Optimal Cascade Linguistic Attribute Hierarchies for Information Propagation

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Abstract— **A hierarchical approach, in which a high-dimensional model is decomposed into series of low-dimensional sub-models connected in cascade, has been shown to be an effective way to overcome the 'curse of dimensionality' problem. The upwards propagation of information through a cascade hierarchy of Linguistic Decision Trees (LDTs) based on label semantics forms a process of cascade decision making. In order to examine how a cascade hierarchy of LDTs works compared with a single LDT for multiple attribute decision making, we developed genetic algorithm with linguistic ID3 in wrapper to find optimal cascade hierarchies. Experiments have been carried out on the two benchmark databases, Pima Diabetes and Wisconsin Breast Cancer databases from the UCI Machine Learning Repository. It is shown that an optimal cascade hierarchy of LDTs has better performance than a single LDT. The use of attribute hierarchies also greatly reduces the number of rules when the relationship between a goal variable and input attributes is highly uncertain and nonlinear. Moreover, the cascade linguistic attribute hierarchy presents cascade transparent linguistic rules, which will be useful for analyzing the effect of different attributes on the decision making as a reference in a special application.**

Keywords: cascade linguistic attribute hierarchy, information propagation, cascade decision making, Genetic algorithm in wrapper, Linguistic ID3

1 Introduction

For multiple attribute decision making, the underlying relationship between attributes and the classification or decision variable is often highly uncertain and imprecise. This requires an integrated treatment of uncertainty and fuzziness when modeling the propagation of information from low-level attributes to high-level goal variables. One of the main drawbacks to fuzzy modeling of systems is known as the 'curse of dimensionality', which is the exponential growth in the number of possible fuzzy rules as a function of the dimension of model input space. A hierarchical approach in which the original high-dimensional model is decomposed into series of low-dimensional sub-models connected in cascade, has been shown to be an effective way to overcome this problem since it provides a linear growth in the number of rules and parameters as the input dimension increases [12]. Campello and Amaral presented a unilateral transformation that converts the proposed hierarchical model into a mathematically equivalent non-hierarchical one [2]. As a result of the uncertainty and non-linear relationship between different attributes and a goal variable, different cascade hierarchies will have different performance on decision making procedures. We have proposed a general multiple attribute hierarchy embedded with Linguistic Decision Trees (LDTs) based on Label Semantics [7]. In this paper, we propose a cascade hierarchy approach embedded with LDTs representing transparent rules, and describe the process of information propagation through a cascade hierarchy. We then develop a genetic algorithm with the Linguistic ID3 (LID3) [9] algorithm in wrapper to optimise cascade hierarchies. The experiments are performed on benchmark databases from the UCI Machine Learning Repository.

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2 Label Semantics

Label semantics [5, 6] proposes two fundamental and interrelated measures of the appropriateness of labels as descriptions of an object or value. Given a finite set of labels $\mathcal{L}$ from which can be generated a set of expressions LE through recursive applications of logical connectives, the measure of appropriateness of an expression $\theta \in LE$ as a description of instance x is denoted by $\mu_\theta(x)$ and quantifies the agent's subjective belief that θ can be used to describe x based on his/her (partial) knowledge of the current labelling conventions of the population. From an alternative perspective, when faced with an object to describe, an agent may consider each label in $\mathcal{L}$ and attempt to identify the subset of labels that are appropriate to use. Let this set be denoted by $\mathcal{D}_x$. In the face of their uncertainty regarding labelling conventions the agent will also be uncertain as to the composition of $\mathcal{D}_x$, and in label semantics this is quantified by a probability mass function $m_x : 2^{\mathcal{L}} \rightarrow [0, 1]$ on subsets of labels. The relationship between these two measures will be described below.

Unlike linguistic variables [14], which allow for the generation of new label symbols using a syntactic rule, label semantics assumes a finite set of labels $\mathcal{L}$. These are the basic or core labels to describe elements in an underlying domain of discourse Ω. Based on $\mathcal{L}$, the set of label expressions LE is then generated by recursive application of the standard logic connectives as follows:

Definition 2.1 *Label Expressions*
The set of label expressions LE of $\mathcal{L}$ is defined recursively as follows:

• *If* $L \in \mathcal{L}$ *then* $L \in LE$
• *If* $\theta, \varphi \in LE$ *then* $\neg\theta, \theta \wedge \varphi, \theta \vee \varphi \in LE$

A mass assignment m_x on sets of labels then quantifies the agent's belief that any particular subset of labels contains all and only the labels with which it is appropriate to describe x.

Definition 2.2 *Mass Assignment on Labels*
$\forall x \in \Omega$ *a mass assignment on labels is a function* $m_x : 2^{\mathcal{L}} \rightarrow [0,1]$ *such that* $\sum_{S \subseteq \mathcal{L}} m_x(S) = 1$

Now depending on labeling conventions there may be certain combinations of labels which cannot all be appropriate to describe any object. For example, *small* and *large* cannot both be appropriate. This restricts the possible values of $\mathcal{D}_x$ to the following set of focal elements:

Definition 2.3 *Set of Focal Elements*
Given labels $\mathcal{L}$ *together with associated mass assignment* m_x : $\forall x \in \Omega$, *the set of focal elements for* $\mathcal{L}$ *is given by:*

$$\mathcal{F} = \{S \subseteq \mathcal{L} : \exists x \in \Omega,\ m_x(S) > 0\} \tag{1}$$

The appropriateness measure, $\mu_\theta(x)$, and the mass m_x are then related to each other on the basis that asserting 'x is θ' provides direct constraints on $\mathcal{D}_x$. For example, asserting 'x is $L_1 \wedge L_2$', for labels $L_1, L_2 \in \mathcal{L}$ is taken as conveying the information that both L_1 and L_2 are appropriate to describe x so that $\{L_1, L_2\} \subseteq \mathcal{D}_x$. Similarly, '$x$ is $\neg L$' implies that L is not appropriate to describe x so $L \notin \mathcal{D}_x$. In general we can recursively define a mapping $\lambda : LE \rightarrow 2^{2^{\mathcal{L}}}$ from expressions to sets of subsets of labels, such that the assertion 'x is θ' directly implies the constraint $\mathcal{D}_x \in \lambda(\theta)$ and where $\lambda(\theta)$ is dependent on the logical structure of θ. For example, if $\mathcal{L} = \{low,\ medium,\ high\}$ then $\lambda(medium \wedge \neg high) = \{\{low, medium\}, \{medium\}\}$ corresponding to those sets of labels which include $medium$ but do not include $high$. Hence, the description $\mathcal{D}_x$ provides an alternative to Zadeh's linguistic variables in which the imprecise constraint 'x is θ' on x, is represented by the precise constraint $\mathcal{D}_x \in \lambda(\theta)$, on $\mathcal{D}_x$.

Definition 2.4 λ*-mapping* $\lambda : LE \rightarrow 2^{\mathcal{F}}$ *is defined recursively as follows:* $\forall \theta,\ \varphi \in LE$
• $\forall L_i \in \mathcal{L}\ \lambda(L_i) = \{F \in \mathcal{F} : L_i \in F\}$
• $\lambda(\theta \wedge \varphi) = \lambda(\theta) \cap \lambda(\varphi)$
• $\lambda(\theta \vee \varphi) = \lambda(\theta) \cup \lambda(\varphi)$
• $\lambda(\neg\theta) = \lambda(\theta)^c$

Therefore, based on the λ-mapping we define the appropriateness measure as below:

Definition 2.5 (Appropriateness Measure)
Appropriateness measure $\mu_{\theta(x)}$ *is evaluated as the sum of mass assignment* m_x *over those subsets of labels in* $\lambda_\theta(x)$, *i.e.* $\forall \theta \in LE, \forall x \in \Omega, \mu_{\theta(x)} = \sum_{F \in \lambda(\theta)} m_x(F)$.

For example, if $\mathcal{L} = \{low, medium, high\}$ with focal sets $\{\{l\}, \{l, m\}, \{h\}\}$ and $\theta = low \wedge \neg medium$ then $\mu_{l \wedge \neg m}(x) = \sum_{F : l \in F, m \notin F} m_x(F) = m_x(\{l\})$.

3 A cascade linguistic attribute hierarchy

3.1 Definition of a cascade hierarchy

The process of aggregation of evidence in multi-attribute decision problems based on attributes $x_1, ..., x_n$ can be viewed as a functional mapping between a high level variable y and input attributes, $y = f(x_1, ..., x_n)$, which is often dynamic and nonlinear, and may be imprecisely defined. In some cases, the function f may be approximated by a composition of lower dimensional sub-functions, forming a cascade hierarchy (a binary tree). Each sub-function represents a new intermediate attribute. Figure 1 shows a simple cascade hierarchy. There are $n-1$ intermediate attributes produced. The last intermediate attribute z_{n-1} corresponds to the goal variable y. The cascade relationship is expressed as following:

$$z_i = \begin{cases} F_1(x_1, x_2) & i = 1, \\ F_i(z_{i-1}, x_{i+1}) & n > i > 1. \end{cases} \tag{2}$$

As proposed in [7], in a linguistic attribute hierarchy, func-

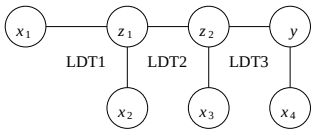

Figure 1: A cascade hierarchy of LDTs

tion mappings between parent and child attribute nodes are defined in terms of weighted linguistic rules which explicitly model both the uncertainty and vagueness which often characterises our knowledge of such aggregation functions. These rules will be defined as conditional expressions in the label semantics framework [6] weighted by conditional probabilities. For each attribute, a set of labels and subsequent label expressions is defined. We assume that expressions describing a parent attribute can be (imprecisely) defined in terms of a description of its children. Let $\mathcal{L}_i$, θ_i and $\mathcal{F}_i$ denote the set of labels, a label expression and focal sets respectively, defined for attribute x_i for $i = 1, ..., n$. Similarly, let $\mathcal{L}_y$, θ_y and $\mathcal{F}_y$ denote the label set, a label expression and focal set for describing the goal variable y, respectively.

More precisely, the weighted conditional rules can take the form of an LDT. In an LDT, the nodes are attributes, and the edges are label expressions describing each attribute. The depth of an LDT with two input attributes is at most 2. A branch B is a conjunction of expressions $\theta_1 \wedge \theta_2$, where θ_1 and θ_2 are the label expressions of the two edges on the branch B, respectively. Each branch also is augmented by a set of conditional mass values $m(F|B)$=$P(C_x = F|B)$, for each output focal element $F \in \mathcal{F}_y$. Then the rules corresponding to the

branch B would be: $\theta_1 \wedge \theta_2 \rightarrow F : m(F|B)$ for each focal element $F \in \mathcal{F}_y$.

3.2 Upwards propagation of information

The upwards propagation of information through a cascade hierarchy of Linguistic Decision Trees (LDTs) based on label semantics forms a process of cascade decision making. Figure 1 shows the process of bottom-up information propagation through the cascade hierarchy. The only information available regarding the mappings F_1, F_2 and F_3 is in the form of decision trees LDT_1, LDT_2 and LDT_3, which define mapping functions for z_1 in terms of those for x_1 and x_2, for z_2 in terms of those for z_1 and x_3, and for y in terms of those for z_2 and x_4.

However, it is not easy to define the labels for intermediate attributes in terms of their children, as the intermediate attributes are not directly related to basic attributes in the system [2]. Therefore, we suppose all intermediate attributes are approximations of the decision variable y with the same domain and description labels. According to Jeffrey's rule [4], given an LDT, the mass assignment of the decision variable can be calculated by:

$$m_{z_i}(F_y) = \begin{cases} \sum_{j=1}^{t_1} \mu_{\theta_1}(x_1)\mu_{\theta_2}(x_2)m(F_y|B_{i_j}), & i = 1 \\ \sum_{j=1}^{t_i} \mu_{\theta_1}(z_{i-1})\mu_{\theta_2}(x_{i+1})m(F_y|B_{i_j}), & i > 1 \end{cases} \quad (3)$$

where, B_{i_j} is the j^{th} branch in the i^{th} LDT, and $\mu_\theta(x)$ is appropriateness measure, quantifying the degree of our belief that label expression θ is appropriate for x [6]. The appropriateness measure can be calculated with mass assignments of attribute x according to Definition 2.5.

Information is propagated along the cascade LDTs from low level to high level. For the example in Figure 1, given mass functions m_{x_1}, m_{x_2},m_{x_3}, and m_{x_4}, the mass function m_{z_1} is determined by propagating m_{x_1} and m_{x_2} through LDT_1, m_{z_2} is determined by propagating m_{z_1} and m_{x_3} through LDT_2, and finally, m_y is determined by propagating m_{z_2} and m_{x_4} through decision tree LDT_3 (see Figure 2). Here we consider only classification problems where the goal variable y belongs to the finite set of classes $\{C_1, ..., C_t\}$. In this case, $\mathcal{F} = \{\{C_1\}, ..., \{C_t\}\}$, and for input vector $\vec{x}$, $m_y(\{C_i\}) = P(C_i|\vec{x})$.

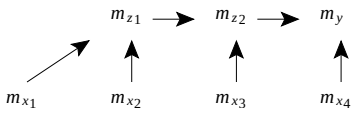

Figure 2: The cascade upwards information propagation

4 GA in wrapper to optimise cascade hierarchies

4.1 Chromosomes and Reproduction

To learn a linguistic cascade hierarchy, we use a genetic algorithm as a search agent with the LID3 as an induction algorithm in wrapper. For the optimisation of cascade hierarchies with n attributes, the size of whole search space is $\frac{n!}{2}$. The performance of different hierarchies is judged on the basis of the accuracy for the given classification task.

Chromosomes: The purpose of a GA is to evolve a population of potential solutions each corresponding to the cascade hierarchies in a multiple-attribute space. Therefore, the GA in wrapper approach conducts a search in the space of possible cascade hierarchies. Different attribute orderings define different cascade hierarchies. So we define any possible permutation of all attributes, $\pi = \{x_1, ...x_n\}$, and $\pi \rightarrow \mathcal{H}$ as a genome of the genetic algorithm.

Reproduction: We use "*roulette-wheel*" selection, according to which, an individual with better fitness has higher probability of being selected. The probability that hierarchy $\mathcal{H}_i$ is selected is given by the nominalised fitness:

$$p_i = \frac{f_i(\mathcal{H}_i)}{\sum_{j=1}^{\Gamma} f_j(\mathcal{H}_j)}. \quad (4)$$

A one-elitism strategy is included since it keeps the current best individual in the next generation, and speeds up the convergence of the evolution process. On the other hand, in order to keep the diversity of solutions, a random hierarchy is generated in each generation.

We use two-point order crossover as follows (Figure 3): two parental permutations, π_1 and π_2, are chosen randomly depending on the probability chosen in 4. A continuous interval of the permutation π_1 is chosen, and also an interval starting at the same position and of the same length from π_2. The two parameters, '*starting position*' and '*length of interval*', are produced randomly. Two new permutations, π_1' and π_2', are created such that π_1' contains the interval from π_2 with the rest being the other elements of π_1 in the same order as they appeared in π_1. π_2' contains the interval from π_1 with the rest being the other elements of π_2 in the order as they were in π_2 (Figure 3). Mutation, which is the swapping of two randomly picked elements of a permutation, is carried out with some probability (m_rate) on each child in the population.

4.2 Evaluation and Termination Criteria

Here we only consider binary classification problem with two classes '+' and '-'. First, we investigate the ordinary accuracy on a threshold, which is the ratio of the number of correct classifications to the number of testing samples. When the estimated probability $p(C|\vec{x})$ (equivalent to $m_y(\{C\})$) that a sample with measurement vector $\vec{x}$ belongs to class C is larger than a threshold α, then that sample is classfied as C. Con-

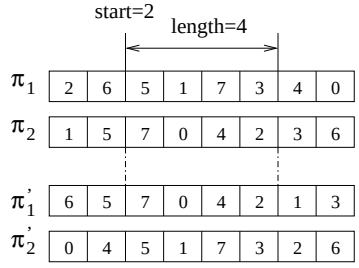

Figure 3: Two-point order crossover

ventionally we use 0.5 as a threshold. Here we consider two measures of accuracy, integrated accuracy and the area under ROC curve, which measures how well the classifier separates the two classes without reference to a decision threshold. The closer the ROC plot is to the upper left corner, the higher the ordinary accuracy of the test results.

For each possible threshold α for discriminating between the two classes, some positive cases will be correctly classified as positive (TP_α=number of True Positive), but some positive cases will be estimated as negative (FN_α=number of False Negative). On the other hand, some negative cases will be correctly classified as negative (TN_α=number of True Negative), but some negative cases will be classified as positive (FP_α=number of False Positive).

Accuracy: For a decision maker, the *Ordinary Accuracy* ($\mathcal{A}_\alpha$) over a threshold α can be calculated as below:

$$\mathcal{A}_\alpha(\mathcal{H}) = \frac{TP_\alpha + TN_\alpha}{\mathcal{M}}, \tag{5}$$

where, $\mathcal{M}$ is the number of test examples. In order to reduce the sensitivity to the threshold α, we define the integrated accuracy to be the integration of accuracies for all $\alpha \in [0.5, 1)$ (Formula (6)):

$$\mathcal{A}_{\tilde{\alpha}}(\mathcal{H}) = \int_{0.5}^{1} \frac{\mathcal{N}_\alpha}{\mathcal{M}} d\alpha \approx \frac{\Delta(\alpha)}{\mathcal{M}} \sum_{i=1}^{m} \mathcal{N}_{\alpha_i}, \tag{6}$$

where, the interval [0.5, 1) is divided into m subintervals with constant step length $\Delta(\alpha)$, and where $\mathcal{N}_{\alpha_i} = TP_{\alpha_i} + TN_{\alpha_i}$.

ROC curve: Receiver Operating Characteristic (ROC) analysis originated from signal detection theory and has been introduced to machine learning in recent years in order to evaluate algorithm performance in an imprecise environment. It is claimed [10] that ROC graphs can offer a more robust framework for evaluating classifier performance than traditional accuracy measure. The true positive rate is calculated with $\eta = \frac{TP}{P}$. The false positive rate is calculated with $\sigma = \frac{FP}{N}$. In a ROC curve, the true positive rate (η) is plotted as a function of the false positive rate (σ) for varing thresholds. Each point on a ROC plot represents a (η, σ) pair corresponding to a particular decision threshold.

Similarly, the integrated accuracy can be defined as the area under ROC curve, which measures how well the decision maker separates the two classes without reference to a decision threshold, as follows:

$$\mathcal{A}_{ROC}(\mathcal{H}) = \int_0^1 \eta d\sigma \tag{7}$$

Let $p(+|\vec{x})$ be the estimation of the probability that an instance with measurement vector $\vec{x}$ is positive. If we rank test instances according to increasing positive probabilities, then the area under the ROC curve ($\mathcal{A}_{ROC}$) for a decision making problem with two classes +,- can be calculated [3] by:

$$\mathcal{A}_{ROC} = \frac{\sum_{i=1}^{P} r_i - P(P+1)/2}{PN}, \tag{8}$$

where, P and N are the numbers of positive and negative samples, r_i is the rank of the i^{th} positive instance in the rank list according to the probabilities of the positive class.

Termination criteria: Termination is an important parameter, which affects the running time and quality of solutions. Generally it heavily depends on the size of the chromosome. The maximum generations max_gen is linear function of the number of basic attributes. The evolution procedure will be repeated until the maximum number of generations is reached.

4.3 LID3 algorithm for the induction of an LDT

In order to obtain an LAH embedded with LDTs, we need to train in turn all LDTs in the hierarchy. The LID3 algorithm [9] for training cascade LDTs is a black box as part of evaluation in the wrapper of the Genetic Algorithm. LID3, an extension of well-known ID3 algorithm [11], is used to build an LDT based on a given linguistic database. The search is guided by a modified measure of information gain in accordance with label semantics.

Definition 4.1 (Branch Entropy) *The entropy of branch B, for a given goal variable belonging to class set* $C = \{C_1, ..., C_t\}$*, is*

$$E(B) = -\sum_{i=1}^{t} P(C_i|B) log_2 P(C_i|B) \tag{9}$$

Given a branch B, suppose x_j is expanded to the branch B, then the Expected Entropy is defined as follows:

Definition 4.2 (Expected Entropy)

$$EE(B, x_j) = \sum_{F_j \in \mathcal{F}_j} E(B \cup F_j) P(F_j|B). \tag{10}$$

where, $B \cup F_j$ represents the new branch obtained by appending the focal element F_j to the end of branch B. The probability of F_j given B can be calculated as follows:

$$P(F_j|B) = \frac{\sum_{\vec{x} \in \mathcal{D}} P(B \cup F_j|\vec{x})}{\sum_{\vec{x} \in \mathcal{D}} P(B|\vec{x})}, \tag{11}$$

where, $P(B|\vec{x}) = \mu_B(\vec{x}) = \mu_{\theta_1}(x_1) * \mu_{\theta_2}(x_2)$, θ_1 and θ_2 are two label expressions associated with the two edges in the branch B, and x_1 and x_2 are incident to the two edges. Hence, the *Information Gain* can be calculated by:

$$IG(B, x_j) = E(B) - EE(B, x_j). \quad (12)$$

The most informative attribute will form the root of an LDT, and the tree will expand into branches associated with all possible focal elements of this attribute. For each branch, the free attribute with maximal information gain will be next node until the branch reaches the specified maximum depth or the maximum class probability arrives the given threshold. The process forms a level order traversal.

5 Experiments and Evaluation

All attributes are discretised using an entropy-based approach into three labels ($\mathcal{L} = \{small, medium, large\}$), respectively. Each label corresponds to a trapezoidal fuzzy set, which has 50% overlapping with neighbouring label fuzzy sets. A missing value of an attribute in an instance of the training database is replaced with the mean value of the attribute for the corresponding class.

The experiments are carried out using ten-fold cross validation. Data is split into 10 approximate equal partitions. Each one is used in turn for testing while the remainder is used for training i.e. 9/10 of data is used for training and 1/10 for testing. The whole procedure is repeated 10 times.

A trained hierarchy is evaluated using two types of accuracy measure described in Section 4.2. The ordinary accuracy is evaluated at threshold 0.5. The area under a ROC curve is calculated with Formula (8).

We examine the quality of cascade decision making and the cost of a hierarchy, i.e. the total number of branches from all decision trees in a cascade hierarchy, and compare the performance with that of a single LDT providing a direct mapping between input attributes and a classification variable.

5.1 On the Pima Diabetes database

The Pima database: The Pima Indian data set is a well-known benchmark problem from the UCI repository [1]. The problem relates to incidents of Diabetes mellitus in the Pima Indian population living near Phoenix Arizona. The target attribute is a binary valued decision variable indicating whether or not the patient shows signs of Diabetes according to World Health Organisation criteria. The database of Diabetes includes 768 samples, in which, 268 positive instances (with Diabetes), 500 instances without Diabetes. There are 8 basic attributes.

Solutions and Fitness values: The two orders of attributes corresponding to the optimal cascade hierarchies ($\mathcal{H}_1$ and $\mathcal{H}_2$) obtained by the GAW with fitness values evaluated by $\mathcal{A}_a$ and $\mathcal{A}_{ROC}$ respectively, are: $\mathcal{H}_1$: 3, 4, 2, 5, 6, 7, 0, 1; $\mathcal{H}_2$: 2, 4, 0, 6, 3, 5, 7, 1. Table 1 lists the accuracies at threshold 0.5 ($\mathcal{A}_a$), the integrated accuracies ($\mathcal{A}_{\tilde{a}}$), the areas under ROC curves ($\mathcal{A}_{ROC}$) and the numbers of branches (β) for $\mathcal{H}_1$, $\mathcal{H}_2$ and the single LDT. It can be seen that $\mathcal{H}_1$ and $\mathcal{H}_2$ achieve similar performance in $\mathcal{A}_a$, $\mathcal{A}_{\tilde{a}}$ and $\mathcal{A}_{ROC}$. Their performance in $\mathcal{A}_a$ and $\mathcal{A}_{ROC}$ is better than that of a single LDT, while the single LDT has higher integrated accuracy than $\mathcal{H}_1$ and $\mathcal{H}_2$. The branch numbers for $\mathcal{H}_1$ and $\mathcal{H}_2$ are much less than for the single LDT.

Table 1: Evaluations of hierarchies obtained by GAW on the Pima database

$\mathcal{H}$	$\mathcal{A}_a$	$\mathcal{A}_{\tilde{a}}$	$\mathcal{A}_{ROC}$	β
$\mathcal{H}_1$	0.747396	0.188281	0.783776	115
$\mathcal{H}_2$	0.748698	0.189437	0.790649	115
LDT	0.713542	0.244922	0.769687	14845

Accuracy and ROC curves: Figure 7 (a) and (b) show the accuracy and ROC curves for the two hierarchies and the single LDT, respectively. From the accuracy curves in Figure 7 (a), it can be seen that $\mathcal{H}_1$ and $\mathcal{H}_2$ obtain approximately the same accuracy curves, and achieve higher ordinary accuracies at threshold 0.5 than the single LDT does. But the accuracies obtained by $\mathcal{H}_1$ and $\mathcal{H}_2$ decrease as thresholds increase, and become smaller than for the single LDT when thresholds are over 0.65. Figure 7 (b) shows that the two optimal cascade hierarchies obtain similar ROC curves to the single LDT, although they have different performance in accuracies.

5.2 On the Wisconsin Breast Cancer Database

The Wisconsin Breast Cancer Database: The Wisconsin Breast Cancer (WBC) database [1] was created by Dr. William H. Wolberg from the University of Wisconsin Hospitals, Madison [8]. There are 699 samples, in which 458 samples are Benign, and 241 samples are Malignant. There are nine basic attributes, and each attribute is with lower bound 1 and upper bound 10. There are 16 instances that contain a single missing (i.e., unavailable) attribute value. It is claimed that the best result is 93.7% trained on 200 instances and tested on the other 169 in the first group of 369 samples with the 1-nearest neighbor approach in [1].

Solutions and Fitness values: The two permutations of attributes corresponding to the two optimal cascade hierarchies are: $\mathcal{H}_3$:6,2,4,3,8,7,5,1,0; $\mathcal{H}_4$:6,4,3,8,1,7,5,2,0. Table 2 lists the accuracies at threshold 0.5 ($\mathcal{A}_a$), the integrated accuracies ($\mathcal{A}_{\tilde{a}}$), and the areas under ROC curves ($\mathcal{A}_{ROC}$) and branch numbers (β) for $\mathcal{H}_3$, $\mathcal{H}_4$ and the single LDT. The experiment results show that $\mathcal{H}_3$ and $\mathcal{H}_4$ have similar performance in ordinary accuracies for different thresholds, and the areas under ROC curves. They have ordinary accuracies at threshold 0.5 better than a single LDT, but they lose performance in the integrated accuracy. The best ordinary accuracy at threshold 0.5 is 96.7% obtained by $\mathcal{H}_3$. Both algorithms for learning a single LDT and a cascade hierarchy have computational com-

plexity $O(n\beta)$, where n is the length of a branch and β is the total number of branches. Table 2 shows that the number of branches for the optimal cascade hierarchies $\mathcal{H}_3$ and $\mathcal{H}_4$ are close to that for the single LDT. However, for each LDT in a cascade hierarchy, there are only two input attributes, thus the length of a branch is at most 2. Therefore, the optimal cascade hierarchies have better computational complexity than the single LDT.

Table 2: Evaluations of hierarchies obtained by GAW on the WBC database

$\mathcal{H}$	$\mathcal{A}_a$	$\mathcal{A}_{\tilde{a}}$	$\mathcal{A}_{ROC}$	β
$\mathcal{H}_3$	0.967096	0.409156	0.985831	100
$\mathcal{H}_4$	0.962804	0.408530	0.985867	100
LDT	0.934192	0.441863	0.932976	97

Accuracy and ROC curves: Figure 8 (a) and (b) show the accuracy and ROC curves for the two optimal cascade hierarchies and the single LDT, respectively. From the accuracy curves in Figure 8 (a), it can be seen that the ordinary accuracy at threshold 0.5 of $\mathcal{H}_3$ and $\mathcal{H}_4$ is better than for the single LDT, but their ordinary accuracies when the threshold is larger than 0.6 are worse than for the single LDT. The ROC curves of $\mathcal{H}_3$ and $\mathcal{H}_4$ are slightly better than for the single LDT.

6 Information propagation on the optimal cascade LAHs

Here, we use Pima Diabetes as an example to observe the information propagation on the optimal cascade hierarchy $\mathcal{H}_2$: 2, 4, 0, 6, 3, 5, 7, 1 (Figure 4). Table 3 shows the information for all attributes.

Table 3: Attribute information in the database of Pima Diabetes, including Lower Bounds (LB),Upper Bounds (UB)

x_i	Description	LB	UB
x_0	Number of times pregnant	0	17
x_1	Plasma glucose concentration a 2 hours in an oral glucose tolerance test	0	199
x_2	Diastolic blood pressure ($mmHg$)	0	122
x_3	Triceps skin fold thickness (mm)	0	99
x_4	Two-Hour serum insulin ($mu\ U/ml$)	0	846
x_5	Body mass index (weight in kg/(height in $m)^2$)	0	67.1
x_6	Diabetes pedigree function	0.078	2.42
x_7	Age (years)	21	81
y	+/-. + indicates "tested positive for diabetes"	0	1

For the Pima Diabetes database, the goal should be the function of the eight input attributes. Through the optimal cascade LAH ($\mathcal{H}_2$), the function mapping $y = f(x_0, ..., x_7)$ is broken down to be a cascade of sub-functions as below:

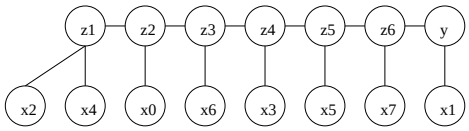

Figure 4: Optimal cascade hierarchy $\mathcal{H}_2$ for the Pima diabetes database

$$
\begin{aligned}
y &= f(x_0, x_1, x_2, x_3, x_4, x_5, x_6, x_7) \\
&= f_7(z_6, x_1) \\
&= f_7(f_6(z_5, x_7), x_1) \\
&= f_7(f_6(f_5(z_4, x_5), x_7), x_1) \\
&= f_7(f_6(f_5(f_4(z_3, x_3), x_5), x_7), x_1) \\
&= f_7(f_6(f_5(f_4(f_3(z_2, x_6), x_3), x_5), x_7), x_1) \\
&= f_7(f_6(f_5(f_4(f_3(f_2(z_1, x_0), x_6), x_3), x_5), x_7), x_1) \\
&= f_7(f_6(f_5(f_4(f_3(f_2(f_1(x_2, x_4), x_0), x_6), x_3), x_5), x_7), x_1)
\end{aligned}
$$

Each sub-function is represented by a trained LDT, and each sub-function decides an intermediate attribute, describing the distributed degrees of belief on difference classes. The calculation is carried out from bottom f_1 to top f_7. Table 5 lists the calculation results of each intermediate attribute for the samples shown in Table 4.

Table 4: Some samples of Pima Diabetes data

S	x_0	x_1	x_2	x_3	x_4	x_5	x_6	x_7	y
s_1	2	174	88	37	120	44.50	0.646	24	+
s_2	1	109	58	18	116	28	0.219	22	-
s_3	3	187	70	22	200	36.40	0.408	36	+
s_4	3	108	62	24	0	26	0.223	25	-

Now, we examine the effects of each attribute in the process of cascade decision making by observing the Table 5. For s_1 and s_3 that are positive samples, the process of decision making are listed as below:

- step 1: The levels of attributes x_2 and x_4 (Diastolic blood pressure and Two-hour serum insulin) do not make the large difference between positive and negative probabilities. But s_1 is with more positive probability, while s_3 is with more negative probability
- step 2: The levels of x_0 (Number of pregnant times) reduce the positive probabilities as the values of x_0 for both samples are small.
- step 3: The larger levels of x_6 (Diabetes pedigree function), the more the positive probabilities increase.
- step 4: The levels of x_3(Triceps skin fold thickness) reduce the positive probabilities.

Table 5: Upwards results for the samples in Table 4

z_i	-/+	s_1	s_2	s_3	s_4
$z_1 = f_1(x_2, x_4)$	-	0.4969	0.7365	0.5567	0.7119
	+	0.5031	0.2635	0.4433	0.2881
$z_2 = f_2(z_1, x_0)$	-	0.7164	0.7585	0.6804	0.6917
	+	0.2836	0.2415	0.3196	0.3083
$z_3 = f_3(z_2, x_6)$	-	0.5967	0.7075	0.6763	0.7040
	+	0.4033	0.2925	0.3237	0.2960
$z_4 = f_4(z_3, x_3)$	-	0.6110	0.7900	0.6854	0.6466
	+	0.3890	0.2100	0.3146	0.3534
$z_5 = f_5(z_4, x_5)$	-	0.5161	0.7093	0.5474	0.8833
	+	0.4839	0.2907	0.4526	0.1167
$z_6 = f_6(z_5, x_7)$	-	0.7761	0.8710	0.5114	0.7730
	+	0.2239	0.1290	0.4886	0.2270
$y = f_7(z_6, x_1)$	-	0.2150	0.7883	0.1804	0.7871
	+	0.7850	0.2117	0.8196	0.2129

- step 5: The levels of x_5 (body mass index) increase the positive probabilities.
- step 6: The level of x_7 (Age) for sample s_1 reduces the positive probability, while the level of x_7 for sample s_3 increases the positive probability. At this step, the negative probabilities are lager than the positive probabilities for both samples, and s_3 has larger positive probability than s_1.
- step 7: However, the results are completely turned down by function f_7, due to the introduce of attribute x_1 (Plasma glucose concentration at 2 hours in an oral glucose tolerance test). The final decision made by the top LDT is that s_1 and s_3 are positive with probability 78.5% and 81.96%, respectively.

Hence, we observe the top LDT representing function f_7(Figure 5). Obviously, if x_1 is $\{m, l\}$ or x_1 is $\{l\}$, then the sample is with larger positive probability than a negative probability (i.e. $p_y(+) > p_y(-)$). Namely, the level of x_1 (Plasma glucose concentration at 2 hours in an oral glucose tolerance test) dominates the final decision.

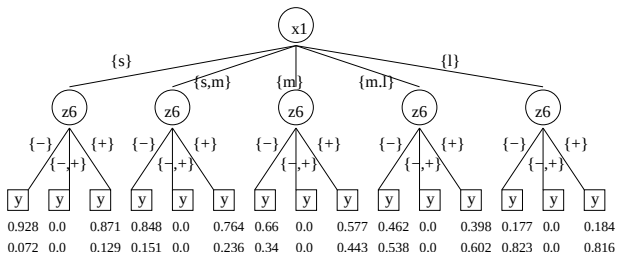

Figure 5: The top LDT in $\mathcal{H}_2$

For s_2 and s_4 that are negative samples, we conclude the effect of each attribute on the positive probability during the process of decision making in the Table 6. From the process of cascade decision making, it can be seen that the decisions have been done clearly at the bottom level, and decision making at the following step only adjusts the probabilities up (↑) or down (↓) slightly.

Table 6: Effect of each attribute on the positive probability in cascade decision making

S	x_2 and x_4	x_0	x_6	x_3	x_5	x_7	x_1
s_2	low p(+)	↓	↑	↓	↑	↓	↑
s_4	low p(+)	↑	↓	↑	↓	↑	↓

Hence, we observe the bottom decision tree (LDT1)(Figure 6) representing function f_1. It can be seen that if x_4 is {s}, $\{s, m\}$, or $\{m\}$, no matter which level x_2 is at, the negative probability on a branch is larger than the positive probability on a branch. The levels of x_4 for s_2 and s_4 are allocated in the range described above, so the results are obvious.

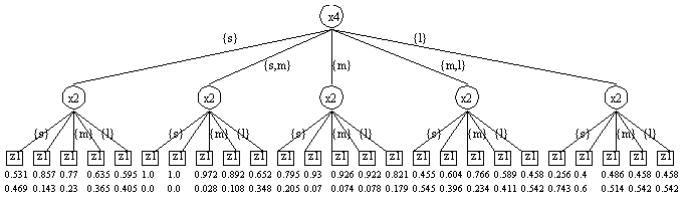

Figure 6: The bottom LDT in $\mathcal{H}_2$

7 Conclusion

In this paper, the process of information propagation through a cascade hierarchy of Linguistic Decision Trees for multi-attribute decision problems is investigated. We develop a genetic algorithm with the training algorithm LID3 in wrapper to optimise cascade hierarchies for decision making, and examine the performance of the optimal cascade hierarchies on two benchmark databases, Pima Diabetes and Wisconsin Breast Cancer databases from UCI machine learning repository. The experimental results show that an optimal cascade hierarchy can achieve better performance in the ordinary accuracy at threshold 0.5 and in the area under ROC curves than a single LDT. The number of rules induced by the optimal cascade hierarchy is much lower than a single LDT, when the relationship between a class and the input attributes is highly uncertain and nonlinear. However, accuracy tends to decrease with higher thresholds. More importantly, the cascade linguistic attribute hierarchy present cascade transparent linguistic rules, which are useful for analyzing the effect of different attributes on the decision making.

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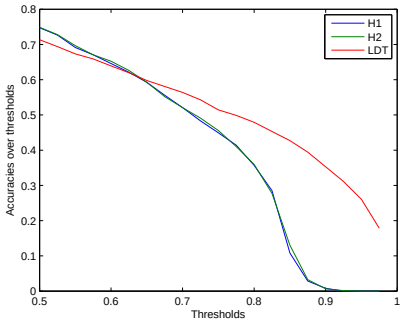
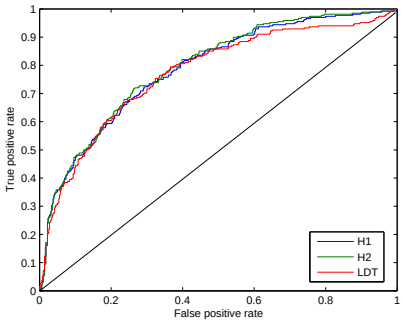
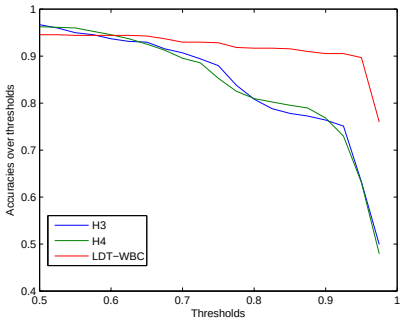


(a) Accuracies at threshold [0.5,1)

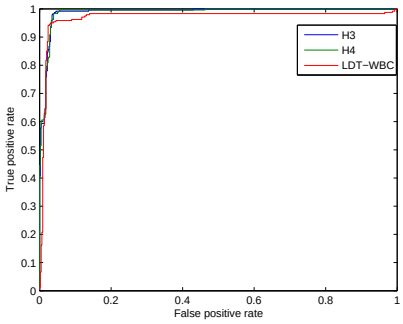


(b) ROC curves

Figure 7: Accuracy and ROC curve for $\mathcal{H}_1$, $\mathcal{H}_2$, and the single LDT on the Pima database



(a) Accuracies on threshold [0.5,1)



(b) ROC curves

Figure 8: Accuracy and ROC curve for $\mathcal{H}_3$, $\mathcal{H}_4$, and the single LDT on the WBC database