Tatami Grammatical Evolution for Feature Extraction with Multi Fitness Evaluation

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Abstract

Feature Extraction is a significant topic in classification problem solving. Until now, there is no such a standard way to determine the best features of a data. In this research, grammatical evolution with multiple fitness evaluation approach (named as *GE Tatami*) has been developed in order to extract best features of the data. The method generate n-1 features which are able to separate data hierarchically, with n is number of classes.

Some methods has been evaluated in this research, including genetics algorithm, grammatical evolution with global fitness measurement, grammatical evolution with multi fitness measurement, grammatical evolution with Tatami fitness measurement, and Gavrilis's grammatical evolution.

It is shown in the experiment that Tatami method produces a better result compared to the four other methods for synthesis data using decision tree classifier. The synthesis data is hierarchically separable. However Tatami method shows a bad result when it is failed to determine ideal features or using SVM classifier.

Index Terms — Keywords: feature extraction, grammatical evolution, classification, multi-fitness.

I. INTRODUCTION

Feature Extraction is a process to determine transformation mapping of original features set into new features set that will produce better class separability [5]. Feature extraction is a significant topic in classification problem, since good feature set can boost classification accuracy, while bad feature set tend to make classification accuracy worse.

Some genetics algorithm based method has been in order to make good feature sets. In [3] and [4], grammatical evolution has been conducted for feature extraction purpose. The authors create a method that produces a set of new feature with classifier's accuracy as fitness function. In [5] and [6], similar method has also been used for different cases. However, sometime there are several irrelevant features also generated and attached to the feature set.

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In [1], the authors create a new approach by measure perfeature accuracy rather than using a set of features altogether as a goodness measurement. However, this approach tends to produce bad accuracy since only one feature used to separate all classes.

In this paper, we propose a multi fitness evaluation to hierarchically separate the data. This multi fitness evaluation is named as Tatami Grammatical Evolution (GE Tatami) since it shows a figure looks like Japanese traditional *tatami*. Several previous methods also used as comparison.

II. DATA AND FEATURE SPACE

A data usually consists of several. Given a set of data, as in table 1.1, one can say that there are two features, x and y, and 3 classes (A, B and C).

Since the data consists of 2 original features, it is possible to plot it in *Cartesian Diagram* to produce better visualization. Figure 1.1 shows how the data plotted.

As shown in the figure 1.1, it is impossible to separate the data by using just one of the features. The two features should be used altogether, producing a feature space to make data separation possible.

Table 2.1 Example of Numeric Data

| Original Features | | Class | |
|-------------------|-----|-------|--|
| X | y | | |
| 0.3 | 0.5 | A | |
| 0.4 | 0.9 | В | |
| 0.6 | 0.2 | A | |
| 0.9 | 1.0 | С | |
| 1.0 | 0.3 | С | |
| 8.0 | 0.2 | В | |
| | | ••• | |

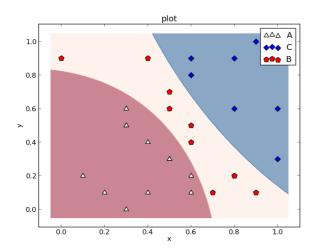


Figure 2.1 Feature Space Produced by Original Features and Classification Process by Using RBF SVM

A commonly used classifier such a SVM or neural network can use the feature space to separate the data very well. However the separation cannot be done linearly. The separator line should be a bit curvy which is mathematically more complex than a simple linear line.

III. FEATURE EXTRACTION

Feature Extraction is basically a mapping from original feature space to another one. The mapping can produce higher dimension, or lower dimension.

In classification problem, it is intuitive to map any inseparable (or difficultly separated) data into higher dimension. Higher dimension tend to produce more possibility to separate the data. However, this will also lead to more complex calculation as well.

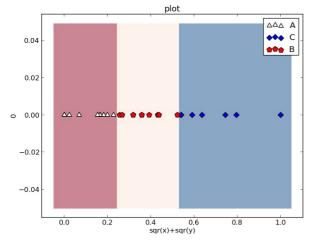


Figure 3.1 Feature Space Produced by New Feature (sqr(x)+sqr(y))

The goal of feature extraction is to produce a feature set that consist of as few features as possible. The generated feature set should also able to produce good data separability in relatively simple way (i.e.: such as using linear lines).

In order to explain the purpose of feature extraction, one can transform the data on table 2.1 which consists of 2 into features (x and y) into a new feature space containing just 1 feature, sqr(x)+sqr(y). The feature space is shown as in figure 3.1

This transformation allows us to separate data by using a linear line, which is mathematically simpler than the previous one.

IV. GRAMMATICAL EVOLUTION

Grammatical Evolution is an evolutionary algorithm based on genetics algorithm. This method takes empowered by a predefined context free grammar to transform an individual into anything allowed by the grammar.

Each individual contains of a binary (or integer) string called genotype. The genotype is then transformed by using the grammar into a phenotype. The phenotype can be a mathematics operation, a function, or even a whole computer program, depend on the grammar used.

For example, one uses a grammar as defined in table 4.1. Let's say an individual contains an integer string 220, 203, 51, 123, 2, 45 as genotype. The process started by taking <expr> as start symbol. <expr> has 4 possible evolution rule, therefore, we take the first segment of the integer string (in this case 220), and do modulo operation. Since 220 mod 4 produce 0, we then take the 0th rule. This make <expr> evolved into <expr><op><expr>. Next, we go with the second segment of integer string (which is 203) and choose the first non-terminal of <expr><op><expr> (which is <expr>). Again, we do a module operation. Since <expr> has 4 possible evolution rule, and 203 mod 4 produce 3, we take the 3rd rule (which is <var>). Now we have <var><op><expr>. The process continued until we get x*x as phenotype. Figure 4.2 shows the complete transformation process.

| Table 4.1 Grammar Example | | | |
|---------------------------|--|--|--|
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |

Figure 4.1 Transformation Process

V. GE MULTI

VI. GE TATAMI

VII. RESULT AND ANALYSIS

VIII. CONCLUSION

The conclusion goes here.

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