Fitness Landscape of the Hopfield Model of Associative Memory

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Abstract— **We apply evolutionary computations to Hopfield's neural network model of associative memory. In the model, some of the appropriate configurations of the synaptic weights give the network a function of associative memory. One of our goals is to obtain the distribution of these configurations in the synaptic weight space. For the purpose, we explore a fitness landscape defined on the weight space. So far, there have been a fair amount of studies regarding the ruggedness of the fitness landscape. These studies, however, are for discrete genes. In this paper, we apply these methods to our continuous genes which represent the synaptic weights of the Hopfield network.**

I. Introduction

Associative memory is a dynamical system which has a number of stable states with a domain of attraction around them [1]. If the system starts at any state in the domain, it will converge to the stable state. In 1982, Hopfield [2] proposed a fully connected neural network model of associative memory in which information is stored by being distributed among neurons and retrieved by being relaxed dynamically.

The dynamical behavior of its neuron states strongly depends on synaptic strength between neurons. The synaptic strength from neuron j to neuron i is called *weight* and denoted as w_{ij} in this paper.

Hopfield used the Hebbian rule [3] to determine the synaptic weights, whilst we specify them with using evolutionary computations (see, e.g., [4], [5], [6], [7]).

For the fully connected neural networks with N neurons, all the possible combinations of w_{ij} construct N^2-dimensional Euclidean space. Hereafter, we will call this (synaptic) weight space. Every configuration of w_{ij} is represented as a point in the weight space. Fitness values of all the points in the space are estimated according to the capability of the network that is determined by each configuration. Therefore, the task of our evolutionary computations is to locate the points of the highest fitness value.

Our previous results show that the task to locate one of the optimum solutions becomes difficult as the number of patterns to be stored is increased. We conjecture that this phenomenon is due to the increased ruggedness of the fitness landscape.

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II. Related Works

As many authors pointed out, the concepts of the fitness landscape were first introduced by Wright [8] to study biological evolutionary process. Since then, this concept has been used not only in biology but also in physics and computer science to investigate various fitness landscapes, for example: the free energies of RNA folding into secondary structures [9]; the chemical affinity of the antibody for the antigen in immune response [10]; the Hamiltonian energy of disordered system [11] (we return to this issue later); traveling salesman problem [12]; elementary cellular automata [13]; and of Kauffman's M-K model [14], [15], [16], [17] as the more general form of fitness landscape [18], [19], [20], [21], [22], [23].

They provide a way to tune the degree of ruggedness. Then their ruggedness are investigated by statistical measures such as: autocorrelation function of a landscape [12], [13]; correlation coefficient of a genetic operator (as a function of distance between parent and child [12], [13]; correlation length [12], [13]; mean hill-climbing/random walk length to a peak [19], [22], [10], [13]; the Fox-Jenkins approach to statistical time series of fitness [18]; the information content and stability [23]; and so on.

The Hopfield model described in this paper, when synaptic weights are selected randomly, can be considered as the Sherrington-Kirkpatrick model of Ising spin-glasses (SK-model) [24]. The number of meta-stable states of the SK-model were analytically studied by Bray et al. [25], [26], using correlations between the Hamiltonian energies of the meta-stable states. Or, the number of meta-stable states in one dimensional spin-glass chain was exactly solved by Derrida et al. [27], answering the question: if a spin configuration is evolve in time, what stable state will it fall into? Bray et al. and Derrida et al. did not use *the concept of the correlation of a fitness landscape* in the sense of Kauffman [14], [15], [16], [17]. Amitrano et al. [28], on the other hand, used this concept to analyze the Hamiltonian energy landscape in the study of chemical evolution of *information-carrying macromolecules* represented by a set of Ising-spin.

However all these landscapes were defined on the *discrete* configuration space of spin glasses. We are exploring the fitness landscape defined on the *continuous* synaptic weight space. As far as we know, there has been no research from this point of view, except that Gardner represented synaptic weight configurations as a volume in the space [29].

III. EVOLUTIONARY PATH & FITNESS EVALUATION

To study ruggedness of a fitness landscape of the Hopfield model, we need both a rule which determines the possible evolutionary paths in the weight space and a rule which determines the fitness of each point in the path, as Macken wrote [10]. In the following two subsections we describe these two rules.

A. Random Gaussian Mutation

In this paper, when point needs to be moved along an evolutionary paths, random Gaussian Mutation is applied to the point. A point

$$(x_1, x_2, \cdots, x_N)$$

is mutated by adding a random Gaussian variable to each coordinate x_i, i.e.,

$$x_i' = x_i + \sigma \cdot N_i(0,1)$$

where $N_i(0,1)$ is normally distributed random variable of mean 0 and standard deviation 1 sampled for each individual i. Note that the step length in Euclidean distance between parent and child is

$$\left(\sum_{i=1}^{N} (\sigma \cdot N_i(1,0))^2 \right)^{1/2}$$

B. Fitness Evaluation

Assume that p random bipolar patterns ξ^ν:

$$\xi^\nu = (\xi_1^\nu, \cdots, \xi_N^\nu), \qquad \nu = 1, \cdots, p$$

are stored as an associative memory in the network. Note that *bipolar* means:

$$\xi_i^\nu \in \{-1, 1\}, \qquad i = 1, \cdots, N.$$

When one of memorized patterns ξ^ν is given to the network as an initial state, the state of neurons varies from time to time afterwards (unless ξ^ν is stored as a fixed point). In order for the network to function as an associative memory, the instantaneous network state must be similar to the input pattern ξ^ν. The similarity is defined by,

$$m^\nu(t) = \frac{1}{N} \sum_{i=1}^{N} \xi_i^\nu \, s_i^\nu(t),$$

where $s_i^\nu(t)$ is the state of neuron i at time t. This $m^\nu(t)$ is referred to as *overlap*. The quality of retrieval of memorized patterns are represented by $\langle m^\mu \rangle$, a temporal average of $m^\nu(t)$ over certain time interval t_0. We evaluate the fitness value of each network by further averaging these $\langle m^\mu \rangle$'s over all p memorized patterns. Namely, the fitness f is

$$f = \frac{1}{t_0 \cdot p} \sum_{t=1}^{t_0} \sum_{\nu=1}^{p} m^\nu(t).$$

In this paper, t_0 is set to $2N$, twice the number of neurons. Then the fitness 1 implies all the p patterns are stored as fixed points, while all other cases have a fitness less than 1.

IV. AN EXAMPLE OF EVOLUTION

In this section, we show a result of evolving the Hopfield model of associative memory using a genetic algorithm as an example.

All simulations were carried out on networks with 49 neurons. The genetic algorithm used in this example is as follows. Before each run, p random bipolar patterns which are to be memorized, are produced. Using these patterns, a weight matrix is calculated by the Hebbian learning rule. In each generation 256 chromosomes modify this original Hebbian matrix, and produce 256 copies which are slightly different from the original. Each chromosome is made up of $2401 (= 49^2)$ Gaussian random variables of mean zero and standard deviation 0.01 which are to be added to the corresponding component of the original Hebbian matrix. These produced copies are evaluated fitness values by the method mentioned in the previous section. Then the chromosomes are ranked according to the fitness value of the copies they produced. Two chromosomes are chosen randomly from the best 40% and are recombined with discrete crossover[1], which makes one child chromosome. Mutation is given to the child chromosome by randomly picking up its allele with the probability 0.01, and replacing it with uniformly random number chosen from $[-0.1, 0.1]$. The process of producing child chromosome is repeated until the worst 60% of the chromosomes are replaced with the children. Thus the best 40% of the population and the produced children of the rest 60% construct the next generation. The cycle of reconstructing the new population and restarting the search is repeated until a perfect solution is found or generation 12000 has been reached.

We repeated each run 30 times with different random number seed for fixed p, the number of patterns to be stored. In Fig. 1, we show results of the fastest convergence out of each 30 runs for p from 14 to 19. The statistics of each 30 runs are shown in Table I.

TABLE I
Statistics of Each 30 Runs

number of patterns	avg of best-fit	std-dev of best-fit	fastest convergence (generation)	number of success
14	.999281	.000237	226	22
15	.998330	.000411	415	17
16	.996560	.000541	2590	5
17	.995294	.000671	3273	5
18	.990218	.000806	3760	1

The results shows that the more the number of patterns to be stored, the more difficult the task to locate one of the optimum will become. This is probably due to both of the

[1] Discrete crossover is a continuous version of uniform crossover [30], i.e., two parents $(u_1, \cdots, u_n)$ and $(v_1, \cdots, v_n)$ produce an offspring $(w_1, \cdots, w_n)$ such that w_i is either u_i or v_i with equal probability.

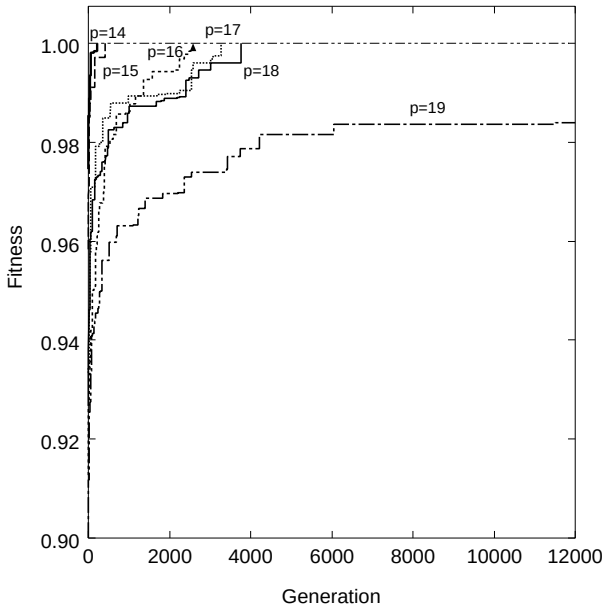

Fig. 1. **Fitness of the Best of Generation**

increasing local optima and the decreasing global optima.

The question now is how many local/global optima are, how they distributed, how large their basin of attraction, and so on. The ultimate goal of the following study to investigate the ruggedness of the fitness landscape is to know these information.

V. Experiments

The simplest way of specifying a fitness distribution would be by enumerating the fitness of each point of the weight space. This, however, is not realistic due to the huge number of points in our weight space. In the current problem, even if we restricted each weight value to the floating-point number from $\{-1.00, -0.99, -0.98, \cdots, 1.00\}$ the weight space is constructed with 201^N points. As such, statistic properties of a collection of randomly sampled points through the landscape, or points along an evolutionary paths are used.

In the following three subsections, we apply the method to obtain statistical properties of landscapes, which are originally devised for discrete genes, to our fitness landscape defined on continuous genes. The measurements were made on two fitness landscapes constructed by $p = 6$ and $p = 49$ as a first step to the whole comparisons.

A. Correlation Coefficient & Correlation Length

A.1 Correlation Coefficient of Gaussian Random Mutation

Both Manderick et al. [12] and Lipsitch [13] proposed a similar method to calculate the correlation coefficient of a single evolutionary operator. We use this method to calculate the correlation coefficient ρ of random Gaussian mutation. From the weight space, q points are randomly chosen as parents. Then, by applying a random Gaussian mutation of mean zero and standard deviation σ to each point, q points of mutant are obtained as children of the original points. Fitness values of both parents and children are denoted as $f_p^i(\sigma)$ and $f_c^i(\sigma)$ $(i = 1, 2, \cdots, q)$, respectively. These are repeatedly evaluated for the value of σ from 0.001 to 0.5. And the correlation coefficient as a function of σ is obtained as follows:

$$\rho(\sigma) = \frac{\sum_{i=1}^{q} (f_p^i(\sigma) - \overline{f_p})(f_c^i(\sigma) - \overline{f_c})}{\left(\sum_{i=1}^{q} (f_p^i(\sigma) - \overline{f_p})^2\right)^{1/2} \left(\sum_{i=1}^{q} (f_c^i(\sigma) - \overline{f_c})^2\right)^{1/2}}$$

where $\overline{f_p}, \overline{f_c}$ denotes average over q samples of parents and children, respectively.

In Fig. 2, we show two examples of correlation coefficient of the landscapes constructed by the fitness evaluation for $p = 6$ and $p = 49$, as a function of step length by a Gaussian mutation. The number of sampled points q was 600. As Lipsitch wrote: correlation provides a measure of how rugged a given landscape is. Highly correlated landscapes are smooth because nearby points have similar fitness values while less correlated landscapes are more rugged having larger fluctuations in fitness over short distance.

We see in the figure that the landscape for $p = 49$ is more correlated than for $p = 6$. This is oposit to our conjecture that the landscape for higher p is more rugged.

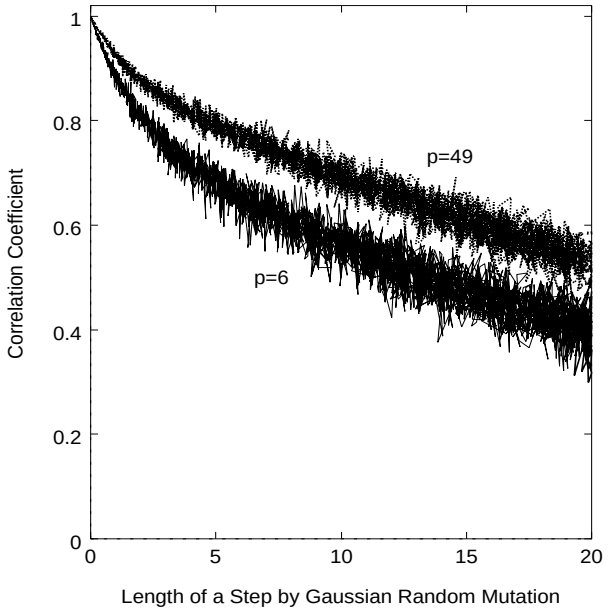

Fig. 2. **Correlation Coefficient**

A.2 Correlation Length

Lipsitch defined the correlation length of a landscape as the length less than the value of σ at which $\rho(\sigma)$ first becomes non-positive [13]. The calculation is very time consuming.

At the point of writing this early version of draft, we have not completed the calculation to obtain the σ whose correlation coefficient becomes 0. However, the figure suggests that the correlation length for $p = 49$ is longer than for $p = 6$. This is also against our intuition.

B. Autocorrelation function & Correlation Length

B.1 Autocorrelation function of the Landscape

In this subsection, we apply the autocorrelation function proposed by Manderick et al. [12] to landscapes given by the Hopfield model.

Firstly, we produce a random walk on the search space. It starts with a point chosen at random and the next point in the walk is determined repeatedly by adding a Gaussian random variable of mean zero and standard deviation σ to each coordinate of current point. The walk lasts q steps. At each point, fitness value is calculated. Then we obtain a sequence of fitness values:

$$f_0, f_1, f_2, \cdots, f_q$$

where f_0 is a fitness value of the starting point. The autocorrelation function $\rho(h)$ of the fitness sequence represents the correlation coefficient between a pair of fitness values of two points separated by h steps of the random walk, and is calculated as follows:

$$\rho(h) = \frac{R(h)}{R(0)}$$

where

$$R(h) = \frac{1}{M}\sum_{i=0}^{q-h}(f_i - \overline{f})(f_{i+h} - \overline{f}),$$

$$\overline{f} = \frac{1}{q+1}\sum_{i=0}^{q} f_i.$$

And roughly corresponds to the distance one can jump maintaining some information about the fitness.

In Fig. 3, we show the results. Again for the fitness landscape constructed for $p = 6$ and $p = 49$. Random walk was continued until 12000 steps (i.e. $q = 12000$). As we can see in the figure, the autocorrelation function defined as above does not work to characterize the feature of the landscapes in our problem. We are making the experiment with different values of step size σ, though we have not yet obtained sufficient results.

B.2 Correlation Length

Manderick et al.[12] also defined the correlation length τ as the distance where the autocorrelation function

$$\rho(\tau) = 1/2.$$

As the figure says, the correlation lengths of the two landscapes above are both around 1000 steps. Probalbly they are too long as the number of steps keeping the information of the initial points. This also suggests that experiment shoud be done with different step size σ.

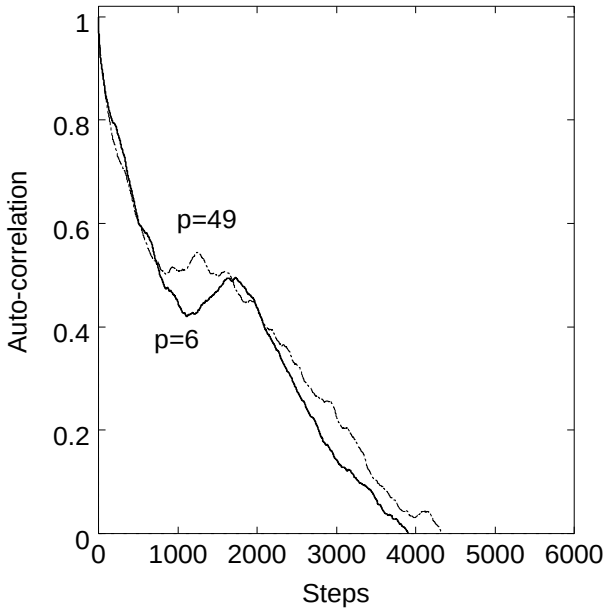

Fig. 3. **Autocorrelation Function**

C. Information Measure

With a sequence of fitness values along a q steps of random walk, Vassilev [23] measured some information characteristics of the fitness landscapes. First, a string $Q(\epsilon) = q_0 q_1 q_2 \cdots q_{q-1}$ is produced where,

$$q_i = \begin{cases} -1 & \text{if} \quad f_{i+1} - f_i < -\epsilon \\ 0 & \text{if} \quad |f_{i+1} - f_i| \leq -\epsilon \\ 1 & \text{if} \quad f_{i+1} - f_i > -\epsilon \end{cases}$$

He wrote that the $Q(\epsilon)$ contains information about the structure of the landscape. Then he defines the function, which he calls information content, as:

$$H(\epsilon) = -\sum_{p \neq q} P_{pq} \log P_{pq},$$

where p and q represent a pair $q_i q_{i+1}$ $(i = 0, 1, \cdots, q)$ in the string $Q(\epsilon)$[2], and P_{pq} is the probability of an occurrence of a specific pair of p and q from the set $\{-1, 0, 1\}$. Since the number of all the possible combination of p and q $(p \neq q)$ is six, the vase of the logarithm is six[3]. To estimate the ruggedness of the fitness landscape, he used an averaged value of $H(\epsilon)$ over m random walks. He also defines *information stability* $e^\star$ as $H(\epsilon^\star) = 0$ for each ϵ greater than $\epsilon^\star$. He suggest that the information content $H(\epsilon)$ represents the degree of diversity of the local optima, namely, that it increases when a landscape is tuned from smooth to rugged.

We can apply this method to the continuous genes without modifying any details. We show the results in Fig. 4. The experiment was made with 256 random walks, averaging

[2] $q_{q+1} = q_0$ (Personal communication with Vassilev.)
[3] Also from personal communications with Vassilev.

each $H(\epsilon)$ over them. The total steps of each random walk was 12000, and Gaussian mutation is with the standard deviation 0.002. As Vassilev wrote, the steepest information content $H(\epsilon)$ presents the smoothest landscape and less steep $H(\epsilon)$ presents more rugged landscape. Hence the figrue shows the same result as the correlation coefficient of Gaussian random mutation described in section A.1, that is, oposit to our conjecture.

It might be interesting to quate Vassilev's note here that sometimes high correlate (smooth) landscape is difficult to search optimum and less correlated (rugged) landscape are easy. He suggested that the information content $H(\epsilon)$ and the information stability $\epsilon^\star$ allow us to understand these phenomena. Since the information stability of a landscape whose optimum is an isolated point, can be comparatively high, and its information content is almost 0.

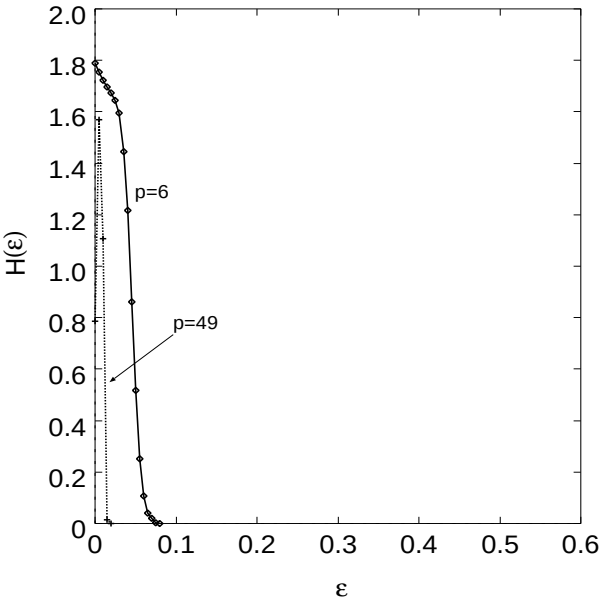

Fig. 4. **Information Content**

VI. Conclusion

We have described the possibility of using some methods which have been used so far to measure the ruggedness of fitness landscapes difined on discrete space, in our fitness landscape of the Hopfield model defined on continuous space. Some of them were found not to work in our problem, and others showed the oposite result to our conjecture. Our conjecture is that the ruggedness of the fitness landscape is increased as the number of patterns to be stored is increased. Namely, the number and the diversity of local optima is increased and their basin of attraction becomes smaller as the number of patterns is increased.

All those method described here to obtain the information about the ruggedness of the fitness landscape is far from being perfect, at least in our problem. Since our weight space is so huge, it is almost impossible for the sample points to include the global optimum solution(s), or even a local optima, whichever those sample points may be taken uniformly at random from the space, or along a random walk. It is less possible for them to represent the whole fitness landscape. Hence our future work should explore how to gather samples which can represent the whole fitness landscape including the information about the local and global optimum. Therefore the next step would be to use statistics for samples along evolutionary paths to the global optimum from a random point.

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