Abstract

Studying the diversity of genetic algorithms is the most important topic to prevent the problem of premature convergence of the population. In general diversity study can be divided into, measuring diversity of the population and maintaining the diversity of the population. This paper is interested in measuring the diversity. Measuring population diversity can be categorised into genotype diversity measure and phenotype diversity measure. Most of the previous research was devoted to measure diversity of genetic programming and genetic algorithms in general. The present paper introduces a dedicated study to measure and analyse the genotype or structure diversity of evolvable neural networks. A new metric is introduced to measure the genotype diversity of evolvable neural networks based on genetic operations required to transform one neural network to another one. This method is called neuro-edit, it is inspired on edit distance measure and genetic operations used to evolve neural networks. This metric measures the distance between neural networks in terms of connection genes addition, deletion, and substitution.

1. Introduction

Although there are many methods to measure genotype and phenotype diversity of a population, all these methods are devoted to genetic programming (GP) and genetic algorithms (GA) in general. There is no an indication on the applicability of these methods to measure the diversity of a population of Evolvable Neural Networks (ENNs), especially measuring the genotype diversity. Already existing methods to measure phenotype diversity can be applied to measure phenotype diversity of population of ENN’s. Since, these methods are based on the performance of the population. However, the methods which are used to measure the genotype diversity, such as Hamming distance and edit distance can not be used to measure genotype diversity of ENN’s since, as a result of evolution, chromosomes have different lengths, the same genes may have different locations in different chromosomes, and some genes may be enabled or disabled. So, there is the need of a genotype diversity measure that fits the dynamic nature of evolving neural networks. Searching for a method to measure the genotype diversity of neural networks is important to explore the evolution of neural networks. The effect of genetic operators and initial settings of evolutionary algorithms on the evolvability of neural networks can be investigated by measuring and analysing the population diversity.

Measuring the genotype diversity of a population is important as, genotype diversity is a sufficient upper bound of population diversity [1]. In general, two identical genotypes will produce the same fitness value, this means that a decrease in genotype diversity (unique individual genotypes) leads to a decrease in phenotype diversity (unique fitness values) [2]. Diversity can be defined as the amount of variety in a population and measuring diversity is an attempt to quantify the variety in that population [1]. There is a large number of researches that discuss diversity in general from different points of view, such as survey and analysis of diversity measures in GP [1], [3], [4], population diversity in genetic algorithms [5] [6], [7], the effect of population diversity on the premature convergence in GA [8], methods of creating diversity [9], correlation between diversity and fitness [1], diversity of multiobjective evolutionary algorithms based on the immune and entropy principle [10], and the relationship between genetic crossover and diversity [11]. Next discussion will be limited to methods of measuring genetic diversity, especially Hamming distance, section 2 and edit distance, section 3 since the proposed method is considered an extension of these methods. Section 4, gives a brief review about ENNs. Section 5 discusses the proposed method. Section 6 is experimental results and finally the conclusion, section 7.

2. Hamming distance

Hamming distance is initially used in communications to detect errors. Hamming distance of an error code is the minimum number of bits errors that must be present in string to make the error undetected [12], [13]. In information theory, Hamming distance between two strings of equal length is the number of positions for which the corresponding symbols are different. For genomes that have fixed length and uniform structure, the definition of a diversity measure for two individuals is
typically based on the use of the Hamming distance [14]. Uniform structure means that all the individuals have a genome with the same number of genes, with the same phenotypic meaning for the genes, and genes are arranged in the same order in genomes.

In the case of ENNs, both of fixed length and uniform structure are not satisfied. Evolving neural networks are based on genetic operations which add nodes and connections randomly to chromosomes so that, the length of chromosomes is usually different and genes have different locations inside chromosomes. In measuring population diversity Hamming distance is used to calculate the difference between every possible pair of chromosomes in the population [2], [14]. If all chromosomes in a population are identical, then there is no difference between any two chromosomes and hence there is no diversity in the population. On the other side, if there is no similarity between chromosomes of a population, then those differences add, and the population should be maximally diverse [2]. Based on, Hamming distance is symmetric, and is equal to zero if the strings are the same, only the lower triangle in a chromosome-pairs table need be considered when computing the diversity [1]. A diversity measure for the whole population p can be then obtained from the diversity measure for pairs of individuals by combining all the pairwise distances between individuals [14]:

\[ \text{div} = \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} h(c_i, c_j) \]

where \( n \) is the population size and \( c_i \) and \( c_j \in p \).

3. Edit distance

Measuring the difference between two individuals based on string edit distances has been used several times in genetic programming [1]. Strings with variable length but still with uniform structure can be treated in a similar way, by generalizing Hamming distance to permit the comparison of strings having different lengths [1], [12], [14]. Edit distance between two strings of characters is the minimum number of operations required to transform one of them into the other [13]. For genetic programming, edit distance based on single node insertion, deletion, and substitution to transform two trees to be equal in structure and content [1]. There are several different algorithms to define or calculate this metric such as edit distance 1 and edit distance 2. Edit distance 1 is based on the use of three elementary operations, “insertion, deletion, and substitution of nodes”, to bring two trees to the same structure. The distance between two nodes is 1 if they are not equal and 0 if they are equal. The distance between two trees is summation of distance between their nodes, normalized by dividing by the smaller tree size. Edit distance 2, divides the total distance, calculated as in edit distance 1, within the same depth by an increasing weight. The distance between two trees is then the total distance within each depth, placing more weight on the distances near the root of the trees [14].

In, traditional neural networks a population of neural networks, that have the same structure, is trained to adjust the weights. Based on edit distance measure, the distance between neural networks of that population will be zero. Since edit distance is based on measuring the difference between structures in terms of nodes. In the case of ENNs, if it is assumed that edit distance operations can be used to make a pair of neural networks of different structures (see figure 1) to have the same structure, and the distance between two neural networks will be the number of operations that are required to edit one neural network to the other. This method does not reflect the actual distance between neural networks since; the weights of the connections are not taken into account. So, using edit distance measure is not enough to measure the diversity of neural networks. Problem specific measure can allow additional insight into population diversity, especially on novel and non-traditional problems [1].

![Figure 1. Example of two neural networks NN1 and NN2](image)

4. Evolvable Neural Networks (ENNs)

ENNs, start initially with chromosomes of the same length, all chromosomes map to the same minimal topology i.e. the same number of input and output nodes, no hidden nodes, and input nodes are fully connected to output nodes. The connections have randomly initialized weights. Through evolution hidden nodes and new connection genes are added to chromosomes. So, chromosomes can have different lengths. This type of neural networks evolution is known as NeuroEvolution through Augmented Topology, (NEAT) [15]. A chromosome is a set of connection genes which could be mapped into a completely functioning neural network as shown in figure 2. Each connection gene has a unique id number or innovation number as defined by Kenneth O. Stanley [15]. Connection gene specifies the in-node,
the out-node, the weight of the connection, and the status of the connection (enabled, or disabled) as shown in F.g.2. Connection genes with same id number in different genomes refer to the same in-node and out-node, but may have different weights or states. So, connection genes are ordered but may be not in sequence. With this structure, edit distance is not a suitable measure for genotype diversity of ENNs, since there is no sense to calculate the distance between two neural networks in terms of genetic operations, which are required to transform one neural network to the other, it is preferable to use mutation operation as a unit of genetic operations.

5. Proposed Method

Based on the nature of ENNs, a new measure defined as “neuro-edit” is proposed to measure the distance between neural networks based on measuring similarity between neural networks in terms of connection genes. But, it is not enough that a connection gene in one genome be similar to a connection gene in another genome, although they have the same in-node and out-node, since the weights and states of such genes may be different. If they have the same weight and status, then they are completely similar and distance between them equals to 0, otherwise the distance will not be 0. The computation of distance between two chromosomes can be divided into two parts. The first part measures the distance between common genes (i.e. genes that have the same id), and the other part measures distance between uncommon genes.

Common genes distance: to calculate the distance between two genes with the same id (genes exist in both chromosomes), the status of each gene is checked, if both genes are enabled, then distance between them will depend on their weights. In the case of similar weights, the distance will equal to 0. While in the case of dissimilar weights, the distance will equal to the absolute difference between weights normalized by the maximum of absolute value of weights. In the case of, one of the genes has a
The distance between two neural networks can be edited in terms of adding (enabling) connection genes, removing (disabling) connection genes, and substituting connection genes. A connection gene for a neural network can be seen as a character for string or node for genetic programming tree. This means that adding a connection gene to a neural network between two given nodes is the same as inserting a character into a string at a given position, removing a connection gene from a neural network between two given nodes is the same as deleting a character from string at a given position, and substituting a connection by another connection is the same as substitute a character another character.

To relate the neuro-edit to genetic operations, let's firstly assume that, at the beginning of the evolution there is a set of hidden nodes which are fully connected to input and output nodes by a set of disabled connections. Based on this assumption some rules can be defined:

1. A given hidden node is activated (added) when at least one in-connection and one out-connection are enabled.
2. By the same meaning an active hidden node is deactivated (removed) when all come-in connections and all come-out connections are disabled.
3. A connection is added between two active unconnected nodes when it is enabled.
4. A connection between two nodes can be replaced by another connection by just replacing the weight of the old connection by the weight of the new connection.

By this set of rules the distance between two neural networks can be edited in terms of adding (enabling) connection genes, removing (disabling) connection genes, and substituting connection genes. A connection gene for a neural network can be seen as a character for string or node for genetic programming tree. This means that adding a connection gene to a neural network between two given nodes is the same as inserting a character into a string at a given position, removing a connection gene from a neural network between two given nodes is the same as deleting a character from string at a given position, and substituting a connection by another connection is the same as substitute a character another character. The above rules are summarized as in Table 1.

Each neuro-edit operation has a weight, both of enabling and disabling a connection has a weight equal to 1, and substitute operation has a weight depends on the weights of connections to be substituted. For relating the neuro-edit operations to the mathematical equations (2) and (3):

Equation (2) calculates the distance between chromosomes by counting the number of substitution operations between common genes (genes that have the same id number). Equation (3) has two terms, each term calculates the number of connections to be deleted from one neural network (which has these connection genes) or inserted to another neural network (which does not have these connection genes). I.e. this equation combines the calculations of enabling and disabling of connection genes.
Table 1 Operations of Edit distance and Neuro-edit

<table>
<thead>
<tr>
<th>Operation</th>
<th>Edit dist.</th>
<th>Neuro-edit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Insert</td>
<td>$a \rightarrow 0$</td>
<td>Enable a connection, $0 \xrightarrow{\text{status}} 1$</td>
</tr>
<tr>
<td>Delete</td>
<td>$0 \rightarrow a$</td>
<td>Disable a connection, $1 \xrightarrow{\text{status}} 0$</td>
</tr>
<tr>
<td>Substitute</td>
<td>$a \rightarrow b$</td>
<td>Substitute connection, $w_i \rightarrow w_j$</td>
</tr>
</tbody>
</table>

6. Experimental Results

Neuro-edit measure is used to measure the genotype diversity of a population of 100 neural networks that are evolved to classify two different problems, Iris data set and Glass data set\(^1\). Iris data includes 150 instances of, 4 attributes and 3 classes. Glass data includes 214 instances of, 9 attributes and 7 classes. The genotype diversity of a population is measured by measuring the neuro-edit distance between each pair in the population and the population diversity is given by equation (6).

In experiments, for each data set a population of neural networks is evolved for 100 generations. The population genotype diversity corresponding to each data set is calculated and plotted per generation as shown in figure 3. It is clear that the diversity of the first generation is very small, since all individuals of the initial population have the same structure and they differ only in weights. Diversity begins to increase after the first generation depending on genetic operations which change the structure and weights. The goodness of neuro-edit is also proved by the fact that it exhibits good degree of correlation with the mean fitness of the population, as shown in figure 4. Further studies will be conducted to confirm this preliminary observation.

7. Conclusion and Future Work

In this paper a new metric “Neuro-edit” is presented to measure the genotype diversity of evolvable neural networks (ENNs). This measure inspired on edit distance measure and genetic operations used to evolve neural networks. Neuro-edit is a specific measure for diversity of ENN’s since, it based on the semantics of neuroevolution operations, crossover and mutation. Neuro-edit measures the distance between neural network structures in terms of connection genes “addition, removing, and substitution” on contrary to edit distance which measures the distance between genetic programming trees in terms of nodes “addition, removing, and substitution”. The main advantage of neuro-edit is its simplicity, since it is based on direct comparison of connection genes. Our future work will be concentrated on using this metric to study the effect of genetic operators on the diversity and evolvability of neural networks.

References


\(^1\) Freely available from http://archive.ics.uci.edu/beta/datasets.html