-0.375	-0.25	0	-0.5	0
R-oLAL	-0.25	0.875	0.125	-0.625	-0.75
R-iLAL	-0.75	0.375	-0.25	-0.375	-0.25
R-iVPC	-0.25	0	0.625	-0.375	-0.25
R-oVPC	-0.25	0	-0.5	-0.25	0.625
R-aiVPC	0.625	0.125	0.375	0.5	-0.375

to \ from	R-oLAL	R-iLAL	R-iVPC	R-oVPC	R-aiVPC
L-oLAL	-0.25	0.875	0.125	-0.625	-0.75
L-iLAL	-0.75	0.375	-0.25	-0.375	-0.25
L-iVPC	-0.25	0	0.625	-0.375	-0.25
L-oVPC	-0.25	0	-0.5	-0.25	0.625
L-aiVPC	0.625	0.125	0.375	0.5	-0.375
R-oLAL	0	-0.875	-0.625	-0.75	-1
R-iLAL	-1	0	0.875	0.125	-0.625
R-iVPC	-0.625	-0.75	0	-0.25	-0.375
R-oVPC	-0.375	-0.25	0	0	-0.375
R-aiVPC	-0.375	-0.25	0	-0.5	0

larger. This shows that the design process is proper.

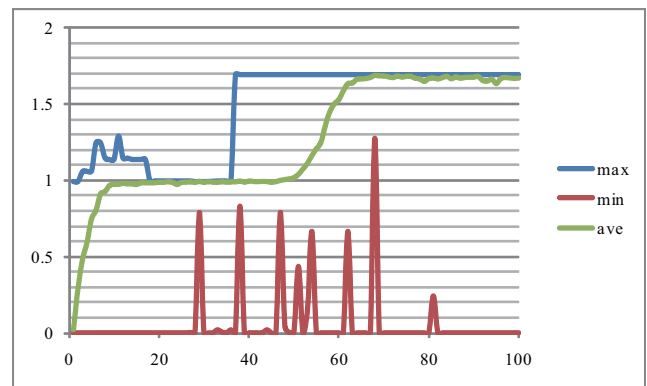


Fig. 12. Transition of fitness value

### C. discussion

From the results of the simulations in the previous subsection, the connections in the active regions can be shown in Fig.13.

From this figure, we can senn that the input region (oLAL) make the opposite output region (aiVPC) be excited. And the buffer region (oVPC) and the output region (aiVPC) in the same side are excited each other. The other connections are inhibition. Especially, the input regions are inhibited from all the other regions.

The dynamics of this network is shown in Fig.14. It can be seen that the right input region is activate by the stimulation at first. And the activation transmits to the opposite output region. Next, the excitation of the output region makes the opposite buffer region fire. For a while, both buffer and output regions fire because of each excitation and inhibit the input regions at the same time. And then, the threshold of

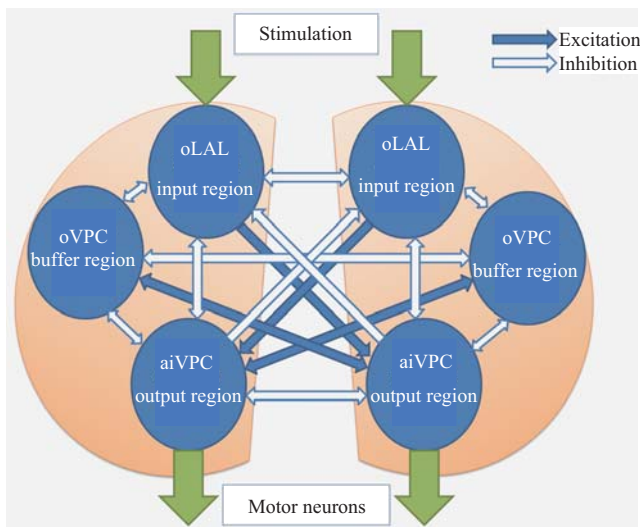


Fig. 13. Obtained model of LAL-VPC

both regions becomes high and both regions stop firing. The input region can fire because of the no inhibition and transmit the excitation to opposite output region. The flip-flop output can be obtained by repeated this dynamics.

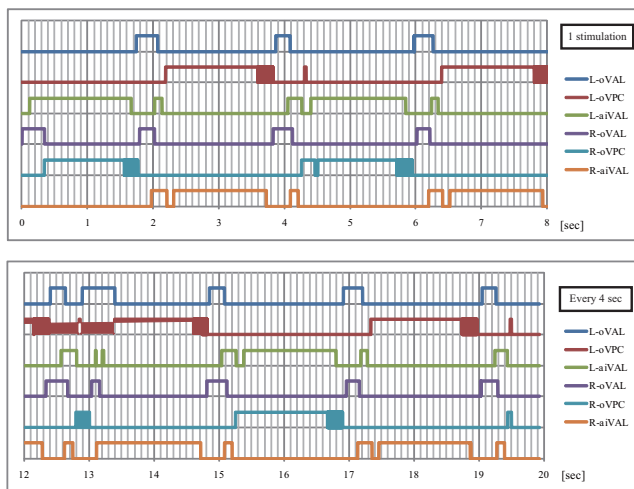


Fig. 14. All regions responses : upper one is 1 stimulation and lower one is every 4 sec. The lower one starts at the last stimulaiton.

The reason why the turn duration times become short at every 4 sec condition is that input region is inhibited by the buffer and output regions and get new stimulation from antenna. The firing input region try to excite the opposite output region and inhibit the same side output region. However, the transmission has delay time. Therefore, both the input and the output regions fire and make each other turn over. In other words, all regions are not stabilized because of time delay.

This phenomenon is like "chattering" and is very interesting for biology because this is new hypothesis. Sikmoth may use the time delay effectively.

## V. CONCLUSIONS AND FUTURE WORKS

In this research, we proposed new model of silkmoth small brain for the analysis of silkmoth behaviour. The model and connection design can estimate the silkmoth inner neurons.

At the modeling, the 10 regions model of LAL-VPC region is proposed based on the biological knowledge. The neuron response is extended from the previous proposed method to fit our model. And, the network connection is estimated using Genetic Algorithm.

Our proposed method can make the flip-flop circuit by the appropriate connections. And, in repeated stimulation, the turn duration times can be short comparing with 1 stimulation in the simulation. This is because of delay time of the transmission between regions.

Using the engineering approach, the biological inspired may be able to be obtained.

As a future work, we consider and discuss the biological meanings of the results more and more. For example, there are no functional difference between regions except oLAL and aiVPC. However, there should be the meanigs of the regions, as time delay may be different.

And the application of GA should be improved because current method is a little redundant. We consider the search space can be reduced.

With the consideration and discussion, we will try various experiments more with and, from data of the experiments, hypothesis of meanings of the regions will be obtained.

## VI. ACKNOWLEDGMENTS

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