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Computational Approaches for Biomarker Discovery

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Abstract

Computational biology plays a significant role in the discovery of new biomarkers, the analyses of disease states and the validation of potential biomarkers. Biomarkers are used to measure the progress of disease or the physiological effects of therapeutic intervention in the treatment of disease. They are also used as early warning signs for various diseases such as cancer and inflammatory diseases. In this review, we outline recent progresses of computational biology application in research on biomarkers discovery. A brief discussion of some necessary preliminaries on machine learning techniques (e.g., clustering and support vector machines—SVM) which are commonly used in many applications to biomarkers discovery is given and followed by a description of biological background on biomarkers. We further examine the integration of computational biology approaches and biomarkers. Finally, we conclude with a discussion of key challenges for computational biology to biomarkers discovery.

Keywords

Computational Biology, Biomarker Discovery, Machine Learning

1. Introduction

Machine learning is the subfield of artificial intelligence which focuses on methods to construct computer programs that learn from experience with respect to some class of tasks and a performance measure [1].

Machine learning enables one to generate automatic rules based on observation of the appropriate examples

by the learning machine. However, the selection and design of the features that will be considered in order to represent each example for the learning process are very important and influence the classifier performance [2].

Each instance in any dataset used by the machine learning methods is presented by a sequence of features, where each instance has the same number and types of features. The features can be categorical (*i.e.* gender), numerical (*i.e.* weight, size, age), and Boolean (*i.e.* sick? married?). So, the algorithms of the machine learning were asked to explain the relationships between the features in the data.

There are two major settings of learning schemes in machine learning. One is called unsupervised learning, where no prior information is given to the learner regarding the data or the output. It studies how systems can learn to represent particular input data in a way to find natural partitions (grouping/clustering) of patterns. Clustering is a simple classical method of the unsupervised learning, which partitions the data set into clusters, so that the data in each subset share some common trait according to some defined distance measure.

The main goal of clustering is to reduce the amount of data by grouping similar data items together. Most of the unsupervised learning methods use a measure of similarity between patterns in order to group them into clusters. The simplest of these involves defining a distance between patterns. For patterns whose features are numeric, the distance measure can be ordinary Euclidean distance between two instances, or Manhattan distance or any other similarity function. **Figure 1** describes a simple example where a given set of sample points is clustered into three clusters around three different centers. It was noted that the clustering algorithm got data where no prior information was given. Moreover, the centers and clusters shapes were unknown, and then the learner studied the data and clustered it into three clusters as shown in the example.

Clustering methods [3]-[8] can be divided into four basic types:
- Exclusive clustering (e.g., K-means algorithm [9]).
- Overlapping clustering (e.g., fuzzy C-means algorithm [10] and improved by Bezdek [11]).
- Hierarchical clustering (e.g., hierarchical clustering algorithm which was defined by Johnson in 1967 [12]).
- Probabilistic (e.g., expectation-maximization (EM) algorithm [13]).

In the other setting, which is a termed supervised learning, the instances are given with known labels; its main goal is to build a classifier which then makes predictions about future instances to assign their class labels. The dataset will be divided into two partitions: one as a training dataset, and the second as a testing data set. The classifier was built according to the training dataset and its performance was measured by the performance of the classifier over the testing dataset. The example in **Figure 2** has two classes (red class and blue class) and the classifier was asked to classify the black square point. In this case, if the classifier classifies the new instances according to the first nearest neighbor, then the black square will be classified as a blue class.

Some of the popular classification algorithms are:

Decision trees are trees that classify instances by sorting them based on feature values. Each node in a decision tree represents a feature in an instance to be classified, and each branch represents a value that the node can assume. Instances are classified starting at the root node and sorted based on their feature values [14].

Support vector machines (SVMs) are a learning machine developed by Vapnik [15]. The performance of this algorithm, as compared to other algorithms, has proven to be particularly useful for the analysis of various classification problems, and has recently been widely used in the bioinformatics field [16]-[18]. Linear SVMs are usually defined as SVMs with linear kernel. The training data for linear SVMs could be linear non-separable and then soft-margin SVM could be applied. Linear SVM separates the two classes in the training data by producing

Figure 1. Data samples clustered into three clusters around three different centers.

the optimal separating hyper-plane with a maximal margin between class 1 and class 2 samples (**Figure 3**). Given a training set of labeled examples (x_i, y_i) $i = 1, \cdots, l$ where $x_i \in R^t$ and $y_i \in \{+1, -1\}$, the support vector machines (SVMs) find the separating hyper-plane of the form $w \cdot x + b = 0$ $w \in R^t, b \in R$.

Here, w is the "normal" of the hyper-plane. The constant b defines the position of the hyper-plane in the space. One could use the following formula as a predictor for a new instance: $f(x) = \text{sign}(w \cdot x + b)$ (for more information see Vapnik [15]).

2. Biomarker-Biological Background

A biomarker is a gene, protein/peptide or metabolite present in a biological system, used to indicate a physiological or pathological state that can be recognized or monitored [19]-[21]. Biomarker discovery is a challenging process; a good biomarker has to be sensitive, specific and its test highly standardized and reproducible.

Genomic studies provide scientists with methods to quickly analyze genes and their products en masse. DNA microarray technologies permit systematic approaches to biological discovery that has begun to have a profound impact on biological research, pharmacology, and medicine. The ability to obtain quantitative information about the complete transcription profile of cells promises to be an exceptionally powerful means to explore basic biology, diagnose disease, facilitate drug development, tailor therapeutics to specific pathologies, and generate databases with information about living processes [22].
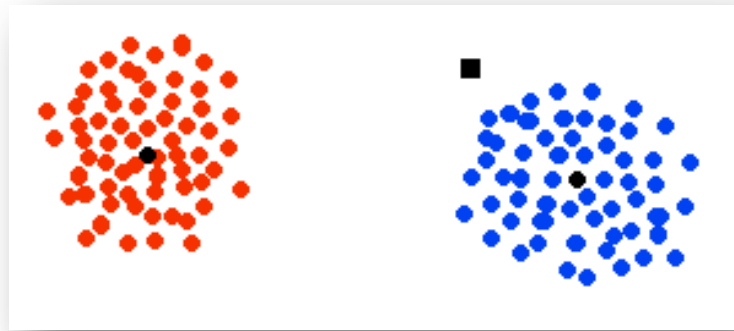
Figure 2. An example of how the classifiers work.
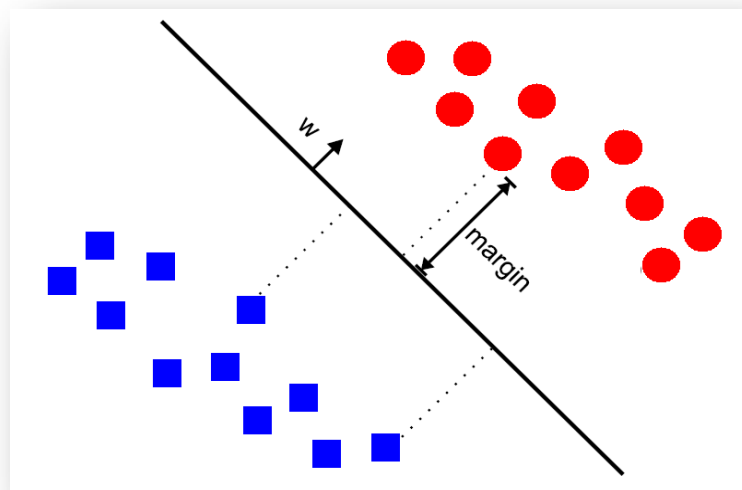
Figure 3. A simple linear support vector.

Gene expression studies bridge the gap between DNA information and trait information by dissecting biochemical pathways into intermediate components between genotype and phenotype. These studies open new avenues for identifying complex disease genes and biomarkers for disease diagnosis and for assessing drug efficacy and toxicity.

For years, scientists studied one gene at a time and genes were indeed studied in isolation from the larger context of other genes. Nowadays, genomics studies the genome of organisms as a whole. It is based on high-throughput techniques allowing a wide picture of gene characteristics. The most popular high throughput techniques are arrays, which are an orderly arrangement of a great number of samples allowing large-scale studies (http://www.gene-chips.com/).

The first arrays were made using DNA samples. This is the genomic area, which emerged from the sequencing of genomes from many organisms. The development of the first arrays to study a great number of genes at a time started many years ago [23] and has widely expanded since then. But now, we can array DNA and RNA probes, proteins, antibodies and even biological samples allowing new types of research. Furthermore, other types of high throughput techniques are currently developing, for instance to study metabolites.

Genomics is thus linked to the development of new biotechnology which covers a broad field of disciplines (biology, computer science, chemistry, physics, and engineering) and which converge and work in synergy to advance rapidly. Genomics involves the identification of organism's genes and understanding how the genes work using new biotechnological approaches [24].

Recent advances in genomics are bringing about a revolution in our understanding of the molecular mechanisms of phenotypes, including the complex interplay of genetic and environmental factors [25].

Genomics divided into two basic areas, structural genomics and functional genomics (also called post-genomic area) [26]. In the former, the target of research is DNA which corresponds to the genetic background of organisms. Structural genomics is therefore clearly related to genetics. In functional genomics, the targets of research are the key molecules which give life to the cells: RNA, proteins and also metabolites (which are both biologically active molecules within cells and tissues). Functional genomics allows the detection of genes that are turned on/off at any given time depending on environmental factors.

Today, genomics has induced two new paradigms in biology. The first paradigm is a new approach allows the study of the complex network through which genes and proteins communicate. It implies the combination of expertise from biologists, engineers, chemists, and computer scientists. This multidisciplinary approach allows the development of systems biology. The second paradigm is a direct consequence of more available information derived from genomics studies. The raw data needs to be analyzed and then to be used in the systemic approach indicated above. This led the development of bioinformatics which needs the use of computers to manage biological information.

The practical applications of gene expression analyses are numerous and only beginning to be realized. One particularly powerful application of gene expression analyses is biomarker identification, which can be used for disease risk assessment, early detection, prognosis, prediction response to therapy, and preventative measures is a challenging task for cancer prevention and the improvement of treatment outcomes. Approaches to cancer biomarker discovery include genomic, epigenomic, transcriptomic, and proteomic analyses.

Current efforts in the laboratory focus on the identification of biomarkers in chronic lymphocytic leukemia, lung cancer and colon cancer. Among the biomarkers we consider are plasma microRNAs (miRNAs). miRNAs are a class of small RNAs that function as regulators of gene expression. Alteration of gene expression patterns due to dysregulation of miRNAs is a common theme in tumorigenesis. High concentrations of cell-free miRNAs originating from the primary tumor have been found in the plasma of cancer patients, and several lines of evidence indicate that plasma miRNAs are associated with specific vesicles called exosomes. Plasma miRNAs have emerged as a promising source of cancer biomarkers [27].

A recent discovery of quantifiable circulating cancer-associated miRNAs, expose the immense potential for their use as novel minimally invasive biomarkers for breast and other cancers [28].

In this section, structural genomics and the different fields of functional genomics (RNA studies, proteomics, metabolomics) will be first detailed for the reader to better understand what genomics is, before the description of the two new paradigms in biology derived from genomics (systemic approaches, bioinformatics).

3. Computational Approaches for Biomarker Discovery

DNA microarray technologies permit systematic approaches to biological discovery that has begun to have a

profound impact on biological research, pharmacology, and medicine. The ability to obtain quantitative information about the complete transcription profile of cells promises to be an exceptionally powerful means to explore basic biology, diagnose disease, facilitate drug development, tailor therapeutics to specific pathologies, and generate databases with information about living processes [22].

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4. Computational Biomarker (Features) Selection

Classification of samples from gene expression datasets usually involves small numbers of samples and tens of thousands of genes. The problem of selecting those biomarker genes that are important for distinguishing the different sample classes being compared poses a challenging problem in high dimensional data analysis and the potential biomarkers are important in improvement in diagnostics and therapeutics development. A variety of methods to address these types of problems have been implemented [29]-[35]. These methods can be divided into two main categories: those that rely on filtering methods and those that are model-based or so-called wrapper approaches [29] [31].

W. Pan [35] has reported a comparison of different filtering methods, highlighting similarities and differences between three main methods. The filtering methods, although faster than the wrapper approaches, are not particularly appropriate for establishing rankings among significant genes, as each gene is examined individually and correlations among the genes are not taken into account. Although wrapper methods appear to be more accurate, filtering methods are presently more frequently applied to data analysis than wrapper methods [31].

Li and Yang [36] compared the performance of support vector machine (SVM) algorithms and ridge regression (RR) for classifying gene expression datasets and also examined the contribution of recursive procedures to the classification accuracy. Their study explicitly shows that the way in which the classifier penalizes redundant features in the recursive process has a strong influence on its success. They concluded that RR performed best in this comparison and further demonstrate the advantages of the wrapper method over filtering methods in these types of studies.

Guyon *et al.* [37] compared the usefulness of RFE (for SVM) against the "naïve" ranking on a subset of genes. The naïve ranking is just the first iteration of RFE to obtain ranks for each gene. They found that SVM-RFE is superior to SVM without RFE and also to other multivariate linear discriminant methods, such as linear discriminant analysis (LDA) and mean-squared-error (MSE) with recursive feature elimination. See **Figure 4(b)** for the procedure of SVM-RFE.

Xiong, Fang *et al.* [38] Propose a general framework to incorporate feature (gene) selection into pattern recognition in the process to identify biomarkers. Using this framework, they develop three feature wrappers that search through the space of feature subsets using the classification error as measure of goodness for a particular feature subset being "wrapped around": linear discriminant analysis, logistic regression, and support vector machines.

Yousef, Jung *et al.* [39], describe a new method for gene selection and classification, which is comparable to or better than some methods which are currently applied. Their method (SVM-RCE) combines the K-means algorithm for gene clustering and the machine learning algorithm, SVMs [15], for classification and gene cluster ranking. The SVM-RCE method differs from related classification methods in that it first groups genes into correlated gene clusters by K-means and then evaluates the contributions of each of those clusters to the classification task by SVM. One can think of this approach as a search for those significant clusters of gene which have the most pronounced effect on enhancing the performance of the classifier. See **Figure 4(a)** that illustrates the procedure of SVM-RCE. Moreover, Lin-Kai [40] propose an improved method of SVM-RCE called ISVM-RCE. ISVM-RCE eliminates genes within the clusters instead of removing a cluster of genes when the number of clusters is small. Six data sets are used to test the performance of ISVM-RCE and compared their performances with SVM-RCE and linear-discriminant-analysis-based RFE (LDA-RFE). The results show that ISVM-RCE
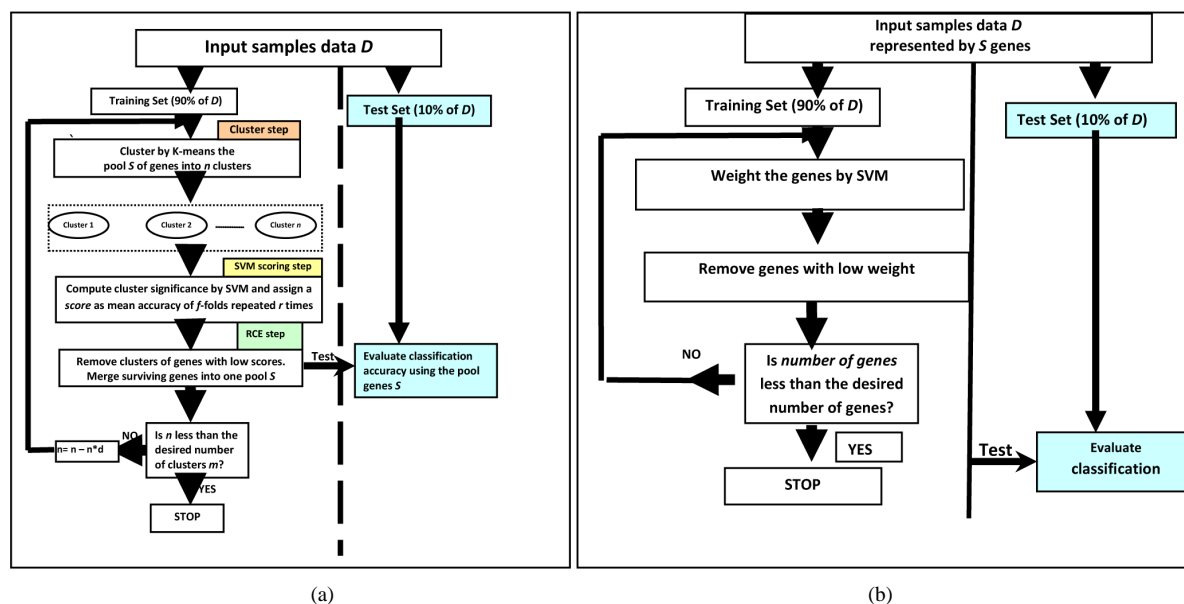
Figure 4. (a) Recursive cluster elimination (RCE) procedure with SVM; (b) Recursive feature elimination (RFE) procedure with SVM.

greatly reduces the time cost of SVM-RCE, meanwhile obtains comparable classification performance as SVM-RCE, while LDA-RFE is not stable.

Recently, Grate [41] has described a technique for discovering small sets of genes (3 or less). The technique is based on brute force approach of exhaustive search through all genes, gene pairs and some cases triple of genes. The combination is analyzed with classification method looking for those combinations that form training error-free classifiers.

Robustness of biomarkers is an important issue, as it may greatly influence subsequent biological validations. In addition, a more robust set of markers may strengthen the confidence of an expert in the results of a selection method. Abeel [42] has proposed a general framework for the analysis of the robustness of a biomarker selection algorithm. The framework is based on ensemble feature selection, where multiple feature selections are combined in order to increase the robustness of the final set of selected features. The proposed methodology is evaluated on four microarray datasets showing increases of up to almost 30% in robustness of the selected biomarkers, along with an improvement of about 15% in classification performance. A different approach to deal with inconsistent cancer biomarkers due to bioinformatics artifacts, was proposed by [43]. The approach is based on using multiple data sets from microarrays, mass spectrometry, protein sequences, and other biological knowledge in order to improve the reliability of cancer biomarkers. The study presents a novel Bayesian network (BN) model which integrates and crosses-annotates multiple data sets related to prostate cancer. The computational results show that the method is able to find biologically relevant biomarkers with highest reliability [44].

Some data is composed from multiple category or classes. For such a data a special methods of biomarker selection is required. [45] has proposed classification method is based on two schemes: error-correcting output coding (ECOC) and pairwise coupling (PWC). The biomarker pattern for distinguishing each disease category from another one is achieved by the development of an extended Markov blanket (EMB) feature selection method.

The study of [46] demonstrates that the machine learning approach can be used to detect a small subset of biomarker genes from high dimensional datasets and generate a classifier for multiple classes. A multiclass support vector machine (MC-SVM) method and an unsupervised K-mean clustering method were applied to independently refine the classifier, producing a smaller subset of 39 and 30 classifier genes, separately, with 11 common genes being potential biomarkers.

Yousef *et al.* [47] developed a new algorithm called recursive network elimination (RNE) with SVM. The main idea is to integrate network information with recursive feature elimination based on SVM. First, filter one

thousand genes selected by t-test from training set so that only genes that map to a gene network database remain. Then to the remaining genes the gene expression network analysis tool (GXNA) [48] is applied to form n clusters of genes that are highly connected in the network. Using these clusters linear SVM is used to classify the samples and a weight is assigned to each cluster based on its significance to the classification. The clusters with less information are removed while retaining the remainder for the next classification step. This process is repeated until an optimal classification result is attained.

5. A Comparative Performance

Pirooznia, M. *et al.* [49] conducted a study to compare the performance (with cross validation) of different machine learning algorithm such as SVM, RBF Neural Nets, MLP Neural Nets, Bayesian, Decision Tree and Random Forrest methods. Additionally, the efficiency of the feature selection methods including support vector machine recursive feature elimination was compared. The data set consists from eight different binary (two class) microarray datasets. The performance was very well and in average higher than 90%. As expected, this study shows that in most cases the accuracy is improved with feature selection. Additionally, this study reports about stability of the top 50, 100, 200 genes with SVM-RFE. Actually those genes will be serving later as a biomarker for diagnostic diseases.

Yousef *et al.* [39] compare the performance of SVM-RCE against the popular SVM-RFE method to reported in most cases that SVM-RCE is with better results as in average of 6 datasets is 96% while SVM-RFE with 92% accuracy.

6. Conclusions

In this review, we proposed many computational approaches which are critical for mining high-dimensional data in order to effectively discover biomarkers. Best data mining approach would to integrate different approaches to arrive at an effective algorithm; however most of the suggested methods ignore existing biological knowledge and treat all the genes equally. Information about gene networks or pathways should be incorporated into a classifier to improve both the predictive performance and interpretability of the resulting biomarker genes as suggested by [47] and [50].

Moreover, we suggest developing more algorithms that incorporate biological knowledge, extracted from existing database with the procedure of feature selection to have more accurate biological results.

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Competing Interests

No competing interests.

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Scientific Research

Application of the Adaptive Neuro-Fuzzy Inference System for Optimal Design of Reinforced Concrete Beams

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Abstract

Using a genetic algorithm owing to high nonlinearity of constraints, this paper first works on the optimal design of two-span continuous singly reinforced concrete beams. Given conditions are the span, dead and live loads, compressive strength of concrete and yield strength of steel; design variables are the width and effective depth of the continuous beam and steel ratios for positive and negative moments. The constraints are built based on the ACI Building Code by considering the strength requirements of shear and the maximum positive and negative moments, the development length of flexural reinforcement, and the serviceability requirement of deflection. The objective function is to minimize the total cost of steel and concrete. The optimal data found from the genetic algorithm are divided into three groups: the training set, the checking set and the testing set for the use of the adaptive neuro-fuzzy inference system (ANFIS). The input vector of ANFIS consists of the yield strength of steel, compressive strength of concrete, dead load, span, width and effective depth of the beam; its outputs are the minimum total cost and optimal steel ratios for positive and negative moments. To make ANFIS more efficient, the technique of Subtractive Clustering is applied to group the data to help streamline the fuzzy rules. Numerical results show that the performance of ANFIS is excellent, with correlation coefficients between the three targets and outputs of the testing data being greater than 0.99.

Keywords

1. Introduction

Genetic algorithms are search algorithms based on the mechanics of natural selection and natural genetics. They have been developed and were formally introduced in 1970s by Professor John Holland at the University of Michigan, who in 1975 published the ground-breaking book "Adaptation in Natural and Artificial System" [1]. In 1989, Goldberg described in more detail the theory of genetic algorithms and their applications [2]. From then on, genetic algorithms become more attractive and popular. Genetic algorithms have a number of applications in many fields, such as engineering, economics, chemistry, manufacturing, mathematics, physics and so on. Especially in the areas of civil engineering, there are reinforced concrete beams [3], multiobjective optimization of trusses [4], reliability analysis of structures [5], global optimization of grillages [6], global optimization of trusses with a modified genetic algorithm [7] and optimization of pile groups using hybrid genetic algorithms [8], to name just a few.

The artificial neural network was originated by McCulloch and Pitts in 1943 [9], who claimed that neurons with binary inputs and a step-threshold activation function were analogous to first-order systems. In 1986, Rumelhart *et al.* [10] proposed the theory of parallel distributed processing and developed the most famous learning algorithm in ANN-backpropagation, which uses a gradient descent technique to propagate error through a network to adjust the weights in an attempt to reach the global error minimum, marking a milestone in the current artificial neural networks.

Fuzzy sets were introduced by Zadeh [11] and Klaua [12] in 1965 as an extension of the classical set, where the membership of elements in a set is assessed in binary terms according to whether the element belongs to the set or not. In contrast, fuzzy set theory permits the gradual assessment of the membership of elements in a set, which is described with the degree of a membership function whose value is in the real interval [0, 1]. Fuzzy set theory is used now in many areas, such as clustering [13], building group decision [14] and linguistic expressions [15], etc.

Neuro-fuzzy systems are fuzzy systems which use ANNs theory in order to determine their membership functions and fuzzy rules by processing data samples. A specific approach in neuro-fuzzy development is the adaptive neuro-fuzzy inference system (ANFIS) first proposed by Jang [16], which has shown significant results in modeling nonlinear functions. ANFIS integrates both neural networks and fuzzy logic principle, whose inference system corresponds to a set of fuzzy rules [17] that have learning capability to approximate nonlinear functions. Successful implementations of ANFIS in many fields have been reported, such as prediction of water level in the reservoir [18] [19], forecasting of water discharge in a river [20], sea level prediction considering tide-generating forces and oceanic thermal expansion [21], prediction of flow through rockfill dams [22], downstream water level forecasting [23], flood forecasting [24], generation of customer satisfaction models [25], speech recognition [26], chaotic traffic volumes forecasting [27], etc.

Distinct from other authors' works, this paper tries to combine the techniques of the genetic algorithm and ANFIS to optimally design reinforced two-span continuous reinforced concrete beams with rectangular cross-section. Based on the provisions of the ACI Building Code Requirements for Structural Concrete and Commentary [28], the constraints are built, considering the strength requirements of the maximum positive and negative moments and shear, the development length of reinforcement as well as the serviceability requirement of deflection. Design variables are the width and effective depth of the continuous beam and the steel ratios for positive and negative moments. The objective function is to find the minimum cost of steel and concrete in the continuous beam.

2. Genetic Algorithms

Genetic algorithms were inspired by the evolution theory of "survival of the fittest", proposed by Charles Darwin in 1860s. They simulate the survival of the fittest among individuals over consecutive generation and can solve both constrained and unconstrained optimization problems according to the "natural selection". Genetic algorithms are less susceptible to getting stuck at local optima than traditional gradient search methods. This paper uses the Global Optimization Toolbox based on MATLAB [29] to carry out the genetic algorithm. It begins by creating a random initial population, and then creates a sequence of new populations. At each step, the algorithm uses the individuals in the current generation to create the next population. To create the new population, the algorithm performs the following steps: 1) score each member of the current population by computing its fitness value; 2) scale the raw fitness scores to convert them into a more usable range of values; 3) select members, called parents, based on their fitness. The lower the value of the fitness function, the more opportunity

it has to be selected; 4) choose some elites from the current population that have lower fitness function values. These elite individuals are just passed to the next population; 5) produce children from the parents. Children are produced either by making random changes to a single parent—mutation—or by combining the vector entries of a pair of parents—crossover; 6) replace the current population with the crossover and mutation children and elites to form the next generation. The algorithm stops when one of the stopping criteria is met, such as the number of generation, the weighted average change in the fitness function value over some generations less than a specified tolerance, no improvement in the best fitness value for an interval of time, etc.

Supposed that x is the vector of design variables. The optimization problem of two-span continuous reinforced concrete beams can generally be described as

Minimize $f(x)$ (the fitness function)

Such that

$$
\begin{aligned}
g_i(x) \leq 0, & \quad i = 1, \cdots, m, \\
h_j(x) = 0, & \quad j = 1, \cdots, n, \\
\boldsymbol{LB} \leq x \leq \boldsymbol{UB}.
\end{aligned}
\tag{1}
$$

where $g_i(x)$ represents the inequality constraints and $h_j(x)$ represents the equality constraints, m is the number of inequality constraints and n is the number of equality constraints, $f(x)$ is the total cost of concrete and tension steels in the continuous beam, and $\boldsymbol{LB}$ and $\boldsymbol{UB}$ are vectors of lower and upper bounds of design variables, respectively. The constraints divide the design space into two domains, the feasible domain where the constraints are satisfied, and the infeasible domain where at least one of the constraints is violated. In most practical problems the minimum is found on the boundary between the feasible and infeasible domains, that is at a point where $g_i(x) = 0$ for at least one i. In most structural optimization problems the inequality constraints prescribe limits on sizes, stresses, displacements, etc. These limits have great impact on the design, so that typically several of the inequality constraints are active at the minimum.

Most of the constraints built in this paper are nonlinear. The Global Optimization Toolbox based on MATLAB uses the augmented Lagrangian genetic algorithm [30] [31] to solve nonlinear constraint problems with bounds. A subproblem is formulated by combining the fitness function and nonlinear constraint functions using the Lagrangian and the penalty parameters. When the subproblem is minimized to a required accuracy, the Lagrangian multiplier estimates are updated, or the penalty parameter is increased by a penalty factor. These steps are repeated until one of the stopping criteria of the genetic algorithm is met.

3. The Adaptive Neuro-Fuzzy Inference System

The adaptive neuro-fuzzy inference system (ANFIS) consists of two components: fuzzy inference systems and neural networks. Using a given input/output data set, ANFIS constructs a fuzzy inference system whose membership function parameters are adjusted by a hybrid learning algorithm to approximate the precise value of the model parameters [16] [32]. The hybrid algorithm is a combination of gradient descent and the least-squares method. The gradient descent updates the premise parameters; the least squares method finds a proper set of consequent parameters. For an ordinary fuzzy inference, the parameters associated with a given membership function are usually predetermined by the user's experience or the trial-and-error method. Rather than choosing the membership function parameters at random, ANFIS can scientifically obtain the parameters through the process of learning to tailor the membership functions to the input/output data to account for variations in the data values. This learning methods work similarly to those of neural networks. The fuzzy inference ANFIS operates on is the first- or zeroth-order Sugeno-type system [33]. For example, if there are only two inputs x and y, the general first-order Sugeno-type fuzzy inference has rules of the form

$$
\text{If } x \text{ is } A \text{ and } y \text{ is } B, \text{ then } z = px + qy + c
\tag{2}
$$

where A and B are the linguistic values defined by fuzzy sets in the antecedent, while p, q and c are constants. In Equation (2), the output z in the consequent is weighted by the firing strength w, which is

$$
w = \text{Min}\left(F_A(x), F_B(y)\right)
\tag{3}
$$

where $F_A(x)$ and $F_B(y)$ are the membership functions of inputs x in A and y in B, respectively. If there

are N rules in the inference system, the output of the inference system is given by

$$\overline{Z} = \frac{\sum\limits_{i=1}^{N} w_i z_i}{\sum\limits_{i=1}^{N} w_i} \tag{4}$$

If the fuzzy inference is zeroth-order, then $p = q = 0$ in Equation (2). The typical structure of ANFIS looks like that in **Figure 1**, where the output membership function is limited to the linear or constant Sugeno-type fuzzy inference. This paper uses the linear Sugeno-type system.

Data clustering specifying each data point belonging to a cluster to some degree by a membership grade can identify natural groupings of data from a large data set to produce a concise representation of a system's behavior. Based on the cluster information, a Sugeno-type fuzzy inference system that best models the data behavior can be generated. The data clustering technique adopted in this paper is "Subtractive Clustering" [34] [35]. Based on the density of surrounding data points, it can estimate the number of clusters and the cluster centers in a set of data. The fuzzy rules found by clustering data are more tailored to the input data; therefore, the fuzzy inference system will have much fewer rules than that without data clustering. This algorithm works like a pre-processor to ANFIS for determining the initial rules. When the fuzzy inference system is generated, four parameters for "Subtractive Clustering" need to be specified [29] [34]: 1) range of influence q_1 (default 0.5), to specify the range of influence of a cluster center. The more neighboring data points a data point can enclose, the higher potential it has as a cluster center; 2) squash factor q_2 (default 1.25), multiplying q_1 to determine the neighborhood of a cluster center within which the existence of other cluster centers are discouraged; 3) accept ratio q_3 (default 0.5), to set the potential above which another data point will be accepted as a cluster center; 4) reject ratio q_4 (default 0.15), to set the potential below which a data point will be rejected as a cluster center.

4. Design of Two-Span Continuous Reinforced Concrete Beams

The two-span continuous reinforced concrete beams with a rectangular section are subjected to a uniformly distributed load $w = 1.2w_D + 1.6w_L$, where w_D and w_L are dead load and live load, respectively. Each span has length L. The shear and moment diagrams are shown in **Figure 2(a)**. The beams are designed with tension reinforcement only. Top reinforcement in the negative moment region will be cut off, while there are no cutoffs for the bottom reinforcement, as shown in **Figure 2(b)**. The objective function is to minimize the total cost of concrete and the tension reinforcement in the positive and negative moment regions, and vertical stirrups along the beam. All the constraints comply with the ultimate-strength design of the ACI 318-08 Code, considering shear, bending moment and the development lengths, and immediate and long-term deflections. The units of force and length in the following formulas are kgf (=9.81 N) and cm, respectively, which are the units of measurement in Taiwan.
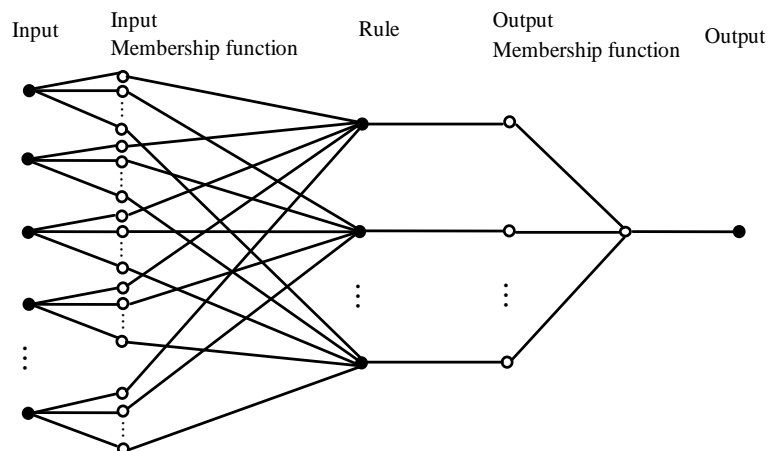
Figure 1. The structure of the adaptive neuro-fuzzy inference system.
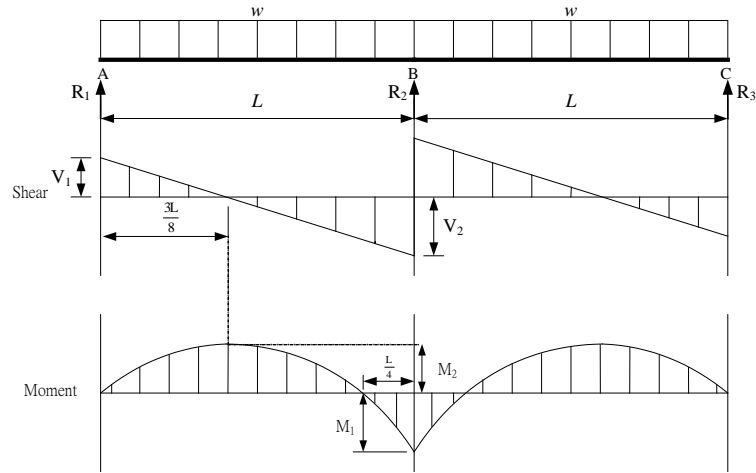
$$R_1 = V_1 = R_3 = V_3 = \frac{3\,wL}{8} \qquad ; \qquad R_2 = \frac{10\,wL}{8}$$

$$V_2 = V_{max} = \frac{5\,wL}{8} \qquad ; \qquad M_1 = \frac{wL^2}{8}$$

$$M_2 \left(at \quad \frac{3L}{8} \; from \quad A \; or \; C \right) = \frac{9\,wL^2}{128} \qquad ;$$

$$\Delta_{max} \left(at \; 0.4215 \; L \; from \quad A \; or \; C \right) = \frac{wL^4}{185\,EI}$$

(a)

$$\max \; \left(d, 12\,d_b, \frac{L_n}{16} \right)$$
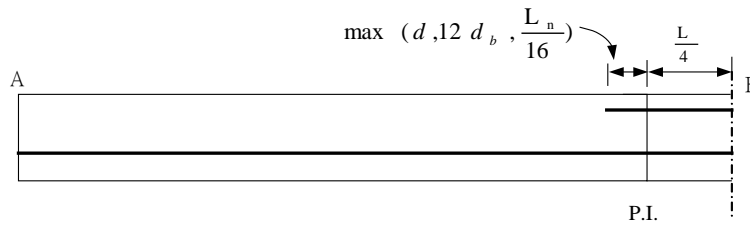
(b)

Figure 2. The two-span continuous beam. (a) Shear and moment diagrams; (b) Reinforcement for the positive and negative moments.

4.1. Shear

Suppose that V_c is the shear capacity of the plain web concrete and V_u is the factored shear force. The design for shear may be separated into the following categories:

1) Region I: If $V_u \leq 0.5\phi V_c$, where $\phi = 0.75$ is the strength reduction factor, there is no shear reinforcement;

2) Region II: If $\phi V_c \geq V_u > 0.5\phi V_c$, a minimum web steel

$$A_v \geq \text{Max}\left(0.2\sqrt{f_c'}\frac{bs}{f_y}, \frac{3.5bs}{f_y} \right) \tag{5}$$

needs to be provided, where b is the width of the beam and s is the spacing of vertical stirrups. The spacing must not be larger than $\text{Min}(d/2, 60)$ cm;

3) Region III: If $3\phi V_c \geq V_u > \phi V_c$, shear reinforcement

$$V_s = \frac{A_v f_y d}{s} = \frac{V_u}{\phi} - V_c \tag{6}$$

has to be provided to carry the difference and the spacing s must not be larger than $\text{Min}\left(d/2, 60, \dfrac{A_v f_y}{0.2\sqrt{f_c'}b}, \dfrac{A_v f_y}{3.5b}\right)$ cm;

4) Region IV: If $5\phi V_c \geq V_u > 3\phi V_c$, similarly the shear reinforcement in Equation (6) has to be provided to carry the difference, but the spacing s must not be larger $\text{Min}\left(d/4, 30, \dfrac{A_v f_y}{0.2\sqrt{f_c'}b}, \dfrac{A_v f_y}{3.5b}\right)$ cm.

The above statements can be summarized in **Figure 3**. From the maximum spacing limitations in different regions computed by the self-written MATLAB program, the total number of vertical stirrups can be obtained.

Because the reaction, in the direction of applied shear, introduces compression into the end regions of a member, the critical section can be assumed at a distance of d from the support, provided that no concentrated loads acts between support face and distance d thereafter. If the factored shear force V_{ud} at a distance d from the face of the support is larger than $5\phi V_c$, the beam section must be enlarged. Therefore, the constraint for shear takes the form

$$V_{ud} \leq 5\phi V_c \tag{7}$$

4.2. Bending Moment

For simplicity, this paper assumes that the strain in the tension reinforcement is equal to 0.005; therefore, the section is tension-controlled, that is, the strength reduction factor for moment is fixed at 0.9, not a function of strain in the tension reinforcement any more. Accordingly, the constraint for both positive and negative moment takes the form

$$M_u \leq 0.9 M_{n,0.005} \tag{8}$$

where M_u is the factored moment M_1 at the middle support section (negative moment) or the maximum pos-
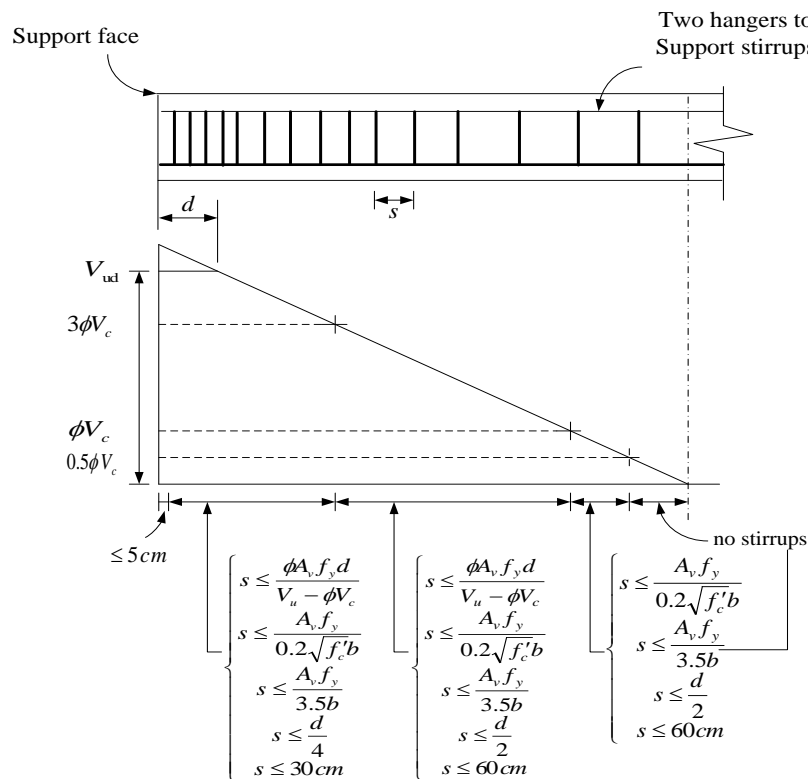
Figure 3. Maximum spacing limitations for vertical stirrups in different regions.

itive moment M_2 at $(3L/8)$ from point A or C, as shown in **Figure 2(a)**, and

$$M_{n,0.005} = A_s f_y \left(d - \frac{1}{2} \times \frac{A_s f_y}{0.85 f_c' b} \right);$$ (9)

When the strain in the tension reinforcement is equal to 0.005, the area of the reinforcement is of the form

$$A_s = \frac{0.85 f_c' \beta_1}{f_y} \times \frac{3db}{8}$$ (10)

where β_1 is the stress block depth factor. To prevent sudden failure with little or no warning when the beam cracks or fails in a brittle manner, the ACI Code also limits the minimum and maximum amount of steel to be

$$A_{s,\min} \le A_s \le A_{s,\max}$$ (11)

where

$$A_{s,\max} = \frac{0.85 f_c' \beta_1 bd}{f_y} \left(\frac{3}{7} \right)$$ (12)

and

$$A_{s,\min} = \max \left(\frac{0.8 \sqrt{f_c'}}{f_y} bd, \frac{14bd}{f_y} \right)$$ (13)

$A_{s,\max}$ in Equation (12) is derived based on the requirement that the tensile strain be equal to 0.004.

4.3. Development of Reinforcement

According to the ACI Code, at least one-third of the total tension reinforcement provided for negative bending moment at the support should extend beyond the inflections point not less than the effective depth d of the member, $12d_b$, or $1/16$ of the clear span. For practical purposes, let span $L \approx$ clear spam L_n. Hence the constraint for the length of the top reinforcement in **Figure 2(b)** can be expressed as

$$\ell_t = \frac{L}{4} + \text{Max} \left(d, 12d_b, \frac{L}{16} \right) \ge \ell_d$$ (14)

where ℓ_d is development length of tension reinforcement and d_b is the nominal diameter of the bar.

4.4. Deflections

The ACI Code indicates that wherever excessive deflection may adversely affect the service-ability of the structure at service loads, deflections under service load conditions must be computed. Creep and shrinkage will magnify the magnitude of deflection with time. Consequently, design engineers have to evaluate immediate as well as long-term deflection in order to ensure their values satisfy the maximum permissible criteria for the particular structure and its particular use. The additional deflection under sustained loading and long-term shrinkage in accordance with ACI procedure can be calculated by multiplying the immediate deflection by a factor

$$\lambda = \frac{T}{1 + 50\rho'}$$ (15)

where ρ' is the compression reinforcement ratio calculated at midspan for simple and continuous beams and T is a factor that is taken as 1.0 for loading time duration of 3 months, 1.2 for 6 months, 1.4 for 12 months and 2.0 for 5 years or more. Because the beam considered in this paper supports partitions and other construction likely to be damaged by large deflections, the ACI code requires that the long-term deflection

$$\Delta = (\Delta_i)_L + \lambda (\Delta_i)_D \le \frac{L}{480}$$ (16)

where $(\Delta_i)_L =$ immediate live-load deflection and $(\Delta_i)_D =$ immediate dead-load deflection. The formula for

the maximum deflection in the beam can be found in **Figure 2(a)**.

5. Numerical Results

The given conditions for the optimal design of two-span continuous singly reinforced rectangular concrete beams with a rectangular cross-section are the span length L, uniformly distributed dead w_D and live load w_L, compressive strength of concrete f_c' and yield strength of steel f_y. Design variables are the width b and effective depth d of the beam, the steel ratio ρ_1 for the positive moment and the steel ratio ρ_2 for the negative moment. The concrete cover for the reinforcement is 4 cm and No. 3 vertical stirrups are used. The objective function is to find the minimum cost in New Taiwan Dollars of concrete and steel used in the two-span continuous beam. In Taiwan, the unit price of concrete is 1800 NT\$/m^3 and the unit price of steel is 19.5 NT\$/kgf. The optimal results found by the genetic algorithm consist of the minimum cost of the two-span continuous beam, the width b and effective depth d of the beam, and the steel ratios for the positive and negative moments. Based on the often-used materials and customs in Taiwan, this paper selects three kinds of yield strength f_y of the tension reinforcement: 2800 kgf/cm^2 (40 ksi), 3500 kgf/cm^2 (50 ksi) and 4200 kgf/cm^2 (60 ksi) as well as three kinds of compressive strength f_c' of the concrete: 210 kgf/cm^2 (3000 psi), 280 kgf/cm^2 (4000 psi) and 350 kgf/cm^2 (5000 psi). Three kinds of span length are chosen: 6 m, 8 m and 10 m; four kinds of uniformly distributed dead load w_D are chosen: 2100 kgf/m, 2300 kgf/m, 2500 kgf/m and 2700 kgf/m; uniformly distributed live load w_L is fixed at 1800 kgf/m. From the combinatorial analysis, there are totally 108 cases to be designed. This paper adopts the MATLAB toolbox for genetic algorithm [29] to carry out the genetic algorithm. All the constraints are built according to the formulas discussed in Section 4, most of which are highly nonlinear and cause the difficulty using the traditional gradient-based methods to find the optimal solution.

5.1. Genetic Algorithms

To run the genetic algorithm of the MATLAB software, some parameters need to be selected. Here are the values used in this paper: after a number of trials, the population size is set to be 20, crossover rate 0.8, and elite number 2. Furthermore, all the individuals are encoded as real numbers; "Rank" is used as the scaling function that scales the fitness values based on the rank of each individual; "Roulette" is the selection function to choose parents for the next generation; "Two-Point Crossover" is used as the crossover method to form a new child for the next generation; the "Adaptive Feasible Function" is chosen as the mutation function to make small random changes in the individuals and ensure that linear constraints and bounds are satisfied. The genetic algorithm is executed 30 times for each case, from which the best is selected. For the use of ANFIS, the total 108 cases of data are divided into 3 groups randomly by a computer algorithm: 64 cases of training data (60%), 22 cases of checking data (20%) and 22 cases of testing data (20%).

5.2. Adaptive Neuro-Fuzzy Inference Systems

When using ANFIS with MATLAB, there are some restrictions: 1) only first- or zeroth-order Sugeno-type systems are supported; 2) there is only one single output; 3) each rule is of unit weight. The inputs of the adaptive neuro-fuzzy inference system consist of six elements: f_y, f_c', w_D, L, b and d. There are three targets: the minimum cost, the steel ratios ρ_1 and ρ_2. Because only one output is allowed, ANFIS must be executed for each target individually. To make the Sugeno-type fuzzy inference system more efficient, the "Subtractive Clustering" technique is employed. During the training process, the checking data is also loaded to ANFIS to avoid the overfitting problem. When the model begins to overfit the data, the error on the checking set will typically to rise. When the checking error increases for a specified number of epochs, the training is stopped. The membership function parameters associated with the training epoch that has a minimum checking error are returned. To evaluate the performance of ANFIS, this paper makes use of a linear regression analysis between outputs and targets. While training ANFIS, four algorithm parameters for "Subtractive Clustering" must be provided. This paper uses the default values for the squash factor, accept ratio and reject ratio. As to the range of influence q_1, this paper tries a variety of values from 0.1 to 1.5 to obtain the best one because of the complexity of the 7-dimensional data points. Among them, the value of 1.4 is found to have the best results on the whole. The results for the three outputs of the testing data are listed in **Tables 1-3**, where the symbols *m*, *b* and *r* stand for the slope, the *y*-intercept and correlation coefficient, respectively. The scatter plots corresponding to

Table 1. The linear regression results of the steel ratio ρ_1 for the testing data.

Parameters Influence Range	m	b	r
0.1	0.7774	0.0011	0.8256
0.2	0.9005	0.0008	0.8211
0.3	0.9337	0.0006	0.8121
0.4	0.8988	0.0008	0.8474
0.5	0.8318	0.0012	0.8882
0.6	0.6519	0.0018	0.6029
0.7	1.0316	−0.0003	0.9380
0.8	0.8869	0.0004	0.8208
0.9	0.9529	0.0003	0.9570
1.0	0.9106	0.0006	0.9745
1.1	1.0241	−0.0001	0.9972
1.2	0.9946	0.0000	0.9958
1.3	0.9953	0.0000	0.9944
1.4	1.0087	−0.0001	0.9983
1.5	1.0397	−0.0002	0.9882

Table 2. The linear regression results of the steel ratio ρ_2 for the testing data.

Parameters Influence Range	m	b	r
0.1	0.9119	0.0014	0.8175
0.2	0.9389	0.0003	0.6480
0.3	0.9165	0.0011	0.8494
0.4	0.9068	0.0011	0.7426
0.5	0.5709	0.0054	0.5486
0.6	0.7702	0.0026	0.8936
0.7	1.1192	−0.0031	0.7251
0.8	0.7186	0.0028	0.7531
0.9	0.9394	0.0007	0.9334
1.0	0.9221	0.0009	0.9799
1.1	1.0350	−0.0005	0.9888
1.2	0.9325	0.0008	0.9939
1.3	1.0109	0.0000	0.9970
1.4	1.0038	0.0000	0.9984
1.5	0.9484	0.0005	0.9751

$q_1 = 1.4$ for the steel ratios ρ_1 and ρ_2 and the minimum cost (10^3 NT$) are shown in **Figures 4-6**, respectively. The correlation coefficients between the network outputs and targets are 0.9983, 0.9984 and 0.9996 for the steel ratios ρ_1 and ρ_2 and the minimum cost, respectively. Besides, the slope m is close to 1 and y-

Table 3. The linear regression results of the minimum cost for the testing data.

Parameters Influence Range	m	b	r
0.1	0.9855	0.0505	0.9944
0.2	0.9736	0.1458	0.9925
0.3	0.9582	0.2669	0.9858
0.4	0.9832	0.0934	0.9912
0.5	0.9478	0.4552	0.9916
0.6	0.9431	0.3981	0.9919
0.7	1.0030	0.1634	0.9951
0.8	1.0744	−0.6299	0.9962
0.9	0.9643	0.3517	0.9982
1.0	1.0350	−0.1380	0.9959
1.1	1.0067	−0.0733	0.9998
1.2	0.9931	0.0621	0.9994
1.3	1.0014	0.0182	0.9996
1.4	1.0012	−0.0241	0.9996
1.5	0.9943	0.0509	0.9989
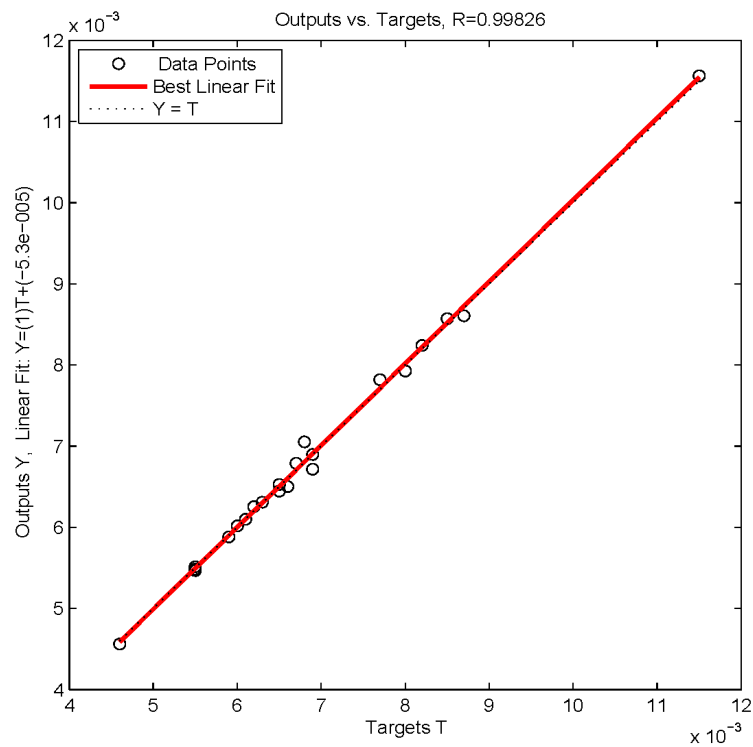
Figure 4. The scatter plot of the steel ratio ρ_1 for the testing data.

intercept *b* approximately equals 0.

Based on **Figures 4-6** and **Tables 1-3**, the performance of ANFIS is satisfactory and considered to be excellent. **Table 4** lists the number of fuzzy rules for the three outputs with the influence ranges changing, which indicates that the larger the influence range of a cluster center becomes, the fewer fuzzy rules ANFIS results in. Taken as example, the inputs, targets and outputs of ANFIS for some cases of the testing data are shown in **Table 5**.
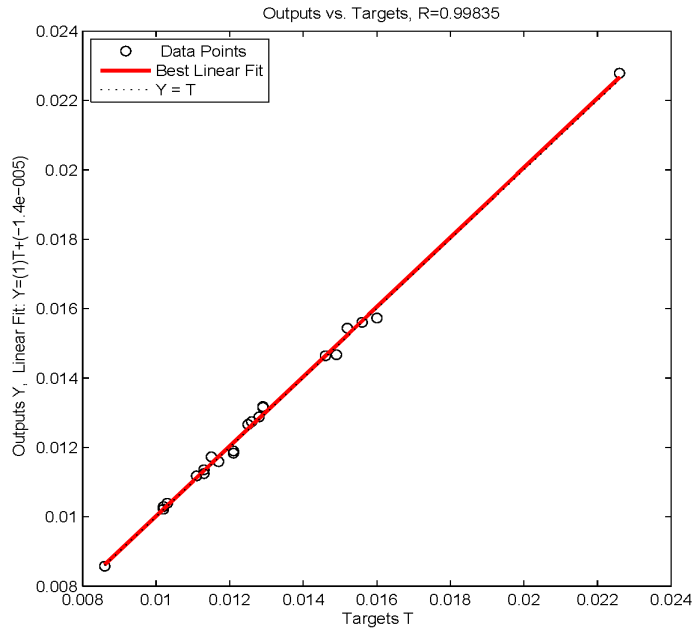
Figure 5. The scatter plot of the steel ratio ρ_2 for the testing data.
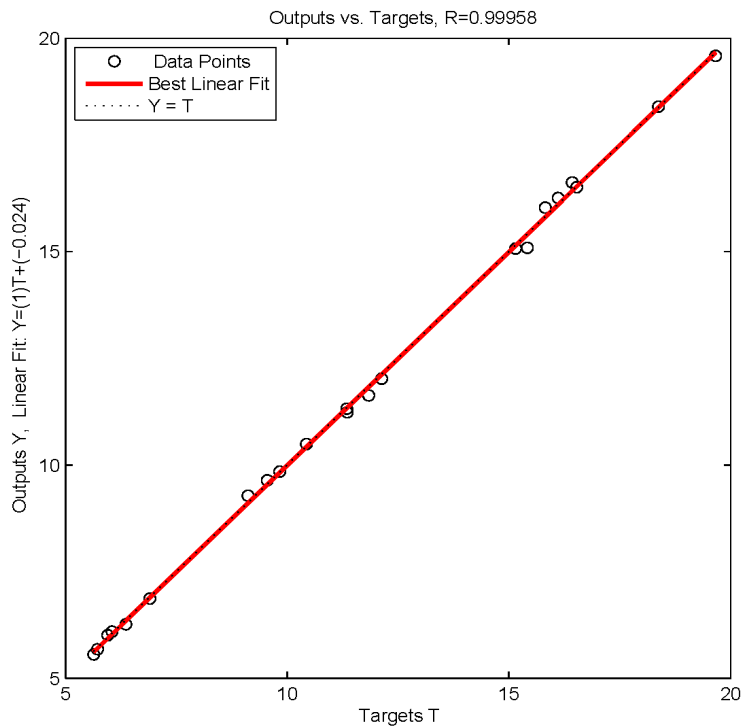
Figure 6. The scatter plot of the minimum cost (10^3 NT\$) for the testing data.

Table 4. The number of fuzzy rules for the three outputs: steel ratios ρ_1 and ρ_2 and the minimum cost with the influence range changing.

Outputs Influence Range	ρ_1	ρ_2	Cost
0.1	64	64	64
0.2	64	64	64
0.3	64	64	64
0.4	64	64	64
0.5	64	64	61
0.6	47	47	46
0.7	34	34	33
0.8	25	26	23
0.9	16	16	16
1.0	11	11	12
1.1	7	7	8
1.2	7	7	7
1.3	4	4	5
1.4	3	3	3
1.5	2	2	3

Table 5. Inputs, targets and outputs of ANFIS for some cases of testing data.

Inputs						Targets			Outputs		
f_y (ton/cm^2)	f_c' (ton/cm^2)	w_d (ton/m)	L (m)	b (m)	d (m)	ρ_1	ρ_2	Cost (10^3 NT\$)	ρ_1	ρ_2	Cost (10^3 NT\$)
2.8	0.28	2.7	6	0.2018	0.6309	0.0080	0.0149	6.904	0.0079	0.0147	6.870
3.5	0.21	2.3	6	0.2000	0.6617	0.0055	0.0102	6.051	0.0055	0.0103	6.094
4.2	0.35	2.1	8	0.2006	0.7178	0.0065	0.0121	9.115	0.0065	0.0118	9.279

6. Conclusion

This paper first uses the genetic algorithm to work on the optimal design of two-span continuous reinforced concrete beams with a rectangular section. The adaptive neuro-fuzzy inference system (ANFIS) is then built based on the data of the given conditions and optimal results of the genetic algorithm. The inputs of this model are the yield strength of steel, compressive strength of concrete, dead load (live load is fixed) and span length, width and effective depth of the beam; targets are the minimum cost, the steel ratios for the positive and negative moments. The inputs of ANFIS are different from the given conditions of the genetic algorithm, which makes ANFI more useful and flexible in the design of beams. This paper proves that ANFIS has excellent performance with correlation coefficients between outputs and targets of the steel ratios for positive and negative moments and the minimum cost of the testing data being 0.9983, 0.9984 and 0.9996, respectively. In addition, the influence ranges of a cluster center from 0.1 to 1.5 for "Subtractive Clustering" to estimate the number of clusters and the cluster centers are explored, among which the value of 1.4 can lead to the best results as a whole, as far as the performance of ANFIS is concerned. In the future, once the input data are provided, ANFIS could quickly yield the minimum cost, steel ratios for the positive and negative moments as well as the spacing of vertical stirrups in each region with high precision, which automatically accomplish the design of the continuous reinforced concrete beams. The ANFIS model for the design of beams is easily implemented and timesaving,

because it does not need to build the tedious and complex constraints.

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A Reinforcement Learning System to Dynamic Movement and Multi-Layer Environments

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Abstract

There are many proposed policy-improving systems of Reinforcement Learning (RL) agents which are effective in quickly adapting to environmental change by using many statistical methods, such as mixture model of Bayesian Networks, Mixture Probability and Clustering Distribution, etc. However such methods give rise to the increase of the computational complexity. For another method, the adaptation performance to more complex environments such as multi-layer environments is required. In this study, we used profit-sharing method for the agent to learn its policy, and added a mixture probability into the RL system to recognize changes in the environment and appropriately improve the agent's policy to adjust to the changing environment. We also introduced a clustering that enables a smaller, suitable selection in order to reduce the computational complexity and simultaneously maintain the system's performance. The results of experiments presented that the agent successfully learned the policy and efficiently adjusted to the changing in multi-layer environment. Finally, the computational complexity and the decline in effectiveness of the policy improvement were controlled by using our proposed system.

Keywords

Reinforcement Learning, Profit-Sharing Method, Mixture Probability, Clustering

1. Introduction

Along with the increasing need for rescue robots in disasters such as earthquakes and tsunami, there is an urgent

need to develop robotics software for learning and adapting to any environment. Reinforcement Learning (RL) is often used in developing robotic software. RL is an area of machine learning within the computer science domain, and many RL methods have recently been proposed and applied to a variety of problems [1]-[4], where agents learn the policies to maximize the total number of rewards decided according to specific rules. In the process whereby agents obtain rewards; data consisting of state-action pairs are generated. The agents' policies are effectively improved by a supervised learning mechanism using the sequential expression of the stored data series and rewards.

Normally, RL agents need to initialize the policies when they are placed in a new environment and the learning process starts afresh each time. Effective adjustment to an unknown environment becomes possible by using statistical methods, such as a Bayesian network model [5] [6], mixture probability and clustering distribution [7] [8], etc., which consist of observational data on multiple environments that the agents have learned in the past [9] [10]. However, the use of a mixture model of Bayesian networks increases the system's calculation time. Also, when there are limited processing resources, it becomes necessary to control the computational complexity. On the other hand, by using mixture probability and clustering distribution, even though the computational complexity was controlled and the system's performance was simultaneously maintained, the experiments were only conducted on fixed obstacle 2D-environments. Therefore, examination of the computational complexity load and the adaptation performance in dynamic 3D-environments is required.

In this paper, we describe modifications of profit-sharing method with new parameters that make it possible to work on dynamic movement of multi-layer environments. We then describe a mixture probability consisting of the integration of observational data on environments that agent learned in the past within framework of RL, which provides initial knowledge to the agent and enables efficient adjustment to a changing environment. We also describe a novel clustering that makes it possible to select fewer elements for a significant reduction in the computational complexity while retaining system's performance.

The paper is organized as follows. Section 2 briefly explains the profit-sharing method, the mixture probability, the clustering distribution, and the flow system. The experimental setup and procedure as well as the presentation of results are described in Section 3. Finally, Section 4 summarizes the key points and mentions our future work.

2. Preparation

2.1. Profit-Sharing

Profit-sharing is an RL method that is used as a policy learning mechanism in our proposed system. RL agents learn their own policies through "rewards" received from an environment.

2.1.1. 2D-Environments

The policy is given by the following function:

$$w : S \times A \to R \tag{1}$$

where S and A denote a set of state and action, respectively. Pair $(s,a)(\forall s \in S, \forall a \in A)$ is referred to as a rule. $w(s,a)$ is used as the weight of the rule ($w(s,a)$ is positive in this paper). When state s^0 is observed, a rule is selected in proportion to the weight of rule $w(s^0, a^0)$. The agent selects a single rule corresponding to given state s^0 using the following probability:

$$P(s^0, a^0) = \frac{w(s^0, a^0)}{\sum_{s' \in S, a' \in A} w(s', a')} \tag{2}$$

The agent stores the sequence of all rules that were selected until the agent reaches the target as an episode.

$$L = \{(s_1, a_1), \cdots, (s_L, a_L)\} \tag{3}$$

where L is the length of the episode. When the agent selects rule (s_L, a_L) and requires reward r, the weight of each rule in the episode is reinforced by

$$w(s_i, a_i) \leftarrow w(s_i, a_i) + f(i) \tag{4}$$

$$f(i) = r\gamma^{L-i} \tag{5}$$

where $f(i)$ is referred to as the reinforcement function and $\gamma (\in (0,1])$ is the "learning rate". In this paper, the following nonfixed reward is used:

$$r = r_0 + (t-n) \tag{6}$$

where r_0 is the initial reward, t is the action number limit in one trial and n is the real action number until the agent reaches the target. We expect that the agent can choose a more suitable rule to reach the target in a dynamic environment by using this nonfixed reward.

2.1.2. 3D-Environments

The weight $w(s,a)$ becomes $w(z,s,a)$ where $z = 1, \cdots, n$ (n is number of layers in this paper). The probability of the rule (z^0, s^0, a^0) becomes to this following function:

$$P(z^0, s^0, a^0) = \frac{w(z^0, s^0, a^0)}{\sum_{s' \in S, a' \in A} w(z^0, s', a')} \tag{7}$$

and the new episode is given in the following function:

$$\mathcal{L} = \begin{Bmatrix} (z_1, s_1, a_1) & (z_1, s_2, a_2) & \cdots & (z_1, s_{L_1}, a_{L_1}) \\ (z_2, s_1, a_1) & (z_2, s_2, a_2) & \cdots & (z_2, s_{L_2}, a_{L_2}) \\ \vdots & \vdots & \ddots & \vdots \\ (z_n, s_1, a_1) & (z_n, s_2, a_2) & \cdots & (z_n, s_{L_n}, a_{L_n}) \end{Bmatrix} \tag{8}$$

$$L = \sum_{i=1}^{n} L_i \tag{9}$$

By the movement on z, we can set the pseudo-reward [11] by using the following function:

$$r_i = r\gamma_z^{n-i} \quad (i = 1, \cdots, n), \quad (0 < \gamma_z \le 1) \tag{10}$$

and update the weights according to the following function by using function (10):

$$w(z_i, s_j, a_j) \leftarrow w(z_i, s_j, a_j) + f(i, j) \tag{11}$$

$$f(i, j) = r_i \gamma^{L_i - j} = r\gamma_z^{n-i} \gamma^{L_i - j} \quad (i = 1, \cdots, n), \quad (j = 1, \cdots, L_i) \tag{12}$$

2.1.3. Ineffective Rule Suppression

As **Figure 1**, agent selects rule (z_1, s_{L_1}, a_{L_1}) in z_1 then moves to z_2. When agent selects any rule in z_2 and finally moves back to state (z_1, s_{L_1}), the rules were selected on z_2 are became detour rules which may not contribute to the acquisition of the reward and these detour rules are called as ineffective rule [12] [13].

The ineffective rule has more negative effect such as the rules continue being selected repeatedly on the movement of z and agent cannot avoid from that situation. And this may make the policy learning become stagnation. From these reasons, the suppression of ineffective rule becomes necessary.

In this paper, we use this following method to suppress the ineffective rule:

Here, we use L_i as the length of episode $\mathcal{L}_i$ and L_C as a fixed number for determination ineffective rule. When $L_i \le L_C \cap z_i = z_{i+1}$, all rules in $\mathcal{L}_i$ are decided to be ineffective rule. Here, all rules in $\mathcal{L}_i$ and the final rule in $\mathcal{L}_{i-1}(z_{i-1}, s_{L_{i-1}}, a_{L_{i-1}})$ will be excluded from $\mathcal{L}$ as shown on **Figure 1**.

2.2. Mixture Probability

Mixture probability is a mechanism for recognizing changes in the environment and consequently improving the agent's policy to adjust to those changes.

The joint distribution [14] $P(z, s, a)$, consisting of the episode observed while learning an agent's policy, is
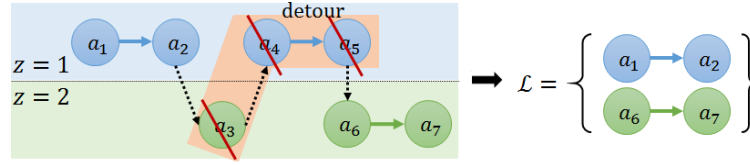
Figure 1. Example of ineffective rule.

probabilistic knowledge about the environment. Furthermore, the policy acquired by the agent is improved by using the mixture probability of $P_i (i = 1, \cdots, m)$ obtained in multiple known environments. The mixing distribution is given by the following function:

$$P_{\text{mix}}(z, s, a) = \sum_{i=1}^{m} \beta_i P_i (z, s, a) \tag{13}$$

where m denotes the number of joint distributions, and β_i is the mixing parameter $\left(\sum_i \beta_i = 1, \beta_i \geq 0 \right)$. By adjusting the environment subject to this mixing parameter, we expect appropriate improvement of the policy on the unknown dynamic environment.

In this paper, we use the following Hellinger distance [15] function to fix the mixing parameter:

$$D_H (P_i, Q) = \left\{ \sum_x \left[P_i(x)^{\frac{1}{2}} - Q(x)^{\frac{1}{2}} \right]^2 \right\}^{\frac{1}{2}} \tag{14}$$

where D_H is the distance between P_i and Q, and D_H is set to 0 when P_i and Q are the same. P_i is joint distributions obtained in m different environments that an agent has learned in the past, Q is the sample distribution obtained from the successful trial of τ times in an unknown environment, and x is the total number of rules. Given that $D_H (P_i, Q) \leq \sqrt{2}$ is established, the mixing parameter can be fixed by the following function:

$$\beta_i = \frac{\sqrt{2} - D_H (P_i, Q)}{\sum_{j=1}^{m} \left[\sqrt{2} - D_H (P_j, Q) \right]} \tag{15}$$

However, when $\sum_{j=1}^{m} \left[\sqrt{2} - D_H (P_j, Q) \right] = 0$, $\beta_i = \frac{1}{m}$, and when all distributions are equal, the mixing parameter is evenly allotted.

2.3. Clustering Distributions

We expect that the computational complexity of the system can be controlled and it will be possible to maintain the effectiveness of policy learning by selecting only the suitable joint distributions as the mixture probability elements based on this clustering method.

In this study, we used the group average method as opposed to the clustering method. The distance between the clusters can be determined by the following function:

$$D(Cl_i, Cl_j) = \frac{1}{n_i n_j} \sum_{P_i \in Cl_i, P_j \in Cl_j} D_H (P_i, P_j) \tag{16}$$

where n_i; n_j are the number of joint distributions contained in Cl_i and Cl_j, respectively. In this study, we used the Hellinger distance function $D_H (P_i, P_j)$. After completing the clustering, element P_i having the minimum $D_H (P_i, Q)$ will be selected as the mixture probability element from each cluster.

2.4. Flow System

The system framework is shown in **Figure 2**. A case involving the application of mixture probability and clustering distributions to improve the agent's policy is explained in the following procedure:
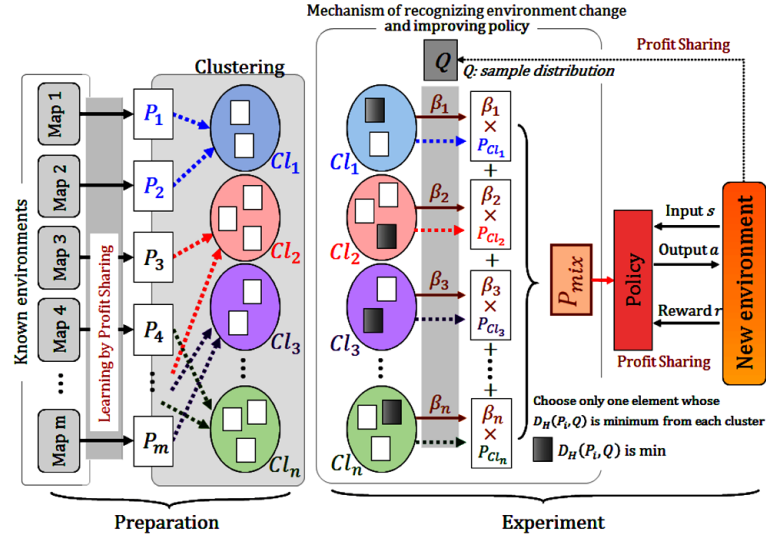
Figure 2. System framework.

Step 1 Learn the policy in m environments by using the profit-sharing method to make the joint distributions $P_i = (i = 1, \cdots, m)$;

Step 2 Cluster m distributions into n clusters;

Step 3 Calculate the Hellinger distance D_H of distributions P_i and sample distribution Q;

Step 4 Select the element having the minimum $D_H(P_i, Q)$ from each cluster;

Step 5 Calculate the mixing parameter β_i;

Step 6 Mix probability P_{mix};

Step 7 Update the weight of all rules by using the following function:

$$w^{\text{new}} \leftarrow w^{\text{old}} + w^{\text{old}} \times P_{\text{mix}} \tag{17}$$

and then continue learning the updated weight by using the profit-sharing method.

3. Experiments

We performed an experiment to demonstrate the agent navigation problem and to illustrate the applied improvement in the RL agent's policy through the modification of parameters of the profit-sharing method and using the mixture probability scheme. The purpose of this experiment was to evaluate the adjustment performance in the unknown dynamic 3D-environment by applying the policy improvement, and to evaluate its effectiveness by using mixture probability.

3.1. Experimental Setup

The aim in the agent navigation problem is to arrive at the target from the default position of the environment where the agent is placed. In the experiment, the reward is obtained when the agent reaches the target by avoiding the obstacle in the environment, as shown in **Figure 3**.

The types of state and action are shown in **Table 1** and **Table 2**, respectively. **Table 1** shows the output actions of an agent in 8 directions and **Table 2** shows 256 types of the total input states coming from the combination of existing obstacles in 8 directions. The 8 directions are the top left, top, top right, left, right, bottom left, bottom, and bottom right. The agent has 2048 (8 actions × 512 states) rules in total that result from a combination of input states and output actions in a layer. The size of agent, target, and environment are 1×1, 5×5, and 50×50, respectively.

3.2. Experimental Procedure

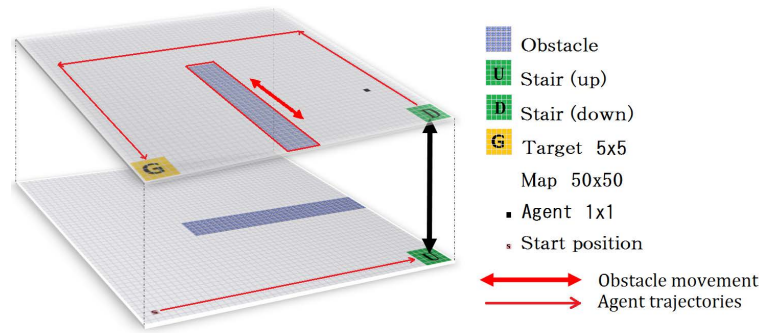The agent learns the policy by using the profit-sharing method. A trial is considered to be successful if an agent

Figure 3. Environment of agent navigation problem.

Table 1. Types of action.

Direction of action			Value		
↖	↑	↗	0	1	2
←	Ⓐ	→	3	Ⓐ	4
			5	6	7
↙	↓	↘			

Table 2. Some types of state.

Position of obstacle and value						

reaches the target at least once out of 200 action attempts. The action is selected by randomization and that action continues until the state is changed.

The purpose of the experiment is to learn the policy in unknown dynamic environments E_A, E_B and E_C in three cases (fixed obstacle, periodic dynamic and nonperiodic dynamic environments), by employing only the profit-sharing method and the mixture probability scheme (elements are m and n); the evaluation is based on the success rate of 2000 trials. The experimental parameters are shown in **Table 3**. Some of known environments that became mixture probability elements, and the unknown dynamic environments (E_A, E_B, E_C) used to evaluate the policy improvement are shown in **Figure 4** and **Figure 5**, respectively.

3.3. Discussion

The success rate of policy improvement in E_A, E_B and E_C by using only profit-sharing method and using mixture probabilities and clustering is shown in **Figure 6**, and the processing time from **Step 3** (system flow) until experiment finish in cases using all 50 elements and using only 35, 25 and 15 elements is shown in and **Table 4**, respectively

Figure 6 shows that the immediate success rate obtained by policy improvement is higher than that obtained by only the profit-sharing method in all environments. This means the speed of adaptation in unknown environment is higher and the higher success rate continues until the experiments end. This results shows the success rate by policy improvement is higher than using only the profit-sharing more than 20% in E_A and E_C, and more than 30% in E_B. So, we can say the policy improvement is effective in all environments.

Even the success rate by using only 15 elements is also higher than that using only the profit-sharing method, but is still lower compared to the results using 25 and 35 elements. Hence, we can say by reducing the number of elements too much, the influence on policy improvement is apparent in all environments. However, although
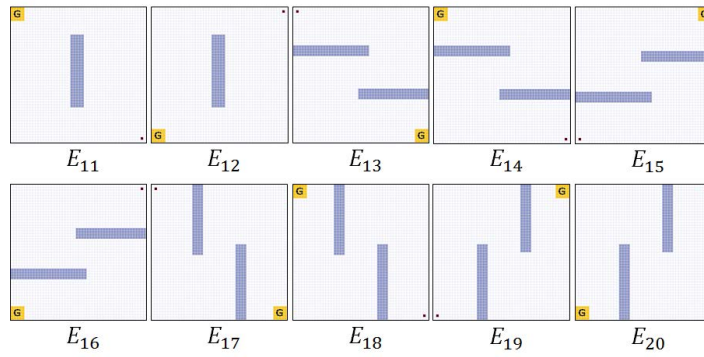
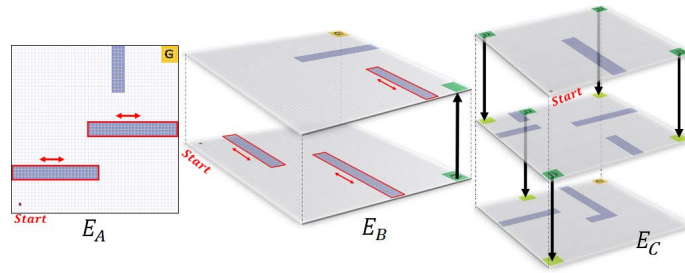**Figure 4.** Some of known environments.

Figure 5. Unknown environments.
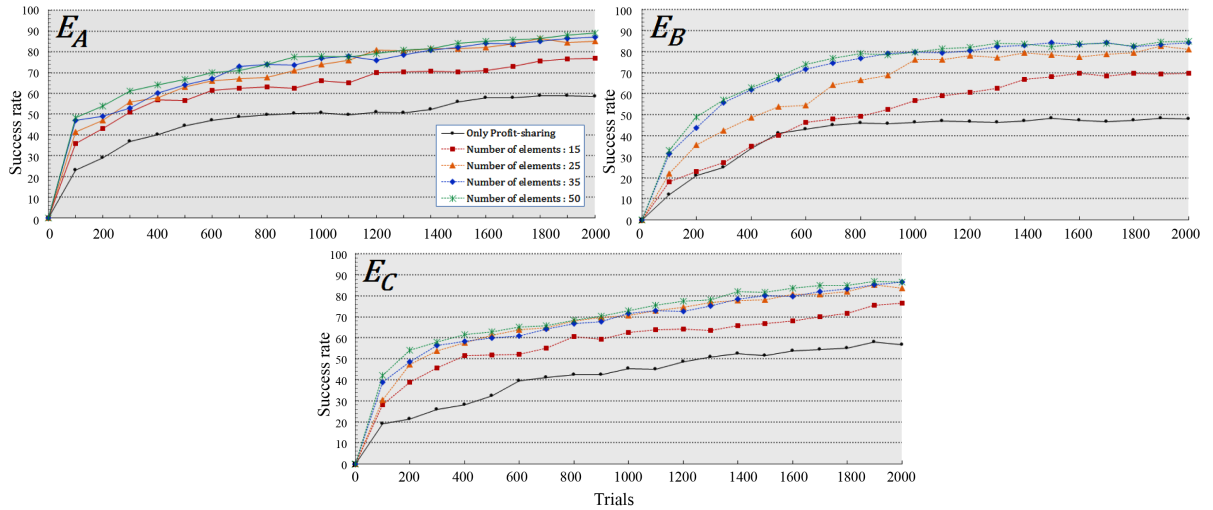
Figure 6. Transition of success rate.

Table 3. Experimental parameters.

Variable	Value	Variable	Value
t	200	τ	20
γ	0.8	w_0	10.0
r	Nonfixed	n	15, 25, 35
r_0	100	m	50
L_i	≤ 3	L_C	6

Processing time.

	Element number and processing time (s)			
	50	35	**25**	15
E_A	26.541	21.047	**18.241**	13.114
E_B	29.247	24.169	**21.374**	18.471
E_C	32.311	28.697	**24.417**	20.381

the success rate using all 50 elements was the highest, but that obtained using 25 elements was almost the same as that using all the elements in this result. So, the decline in effectiveness can still be controlled even if the number of mixture probability elements is reduced to half.

Furthermore, from the results in **Table 4**, we can see that by reducing the number of elements, the processing time was reduced considerably. Hence, we can say by using 25 elements, we can reduce the processing time without declining in policy improvement performance.

Figure 7 shows the typical trajectories of agent following the policy acquired while selecting data in environment E_C in cases 1 - 500, 501 - 1000 and 1001 - 2000 trials. The intensity of color (from light red to dark red) show the frequency of agent's trajectories when they reached to target in each layers.

In these results, we can see in the first 500 trials, agent reached to all sub-targets in top layer. But due to the agent which started from sub-target 1 was the most difficult for reaching next sub-target, the number of time that agent reached to sub-target 1 became fewer in 501 - 1000 trials and finally almost reached to sub-target 2 and 3 in 1001 - 2000 trials. Also in middle layer, agent reached to all sub-targets in first 500 trials. But due to the agent which started from sub-target 5 was more easily for reaching to the final goal, the more number of trials there are, the more frequency of agent's trajectories from sub-target 5 to the final goal increased clearly.

From the results of typical agent', we can say by using the pseudo-reward, the agent can choose more suitable rules to reach the target in each layers even agent might be sometimes more difficult to reach in some layer, but more easily to reach to the final goal.

3.4. Supplemental Experiments

These experiments were conducted to compare the performance of the policy improvement in cases of fixed obstacle, periodic dynamic movement and nonperiodic dynamic movement on E_A and E_B by using 25 elements. And experiments in only periodic and nonperiodic cases by using the same parameters were conducted 5 times.

4. Discussion

The results of policy improvement by using 25 elements of mixture probabilities in three cases are shown in **Figure 8**, and the results of five sets of experiments in periodic and nonperiodic dynamic movement are shown in **Figure 9**, respectively.

Figure 8 shows that the success rate in the case of periodic dynamic movement was almost no difference in the early period compared with the fixed obstacle case in both E_A and E_B, and continued to keep abreast of high success rate until the experiments end. On the other hand, in the case of nonperiodic dynamic movement, even the success rate in E_B was almost no difference or sometime was conversely higher compared with the fixed obstacle case. However, as shown in **Figure 9**, even though the experiments were conducted by using the same parameters, the results of nonperiodic case in E_A was quite low compared to periodic case. And the results of nonperiodic case were unstable in all E_A and E_B.

From these results, we can deduce that agent successfully learns the policy in the periodic dynamic movement environment and can more easily reach the target when the obstacle moves out from the trajectory as in E_B. On the contrary, when the obstacle moves into the trajectory, it will be more difficult for the agent to reach the target.

5. Conclusions

In this research, we used the joint distributions $P(z, s, a)$ as the knowledge and the sample distribution Q to
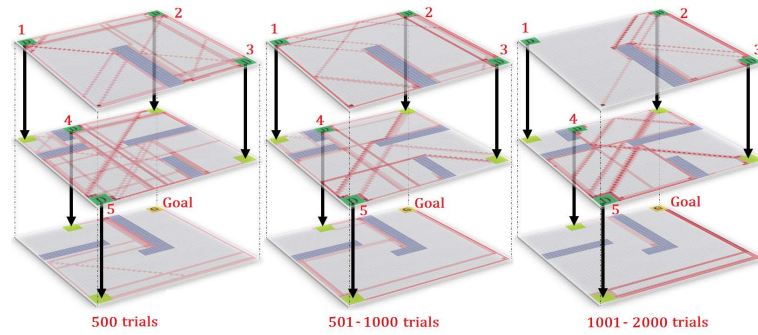
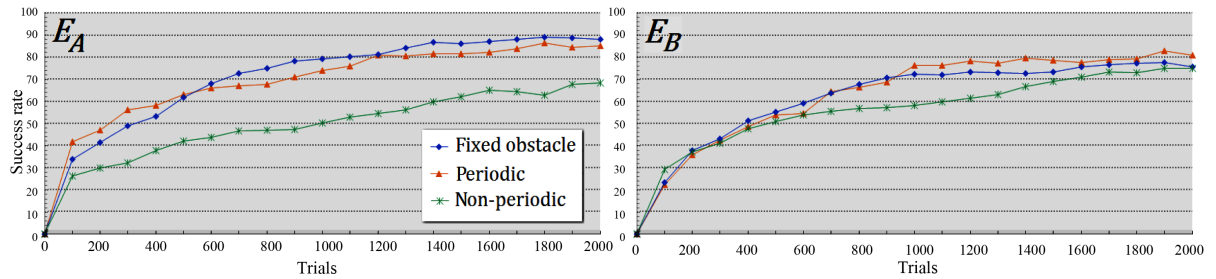Figure 7. Typical agent trajectories in E_C.

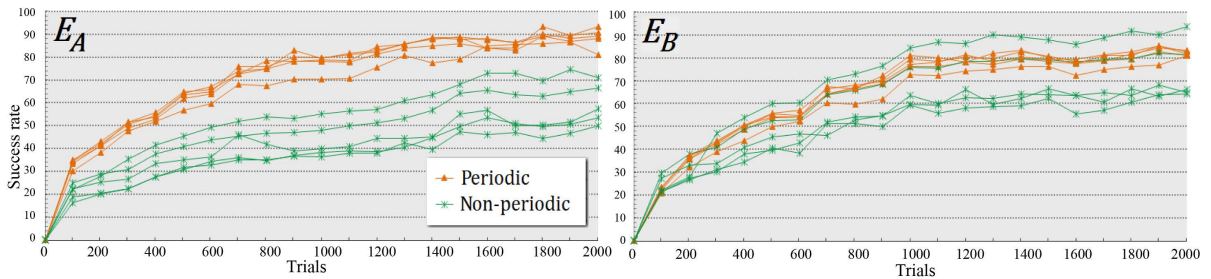Figure 8. Transition of success rate (3 cases).

Figure 9. Five sets of experiments.

find the degree of similarity between the unknown and each known environment. We then used this as the basis to update the initial knowledge as being very useful for the agent to learn the policy in a changing environment. Even if obtaining the sample distribution is time-consuming, it is still worthwhile if the agent can efficiently learn the policy in an unknown dynamic environment.

Also, by using the clustering method to collect similar elements and then selecting just one suitable joint distribution as the mixture probability elements from each cluster, we can avoid using similar elements to maintain a variety of elements when we reduce their number.

From the results of the computer experiment as an example application in the agent navigation problem, we can confirm that the policy improvement in dynamic movement environments is effective by using the mixture probabilities. Furthermore, agent is possible to select suitable rules to reach to the target in multi-layer by using the pseudo-reward. And the decline in effectiveness of the policy improvement can be controlled by using the clustering method. We conclude that the improvement of stability and speed in policy learning, and the control of computational complexity are effective by using our proposed system.

Improvement of the RL policy is also required by using mixture probability with a positive and negative weight value for making the system adaptable to unknown environments that are not similar to any known environments. Finally, a new reward process is needed as well as a new mixing parameter for the agent to adjust to a changing environment more efficiently and to be able to work well in any complicate environments in future work.

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Scientific
Research

Dominant Meaning Method for Intelligent Topic-Based Information Agent towards More Flexible MOOCs

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Abstract

The use of agent technology in a dynamic environment is rapidly growing as one of the powerful technologies and the need to provide the benefits of the Intelligent Information Agent technique to massive open online courses, is very important from various aspects including the rapid growing of MOOCs environments, and the focusing more on static information than on updated information. One of the main problems in such environment is updating the information to the needs of the student who interacts at each moment. Using such technology can ensure more flexible information, lower waste time and hence higher earnings in learning. This paper presents Intelligent Topic-Based Information Agent to offer an updated knowledge including various types of resource for students. Using dominant meaning method, the agent searches the Internet, controls the metadata coming from the Internet, filters and shows them into a categorized content lists. There are two experiments conducted on the Intelligent Topic-Based Information Agent: one measures the improvement in the retrieval effectiveness and the other measures the impact of the agent on the learning. The experiment results indicate that our methodology to expand the query yields a considerable improvement in the retrieval effectiveness in all categories of Google Web Search API. On the other hand, there is a positive impact on the performance of learning session.

Keywords

Massive Open Online Courses, MOOCs, Search Engine, Hypermedia Systems, Web-Based Services, Query Expansion, Probabilistic Model, Information Retrieval, Search Engine

1. Introduction

Agent technology has been suggested by experts to be a promising approach to help in overcoming the challenges of the modern e-learning environment [1]. It is now a very important issue due to the increasing in the use of new technology and distributed artificial intelligence technology for new learning environment. Business Dictionary [2] defines an agent technology as "computer programs that use artificial intelligence technology to 'learn', and automate certain procedures and processes". It uses re-determined inventory levels on the Internet to automate ordering process. It emerges rapidly as one of the leading technologies for overcoming the uncertainty in a dynamic environment to help in improving distributed systems [3]. The domain of information on the web is suitable for an agent-based approach because information online is regularly distributed in dynamic varying environments.

Nowadays, information agent technology has been a long-term development and we still need it to deal with the huge information increasing on the web. One of these new application domains of e-learning is Massive Open Online Courses (MOOCs). Mass [4] found that MOOCs need more learning resources to help students in acquiring more knowledge. The web includes huge and different types of information. A small amount of information is suitable for learners. This is because web search engines are not able to classify such information related to learner's needs. Intelligent Topic-Based Information Agent (ITBIA) offers an updated knowledge including various types of resource (alternative explanations, examples, exercises, images, applets, etc.) for students. The algorithm formulates Hierarchy of Dominant Meanings Tree using a textual course material (e.g., video transcripts) and queries from topics extracted from discussion postings between students in the course. Then it searches Google using these queries, and inserts the resulting content into categorized lists. During the discussion, the ITBIA employs a current topic to recognize the intended meaning of a query. ITBIA offers a top ranked website to students to look at them and enrich the discussion. Various approaches have been introduced in the field of information retrieval. Even though these approaches are successful, from time to time they are not able to offer precise information to the user [5]. This paper presents a mechanism based on a dominant meaning approach for searching the web.

Two experiments were done to measure a precision and to examine the performance of the ITBIA to retrieve relevant documents.

In the rest of the paper, Section 2 details the related work for the topic of MOOCs and search engine. Section 3 introduces Intelligent Topic-Based Information Agent and its frameworks. In Section 4, the methodology used by tutor agent is presented. Finally, Section 5 introduces the results of the experiments and its discussions.

2. Related Work

Because Intelligent Topic-Based Information Agent is first introduced in MOOCs, this section surveys previous work in three folds: agent technology, search engine and MOOCs.

Agent technology and their applications in information retrieval and the web information have been studied for more decades. A number of applications which apply agent technologies have already been reported in the literature such as [1] [3] and [6]. This paper studies the way of presenting more up-to-date web information related to the topic taught on MOOCs to be used as learning recourse. Usual search engines store the textual content of the web pages in a database and they revisit a prearranged record of files including keywords suggested during a query. Agent seeker [7] is a multi-agent platform that helps users to retrieve and index, web documents based on meta-search engine. The ITBIA is also devoted to practically execute a query coming from the rest of the platform, in particular from the query agent [7]. Our type of agent follows the four type of activity such as aggregation, remixing, repurposing, and sharing [8] to describe information retrieved from the web. Lin *et al.* [9] proposes a query expansion technique by mining extra query terms. They depend on the fuzzy rules to compute the weights of the additional query terms. They use these additional query terms along with the original query terms for refining the performance of search systems. Ciaramita *et al.* [10] uses a hierarchical learning architecture to define lexical semantic classification for formulate a semantic query by mining training sentences from a dictionary ontology—Word Net. Akrivas *et al.* [11] based on an inclusion relation, suggest a query expansion method which is built as a fuzzy set of semantic entities. They use the user's profile to personalize the query. In contrast, Razek *et al.* [12] uses dominant meaning to determine the meaning of text retrieved from Google. Based on dominant meaning, he used dominant meaning to individualize a query and search result. Google uses query expansion to enable the search to routinely give additional terms to a user's search query. When query

expansion is enabled, the appliance can expand two types of terms: words that share the same word stem as the word given by the user. For example, if a user searches for "engineer", the appliance could add "engineers" to the query. Terms of one or more space-separated words those are synonymous or closely related to the words given by the user. For example, if a user searches for "office building", the query could expand to include "office tower" [13]. In contrast, our methodology of expansion is built on the dominant meaning of the query. Accordingly, if the query is about "engineer", the proposed search engine combines "computer engineer" to the query.

MOOCs is an open access web-based courses built on the typical quality of a behaviorist, cognitivist, and connectivist philosophy. MOOCs are built upon conventional online learning techniques but, scaled to a large number of students and backed up by a strong technology medium. Daniel [14] divides MOOCs into two categories: one is connectivism-based and the second is extensions of conventional online courses. Kop *et al.* [8] emphasizes that connectivist MOOCs have four types of activity, such as aggregation, remixing, repurposing, and sharing. Based on the same idea, our proposed agent has a typical action. MOOCs' students feel to be alone in the process of learning because MOOCs focus on teaching more than learning. With MOOCs, the interaction between students and teacher is lost, overcome this interaction with peer forums, where student can contribute with questions and receive answers from their classmates.

Based on similar methods for social networking strategies, MOOCs use benefits of subject matter experts to engage students with others throughout the world with some organizing subgroups specific to their learning goals [15]. The first trying to offer a free MOOC course was in 2011 by a group of universities such as the University of Pennsylvania, Princeton University, Stanford University, and the University of Michigan [16]. In 2012, the MIT and Harvard University came mutually to offer a free course with the same manner. In 2013, the American Council on Education (ACE) recommended that institutions grant credit for five online courses on Coursera [3]. These collections of world-class universities have caused the start of increasingly greater interest among higher education leaders in such massive open online courses. However, video lectures are the fundamental of MOOCs, there are other technologies used to create a rich learning environment by combining PowerPoint slides, notes, or animated illustrations on digital whiteboards [17].

MOOCs try to maximize the usage of the asynchronous discussion forums to reimburse for the lack of synchronous interaction [17]. Other than video lectures, one of the characteristics of MOOCs is reducing instructor contact with individual students; students frequently depend on self-organized study and collaborative learning [16]. Gillet [18] uses a Connectivist MOOCs platform to create Personal Learning Environments (PLE). PLE platform is designed for fully self-regulated learning activities. The social media features are built-in PLE to boost opportunistic interaction and informal exchanges between students. PLE satisfies Kop activities and presents more media related to the topic taught. MOOCs provide influence technologies to create a rich learning environment by adding in some components, such as, professor speaking directly to the camera while accompanied by PowerPoint slides, notes, or animated illustrations on digital whiteboards [17]. Massis [4] mentions that MOOCs may give students the chance to offer the learning for all people anytime and anywhere. He also discovers that the development of MOOCs is built as an integral component and librarians have a chance to extend their influence. He finds that MOOCs is in need for more learning resources to help students in acquisition more knowledge.

3. Intelligent Topic-Based Information Agent Overview

The goal this section is to present the roles of the proposed intelligent agents to create advanced AI programs that can function usefully in web environment. Agent technologies are applied successfully on environments where it is dangerous or where it is difficult to place human being. It is clear that the choice of information agents to help in retrieving learning recourses from the internet is because the internet is virtual environment which do not exist in our physical live. The human needs huge amount of time to just read or analysis, remark a part of the information coming from the internet. Such environment needs an intelligent agent to retrieve suitable information to meet every user's needs.

The Intelligent Topic-Based Information Agent (ITBIA) is devoted to control the metadata coming from the internet of the topic domain, and organize the results of a topic's query. This mechanism is a conceptual model that defines the structure and behavior of the ITBIA agent. **Figure 1** illustrates ITBIA architecture and the flow of how it works. ITBIA platform works like a meta-search engine. Intelligent Topic-Based Information Agent follows the following stages:
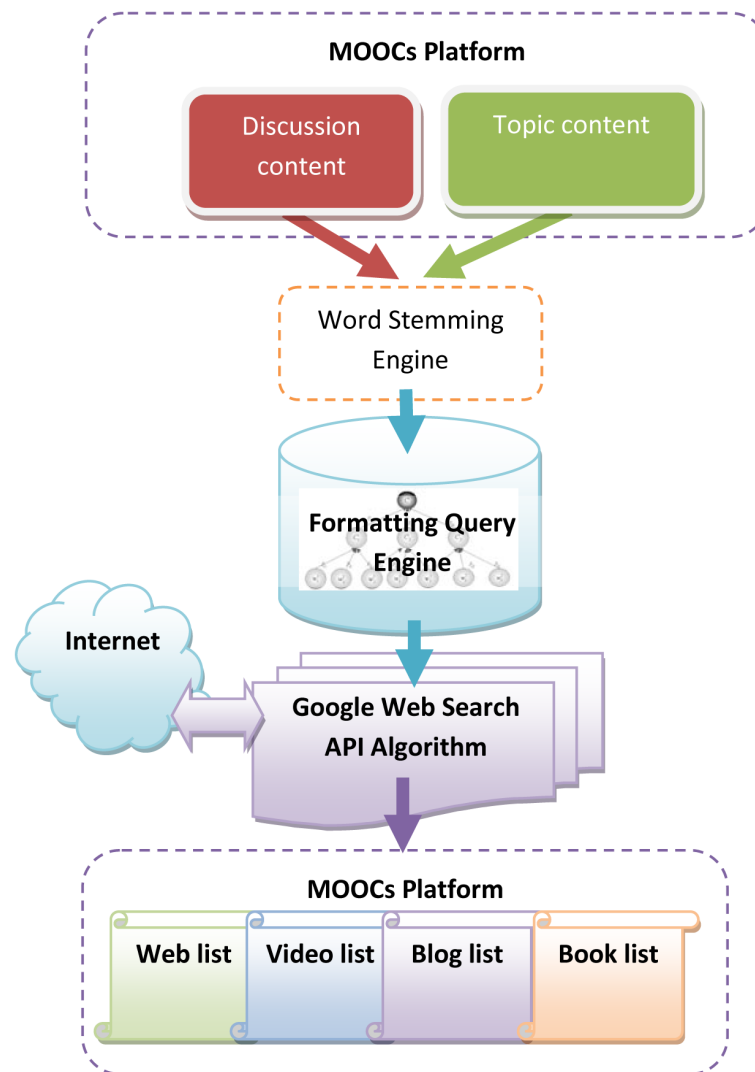
Figure 1. Intelligent topic-based information agent.

- **Extracting Query**—this is to extract some words from the discussion between learners, stem, filter, and eliminate stop words. All MOOCs courses include pre-recorded video lectures, and almost all courses have textual course material (e.g. video transcripts) included blank-audio described the video lectures. In each course, students will also have access to a discussion forum, where he/she can ask questions of course staff and discuss the course topics with his/her peers. The ITBIA has two tasks: building hierarchy of dominant meanings, and constructing a query. The methodology of building hierarchy of dominant meanings, and constructing a query are described on the next section.
- **Formatting Query**—this is to reformulating the query based on the dominant meaning technique. The concept of the query is constructed from a discussion between MOOCs' students and the application domain of the topic taught.
- **Dispatch Query**—this is to send the query to. It uses Google Web Search API, rather than using a set of online engines. ITBIA is configured search across Google for different types of search such as local search, web search, video search, blog search, news search, image search, and book search [13].
- **Display Results**—this is to employ and re-rank the results into a uniform format for displaying to learners and deleting duplicates. According to the versatility of the content on the web, it makes sense for us to use Google Web Search API to retrieve a diversity of media related to topic taught in MOOCs. After formatting the query, it is sent to Google by the Google Web Search API Algorithm (GWSAPI). GWSAPI is embedded

as a JavaScript in MOOCs webpage.

The user interface of ITBIA is built as a dynamic search box in a simulation of Coursera webpage downloaded in our Apache server, as pictured in **Figure 2**. The MOOCs platform contains the user interface of ITBIA. The user interface of ITBIA is built as a dynamic search box in a simulation to Coursera webpage downloaded in our Apache server. After formatting the query, it is sent to Google by the Google Web Search API Algorithm (GWSAPI). GWSAPI is embedded as a JavaScript in a tested MOOCs webpage in our server. The course in of Blended Learning: Personalizing Education for Students created by [19]. The ITBIA demonstrates search results in MOOCs webpage classified by its format and its importance.

3.1. Intelligent Topic-Based Information Agent Methodology

The approach described in this section employs the approach used to create dominant meaning query and is similar to the other works cited before, in particular [12] and [20], however, it is inspired by a specific application domain coming from textual course material (e.g. video transcripts) in MOOCs. The framework of MOOCs Tutors Agent consists of the following operations: drag some words from the discussion between learners, get the corresponding dominant meanings of the current concept, build a query related to the set of words reformulated from the dominant meaning tree, and re-rank the results.

3.1.1. Dominant Meaning Method for Constructing Hierarchy Tree

In this subsection, we present methodology of a query construction to retrieve the most likely document on line to match the topic been taught.

The proposed approach is applied on "Blended Learning: Personalizing Education for Students" MOOCs course through Coursera. The course is offered to anyone with a strong interest in blended learning, participants from the education technology sector, or non-profits sectors [21]. It deals with how to explore the topics of blended learning and how to develop blended learning models. It describes some various types of blended learning models and the best practices from real schools using these models.

The course includes pre-recorded video lectures along with video transcripts for the audio-back. In the course, participants have access to a discussion forum, where they can ask questions and discuss topics with other contributors.

To build the dominant meaning tree, we identify the topic of each class, and use video transcripts as a set of documents for each topic in this domain [20]. Stop words are those that occur commonly but are too general—such as "*the*, *is*, *on*, *or*, *of*, *how*, *why*, etc". Those words were developed as a list and removed from the collection. Consider that the course contains m topics $\{T_k\}_{k=1}^{m}$. Each topic is represented by a given set of concepts represented by video transcript $T_k = \{C_{j,k} \mid j = 1, \cdots, r\}$. Each video transcript is represented by a set of words
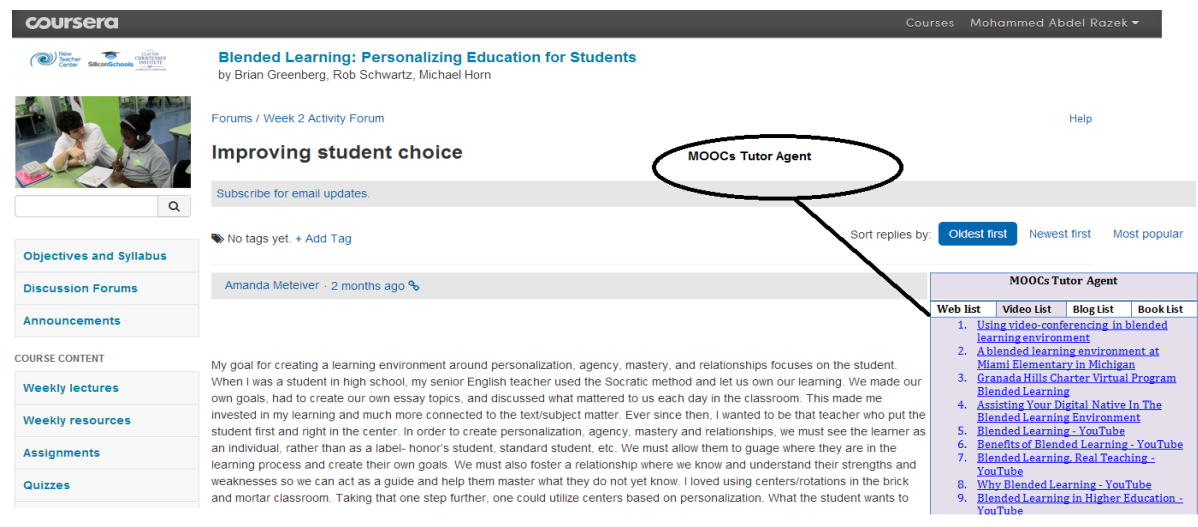
Figure 2. Coursera platform with embedding MOOCs tutors agent.

$C_{j,k} = \{w_{i,j,k} | i = 1, \cdots, n_{j,k}\}$, where $w_{i,j,k}$ represents the frequency of word w_j occurs in document C_k and topic T_k. To formulate the query, we need to choose top five words that match the top values of the Dominant Meaning Probability (DMP). Where the dominant meaning probability is defined as, and as shown in **Figure 3**:

$$P_{i,j,k}\left(w_i | C_j, T_k\right) = 1 - \frac{1}{\ln(2)}\left|\ln\left(\frac{w_{i,j,k}}{n_{j,k}}\right)\right| \tag{1}$$

where $i = 1, \cdots, n_{j,k}$, $j = 1, \cdots, r$, $k = 1, \cdots, m$, and $0 \le P_{i,k,j}\left(w_j | C_k, T_i\right) \le 1$.

Accordingly, a function called $\Psi_{j,k}$ Total Value of the Concept is calculated as follows:

$$\Psi_{j,k}\left(C_j, T_k\right) = \frac{1}{n_{j,k}}\left[\sum_{i=1}^{n_{j,k}} P_{i,j,k}\left(w_i | C_j, T_k\right)\right] \tag{2}$$

where $j = 1, \cdots, r$, $k = 1, \cdots, m$.

3.1.2. How ITBIA Formatting Query

The ITBIA gets some words through discussion between learners; the dilemma is to represent the query and discover which topic properly represents these words. To improve the query, ITBIA do not intentionally give attention to common words called stop words. The stop words are the words that they are not strongly affected on a search, and therefore they can significantly be got rid. To formulate the query, the ITBIA traverses the Dominant Meaning Tree in **Figure 3** using the formatting query algorithm. The algorithm starts with the word represents the topic T_k node as starting point. It choose the concept C_k which has a biggest value of the function $\Psi_{j,k}$, and then choose a word which has a biggest value of a $P_{i,k,j}$ till it find the matching word, and then formulate the query from its siblings.

Formatting Query Algorithm (Word w, Topic T_k, $\Psi_{j,k}$, $P_{i,k,j}$)
1. Sort $\Psi_{j,k}$ Descending according to *j*, Return $\Psi - List$;
2. Sort $P_{i,k,j}$ Descending according to *i*, Return $P - List$;
3. While $\Psi - List \ne$ [ ] do begin
   1. Remove the first concept from $\Psi - List$, call it X.
   2. While $P - List$ in concept X $\ne$ [ ] do begin
      1. Remove the first word from $P - List$ in concept X, call it Wx.
      2. If Word w matches Wx, announce success.
      3. Return words in the list $P - List$.

3.1.3. Re-Ranking Web Objects Results

Our proposed probability definition should improve retrieval effectiveness by making imposing some constraints on submitted queries and retrieved documents. Following the above Formatting Query Algorithm, suppose that the algorithm return the concept C_l, therefore the query is represented by the vector $V\left(w_{1,l,k}, w_{2,l,k}, \cdots, w_{M,l,k}\right)$. In general, the results of the query is represented by web objects $\{D_s\}_{s=1}^{s=R}$. These web objects are divided by four categories based on Google API search such as the images list, web list, video list, and blog list. To filter the stream of the research results, we evaluate the importance of each document
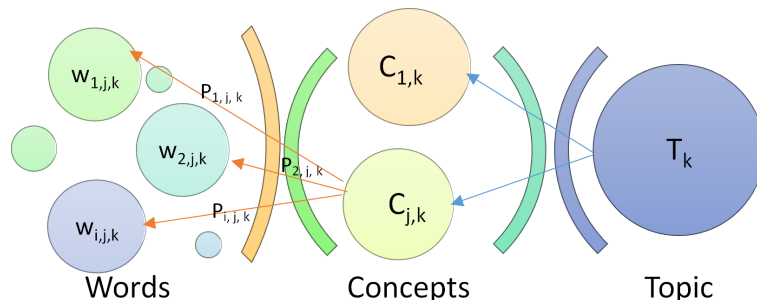

Figure 3. Dominant meaning tree.

against the query. The distance meaning function $Dis(D_s|C_l)$ is to compute the relevance of document D_s to the concept C_l, as follows:

$$Dis(D_s|C_l) = \frac{1}{M}\left[\sum_{j=1}^{j=M}\frac{F(w_{j,l,k}|D_s)}{F_s}\right] \tag{3}$$

where, $F_s = \max_{j=1,\cdots,M}\left\{F(w_{j,l,k}|D_s)\right\}$, $\forall s = 1,\cdots,R$; where, the function $F(w|D)$ represents the frequency of the word w which appears in document.

4. Experimental Evaluation of ITBIA

There are two experiments conducted on the Intelligent Topic-Based Information Agent: one to measure the improvement in the retrieval effectiveness and the other measures the impact of ITBIA on the learning using it through MOOCs and whether retrieved materials are relevant to students. The paper used the distance meaning function defined in the previous section to determine which document is relevant and which is not relevant from the document retrieved using Google Web Search API. Therefore, it used a precision to examine the performance of the ITBIA to retrieve relevant documents. The "Precision" measure can be defined as follows [22]:

$$\text{Precision} = \frac{\text{The number of retrieved relevant documents}}{\text{The number of retrieved documents}}$$

The definition is considered that the precision is the fraction of retrieved documents that are relevant to the find.

4.1. Data Set

The data set is collected using Google Web Search API Google. The dataset collected is contain 697 web objects. We take one month from Feb. 2014 to March 2014 to collect and classify the data. **Table 1** presents their main features and the number of documents and it is categorized into 4 classes and 5 query concepts.

4.1.1. Effectiveness of the Methodology Used in ITBIA

This experiment is conducted to show the effectiveness of the methodology used in searching in ITBIA. The experiment is to compare our different query expansion methods, referring to previous section for the relative performances. We used the materials of a course named "Blended Learning: Personalizing Education for Students" in Coursera [21] to build the dominant meaning tree. We used video transcripts for each six domain in the course as a training set for building the concepts and its related words in the tree.

Based on the definition of the Distance Meaning Function, we consider the document D is relevant if $0.5 \le Dis(D|C) \le 1$ and is irrelevant if $0 \le Dis(D|C) < 0.5$.

The results are filtered and classified based on Google Web Search API, such as web list, video list, blog list, and book list. Later, the distance meaning values are calculated for the four lists for both query without expansion, and query dominant meaning expansion using Equation (2). **Table 2** shows performance improvement when the query is expanded by using dominant meanings.

Table 1. Number of document in data set.

Concepts		Web objects				Total
		Web list	Video list	Blog list	Book list	
Q1	Blended learning models	49	37	25	24	135
Q2	Role of the student	44	38	32	33	147
Q3	Role of the teacher	38	35	31	29	133
Q4	Change at the school level	47	37	33	31	148
Q5	Hardware, software and space	41	35	31	27	134
	Total	219	182	152	144	697

Table 2. Number of document in data set based on the dominant meanings.

	Concepts	Web objects			
		Query without expansion		Query dominant meaning expansion	
		Irrelevant	Relevant	Irrelevant	Relevant
Q1	Blended learning models	55	80	21	114
Q2	Role of the student	80	67	40	107
Q3	Role of the teacher	77	56	34	99
Q4	Change at the school level	83	65	39	109
Q5	Hardware, software and space	89	45	37	97
	Total	384	313	224	473

Figure 4 summarizes the results of using our dominant meaning query expansion methods, measuring their relative performance in terms of the number of relevant documents retrieved. It seems that the dominant meaning methods which take into consideration the meaning of the query are better than the traditional expansion for the query.

Based on these results, the query without expansion did not provide any noticeable performance improvement for any of the five topics. However, the best result for the measure was at the topic "blended learning models" in **Figure 4**. We believe this is because the Blended learning subject is popular topic on the web. In the same result, the topic "hardware, software and space" has the lowest average value among the topics. In general, our expansion using dominant meaning shows high performance, and it improves the results with around 38% more than the result without expansion.

Table 3 and **Figure 5** show the performance of the dominant meaning in terms of the precision of results. They display the precision of the results of the original queries and with the dominant meaning query expansion. In general, the performance of search results with the dominant meaning query expansion has precision higher than the search results without query expansion.

Apparently, the improving in the query of the blended learning concept gains (0.84) considered as a highest value precision. Obviously, the well-known terms online contains more domain knowledge than the small ones. Accordingly, it seems that the performance increases with the importance of the topic online. It is possible to return this growing to the huge number of web sites that contain books related to the subject of the blended learning. Moreover, it can be seen easily that the improvement in the five concepts are 25%, 27%, 32%, 29%, and 38% "blended learning models", "role of the student", "role of the teacher", "change at the school level", "hardware, software and space", respectively. In addition, the average improvement for all topics and lists is around (30%) which is considerable results based on the high quality of the Google search engine and its fast-paced work environment.

4.1.2. The Impact of ITBIA on the Learning Using It through MOOCs

This section investigates ITBIA effectiveness factors influencing learner satisfaction on the learning session through MOOCs. Effectiveness investigation measures how well ITBIA achieves its objective. It is expected that effectiveness investigation is correlated with learner satisfaction. Seventy distance learning students were recruited for this test; all participants were between the ages of 16 and 21 years old with a median age of 19. There were 70 students included 42 girls and 28 boys. A simulation web site was created to mimic coursera course "Blended Learning: Personalizing Education for Students" [21]. The website was hosting on our Apache server, and the students were invited to navigate the course and answer on a questionnaire. An online survey is conducted, and 10 questions are returned, as shown in **Table 4**. The survey included 5-point LIKERT type scale, which has been anchored to measure all of the scales with the statements: "Strongly Disagree" = 5, "Disagree" = 4, "Neutral" = 3, "Agree" = 2 and "Strongly Agree" = 1.

As shown in **Figure 6**, the results indicate that there were significant in the response of the learner that ITBIA gives more courses materials which were relevant and useful. Learners were asked if they thought that ITBIA was valuable for learning session and helped students to have valuable learning experiences during the course. A
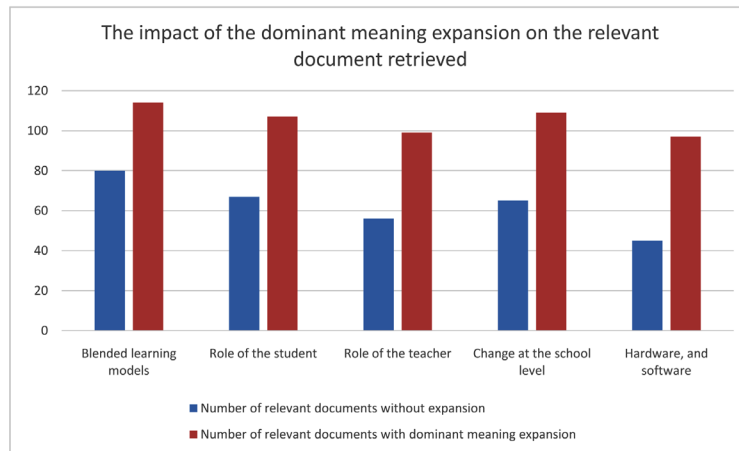
Figure 4. The impact of the dominant meaning expansion on the relevant document retrieved.
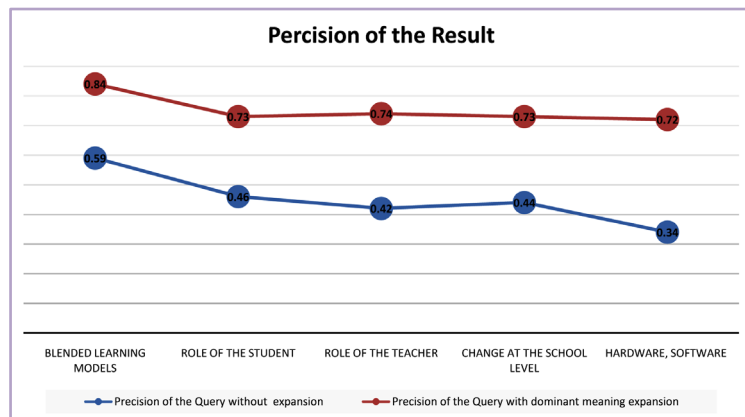

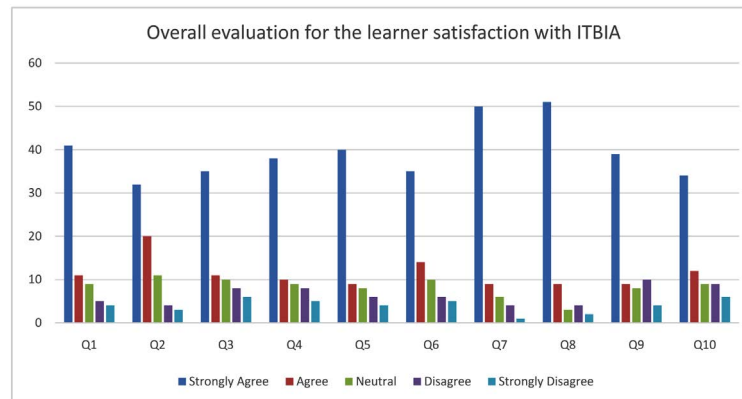**Figure 5.** Precision of the results.

Figure 6. Overall evaluation for the learner satisfaction with ITBIA.

significant majority (84%) included who agreed and strongly agreed confirmed that it is valuable, while seven percent included who strongly disagreed and disagreed responded no.

When learners were asked if the ITBIA's web search results helped them in the learning session. There was 87% included who agreed and strongly agreed reported that it helped them, while 9% included who disagreed and strongly disagreed of learners indicated that the ITBIA could not help them. During the survey, learners

Table 3. Precision of the results.

	Query concept	Precision of the query without expansion	Precision of the query with dominant meaning expansion	Improvement in the precision
Q1	Blended learning models	0.59	0.84	0.25
Q2	Role of the student	0.46	0.73	0.27
Q3	Role of the teacher	0.42	0.74	0.32
Q4	Change at the school level	0.44	0.73	0.29
Q5	Hardware, software and space	0.34	0.72	0.38

Table 4. Criteria of evaluating learner satisfaction for ITBIA.

Question number	Criteria
Q1	I think ITBIA gives more courses materials which were relevant and useful
Q2	I think ITBIA helps me to have valuable learning experiences from my courses
Q3	I think ITBIA's web search results helped me in the learning session
Q4	The procedure of search in ITBIA was clearly presented
Q5	It is easy for me to complete the learning session by using ITBIA
Q6	The ITBIA encouraged me to become actively involved in the Coursera discussions
Q7	I think ITBIA is needed to massive open online courses
Q8	I think ITBIA's features are reliable
Q9	I think ITBIA's features are accessible
Q10	I can accomplish ITBIA tasks quickly

were asked if they thought that if it was easy for him to complete the learning session by using ITBIA. Results revealed 73% confirmed that it has flexible navigation. Where there was 15% responded no. Moreover, the respond on "the ITBIA encouraged me to become actively involved in the Coursera discussions" has an average of 70% on a scale of 1 (strongly agree) along with the scale of "agree" while there was 16% who do not agree along with strongly disagree.

Finally, to test the entire survey, we use Cronbach's alpha. The test is to be conducted on all subscales combined. The reliability coefficient for the instructor subscale is for this test is 0.91 which it indicates a good internal consistency.

5. Conclusion

In this paper, we described Intelligent Topic-Based Information Agent that autonomously creates a query, searches the web, retrieves information, resorts the results, and recommends contents to users of the massive open online courses. The research results clearly establish the potential of using agent technology to improve the performance of retrieving well-suited information from the web according to topic which has been taught. Using information agent technology in this paper provides users with an effective way of finding out required results from Google search engine. To overcome these challenges, the framework of Intelligent Topic-Based Information Agent was presented and the algorithm of the query expansion technique was presented and implemented. Two experiments were conducted on the Intelligent Topic-Based Information Agent: one measures the improvement in the retrieval effectiveness and the other measures the impact of ITBIA on the learning using it through MOOCs. The first experiment gave a test query based on the topic taught in the proposed course in Coursera; our result indicated gains in average of roughly 30% with regard to the precision test. The second experiment showed the significance of using ITBIA on the learning session of MOOCs. In general, the result showed that the proposed agent performs efficiently.

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