Artificial Neural Development for Pulsed Neural Network Design

- Generating Place Recognition Circuits of Animats -

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Abstract

We propose the artificial neural development method that generates the three-dimensional multi-regional pulsed neural network arranged in three layers of the nerve area layer, the nerve sub-area layer, and the cell layer. In this method, the neural development process consists of the first genome-controlled spatiotemporal generation of a neural network structure and the latter activity-dependent regulation of it. In the first process, by decoding a genome, 1)a nerve sub-area is generated in each nerve area and neurons are produced in it, 2)axonal outgrowth target sub-areas are recognized according to the attraction and repulsion rule, and 3)synapse formation is controlled under the topology preservation projection rule between origin cells and target cells. In the latter process, 4)programmed cell death occurs under control of spiking activity and a neurotrophic factor, then 5)synaptic efficacy is regulated according to the spike-based hebbian rule and weakened synapses are eliminated as a result of competition of spiking activity. For design of genomes, the steady state genetic algorithm is introduced and it is applied to initial genomes partially designed manually. To evaluate our artificial neural development method, simulation experiments are conducted to generate a pulsed neural network of an animal-like robot (animat) which moves in an environment. We evolve and develop an animat's place recognition circuit that contains the place cell area. The place recognition performance is evaluated in an environment where an animat comes into existence and in another environment where the animat enters after development. Through these experiments, we show our artificial neural development method is useful for generating a biologically realistic pulsed neural network of the animat.

Introduction

The design of artificial neural networks can result in the design of artificial genomes with lowered dimensions by mimicking the neurogenesis process of living things, automatically generating artificial neural networks based on genomes' decoding and neurergic regulation. The neurogenesis process of living things is roughly divided into the first genome-controlled process and the latter activity-dependent process. The first process forms a nerve structure under control of a genome and the latter process regulates it dependent on spiking activity caused by interaction with environments.

Various artificial neural development mechanisms can be formulated according to which part of the neurogenesis process is modeled. For example, (Vaario, Onitsuka and Shimohara 1997), (Rust *et al.* 1997a), (de Garis 1994) have treated mainly axonal outgrowth and synapse formation. (Cangelosi, Parisi and Nolfi 1994), (Eggenberger 1996), (Kitano 1995), (Dellaert and Beer 1996) have modeled cell division, cell differentiation and cell migration in addition to those processes. (Rust *et al.* 1997b), (Vos, Heijst and Greuters 1997) have focused on programmed cell death and synapse elimination especially.

In this paper, we propose the artificial neural development method that generates three-dimensional multi-regional pulsed neural networks arranged in three layers of the nerve area layer, the nerve sub-area layer, and the cell layer. The reason the pulsed neural network is adopted is that it is suitable for synchronous spiking expression within the scale of milliseconds, which is considered to be one of information expression in the brain. The three-layered structure is introduced to model neural structure at a level above that of the individual neuron but below that of an overall neural system, for example modules such as brain regions and their columnar organization of the nerve system of living things. The nerve system is a functional network of those modules, and, in general, modularity and functional connection of modules are indispensable for the design of a complex system. The multi-regional neural structure is designed by providing arrangement, properties, and connections of nerve areas. In our method, the design process is composed of the first genome-controlled process and the latter activity-dependent process by modeling the following features in the neurogenesis process of living things. The features of attention in the first process are as follows. 1) A genome predetermines the spatiotemporal structure of neural development, that is it is predetermined according to a genome when and where neurons are arranged and what properties they possess. 2) As for connection formation by the axon outgrowth among areas, axonal outgrowth targets are recognized according to

attraction and repulsion between receptor factors on axons of presynaptic cells and guide factors on postsynaptic cells, and synapses are formed under the topology preservation projection between origin cells and target cells. The features of attention in the latter process are as follows. 3) For connection regulation among areas, the size of origin cells and target cells is adjusted based on the programmed cell death, and the target government among presynapses is controlled based on the synapse elimination.

By the way, since complex neural networks need complicated genomes, it becomes difficult to design all genomes by hand. So it is useful to apply evolutionary computation to the design of genomes, however it is also difficult to design all the complex genome structure by evolutionary computation because the computation cost is expensive and it often fails due to premature convergence. Accordingly a method for partially applying an evolutionary algorithm to manual coded genomes is introduced in our method, and we use the steady state genetic algorithm as an evolutionary algorithm.

To evaluate our artificial neural development method, simulation experiments are conducted to generate the place recognition circuit of an animal-like robot (animat) which moves in an environment. It is known in rats that assembly of place cells that fires at the same time express a place in an environment. It is also examined that the place recognition circuit is a multi-regional circuit which contains the place cell area, the head-direction cell area, the outer-world sensory area, and so forth. For these reasons, we evolve and develop an animat's place recognition circuit that contains the place cell area. The Bayesian place reconstruction mapping (Zhang *et al.* 1998) from a spiking pattern of place cells to a place in an environment is used for evaluation of animat's place recognition, and the accuracy of this reconstruction is used as fitness for evolution. The place recognition performance is evaluated in an environment where an animat comes into existence and in another environment where the animat enters after development. Through these experiments, we discuss utility of our artificial neural development method and some properties of generated place recognition circuits.

This paper is organized as follows. In section 2, we present our artificial neural development method. Section 3 describes the formation of the animat's place recognition circuit and the genome to generate it genetically. Section 4 describes experimental results on the animat's place recognition circuit genesis and evaluation of place recognition performance. Finally in section 5, we present conclusions and ongoing research.

Artificial Neural Development NEUROGEN'2000

Overview of NEUROGEN'2000

Our artificial neural development method, that is named NEUROGEN'2000, generates pulsed neural networks (Gerstner 1999) arranged in three layers of the nerve area layer, the nerve sub-area layer, and the cell layer, expressed in the three-dimensional coordinate system of the anterior-posterior axis, the dorsal-ventral axis and the right-left axis. As a result, each cell has a three-dimensional coordinate triplet $((X_a,Y_a,Z_a), (X_s,Y_s,Z_s), (X_c,Y_c,Z_c))$, where (X_a,Y_a,Z_a) is a nerve area coordinate, (X_s,Y_s,Z_s) is a nerve sub-area coordinate in the nerve area, and (X_c,Y_c,Z_c) is a cell coordinate in the nerve sub-area.

Our genome represents a schedule of what kind of nerve sub-area is developed in each nerve area at each development stage. Therefore a genome consists of a matrix of genes whose order is defined by the number of nerve areas multiplied by the length of development stages.

The artificial neural development process in NEUROGEN'2000 is outlined as follows. A population of initial genomes is set by manually coding a part of genomes and automatically the rest. For each genome, by decoding a gene for each nerve area at each development stage,

Step 1: a nerve sub-area is generated and neurons are produced in it,

Step 2: axonal outgrowth target sub-areas are recognized according to the attraction and repulsion rule,

Step 3: synapse formation is controlled under the topology preservation projection rule between origin cells and target cells.

Then for a pulsed neural network generated,

Step 4: programmed cell death occurs under control of spiking activity and a neurotrophic factor,

Step 5: synaptic efficacy is regulated according to the spike-based hebbian rule and weakened synapses are eliminated as a result of competition of spiking activity.

Fitness of each neural network is evaluated in an environment, and the steady state genetic algorithm evolves the specified parts in genomes based on fitness values.

Target Recognition and Synapse Formation

The genome is a matrix of genes whose order is defined by the number of nerve areas multiplied by the length of development stages and it represents a schedule of what kind of nerve sub-area is developed in each nerve area at each development stage. Each gene expresses properties of a nerve sub-area and neurons in it, that is developed in a nerve area at a certain development stage. These properties include a direction of nerve sub-area generation in a nerve area, the number of neurons, the neuron's response type of excitation or inhibition, target nerve areas, the guide factor and the receptor factor for target sub-area recognition, the number of axon branches, and the amount of neurotrophic factor.

The artificial neural development is executed by decoding these genes in specified nerve areas at specified development stages. First, a sub-area is generated in the specified direction in a nerve area and neurons of specified number with specified response type are produced. Each

sub-area is assigned a three-dimensional coordinate in the nerve area and each neuron is assigned a three-dimensional coordinate in the nerve sub-area. Second, target nerve sub-areas are selected according to the target recognition rule from among nerve sub-areas in the specified target area. The target nerve sub-area recognition is performed based on attraction and repulsion between the specified receptor factor on axons of presynaptic neurons and the specified guide factor on postsynaptic neurons. The target recognition rule is defined as follows.

[**Target recognition rule**] Let R and G be binary vectors of length n by which the receptor factor and the guide factor are expressed. For $R=(r_1,...,r_n)$ and $G=(g_1,...g_n)$, let define $(R \cap G)_i=1 \Leftrightarrow r_i=1 \wedge g_i=1$, and $R \subseteq G \Leftrightarrow R \cap G=R$. Then the target recognition rule is defined as follows: if $R \subseteq G$ then attraction between R and G occurs else repulsion of R against G occurs. □

Thirdly, axons grow toward the target nerve sub-area and synapses are formed between neurons in the origin nerve sub-area and the target nerve sub-area. The topology among coordinates of neurons in the origin nerve sub-area and the target nerve sub-area is preserved according to the topology preservation projection rule described below.

[**Topology preservation projection rule**] The topology preservation projection from a certain nerve sub-area (S_O) to another nerve sub-area (S_T) is a mapping $M: S_O \rightarrow 2^{S_T}$, from a cell in S_O to a set of cells in S_T, that satisfies the following condition:

for any $c_{O1}(x_{O1},y_{O1},z_{O1})$, $c_{O2}(x_{O2},y_{O2},z_{O2}) \in S_O$, *there exist* $c_{T1}(x_{T1},y_{T1},z_{T1}) \in M(c_{O1})$ *and* $c_{T2}(x_{T2},y_{T2},z_{T2}) \in M(c_{O2})$ *s.t.* $(x_{O1}-x_{O2})(x_{T1}-x_{T2}) \geqq 0$, $(y_{O1}-y_{O2})(y_{T1}-y_{T2}) \geqq 0$, $(z_{O1}-z_{O2})(z_{T1}-z_{T2}) \geqq 0$,

where $c_{ij}(x_{ij},y_{ij},z_{ij})$ represents a cell c_{ij} and its coordinate (x_{ij},y_{ij},z_{ij}) in a nerve subarea. □

Synapse formation is performed by the following procedure under control of this topology preservation projection rule, the number of axon branches, axon concentration parameters, and the amount of a neurotrophic factor on postsynaptic neurons. First of all, a certain neuron is selected as a pioneer neuron, and a pioneer axon's main branch selects a target cell, then its sub-branches select target cells in its neighborhood under the limit in the number of axon branches. Next, neurons around the pioneer neuron grow axons sequentially in the manner that a main branch selects a target cell under the topology preservation projection between main branches, then sub-branches select target cells in its neighborhood under the limit in the number of axon branches. The amount of a neurotrophic factor of target cells limits the number of presynapse formation and axon concentration parameters for a main branch and sub-branches also give a concentration constraint of a main branch and sub-branches on a target nerve sub-area respectively. The axon outgrowth and synapse formation continues for a certain development stages after neuron production.

Activity-dependent Synapse Regulation

We formulate a model of a pulse neuron based on the Spike Response Model proposed by (Gerstner 1999). In our model, activity of a neuron is formulated as follows. Let T be a set of discrete times whose time unit is defined in the scale of one or a few milliseconds. The membrane potential $u_i(t)$ of neuron i at time $t(\in T)$ is formulated by

$$u_i(t) = \begin{cases} \eta(t-t_i^f) + \sum_{j \in \Gamma_i} p_{ij}(t) \cdots\cdots t - t_i^f > \delta_{abs} \\ undefined \cdots\cdots\cdots\cdots\cdots\cdots otherwise \end{cases} \quad (1)$$

where t_i^f*: recent firing time before time* t, $\eta(t-t_i^f)$*: negative contribution to membrane potential that is called a refractory function, and represents negative effect for the relative refractory period,* δ_{abs}*: time length of the absolute refractory period,* Γ_i*: a set of presynaptic neurons of neuron* i, $p_{ij}(t)$*: synaptic potential from presynaptic neuron* $j(\in \Gamma_i)$ *to postsynaptic neuron* i.

The refractory function η is given by

$$\eta(s) = -\eta_0 \exp(-\frac{s-\delta_{abs}}{\tau_{rel}}) \quad (2)$$

where τ_{rel}*: time constant of relative refractoriness,* η_0*: a positive constant that represents the magnitude of relative refractoriness.*

The synaptic potential $p_{ij}(t)$ from presynaptic neuron j to postsynaptic neuron i at time $t(\in T)$ is formulated by

$$p_{ij}(t) = (p_{ij}(t_{ij}^a) + w_{ij}(t_{ij}^a)) \exp(-\frac{t-t_{ij}^a}{\tau_{syn}}) \quad (3)$$

where τ_{syn}*: time constant of synaptic potential,* $w_{ij}(t)$*: synaptic efficacy from presynaptic neuron* j *to postsynaptic neuron* i *at time* t, t_{ij}^a*: recent time of impulse arrival before time* t *from neuron* j, *that is computed as* $t_{ij}^a = t_j^f + \Delta_{ij}^{ax}$ *using the conduction delay* Δ_{ij}^{ax} *of impulse from neuron* j *to neuron* i.

Then, for a threshold θ, a neuron i fires when $u_i(t) \geqq \theta$ and $u_i(t-1) < \theta$ hold. As a result, a set of firing times of neuron i is given by the following expression

$$F_i = \{t + \Delta^{ir} \in T \mid u_i(t) \geq \theta \wedge u_i(t-1) < \theta\} \quad (4)$$

where Δ^{ir} *is an impulse rising period.*

The transmission of impulse takes the conduction delay Δ_{ij}^{ax} proportional to a distance between neurons, and is calculated from three-dimensional coordinate triplets of them.

Next we formulate synaptic efficacy regulation based on the spike-based hebbian rule. Hebbian rule generally says that when both presynaptic neuron and postsynaptic neuron fire synchronously, the synaptic efficacy increases, otherwise decreases. That is, change in synaptic efficacy is

determined according to whether postsynaptic neuron fires for an impulse arrival from presynaptic neuron. Let t_i^f be recent fire time of neuron i, and t_{ij}^a be recent impulse arrival time from neuron j to neuron i. Then

(1)if postsynaptic neuron i fires when an impulse arrives from presynaptic neuron j, all synaptic efficacy w_{ik} for all presynaptic neurons $k(\in \Gamma_i)$ are regulated according to

$$\Delta w_{ik}(t_i^f) = \lambda(|w_{ik}(t_i^f)|)\times|p_{ik}(t_i^f)|\times W(t_i^f - t_{ik}^a), \quad (5)$$

(2)if postsynaptic neuron i don't fire when an impulse arrives from presynaptic neuron j, synaptic efficacy w_{ij} for presynaptic neuron $j(\in \Gamma i)$ is regulated according to

$$\Delta w_{ij}(t_{ij}^a) = \lambda(|w_{ij}(t_{ij}^a)|)\times|p_{ij}(t_{ij}^a)|\times W(t_i^f - t_{ij}^a). \quad (6)$$

In above formulas, λ is a learning rate function dependent on the magnitude of synaptic efficiency and is given by the following expression

$$\lambda(w) = \lambda_0 \exp(-\frac{(w-w_0)^2}{2\lambda_1^2}) \quad (7)$$

where w_0: an initial value of synaptic efficacy, $\lambda_0 (0 \leqq \lambda_0 \leqq 1)$ and $\lambda_1 (\lambda_1 \geqq 0)$: constants.

An initial value of synaptic efficiency can take a different value in excitatory synapse and inhibitory synapse. $W(s)$ is a learning window as a function of the delay s between postsynaptic firing and presynaptic impulse arrival, and expressed as (Gerstner *et al.* 1996)

$$W(s) = \begin{cases} (A_+ - A_-)\exp(-\frac{s-\Delta^{ir}}{\tau_0}) \cdots\cdots\cdots\cdots s \geq \Delta^{ir} \geq 0 \\ A_+ \exp(-\frac{\Delta^{ir}-s}{\tau_+}) - A_- \exp(-\frac{\Delta^{ir}-s}{\tau_-}) \cdots s < \Delta^{ir} \end{cases} \quad (8)$$

where $A_+ > A_- > 0$, $\tau_0 > 0$, and $\tau_- > \tau_+ > 0$.

Parameters A_+, A_-, τ_+, τ_-, and τ_0 can take different values for excitatory synapses and inhibitory synapses respectively, and are set to values in Table 3. As a result, the excitatory synaptic efficiency $w_{ij}(t)(\geqq 0)$ is regulated according to

$$w_{ij}(t) \leftarrow \max(0, w_{ij}(t) + \Delta w_{ij}(t)), \quad (9)$$

and the inhibitory synaptic efficacy $w_{ij}(t)(\leqq 0)$ is regulated according to

$$w_{ij}(t) \leftarrow \min(0, w_{ij}(t) + \Delta w_{ij}(t)). \quad (10)$$

We can see the following properties as for synaptic efficacy regulation from these formulas. (a)For an excitatory synapse $(p_{ij}(t) \geqq 0)$, synaptic efficacy is reinforced when the postsynaptic neuron fires for a presynaptic impulse arrival and weakened when it do not fire. For an inhibitory synapse $(p_{ij}(t) \leqq 0)$, synaptic efficacy is reinforced when the postsynaptic neuron do not fire against a presynaptic impulse arrival and weakened when it fires. (b)Since change in synaptic efficiency is proportional to $|p_{ij}(t)|$, a continuous stimulation like the tetanus stimulation causes large regulation. (c)Since change in synaptic efficiency is large for the first stimulation and gradually becomes small as indicated in $\lambda(w)$, synaptic efficiency becomes steady for repeated reinforcement.

In our artificial neural development method, spiking activity affects the neural network structure through the programmed cell death and the synapse elimination. The programmed cell death adjusts the size of an origin neuron group and a target neuron group in case of living things. It is known that the interception of presynaptic inputs and the loss of connection with target nerve areas cause the programmed cell death (Hall 1992). In our method, the programmed cell death is controlled according to the following rule.

[Programmed cell death rule] (1) If a neuron forms no synapses with target cells, it dies because it is supplied no neurotrophic factor. (2) If a neuron receives no impulses from presynaptic neurons throughout development, it dies because of stimulation interception. □

As for the synapse elimination, it is considered that eliminated synapses are those defeated at the target government competition among presynapses through spiking activity. The synapse elimination can be considered to play the role of selective stabilization of connections between nerve areas. According to this speculation, weakened synapses are considered to be doomed to elimination and the following synapse elimination rule is applied to a set of excitatory presynapses and a set of inhibitory presynapses for each neuron respectively.

[Synapse elimination rule] Let m be a mean of synaptic efficacy of presynapses for each neuron, and σ be their standard deviation. Then synapses with lower efficiency than $(m - k\sigma)$ are eliminated where $k \geqq 0$. □

This rule is an extension of the tree-wide rule of (Rust *et al.* 1997b).

Animat's Neural Structure and Genome for Place Recognition

Animat's Place Recognition Circuit

Activity of neurons that occurs in response to an animal's position is especially observed from neurons of dorsal hippocampus. These neurons are called place cells because it is considered that groups of these neurons code information on places where an animal is situated. From experiments of rats, correlation between a rat's position and activity of an individual place cell is weak but there is a strong correlation between a set of place cell firing and a rat's position (Delcomyn 1998). This means that a rat recognizes his/her location with a place cell assembly. A lot of models of the place recognition circuit that contains

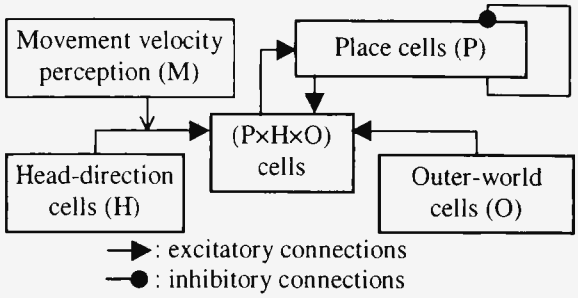


Figure 1: Place recognition circuit

place cells for navigation of animals and robots have been proposed (Trullier *et al.* 1997). In this paper, a model of the artificial place recognition circuit shown in Figure 1 is supposed based on some of these works. As for receptive cells, we suppose outer-world cells (O) and head-direction cells (H). The movement velocity modulates receptor potential of head-direction cells. Central circuits for place recognition are supposed to be the interconnected circuit of place cells with (P×H×O) cells and the lateral inhibitory circuit for place cells. Lateral inhibition is introduced to support place recognition based on the competition principle.

Animat's Neural Structure and Genome

Our animat has a body of the diameter 40 cm and has four sonar sensors and four infrared sensors for outer-world sensing on the frontal right and left body respectively. The infrared sensor measures distance in the range from 0 to 15 inches. The sonar sensor measures distance in the range from 0 to 255 inches. It has also a head-direction sensor as an internal sensor. As an effector, it has two differential-drive wheels. Figure 2 shows the composition of our animat.

One receptive cell is assigned to each infrared sensor and six receptive cells are assigned to each sonar sensor. Infrared receptive cells and sonar receptive cells have the selective reactivity to distance and they selectively generate receptor potential for the specific range of distance measured by sensors. An infrared receptive cell has the reactivity to short distance. Six sonar receptive cells for each sonar sensor have the different reactivity, that is each reacts to one of six ranges for distance from 0 to 255 inches. Sixteen

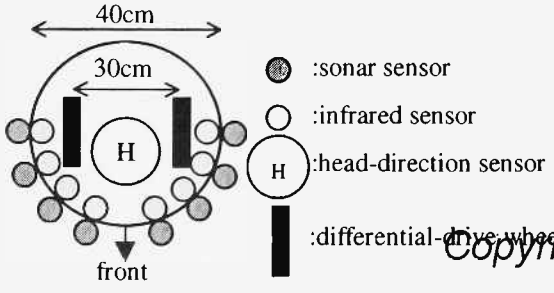
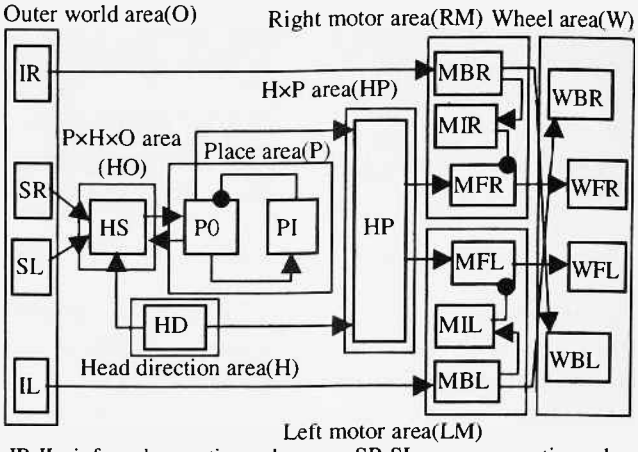


Figure 2: Sensors and actuators of the animat



IR,IL: infrared receptive sub-areas, SR,SL: sonar receptive sub-areas, HD: head-direction receptive sub-area, WFR,WFL: wheel effector sub-areas (forward), WBR,WBL: wheel effector sub-areas (backward), P0,PI: place sub-areas, HS: (P×H×O) sub-area, MFR,MBR,MIR,MFL,MBL,MIL,HP: motor sub-areas

Figure 3: The animat's neural structure

head-direction cells are assigned to the head-direction sensor, and each selectively reacts in one direction of every 22.5° and generates the receptor potential. When membrane potential as the temporal sum of receptor potential exceeds a threshold, a spike is generated. As for the effector, plural effector cells are assigned to right and left wheels respectively. Effector cells compute the velocity of the wheel in proportion to the number of spikes received in a certain interval.

Figure 3 shows a skeleton of the hypothetical neural network of the animat that contains the place recognition circuit shown in Figure 1. The neural network roughly consists of the forward movement controller and the backward movement controller. The forward movement is performed based on place and head-direction recognition by signals from sonar and head-direction sensors. The backward movement is performed based on signals from infrared sensors. Table 1 shows the composition of the

NA	NSA	NOC	RF	NAB	GF	ANF
O	SL	24	1010	4		
	SR	24	1010	4		
	IL	4	0110	6		
	IR	4	0101	6		
H	HD	16	1010	4		
W	WFL	2			0101	5
	WFR	2			0110	5
	WBL	2			1010	5
	WBR	2			1001	5

NA: Nerve Area, NSA: Nerve Sub-Area, NOC: the Number Of Cells, RF: Receptor Factor, NAB: the Number of Axon Branches, GF: Guide Factor, ANF: the Amount of Neurotrophic Factor

Table 1: Composition of receptor and effector areas

NA	DS	DD	NOC	TNA	RT	GF	RF	NAB	ANF	NSA
HO	1	0,0,0	*VAR*	S,H,P	+	1010	0011	*VAR*	*VAR*	HS
P	2	0,0,0	*VAR*	HO,HP,P	+	0011	1010	*VAR*	*VAR*	P0
	3	-1,0,0	*VAR*	P	-	1010	0011	*VAR*	*VAR*	PI
HP	1	0,0,0	20	H,LM,RM	+	1010	0011	2	8	HP
LM	2	0,-,-	10	S,W,LM	+	0110	1001	2	8	MBL
	3	0,+,-	10	W	+	0011	0101	2	16	MFL
	4	0,0,-	10	LM	-	1001	0011	6	8	MIL
RM	2	0,-,+	10	S,W,RM	+	0101	1010	2	8	MBR
	3	0,+,+	10	W	+	0011	0110	2	16	MFR
	4	0,0,+	10	RM	-	1010	0011	6	8	MIR

The left table shows an animat's genome. Each row is a gene indexed by a nerve area(NA) and a development stage(DS). The right table shows the correspondence of genes with nerve sub-areas in Figure 3.

Table2: An animat's genome

DS: Development Stage, DD: Development Direction, TNA: Target Nerve Areas, RT: Response Type, NA,NOC,GF,RF,NAB,ANF,NSA: see table 1

receptor area for sensors and the effector area for wheels.

When a specification of receptor areas and effector areas like Table 1 is given by a user, the artificial neural development of NEUROGEN'2000 can generate a neural network that connects these receptor areas and effector areas by developing genomes evolved automatically. However, it takes enormous computation cost to evolve genomes that generate such a neural network we suppose to construct in this paper, even if it can be done. On the other hand, it requires a serious load to design all the genome for generating a neural network like Figure 3 by hand. In order to design a place recognition circuit of good place recognition performance, there are several difficult problems, for example, how many neurons are necessary in each nerve area, what connections are necessary between nerve areas, and so forth. In NEUROGEN'2000, hybrid manual and evolutionary genome design method resolve these problems.

The genome of the animat is shown in Table 2 by a table form. The number of nerve areas is 5 and the number of development stages is 4, so the gene matrix of (5, 4)-type represents the genome. In the table, the "VAR" sign expresses a part that is determined by evolutionary computation, and these nine values are evolutionally determined in the experiments of the next section. In general, an arbitrary part of genomes can be determined by evolutionary computation.

Experiments

Testbed

As an environment to evaluate the artificial neural development and evolution of the animat's artificial place recognition circuit, we use a simple T-maze in Figure 4. The T-maze has three arms of 120cm in width and 160cm in length. The maze is sectioned in grids of 10cm.

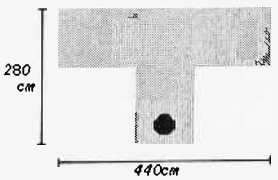


Figure 4: T-maze with 3 arms

The animat can move to an arbitrary direction at a speed within a certain range, and is located on a lattice point that is nearest to the moved point.

Decoding a genome through four development stages develops a neural network. The period of the target recognition for axonal outgrowth is set to 3 development stages. Activity of a neural network is computed at every time unit. The interval of outer-world sensing by sonar and infrared sensors is set to 5 and the interval of movement computation is set to 50. The time length of spiking before synapse elimination is set to 10000. The σ value for synapse elimination is set to 3. Main parameters which characterizes a pulse neuron are shown in Table 3.

Parameters for the steady state genetic algorithm are as follows. The selection method is set to the ranking selection, the replacement method is set to the conditional ranked replacement, and the non-selection age is set to 2. As for genetic operators, the creeping mutation is used for mutations of the number of cells, the number of axon branches, and the amount of a neurotrophic factor. The mutation rate is set to 0.5. These operators change the number of cells, the number of axon branches, and the amount of a neurotrophic factor between 10 and 100, 1 and 10, and 1 to 20 respectively.

The Bayesian place reconstruction mapping from a spiking pattern of place cells to a place as a physical variable in an environment (Zhang *et al.* 1998) is used for evaluation of animat's place recognition. The Bayesian place reconstruction consists of the sampling phase and the

	excitatory	inhibitory
W_0	1.0	3.0
A+	0.5	0.35
A-	0.2	0.3
τ_0	10	10
τ_+	5	5
τ_-	20	20

δ_{abs}	4
η_0	1.5
τ_{rel}	3
τ_{syn}	10
θ	3.0
Δ_{ir}	2
λ_0	0.01
λ_1	0.5

Table 3: Parameters of pulse neurons

reconstruction phase. In sampling, the spatial occupancy $P(X)$ of the animat and the firing rate map $f_i(X)$ are computed. The spatial occupancy is the probability for the animat to visit each spatial position $X=(x, y)$. The firing rate map is the average firing rate of a place cell i while the animat is at each position X. In reconstruction, the one-step reconstruction method and the two-step reconstruction method are used to compute a reconstructed position of the animat from the spatial occupancy and the firing rate map. Let $n_t=(n_1,\ldots,n_N)$ be the numbers of spikes fired within the t-th time window, where n_i is the number of spikes of cell i. The one-step reconstruction method computes the conditional probability $P(X_t|n_t)$ for the animat to be at each position X_t. The two-step reconstruction method introduces a continuity constraint of positions and computes the conditional probability $P(X_t|n_t,X_{t-1})$ for the animat to be at each position X_t, given the preceding position X_{t-1}. In these probability distribution, the most probable position is taken as the reconstructed position of the animat at the t-th time window. In experiments, the time window is set to 50. Since length of the time window for reconstruction is equal to the interval of movement, the pulse assembly of place cells counted in the time window can be considered to code a place where the animat is situated.

As a fitness function for evolution, the following function is used to evolve an animat who can recognize places accurately and move widely.

$$fitness = \frac{(V-1)^{\beta}}{\alpha + E} \tag{11}$$

where V: the number of visit positions, E: the reconstruction error that is computed as the sum of distance between true positions and reconstructed positions, α and β: constants.

In experiments, one-step reconstructed positions are used for the fitness computation, where the sampling time length and the reconstruction time length are set to 10000. The constants α and β are set to 250 and 1 respectively.

Results: Place Recognition Circuit Genesis

We could generate animats that achieve high fitness values by repeated simulations of population size 10 and generation length 15. Figure 5 shows true positions, the one-step reconstructed positions, and the two-step reconstructed positions of an animat with a high fitness value, where the sampling time length is set to 30000 and the reconstruction time length is set to 10000. We can observe several erratic jumps in the trajectory of the one-step reconstruction. These erratic jumps are also observed when positions are reconstructed from firing data of rat's place cells in (Zhang *et al.* 1998), and our reconstructed trajectory is similar to those results. In case of the two-step reconstruction, reconstruction error is less in comparison with the case of the one-step reconstruction. This is also similar to the result in (Zhang *et al.* 1998). As a type of place recognition error, there is so-called perceptual aliasing in which different places are judged to be the same place due to incomplete perception. It is considered that integration of view information and dead reckoning information is necessary to avoid this type of error. Since erratic jumps are resolved by a continuity constraint using information from two consecutive times, it is suggested that erratic jumps are induced by the perceptual aliasing. We guess that place recognition is not complete at hippocampal place cells of rats since erratic jumps are observed in their one-step reconstructed trajectories. It is remarkable that our reconstructed trajectories are similar to those reconstructed from firing data of rat's place cells, including feature of

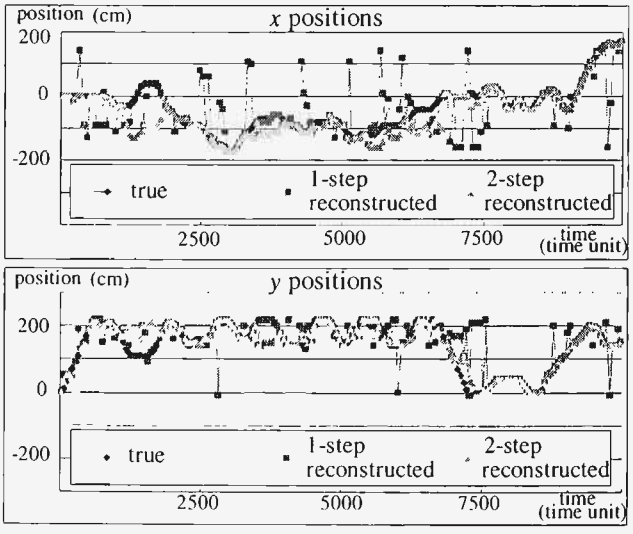


Figure 5: True position, 1-step reconstructed position, and 2-step reconstructed position of an animat with a high fitness value

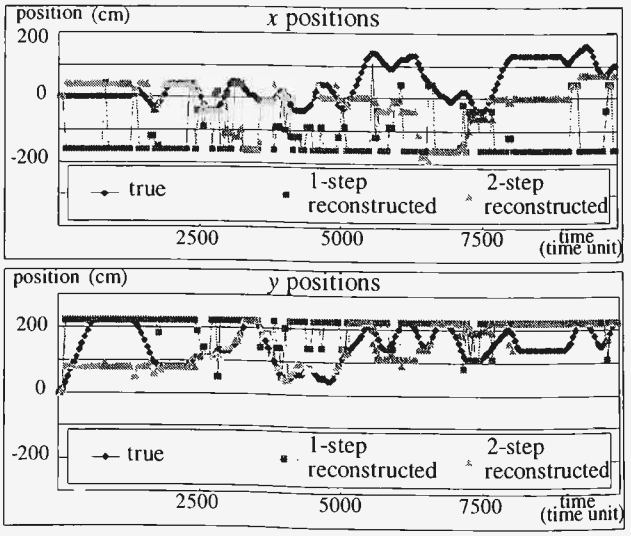


Figure 6: True position, 1-step reconstructed position, and 2-step reconstructed position of an animat with a low fitness value

erratic jumps. Figure 6 shows a place reconstruction result of an animat with a low fitness value, who can not recognize places well. By these experiments, it was confirmed that there were place recognition circuits that were able to reconstruct places well and that were not able to reconstruct places at all. It was also confirmed that the well-cognitive circuits could be designed by evolutionary computation. That is, it was found that the evolutionary design could be achieved as evolutionary search of finding a suitable combination of nine parameters in the genome of Table 2 in combination with the artificial neural development.

Table 4 shows a part of the genome and the neural network composition of the above animat with a high fitness value. Many synapse connections are generated among place recognition nerve sub-areas as assumed in Figure 1. This suggests that the assumed circuit satisfies a necessary condition for place recognition. However, it seemed that it was difficult to distinguish high-fit animats with low-fit animats only by these connections.

It was also observed that the place reconstruction performance of high-fit animats was superior for a short sampling time length but was inferior for a long sampling time length. In fact, the place reconstruction performance was far better for 10000 sampling time length than for 30000 sampling time length and was slightly worse for 50000 sampling time length than for 30000 sampling time length, that is the case in Figure 5. We presume that one cause for decrease in reconstruction accuracy is the increase of visits to the same place from different directions. It is one of typical place recognition errors in which a place is judged to be different places for visiting the place from different directions. Since it is considered that integration of view information and head-direction information is necessary to avoid this type of error, the interconnected circuit of place cells with (P×H×O) cells is supposed to realize the integration to set the equivalence between different views from the same place. That is, it is supposed that a spiking pattern specific to a place occurs in the place cell area as a result of integrating view information and head-direction information in this interconnected circuit. However, it became clear this circuit was insufficient to achieve this information integration. To resolve this problem, it is necessary to evolve more parts of the place recognition circuit structure to find a better one or to assume another place recognition circuit scheme.

NA	DS	NOC	NAB	ANF
HO	1	25	8	10
P	2	72	3	9
	3	63	4	8

NSA
HS
P0
PI

	NOC	the number of synapses(row→column)						
		SR	SL	HD	HS	HP	PI	P0
SR	24	0	0	0	96	0	0	0
SL	24	0	0	0	96	0	0	0
HD	13	0	0	0	32	46	0	0
HS	25	0	0	0	0	0	0	200
HP	17	0	0	0	0	0	0	0
PI	28	0	0	0	0	0	0	107
P0	55	0	0	0	26	85	155	0

The top tables show the animat's genes and their correspondence with nerve sub-areas in Figure 3. Each row is a gene indexed by a nerve area and a development stage. The bottom table shows the number of cells and synapses of the animat.

NA, DS, NOC, NAB, ANF, NSA: see table 1 and 2.

Table 4: A part of the genome and the neural structure

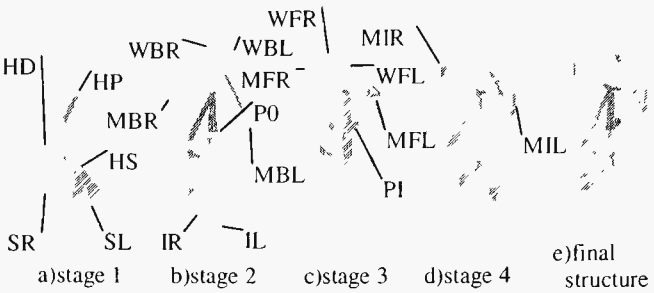


Figure 7: The development of the artificial neural network

The development process of the artificial neural network of the above high-fit animat is shown in Figure 7 and numbers of cells and synapses in the place recognition circuit before and after the programmed cell death and the synapse elimination are shown in Figure 8. It is observed sizes of origin neuron groups and target neuron groups are adjusted by the programmed cell death to meet roughly the size of the nerve sub-area HS.

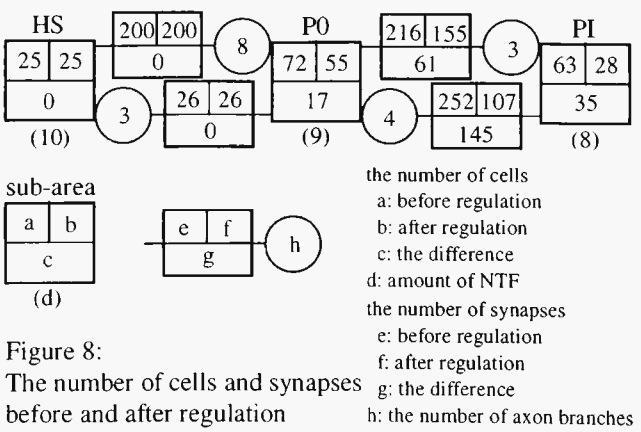
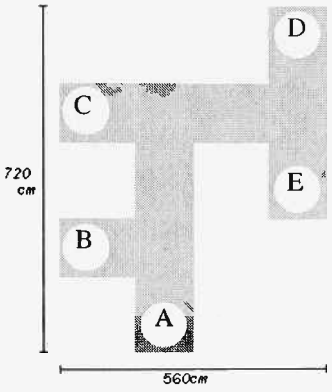


Figure 8:
The number of cells and synapses before and after regulation

Results: Place Recognition Performance

We evaluate the place recognition performance of animats in an environment where they first enter after development, in comparison with the place recognition performance in an environment where they came into existence. It is reported that place cells shows specific spatial firing

after an animal is introduced in a new environment, that is place recognition do not depend on learning. This experiment examines whether our place recognition circuit shows such a characteristic.



A,B,C,D,E: Initial positions

Figure 9: T-maze with 7 arms

For that purpose, we use animats of good place recognition performance and animats of bad place recognition performance in the T-maze with three arms of Figure 5, and measure place recognition performance of these animats in the T-maze with seven arms of Figure 9. In this experiment, animats start from each of initial positions A to E in the T-maze of Figure 9, and moves freely in it. The Bayesian place reconstruction mapping is used for the evaluation of place recognition performance. That is, animats start from each initial position and move freely in the T-maze firstly for the sampling time length 30000 and then for the reconstruction time length 10000, and errors between true positions and reconstructed positions are computed.

	S10000-R10000		S30000-R10000	
	1-step	2-step	1-step	2-step
G1	26.4	11.6	52.9	41.3
G2	15.9	7.3	46.6	26.4
G3	19.3	5.4	47.4	24.1
G4	19.0	11.2	50.5	17.1
Mean	20.2	8.9	49.4	27.2

(a)results of animats with high fitness values

	S10000-R10000		S30000-R10000	
	1-step	2-step	1-step	2-step
B1	96.7	96.9	92.7	75.8
B2	84.4	79.1	183.3	98.1
B3	82.8	98.2	90.5	90.7
B4	89.4	115.4	83.4	98.6
Mean	88.3	97.4	112.5	90.8

(b)results of animats with low fitness values

Average reconstruction error that is the average distance between true positions and reconstructed positions. The unit is the centimeter (cm). The label "S10000-R10000" means that the sampling time length is 10000 and the reconstruction time length is 10000. The label "S30000-R10000" means that the sampling time length is 30000 and the reconstruction time length is 10000. The label "1-step" represents 1-step reconstruction and the label"2-step" represents 2-step reconstruction.

Table 5: Place recognition performance in T-maze with 3 arms where animats came into existence

	Initial positions					
	A	B	C	D	E	
G1	61.0	43.6	45.0	71.8	44.8	53.2
G2	59.5	54.2	37.6	92.0	48.0	58.3
G3	44.3	58.7	75.0	77.4	71.9	65.5
G4	67.4	48.0	52.0	44.5	51.9	52.8
B1	170.8	187.9	180.9	113.1	111.1	152.8
B2	111.0	120.7	106.4	109.0	291.4	147.7
B3	126.5	209.1	108.1	148.2	152.1	148.8
B4	187.3	90.3	136.9	89.3	127.7	126.3

Average reconstruction error in the case of the 1-step reconstruction. The sampling time length is 30000 and the reconstruction time length is 10000. The unit is the centimeter (cm).

Table 6: Place recognition performance in T-maze with 7 arms

Table 5 shows place recognition performance of animats in the T-maze of Figure 5. Four animats in Table 5(a) are high-fit ones and have good place recognition performance. On the other hand, four animats in Table 5(b) are low-fit ones and have bad place recognition performance. Table 6 shows what place recognition performance these animats display in the T-maze of Figure 9. As for animats that had good place recognition performance in the T-maze with three arms, they displayed good place recognition performance in another T-maze with seven arms. As for animats that had bad place recognition performance in the T-maze with three arms, there was a tendency that they displayed worse place recognition performance in another T-maze with seven arms.

These results suggest that the place recognition ability is an innate ability dependent on the composition of the place recognition circuit.

Conclusion and Future Work

We have proposed the artificial neural development method NEUROGEN'2000 that generates the three-dimensional multi-regional pulsed neural network arranged in three layers of the nerve area layer, the nerve sub-area layer, and the cell layer. Then we have applied it to develop an animat's place recognition circuit that focuses on the place cell area. The Bayesian place reconstruction mapping from a spiking pattern of place cells to a place in an environment was used for evaluation of animat's place recognition performance. As a result of simulation experiments, it was found that performance of place recognition depended on the composition of the place recognition circuit and the well-cognitive circuits could be designed by our artificial neural development method in combination with evolutionary computation. That is, we could generate a multi-regional place recognition circuit with the place cell area that showed [illegible] recognition features similar to rat's place cells. Also it was suggested that the place recognition ability was an

innate ability dependent on the composition of the place recognition circuit. By these results, it was confirmed that NEUROGEN'2000 was useful for designing biologically realistic multi-regional pulsed neural networks.

However, there are a lot of future works and the following researches are ongoing at present. The first is to find genetic and/or nerve-structural factors of good place recognition performance by analyzing genomes and nerve circuits of good place recognition performance and bad place recognition performance. This may suggest how the development process contributes to generation of good place recognition circuits. The second is genetically to design the place recognition-triggered navigation circuit, that is the goal-seeking action circuit in combination with the place recognition circuit. As for the goal-seeking behavior, learning after growth plays an important role in addition to development and evolution.

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