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Fuzzy-based concept-cognitive learning: An investigation of novel approach to tumor diagnosis analysis

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ABSTRACT

Medical decision-making with high-dimensional complex data has recently become a focus and difficulty in artificial intelligence and the medical field. Tumor diagnosis using data mining technology, from the perspective of gene analysis, can effectively improve the prediction accuracy of patients. For gene databases of tumors with high-dimensional attributes and small sample sizes, tumor classification based on gene analysis is a significant step in the intervention and treatment of tumors. The existing research on the tumor classification of gene data has one prevalent disadvantage: gene obtained via the classification performance evaluation has weak interpretability and universality. This paper presents a concept-cognitive learning system with the three-way analysis (CCL3S) in the fuzzy context for the problem of tumor diagnosis with high-dimensional data, a new fuzzy classifier good at tumor diagnosis. The main steps of the CCL3S include: designing fuzzy recognition to extract the core gene, constructing a fuzzy three-way concept space via the core gene, and finally completing the tumor diagnosis based on the minimum recognition degree. Experimental results on nine tumor gene expression datasets demonstrate that CCL3S achieves better classification performance than some related methods.

1. Introduction

With the development of biochip technology, thousands of gene expression levels in different samples can be measured simultaneously, providing a basis for studying the relationship between gene expression profiles and tumor disease classification [1]. It is of great significance for the treatment of patients to discover the core genes affecting tumor genesis in the early diagnosis. Tumor genes, however, usually have a small sample size and high-dimension complex data characteristics, which brings new challenges to data analytics.

Tumor diagnosis based on gene expression profiles is viewed as an emerging and recognized effective method to explore the pathogenesis of cancer that implements the analysis and prediction of patients' conditions at the data level. Then, combining machine learning or statistical methods with gene-expression data has become the primary trend in this direction. However, while using these technologies to analyze tumor data, many challenges also arise: 1) redundancy of high-dimensional features; 2) class distribution of small samples is unbalanced; 3) whether the classification results have corresponding explanations that can be interpreted. As we all know, for the characteristics of small samples of gene data, the deep learning method is used to cause the overfitting phenomenon in the process of training models, and the results also lack interpretability. Nevertheless, if just considering the high-dimensional

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characteristics of gene data, it is not easy to understand and interpret the original biological meaning of the feature space after dimensionality reduction, which is not conducive to the in-depth exploration of gene data. While tens of thousands of genes, most of them do not affect the tumor diagnosis or even interfere with the prediction of the disease [2]. Thus, feature selection technology to select core genes related to tumor pathogenesis has become essential for effective tumor diagnosis [3].

As an essential basis to support artificial intelligence and medical decision-making, data is related to the reliability of the whole medical diagnosis system. The data-information-knowledge-wisdom (DIKW) hierarchy is one of the fundamental conceptual models in artificial intelligence and data sciences [6,7]. Currently, data analysis of genes based on feature selection (as an essential tumor diagnosis tool) has received much attention, such as Authors [4] present a locally linear embedding (LLE) and neighborhood rough sets-based gene selection method using Lebesgue measure for cancer classification; Paper [5] propose we have proposed a recursive particle swarm optimization approach (PSO) for gene selection; Authors [8] establish a weighted general group lasso model to select cancer genes in groups. In this process, the feature selection algorithm can reduce the dimension of high-dimension gene data, extract core genes, and improve data quality and classification accuracy. From the perspective of DIKW, preprocessing gene expression data is equivalent to creating information from data, while feature extraction is equivalent to discovering knowledge from information [9,10]. Thus, it is meaningful work for us to obtain the information and knowledge that we can use from the complex genetic data and use it to assist us in making some decisions, which is the fundamental motivation for the work of the current article.

Classification problem, which aims to separate objects into specific classes based on a given information system, is another hot topic in data mining and artificial intelligence. Meanwhile, determining whether a patient has a disease in medical diagnosis can be considered a classification problem. While a gene expression profile often contains many genes that describe a patient, various genes contribute to the disease to varying degrees [11,12]. The feature selection method selects important features from a given information system, eliminates interfering features, and obtains core features with the same or even better classification ability than the entire information system [13–15]. Using the selected core features for data classification and establishing the classifier model can reduce the interference of redundant features to the results, ensure the classification ability of the results, and improve the reliability of the decision-making system. The current article applies this idea to the problem of tumor diagnosis, which has also become a necessary step to ensure the effectiveness of our method.

Moreover, a distinct feature of tumor gene data is its high dimensionality and small sample sizes. Traditional feature selection methods are often prone to overfitting when performing gene selection, resulting in a lack of reliability of results. The challenge lies in selecting beneficial genes (i.e., the genes with biological significance and interpretability) for the following medical diagnosis rather than simply pursuing a single classification accuracy. Some emerging scientific theories, such as cognitive computing and interactive granular computing [16–19], promise to address this challenge due to the basic concept and scientific methodology of cognitive science built on modern scientific analysis and engineering experiments to study cognition [20–23]. So it is beneficial to apply the naive idea of cognitive computing to gene data analysis to think about the utility mechanism of tumor genes and discuss a novel tumor classification method from a cognitive viewpoint. Concept-cognitive learning, as the expansion of intelligent computing systems modeled on the human brain, is an effective cognitive mechanism [24–26]. Recently, the research of CCL has produced many valuable results in a classification problem [27–30]. However, the existing CCL system mainly focuses on the object classification of low-dimensional data, and they are not suitable for gene data analysis. Several mathematical concepts were utilized to illustrate an explicit concept from its extent and intent, including fuzzy concept [31,32], two-way granule concept [33,34] and three-way concept [35,36]. Therefore, how to apply the concept-cognitive learning method to tumor diagnosis to achieve better classification performance is another motivation of the current paper.

Concept-cognitive learning is the science of cognition and learning things via concepts. Generally speaking, from the perspective of cognition, it is not so easy to accurately determine the extent of a concept, which is one of the reasons for the high misclassification of the traditional two-way classification method in the application. In this sense, the three-way decision may be a good choice since it emphasizes introducing a third region as a buffer in the face of uncertain or incomplete information. Three-way decision (3WD) theory based on the symbols-meaning-value concept, coined by Yao in his seminal paper [37,38], is an effective granular computing paradigm for studying knowledge and concept learning. Subsequently, particular models of the three-way decision have been investigated in different fields to address different problem needs [39,40]. Inspired by this theory, the authors [41,42] combine three-way decisions with the formal concept to study formal concept analysis (FCA) from positive and negative perspectives (i.e., positive and negative operators). Through a fruitful marriage of 3WD and FCA, it provides a novel model to investigate the concept analysis mechanism, and we also call it a three-way analysis. Simultaneously, many investigations have shown the effectiveness of the three-way analysis methods for concept knowledge presentation and learning. Drawing on these works, in the current paper, we introduce the thought of three-way analysis into the concept description and use it to learn and recognize concepts.

Following the above analysis, we propose a systematic framework for tumor diagnosis: fuzzy-based concept-cognitive learning system with three-way analysis (CCL3S) by introducing core gene selecting, concept-cognitive learning, and the three-way decision to tumor diagnosis in a fuzzy context. The block diagram of the proposed approach is shown in Fig. 1. Furthermore, we summarize the main contributions of this paper as follows.

- It provides a new thought of tumor diagnosis based on gene data analysis via the core gene for tumor diagnosis and builds a classifier model from a cognitive viewpoint. Furthermore, it attempts to construct a new concept-cognitive learning system from gene data with high-dimension and small sample data. Compared with other CCL models, CCL3S pays more attention to the concept-cognitive learning mechanism of gene data.

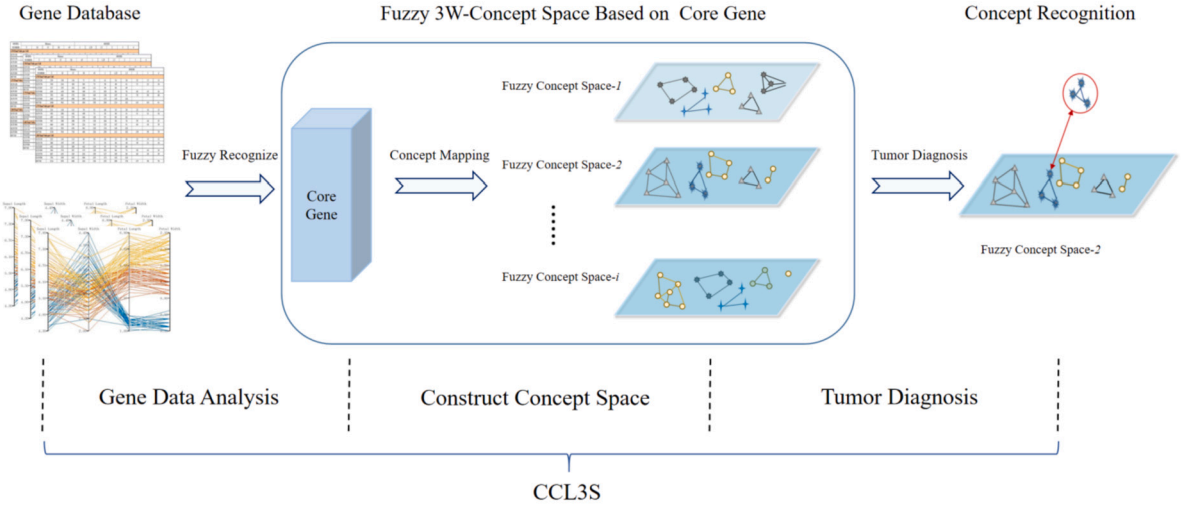


Fig. 1. Block diagram of CCL3S. It consists of three stages: the first stage is designing fuzzy recognition to extract the core gene in the gene database; the second stage is learning fuzzy three-way concept via core gene and constructing concept space; and the third stage is completing the tumor diagnosis based on the minimum recognition degree.

Table 1
Terminology notation.

Terminology	Explanation	Terminology	Explanation
Ω	The nonempty finite set of patient	Λ	The attribute set of gene
R	The attribute set of core gene	$\mu_{\widetilde{O}}$	The membership degree of objects
$\widetilde{T}$	The gene attribute set	$\delta_{\widetilde{T}}(o)$	The neighborhood of o in $\widetilde{T}$
$d(o,o')$	The euclidean distance	$rec_a(o_i,o_j)$	The fuzzy recognition degree
$S(o)$	The fuzzy similar classes	$\widetilde{I}$	The fuzzy binary relation
$\widetilde{I}^-(o,a_j)$	The non-membership degree of (o,a_j) to $\widetilde{I}$	$\widetilde{\mathcal{G}}_i$	The $i-th$ fuzzy 3W-concept space
$\widetilde{\mathcal{G}}_i^F$	The fuzzy 3W-concept fusion	$Rec(o,\widetilde{\mathcal{G}}_i^F)$	The recognition degree
$\widetilde{\mathcal{F}}$, $\mathcal{H}$	The positive cognitive operator	$\widetilde{\mathcal{F}}^-$, $\mathcal{H}^-$	The negative cognitive operator
$\widetilde{\mathcal{F}}^\nabla$, $\mathcal{H}^\nabla$	The fuzzy 3W-concept learning operator	$\widetilde{I}(o,a_j)$	The membership degree of (o,a_j) to $\widetilde{I}$

- It formulates a core gene selection method based on fuzzy recognition relation, and then a novel fuzzy-based concept-cognitive learning model grounded on core gene is presented for tumor classification. The core idea does not focus on researching feature selection and classification mechanisms but provides a new perspective for gene data analysis in medical decision-making.
- It has interpretability on the premise of improving tumor classification performance compared with several popular classification techniques, as it can take full advantage of the object and attribute information simultaneously.

The current article focuses on the problem of tumor diagnosis with high-dimensional data and proposes a fuzzy-based concept-cognitive learning mechanism with three-way analysis. The remainder of the current article is organized as follows. Section 2 briefly reviews basic concepts about fuzzy formal context and the CCL model. Section 3 presents a novel fuzzy concept-cognitive learning system based on the core gene. The tumor diagnosis of CCL3S and its corresponding algorithms are presented in Section 4, and the experimental analysis is given in Section 5. Finally, some concluding remarks of our paper are in Section 6.

2. Preliminaries

This section briefly reviews some necessary notions regarding two related aspects: 1) fuzzy set in formal context; 2) concept-cognitive learning with three-way analysis. The details can be obtained from their corresponding papers.

Before starting this section, it is necessary to claim that the three-way analysis for CCL is discussed in the fuzzy formal context without the regular formal context. The fuzzy pseudo-concept may be called a fuzzy concept when no confusion exists. Necessary symbolic notations are explained in Table 1.

2.1. Fuzzy set in formal context

In this subsection, we start with the notion of a fuzzy formal context [43–45], and several essential notions are presented as follows.

Let W be a whole of a nonempty and finite set, a fuzzy set $\widetilde{O}$ of W can be defined as follows:

$$\widetilde{O} = \{< o, \mu_{\widetilde{O}}(o) > | o \in W\},$$

where $\mu_{\widetilde{O}} : W \to [0,1]$, $\mu_{\widetilde{O}}(o)$ denotes the membership degree of object o with respect to $\widetilde{O}$, and $\mu^c_{\widetilde{O}}(o) = 1 - \mu_{\widetilde{O}}(o)$ is the nonmembership.

A fuzzy decision formal context $(W, M, \widetilde{I}, D, J)$ is a quintuple, where $(W, M, \widetilde{I})$ and (W, D, J) are two formal contexts. A fuzzy formal context $(W, M, \widetilde{I})$ is a triple, where $W = \{o_1, o_2, \ldots, o_n\}$ and $M = \{a_1, a_2, \ldots, a_m\}$ are, respectively, called the object set and the conditional attribute set, and $\widetilde{I} = \{< (o,a), u_{\widetilde{I}}(o,a) > | (o,a) \in W \times M\}$ is a fuzzy binary relation. A fuzzy formal context (W, D, J) is a triple, where $D_1, D_2, \ldots, D_l$ are decision class of D, $D = D_1 \cup D_2 \cup, \ldots, \cup D_l$, $J : W \times D \to \{D_1, D_2, \ldots, D_l\}$ is a binary relation.

For any $(o,a) \in W \times M$ has a membership degree $\mu_{\widetilde{I}}(o,a) \in [0,1]$. We denote $\widetilde{I}(o,a) = \mu_{\widetilde{I}}(o,a)$ for convenience. Given $\widetilde{I}(o,a)$ and $\widetilde{I}(o',a)$, we have $\widetilde{I}(o,a) \geqslant \widetilde{I}(o',a) \Leftrightarrow \mu_{\widetilde{I}}(o,a) \geqslant \mu_{\widetilde{I}}(o',a)$.

A fuzzy formal context $(W, M, \widetilde{I})$. For any $E \subseteq W$, $T \subseteq M$ and $\widetilde{T} \in \Gamma^M$, the derivation operator $(\cdot)^*$ can be defined as follows:

$$E^*(a) = \bigwedge_{o \in E} \widetilde{I}(o,a), a \in M,$$
$$\widetilde{T}^* = \{o \in W | \forall a \in T, \widetilde{T}(a) \leqslant \widetilde{I}(o,a)\},$$

where Γ^M is the union of all fuzzy sets in M.

The triplet $(W, T, \widetilde{I})$ is a fuzzy formal context, for any $E_1, E_2, E \subseteq W, \widetilde{T}_1, \widetilde{T}_2 \subseteq \widetilde{T}$, then we have:

1) $E_1 \subseteq E_2 \Rightarrow E_2^* \subseteq E_1^*, \widetilde{T}_1 \subseteq \widetilde{T}_2 \Rightarrow \widetilde{T}_2^* \subseteq \widetilde{T}_1^*$;
2) $E \subseteq E^{**}, \widetilde{T} \subseteq \widetilde{T}^{**}$;
3) $E = E^{***}, \widetilde{T} = \widetilde{T}^{***}$;
4) $E \subseteq \widetilde{T}^* \Leftrightarrow \widetilde{T} \subseteq E^*$;
5) $(E_1 \cup E_2)^* = E_1^* \cap E_2^*, (\widetilde{T}_1 \cup \widetilde{T}_2)^* = \widetilde{T}_1^* \cap \widetilde{T}_2^*$;
6) $(E_1 \cap E_2)^* \supseteq E_1^* \cup E_2^*, (\widetilde{T}_1 \cap \widetilde{T}_2)^* \supseteq \widetilde{T}_1^* \cup \widetilde{T}_2^*$.

Therefore, $(W, M, \widetilde{I})$ is a fuzzy formal context, a pair $(E, \widetilde{T})$ is called a fuzzy formal concept or fuzzy concept if only $E^* = \widetilde{T}$ and $\widetilde{T}^* = E$ hold, where E is the extent and $\widetilde{T}$ is the intent of the concept $(E, \widetilde{T})$. Obviously (E^{**}, E^*) and $(\widetilde{T}^*, \widetilde{T}^{**})$ are fuzzy concepts. The fuzzy concept lattice $\widetilde{\mathcal{L}}(W, M, \widetilde{I})$ is the union of all fuzzy concepts in $(W, M, \widetilde{I})$. For any fuzzy concept $(E_1, \widetilde{T}_1), (E_2, \widetilde{T}_2) \in \widetilde{\mathcal{L}}(W, M, \widetilde{I})$, the ordered by $(E_1, \widetilde{T}_1) \leqslant (E_2, \widetilde{T}_2) \Leftrightarrow E_1 \subseteq E_2 \Leftrightarrow \widetilde{T}_2 \subseteq \widetilde{T}_1$. Moreover, if the meet and join are given by:

$$(E_1, \widetilde{T}_1) \wedge (E_2, \widetilde{T}_2) = (E_1 \cap E_2, (\widetilde{T}_1 \cup \widetilde{T}_2)^{**}),$$
$$(E_1, \widetilde{T}_1) \vee (E_2, \widetilde{T}_2) = ((E_1 \cup E_2)^{**}, \widetilde{T}_1 \cap \widetilde{T}_2),$$

then the fuzzy concept lattice $\widetilde{\mathcal{L}}(W, M, \widetilde{I})$ is complete lattice.

Considering our paper mainly focuses on applying concept-cognitive learning with three-way analysis to tumor diagnosis rather than analyzing its notion. Thus, we only briefly introduce some related notions in the following subsection.

2.2. Concept-cognitive learning with three-way analysis

Let the complement of $\widetilde{I}$ be denoted by $\widetilde{I}^- = \{< (o,a), 1 - u_{\widetilde{I}(o,a)} > | (o,a) \in W \times M\}$, which reflects the nonmembership degree. Similarly, for any $\widetilde{I}^-(o,a)$ and $\widetilde{I}^-(o',a)$, we have $\widetilde{I}^-(o,a) \geqslant \widetilde{I}^-(o',a) \Leftrightarrow \mu_{\widetilde{I}^-}(o,a) \geqslant \mu_{\widetilde{I}^-}(o',a)$.

Definition 1. Let $(W, M, \widetilde{I})$ be a fuzzy formal context. For any $O \subseteq W$ and $\widetilde{T} \in \Gamma^M$, the positive cognitive operators $\widetilde{\mathcal{F}} : 2^W \to \Gamma^M$ and $\mathcal{H} : \Gamma^M \to 2^W$ of $(W, M, \widetilde{I})$ are defined as:

$$\widetilde{\mathcal{F}}(O)(a) = \bigwedge_{o \in O} \widetilde{I}(o,a), a \in M,$$
$$\mathcal{H}(\widetilde{T}) = \{o \in W | \forall a \in T, \widetilde{T}(a) \leqslant \widetilde{I}(o,a)\}.$$

The $\widetilde{\mathcal{F}}(O)(a)$ shows the learning process from object to attribute, and $\mathcal{H}(\widetilde{T})$ also describes the learning process from attribute to object, which means that we could learn object or attribute information from the given information. Similarly, the negative cognitive operators $\widetilde{\mathcal{F}}^- : 2^W \to \Gamma^M$ and $\mathcal{H}^- : \Gamma^M \to 2^W$ of $(W, M, \widetilde{I}^-)$ can be defined as follows:

$$\widetilde{\mathcal{F}}^-(O)(a) = \bigwedge_{o \in O} \widetilde{I}^-(o,a), a \in M,$$
$$\mathcal{H}^-(\widetilde{T}) = \{o \in W | \forall a \in T, \widetilde{T}(a) \leqslant \widetilde{I}^-(o,a)\},$$

where the 2^W be the power set of W.

Table 2
A fuzzy formal decision context with tumor diagnosis.

Object	a_1	a_2	a_3	a_4	a_5	a_6	a_7	a_8	a_9	a_{10}	a_{11}	a_{12}	a_{13}	a_{14}
o_1	0.76	0.17	0.72	0.33	0.63	0.78	0.97	0.34	0.65	0.58	0.55	0.55	0.97	1
o_2	0.83	0.20	0.72	0.29	0.24	0.48	0.68	0.25	0.65	0.40	0.51	0.86	0.83	1
o_3	0.71	0.26	0.83	0.50	0.85	0.52	0.67	0.27	0.35	0.38	0.56	0.86	0.84	1
o_4	0.95	0.15	0.54	0.24	0.27	0.60	0.83	0.23	0.65	0.39	0.58	0.55	0.61	1
o_5	0.64	0.09	0.60	0.39	0.29	0.67	0.89	0.07	0.60	0.64	0.50	0.84	0.61	1
o_6	0.18	0.09	0.44	0.45	0.34	0.30	0.31	0.77	0.09	0.46	0.47	0.01	0.08	2
o_7	0.56	0.07	0.37	0.53	0.20	0.33	0.43	0.30	0.13	0.22	0.75	0.38	0.24	2
o_8	0.08	0.04	0.53	0.60	0.02	0.87	0.87	0.32	0.61	0.30	0.74	0.56	0.06	2
o_9	0.02	0.11	0.77	0.60	0.44	0.25	0.42	0.59	0.26	0.12	0.87	0.28	0.32	2
o_{10}	0.23	0.31	0.61	0.64	0.32	0.05	0.01	0.66	0.10	0.96	0.12	0.03	0.10	3
o_{11}	0.75	0.33	0.74	0.68	0.12	0.17	0.07	0.57	0.35	0.94	0.06	0.06	0.27	3
o_{12}	0.58	0.79	0.72	0.71	0.22	0.17	0.04	0.75	0.27	0.70	0.08	0.08	0.34	3
o_{13}	0.46	0.63	0.74	0.89	0.39	0.21	0.09	0.55	0.42	0.65	0.15	0.23	0.35	3

The negative cognitive operator shows the learning process between objects and attributes from the non-membership degree, which can realize comprehensive recognition by combining with the positive cognitive operator.

The $\widetilde{F}: 2^W \to \Gamma^M, \mathcal{H}: \Gamma^M \to 2^W, \widetilde{F}^-: 2^W \to \Gamma^M$ and $\mathcal{H}^-: \Gamma^M \to 2^W$ are considered as four set-valued mappings, and they are abbreviated as $\widetilde{F}, \mathcal{H}, \widetilde{F}^-, \mathcal{H}^-$ respectively. The operators $(*,*)$ defined by the basic notions in fuzzy formal context are the cognitive operator $\widetilde{F}$ and $\mathcal{H}$ of $(W, M, \widetilde{I})$, respectively. The following example gives the cognitive learning process in detail.

Definition 2. Let $(W, M, \widetilde{I})$ be a fuzzy formal context, $O \subseteq W$ is an object, and $\widetilde{T_1}, \widetilde{T_2} \in \Gamma^M$ are two fuzzy sets. The fuzzy 3W-concept learning operator $\widetilde{F}^\nabla: 2^W \to \Gamma^M \times \Gamma^M$ and $\mathcal{H}^\nabla: \Gamma^M \times \Gamma^M \to 2^W$ are defined as follows:

$$\widetilde{F}^\nabla(O) = (\widetilde{F}(O), \widetilde{F}^-(O)),$$
$$\mathcal{H}^\nabla(\widetilde{T_1}, \widetilde{T_2}) = \mathcal{H}(\widetilde{T_1}) \cap \mathcal{H}^-(\widetilde{T_2}).$$

Then $(O, (\widetilde{T}_1, \widetilde{T}_2))$ is called a fuzzy three-way concept (fuzzy 3W-concept) when the following statement holds: $\widetilde{F}^\nabla(O) = (\widetilde{T}_1, \widetilde{T}_2), \mathcal{H}^\nabla(\widetilde{T}_1, \widetilde{T}_2) = O$. That is, the $(O, (\widetilde{T}_1, \widetilde{T}_2))$ is a fuzzy three-way concept in the learning process when the information learned by objects is the same as that learned from attributes according to the positive and negative learning operator. Moreover, $(O, (\widetilde{T}_1, \widetilde{T}_2))$ is the supper concept of $(O', (\widetilde{T}'_1, \widetilde{T}'_2))$, denoted as $(O, (\widetilde{T}_1, \widetilde{T}_2)) \leq (O', (\widetilde{T}'_1, \widetilde{T}'_2))$ when $O \subseteq O'$ or $(\widetilde{T}'_1, \widetilde{T}'_2) \geq (\widetilde{T}_1, \widetilde{T}_2)$.

Intuitively, Definition 1 shows that the membership degree of (o, a) to $\widetilde{I}$ on attribute a and the non-membership degree of (o, a) to $\widetilde{I}^-$ on attribute a from the positive and negative perspectives. Thus, positive and negative operators have the same properties. In order to express both positive and negative information simultaneously, we combine the positive and negative operators to form a new operator and concept, which is called the three-way operator and three-way concept, and its corresponding fuzzy concept is the fuzzy three-way concept (as shown in Definition 2). According to paper [30], we know the following property hold:

Property 1. *Let $(W, M, \widetilde{I})$ be a fuzzy formal context. For any $O \subseteq W, (\mathcal{H}\widetilde{F}(O) \cap \mathcal{H}^-\widetilde{F}^-(O), (\widetilde{F}(O), \widetilde{F}^-(O)))$ is a fuzzy 3W-concept.*

Note that fuzzy concept with three-way analysis could depict the relation between objects and attribute more detail to the positive and negative cognitive operator. More definitions and properties of the fuzzy three-way concept and the fuzzy three-way operator can be found in references [30,35,41].

Example 1. Table 2 is a fuzzy formal decision context with $W = \{o_1, o_2, \ldots, o_{13}\}$, $M = \{a_1, a_2, \ldots, a_{14}\}$, where a_{14} is the decision attribute. The whole objects can be divided into three classes, where $D_1 = \{o_1, o_2, \ldots, o_5\}, D_2 = \{o_6, o_7, \ldots, o_9\}, D_3 = \{o_{10}, o_{11}, \ldots, o_{13}\}$. Given the $O = \{o_1, o_2, o_3, o_5\} \subseteq W$ and $\widetilde{T}_1 = \{< a_1, 0.64 >, < a_2, 0.09 >, < a_3, 0.60 >, < a_4, 0.29 >, < a_5, 0.24 >, < a_6, 0.48 >, < a_7, 0.67 >, < a_8, 0.07 >, < a_9, 0.35 >, < a_{10}, 0.38 >, < a_{11}, 0.50 >, < a_{12}, 0.55 >, < a_{13}, 0.61 >\}$, and $\widetilde{T}_2 = \{< a_1, 0.17 >, < a_2, 0.74 >, < a_3, 0.17 >, < a_4, 0.50 >, < a_5, 0.15 >, < a_6, 0.22 >, < a_7, 0.03 >, < a_8, 0.66 >, < a_9, 0.35 >, < a_{10}, 0.36 >, < a_{11}, 0.44 >, < a_{12}, 0.14 >, < a_{13}, 0.03 >\}$.

According to the positive cognitive operator in Definition 1, we could obtain the $\widetilde{F}(O) = \{< a_1, 0.64 >, < a_2, 0.09 >, < a_3, 0.60 >, < a_4, 0.29 >, < a_5, 0.24 >, < a_6, 0.48 >, < a_7, 0.67 >, < a_8, 0.07 >, < a_9, 0.35 >, < a_{10}, 0.38 >, < a_{11}, 0.50 >, < a_{12}, 0.55 >, < a_{13}, 0.61 >\}$ and $\mathcal{H}(\widetilde{T}_1) = \{o_1, o_2, o_3, o_5\}$. In this paper, we could obtain the negative membership degree $\widetilde{I}^-(o, a) = 1 - \widetilde{I}(o, a)$, then, the negative cognitive operator can be obtained similarly, $\widetilde{F}^-(O) = \{< a_1, 0.17 >, < a_2, 0.74 >, < a_3, 0.17 >, < a_4, 0.50 >, < a_5, 0.15 >, < a_6, 0.22 >, < a_7, 0.03 >, < a_8, 0.66 >, < a_9, 0.35 >, < a_{10}, 0.36 >, < a_{11}, 0.44 >, < a_{12}, 0.14 >, < a_{13}, 0.03 >\}$ and $\mathcal{H}(\widetilde{T}_2) = \{o_1, o_2, o_3, o_5\}$. Moreover, we know $\widetilde{F}^\nabla(O) = (\widetilde{T}_1, \widetilde{T}_2), \mathcal{H}^\nabla(\widetilde{T}_1, \widetilde{T}_2) = O$. Thus, the $(O, (\widetilde{T}_1, \widetilde{T}_2))$ is called the fuzzy three-way concept, which indicates that object set $\{o_1, o_2, o_3, o_5\}$ has the lowest membership degree $\widetilde{T}_1$ and highest membership degree of attribute set M, respectively.

3. Fuzzy 3W-concept space based on core gene

There is no doubt that only a few are involved in the thousands of tumor genes. We wish to eliminate the negative influence between genes and disease that redundant genes interfere with disease diagnosis. Thus, we introduce a method through partial genes (i.e., core genes) from gene data and construct the fuzzy concept space for their core gene for the following process of tumor diagnosis. In this section, we introduce the notion of a gene database. Based on a gene database, we suggest a fuzzy 3W-concept space of core genes for tumor diagnosis.

A tumor gene database generally contains three main elements: patient, gene, and diagnosis. From the perspective of the formal context, a gene database is the following quintuple:

Definition 3. A gene database is the following quintuple:

$$GD = (\Omega, \Lambda, \widetilde{I}, D, J),$$

where $\Omega = \{o_1, o_2, \ldots, o_n\}$ is a nonempty finite set of patient, Λ is an attribute set of gene, $u_{I(o,a)}$ is the values of patient o for gene attribute a, that is, $\widetilde{I} = \{< (o,a), u_{\widetilde{I}(o,a)} > |(o,a) \in \Omega \times \Lambda\}$ is a fuzzy binary relation of patient o and gene $a, u_{\widetilde{I}(o,a)} = v$ means that the patient o have the value v on the gene a. Similarly, D is the diagnosis, and J is a binary relation of patient and diagnosis.

For convenience, hereinafter, patient $o \in \Omega$ is called object o, gene $a \in \Lambda$ is the gene attribute a, and diagnosis D is the decision attribute. Without loss of generality, the gene database GD denotes all fuzzy decision formal contexts in this paper.

3.1. Fuzzy recognition of core gene

In this subsection, we introduce a fuzzy recognition relation for the core gene selection to measure the recognition degree of the various gene for the tumor in the diagnosis process. We define a δ neighborhood as follows.

Definition 4. Let $(\Omega, \Lambda, \widetilde{I}, D, J)$ be a gene database. For arbitrary $o \in \Omega$ and $\widetilde{T} \in \Gamma^{\Lambda}$, the neighborhood $\delta_{\widetilde{T}}(o)$ of o in gene attribute set T can be defined as follows:

$$\delta_{\widetilde{T}}(o) = \{o' \in \Omega | d(o,o') \leqslant \delta\},$$

where δ is a threshold and $d(o,o') = \sqrt{\sum_{a \in \widetilde{T}} \|\widetilde{I}(o,a)\|^2}$ is the Euclidean distance.

The core genes have better characterized by their ability to recognize sample objects. We wish to use a standard to detect undesirable genes for recognizing sample objects and selecting desirable genes. Thus, we introduce the concept of fuzzy recognition to obtain core genes for tumor diagnosis.

Definition 5. Given a gene database $(\Omega, \Lambda, \widetilde{I}, D, J)$, for any $o_i, o_j \in \Omega, a \in \Lambda$, the fuzzy recognition relation of gene attribute a on o_i and o_j can be defined as follows:

$$rec_a(o_i, o_j) = \begin{cases} 0, & o_j \in \delta_a(o_i) \\ 0, & J(o_i, D) = J(o_j, D) \\ \dfrac{|\widetilde{I}(o_i,a) - \widetilde{I}(o_j,a)| - \delta}{1-\delta}, & \text{else} \end{cases}$$

where $rec_a : \Omega \times \Omega \to [0,1], rec_a(o_i, o_j)$ denotes the fuzzy recognition degree of the gene attribute a with respect to (o_i, o_j). Obviously, $rec_a(o_i, o_i) = 0$ and $rec_a(o_i, o_j) = rec_a(o_j, o_i)$.

From Definition 5, we can see that for any object, if their decision classes are the same or are similar to each other (i.e., the distance between the object is less than δ), then their fuzzy recognition degree is 0.

Definition 6. Given a gene database $(\Omega, \Lambda, \widetilde{I}, D, J)$, for any $o_i, o_j \in \Omega, a \in \Lambda$, the fuzzy recognition degree of the gene attribute $a \in \Lambda$ and the fuzzy recognition degree of the gene attribute set $\Lambda' \subseteq \Lambda$ with respect to a pair of objects (o_i, o_j) can be calculated as follows::

1) $rec_a = \sum_{i=1}^{n} \sum_{j=i}^{n} rec_a(o_i, o_j)$;
2) $rec_{\Lambda'}(o_i, o_j) = \sum_{a \in \Lambda'} rec_a(o_i, o_j)$.

Hence, for all gene attribute $a \in \Lambda$, the fuzzy recognition degree of a reflects the total distinction of gene attribute a to all objects, and the fuzzy recognition degree of Λ reflects the total distinction of gene attribute set Λ with respect to (o_i, o_j). The larger its value is, the stronger its identification ability is. It can also explain that we can get more information and divide more objects into different classes by considering gene attribute a. Consequently, we have:

Definition 7. Given a gene database $(\Omega, \Lambda, \widetilde{I}, D, J)$, a subset of gene attribute set $R \subseteq \Lambda$ is a core gene attribute set by considering fuzzy recognition degree rec_a, if it satisfies the following two conditions:

1) $\forall o_i, o_i \in \Omega, \exists a \in R$, st. $rec_a(o_i, o_j) > 0$, if $rec_\Lambda(o_i, o_j) \neq 0$;
2) $\forall a \in R, \exists o_i, o_j \in \Omega$, st. $rec_{\Lambda - a}(o_i, o_j) > 0$, if $rec_\Lambda(o_i, o_j) \neq 0$.

According to Definition 7, the first condition ensures that there is always one gene attribute in the core gene attribute set that can identify any two objects. The second condition ensures that any gene attribute in the core gene attribute set has a specific effect on object recognition. Therefore, we can obtain the core gene attribute set R by considering the fuzzy recognition degree. Based on the above discussion, the core gene attributes based on fuzzy recognition relation can be obtained. The detail of the core gene attributes selection method is shown in Algorithm 1.

Algorithm 1 Core gene attribute selection based on fuzzy recognition relation.

Input: A gene database $(\Omega, \Lambda, \widetilde{I}, D, J)$, parameter δ;
Output: Core gene attribute set R;
1: Initial $R = \emptyset$;
2: **for all** $a \in \Lambda$ **do**
3: Compute $\delta_a(o_i)$ according to Definition 4;
4: **for all** $o_i \in \Omega$ **do**
5: **for** $o_j = o_i : o_{|\Omega|}$ **do**
6: Compute $rec_a(o_i, o_j)$, rec_a, $rec_\Lambda(o_i, o_j)$ according to Definition 5-6;
7: **end for**
8: **end for**
9: **end for**
10: **while** $\sum_{a \in \Lambda} rec_a \neq 0$ **do**
11: Let $a^* = argmax_{a \in \Lambda - R} rec_a$;
12: **if** $rec_{a^*}(o_i, o_j) > 0$ **then**
13: $R \leftarrow R \cup a^*$;
14: **for all** $a \in \Lambda$ **do**
15: $rec_a(o_i, o_j) \leftarrow 0$;
16: **end for**
17: **end if**
18: **end while**
19: **return** R.

Given a gene database $(\Omega, \Lambda, \widetilde{I}, D, J)$, we still use $|\Omega|$ and $|\Lambda|$ to represent the number of objects and gene attributes, respectively. Running step 1, take $O(1)$ due to initialized setting. In steps 2-9, the running time is decided by three for-statements. Hence, running the step 2-9 take $O(|\Lambda||\Omega|^2)$. Running steps 10-18 take $O(|\Lambda||\Omega|^2)$ due to a while-statement and a for-statement. Hence, the running time complexity of Algorithm 1 takes $O(|\Lambda||\Omega|^2)$. A more detailed process of the core attribute is shown in Example 2.

Example 2. In this example, we can further select the core attributes of fuzzy formal decision context shown in Table 2 based on fuzzy recognition relation. From Table 2, we calculate the fuzzy recognition relation of attribute according to Definition 5 and select the first core attribute a_7, where $rec_{a_7} = 21.3467$. Then, the second core attribute a_{13} is selected and the $\sum_{a \in \{a_7, a_{13}\}} rec_a = 3.5733$. Moreover, the a_3 is also selected to the core attribute set, and then the fuzzy recognition degree becomes 0. Therefore, the final core attribute set is $\{a_1, a_7, a_{13}\}$. The more detailed process of core analysis can be learned in Algorithm 1.

3.2. Fuzzy 3W-concept generation

Generally speaking, the fuzzy concept with three-way analysis describes a relationship between object and gene attributes from two characteristics: the positive and negative cognitive learning operator. Compared with the classical fuzzy concept, it contains a more comprehensive description of the information. It is more suitable to replace the fuzzy concept with the fuzzy 3W-concept in gene data analysis tasks to improve concept-cognitive learning efficiency. Moreover, considering the concept space is constructed based on object-oriented concept cognitive learning under the fuzzy environment, we believe constructing fuzzy concept space in gene data is generally not feasible. Hence, the core gene should be introduced into the process of concept-cognitive learning of gene data to significantly reduce the amount of calculation.

According to the discussion in subsection 3.1, we can obtain a δ neighborhood to describe similar objects via a gene database $(\Omega, \Lambda, \widetilde{I}, D, J)$ and a parameter δ. And then, we propose a procedure for learning the fuzzy 3W-concept space based on the core gene via the neighborhood information in this subsection.

Given a gene database $(\Omega, \Lambda, \widetilde{I}, D, J)$, the core gene attributes of Λ can be obtained according to Algorithm 1. We wish to use these core gene attribute to construct a fuzzy concept space. Then, we first define a fuzzy formal context via core gene attribute as follows:

Definition 8. Let $(\Omega, R, \widetilde{I}, D, J)$ be a core gene database, $R \subseteq \Lambda$ is the core gene attribute set, $\Omega/D = \{\Omega_1, \Omega_2, \ldots, \Omega_k\}$. For $o \in \Omega_i (i = 1, 2, \ldots, k)$ and $a_j \in R (j = 1, 2, \ldots, r)$, the membership degree of (o, a_j) to $\widetilde{I}$ is $\widetilde{I}(o, a_j)$, non-membership degree is $\widetilde{I}^-(o, a_j)$. Then, its fuzzy similar classes $S(o)$ is described as follows:

$$S(o) = \{o' \in \Omega_i | d(o, o') \le \delta'\},$$

where δ is a threshold and $d(o,o') = \sqrt{\frac{1}{2}(\sum_{a_j \in R} \|\widetilde{I}(o,a_j)\|^2 + \sum_{a_j \in R} \|\widetilde{I^-}(o,a_j)\|^2)}$ is the Euclidean distance.

Generally, we can believe that the objects are considered the same in the δ' neighborhood. In this subsection, we set a specific value as δ', and then we could obtain similar classes for all objects. The notions of the fuzzy 3W-concept of core gene attributes can be defined according to Property 1. Note that the parameter δ' plays an essential role in constructing similar classes. Meanwhile, the membership and non-membership degrees will be different from various objects, and then the intent will change with the extent so that the value of δ' will influence the fuzzy 3W-concept. Furthermore, the tumor diagnosis system presented in the current article is via a fuzzy 3W-concept; Hence, the δ' is the main factor affecting the tumor recognition performance in our method. Then we can get the notions of fuzzy 3W-concept and fuzzy 3W-concept space as follows.

Property 2. *Given a core gene database* $(\Omega, R, \widetilde{I}, D, J)$, $R \subseteq \Lambda$, $\Omega/D = \{\Omega_1, \Omega_2, \dots, \Omega_k\}$. *For a similar class* $S(o) \subseteq \Omega$, $(\mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o)), (\widetilde{\mathcal{F}}(S(o)), \widetilde{\mathcal{F}}^-(S(o))))$ *is a fuzzy 3W-concept.*

Proof: According to Definition 2, we only need to prove $\mathcal{H}^\nabla(\widetilde{\mathcal{F}}(S(o)), \widetilde{\mathcal{F}}^-(S(o))) = \mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o))$ and $\widetilde{\mathcal{F}}^\nabla(\mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o))) = (\widetilde{\mathcal{F}}(S(o)), \widetilde{\mathcal{F}}^-(S(o)))$ are valid.

1) It is immediate from the definition of 3W-concept learning operator, that is

$$\mathcal{H}^\nabla(\widetilde{\mathcal{F}}(S(o)), \widetilde{\mathcal{F}}^-(S(o))) = \mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o)).$$

2) According to Definition 1, we have

$$\begin{aligned}
\mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o)) &= \{o \in \Omega | \widetilde{I}(o,a) \ge \bigwedge_{o \in S(o)} \widetilde{I}(o,a)\} \cap \{o \in \Omega | \widetilde{I^-}(o,a) \ge \bigwedge_{o \in S(o)} \widetilde{I^-}(o,a), a \in R\} \\
&= \{o \in \Omega | \widetilde{I}(o,a) \ge \bigwedge_{o \in S(o)} \widetilde{I}(o,a)\} \cap \{o \in \Omega | 1 - \widetilde{I^-}(o,a) \le 1 - \bigwedge_{o \in S(o)} \widetilde{I^-}(o,a), a \in R\} \\
&= \{o \in \Omega | \widetilde{I}(o,a) \ge \bigwedge_{o \in S(o)} \widetilde{I}(o,a)\} \cap \{o \in \Omega | \widetilde{I}(o,a) \le \bigvee_{o \in S(o)} \widetilde{I}(o,a), a \in R\} \\
&= \{o \in \Omega | \bigwedge_{o \in S(o)} \widetilde{I}(o,a) \le \widetilde{I}(o,a) \le \bigvee_{o \in S(o)} \widetilde{I}(o,a),\ a \in R\}.
\end{aligned}$$

Therefore, we have $\widetilde{\mathcal{F}}(\mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o)))(a) = \bigwedge_{o \in S(o)} \widetilde{I}(o,a) = \widetilde{\mathcal{F}}(S(o))(a)$ for $a \in R$.
Similarly, we also obtain

$$\mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o)) = \{o \in \Omega | \bigwedge_{o \in S(o)} \widetilde{I^-}(o,a)\} \le \widetilde{I^-}(o,a) \le \bigvee_{o \in S(o)} \widetilde{I^-}(o,a), a \in R\}.$$

$$\widetilde{\mathcal{F}}^-(\mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o)))(a) = \bigwedge_{o \in S(o)} \widetilde{I^-}(o,a) = \widetilde{\mathcal{F}}^-(S(o))(a) \quad \forall a \in R.$$

Hence, $\widetilde{\mathcal{F}}^\nabla(\mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o))) = (\widetilde{\mathcal{F}}(S(o)), \widetilde{\mathcal{F}}^-(S(o)))$ holds.

By combining 1) and 2), this property is proven. #

Definition 9. Given a core gene database $(\Omega, R, \widetilde{I}, D, J)$, $R \subseteq \Lambda$, $\Omega/D = \{\Omega_1, \Omega_2, \dots, \Omega_k\}$. For a similar class $S(o) \subseteq \Omega$, the object-oriented fuzzy 3W-concept space $\widetilde{\mathcal{G}_i}$ about $S(o)$ is defined as follows:

$$\widetilde{\mathcal{G}_i} = \{(\mathcal{H}\widetilde{\mathcal{F}}(S(o)) \cap \mathcal{H}^-\widetilde{\mathcal{F}}^-(S(o)), (\widetilde{\mathcal{F}}(S(o)), \widetilde{\mathcal{F}}^-(S(o)))) | o \in \Omega_i\}.$$

From Definition 9, we know that for any object set can also be connected with a label in a real gene database, that is $\{\widetilde{\mathcal{G}_1}, \widetilde{\mathcal{G}_2}, \dots, \widetilde{\mathcal{G}_k}\}$. Then, the complete algorithm of constructing object-oriented fuzzy 3W-concept space is presented in Algorithm 2. Example 3 shows the learning process of fuzzy 3W-concept space.

Example 3. According to the fuzzy formal decision context in Table 2, we first compute the fuzzy similar classes of objects in their corresponding decision class according to Definition 8.

$$\begin{aligned}
&S(o_1) = \{o_1\}, \quad S(o_2) = \{o_2, o_3, o_4\}, \quad S(o_3) = \{o_2, o_3\}, \quad S(o_4) = \{o_2, o_4\}, \quad S(o_5) = \{o_5\}; \\
&S(o_6) = \{o_6\}, \quad S(o_7) = \{o_7\}, \quad S(o_8) = \{o_8\}, \quad S(o_9) = \{o_9\}; \\
&S(o_{10}) = \{o_{10}\}, \quad S(o_{11}) = \{o_{11}, o_{12}\}, \quad S(o_{12}) = \{o_{11}, o_{12}, o_{13}\}, \quad S(o_{13}) = \{o_{12}, o_{13}\}.
\end{aligned}$$

Algorithm 2 Constructing fuzzy 3W-concept space.

Input: A gene database $(\Omega, \Lambda, \widetilde{I}, D, J)$, parameter δ';
Output: Fuzzy three-way concept space $\widetilde{\mathcal{G}} = \{\widetilde{\mathcal{G}}_1, \widetilde{\mathcal{G}}_2, \ldots, \widetilde{\mathcal{G}}_k\}$;
Initial $\widetilde{\mathcal{G}} = \emptyset$;
for all $\Omega_i \in \Omega/D$ **do**
  for all $o \in \Omega_i$ **do**
    Let $\widetilde{\mathcal{G}} = \emptyset$;
    Construct the similar class $S(o)$ of o according to Definition 8;
    Construct the fuzzy 3W-concept $(\mathcal{H}\widetilde{F}(S(o)) \cap \mathcal{H}^{-}\widetilde{F}^{-}(S(o)), (\widetilde{F}(S(o)), \widetilde{F}^{-}(S(o))))$;
    $\widetilde{\mathcal{G}}_i \leftarrow \widetilde{\mathcal{G}}_i \cup (\mathcal{H}\widetilde{F}(S(o)) \cap \mathcal{H}^{-}\widetilde{F}^{-}(S(o)), (\widetilde{F}(S(o)), \widetilde{F}^{-}(S(o))))$;
  end for
end for
return $\widetilde{\mathcal{G}}$.

Table 3
The object-oriented fuzzy 3W-concept space.

$(\{o_1\}, (\{< a_1, 0.97 >, < a_7, 0.97 >, < a13, 0.76 >\}, \{< a_1, 0.03 >, < a_7, 0.03 >, < a_{13}, 0.24 >\}))$,
$(\{o_2, o_3, o_4\}, (\{< a_1, 0.67 >, < a_7, 0.61 >, < a_{13}, 0.71 >\}, \{< a_1, 0.17 >, < a_7, 0.16 >, < a_{13}, 0.05 >\})$,
$(\{o_2, o_3\}, (\{< a_1, 0.67 >, < a_7, 0.83 >, < a_{13}, 0.71 >\}, < a_1, 0.32 >, < a_7, 0.16 >, < a_{13}, 0.17 >))$,
$(\{o_2, o_4\}, (\{< a_1, 0.68 >, < a_7, 0.61 >, < a_{13}, 0.83 >\}, \{< a_1, 0.17 >, < a_7, 0.17 >, < a_{13}, 0.05 >\}))$,
$(\{o_5\}, (< a_1, 0.89 >, < a_7, 0.61 >, < a_{13}, 0.64 >, \{< a_1, 0.11 >, < a_7, 0.39 >, < a_{13}, 0.36 >\}))$,
$(\{o_6\}, (\{< a_1, 0.31 >, < a_7, 0.08 >, < a_{13}, 0.18 >\}, \{< a_1, 0.69 >, < a_7, 0.92 >, < a_{13}, 0.82 >\}))$,
$(\{o_7\}, (\{< a_1, 0.43 >, < a_7, 0.24 >, < a_{13}, 0.56 >\}, \{< a_1, 0.57 >, < a_7, 0.76 >, < a_{13}, 0.44 >\}))$,
$(\{o_8\}, (\{< a_1, 0.87 >, < a_7, 0.06 >, < a_{13}, 0.08 >\}, \{< a_1, 0.13 >, < a_7, 0.94 >, < a_{13}, 0.92 >\}))$,
$(\{o_9\}, (\{< a_1, 0.42 >, < a_7, 0.32 >, < a_{13}, 0.02 >\}, \{< a_1, 0.58 >, < a_7, 0.68 >, < a_{13}, 0.98 >\}))$,
$(\{o_{10}\}, \{< a_1, 0.01 >, < a_7, 0.10 >, < a_{13}, 0.23 >\}, \{< a_1, 0.99 >, < a_7, 0.90 >, < a_{13}, 0.77 >\}))$,
$(\{o_{11}, o_{12}\}, \{< a_1, 0.04 >, < a_7, 0.27 >, < a_{13}, 0.58 >\}, \{< a_1, 0.93 >, < a_7, 0.66 >, < a_{13}, 0.25 >\}))$,
$(\{o_{11}, o_{12}, o_{13}\}, \{< a_1, 0.04 >, < a_7, 0.27 >, < a_{13}, 0.46 >\}, \{< a_1, 0.91 >, < a_7, 0.65 >, < a_{13}, 0.25 >\}))$,
$(\{o_{12}, o_{13}\}, \{< a_1, 0.04 >, < a_7, 0.34 >, < a_{13}, 0.46 >\}, \{< a_1, 0.91 >, < a_7, 0.65 >, < a_{13}, 0.42 >\}))$.

According to Definition 9, the object-oriented fuzzy 3W-concept space can be learned. There are 5, 4 and 4 fuzzy concepts in $\widetilde{\mathcal{G}}_1$, $\widetilde{\mathcal{G}}_2$ and $\widetilde{\mathcal{G}}_3$, which are shown in Table 3.

4. The concept-cognitive learning mechanism of tumor diagnosis system

Note that concepts influence each other in fuzzy 3W-concept space, with much repetitive and interfering information between them. Hence, to verify our proposed method, two tasks need to be done in this section: 1) fuzzy 3W-concept fusion; 2) explore an effective concept-cognitive learning mechanism for the tumor diagnosis system.

4.1. Fuzzy 3W-concept fusion

As we all know, the reliability of information from the different fuzzy 3W-concepts is different, namely the importance of fuzzy 3W-concepts. In order to evolve fuzzy ontologies, a fuzzy concept clustering was proposed in paper [29], and a progressive fuzzy concept was discussed in paper [30]. Meanwhile, to use this idea to facilitate our concept-cognitive learning method, we introduce concept fusion, where the concept is a fuzzy pseudo-concept. Thus, this subsection mainly focuses on fuzzy concept fusion according to the fuzzy 3W-concept space of learning.

Let $(\Omega, R, \widetilde{I}, D, J)$ be a core gene database, $R \subseteq \Lambda$ be a core gene set, $\widetilde{\mathcal{G}}_i$ be a subconcept space of $\widetilde{\mathcal{G}}$. For any fuzzy 3W-concept space $\widetilde{\mathcal{G}}_i$, we say that $\widetilde{\mathcal{G}}_i^F$ is a fuzzy 3W-concept fusion of concept space $\widetilde{\mathcal{G}}_i$ based on core gene attribute if it satisfies the following two settings:

1) For any fuzzy 3W-concept fusion $(S_u, (\widetilde{T}_u(S_u), \widetilde{T}_u^{-}(S_u))) \in \widetilde{\mathcal{G}}_i^F$ is not supper concept of others fuzzy 3W-concept fusion in $\widetilde{\mathcal{G}}_i^F$;
2) For any fuzzy 3W-concept $(S_j, (\widetilde{T}_j(S_j), \widetilde{T}_j^{-}(S_j))) \in \widetilde{\mathcal{G}}_i$, there exists at least one extent of a fuzzy three-way concept fusion S_u such that $S_j \subseteq S_u$.

Definition 10. Given a fuzzy 3W-concept space $\widetilde{\mathcal{G}}_i$. There exists some fuzzy 3W-concept $(S_{\lambda_j}, (\widetilde{T}_{\lambda_j}(S_{\lambda_j}), \widetilde{T}_{\lambda_j}^{-}(S_{\lambda_j}))) \in \widetilde{\mathcal{G}}_i$ such that $S_{\lambda_j} \subseteq S_u$, the fuzzy 3W-concept fusion $(S_u, (\widetilde{T}_u(S_u), \widetilde{T}_u^{-}(S_u))) \in \widetilde{\mathcal{G}}_i^F$ satisfies the following conditions:

1) $S_u = S_{\lambda_1} \cup S_{\lambda_2} \cup \ldots \cup S_{\lambda_t}$;
2) $(\widetilde{T}_u(S_u), \widetilde{T}_u(S_u)^{-}) = \frac{1}{2^{t-1}}((\widetilde{T}_{\lambda_1}(S_{\lambda_1}), \widetilde{T}_{\lambda_1}^{-}(S_{\lambda_1})) + (\widetilde{T}_{\lambda_2}(S_{\lambda_2}), \widetilde{T}_{\lambda_2}^{-}(S_{\lambda_2})) + 2^1(\widetilde{T}_{\lambda_3}(S_{\lambda_3}), \widetilde{T}_{\lambda_3}^{-}(S_{\lambda_3})) + \ldots + 2^{t-2}(\widetilde{T}_{\lambda_t}(S_{\lambda_t}), \widetilde{T}_{\lambda_t}^{-}(S_{\lambda_t})))$;

where $|S_{\lambda_1}| \geq |S_{\lambda_2}| \geq \ldots \geq |S_{\lambda_t}|$.

Table 4
The object-oriented fuzzy 3W-concept space.

$(\{o_1\},(\{<a_1,0.97>,<a_7,0.97>,<a_{13},0.76>\},\{<a_1,0.03>,<a_7,0.03>,<a_{13},0.24>\}))$,
$(\{o_5\},(\{<a_1,0.89>,<a_7,0.61>,<a_{13},0.64>\},\{<a_1,0.11>,<a_7,0.39>,<a_{13},0.36>\}))$,
$(\{o_2,o_3,o_4\},(\{<a_1,0.68>,<a_7,0.67>,<a_{13},0.77>\},\{<a_1,0.21>,<a_7,0.16>,<a_{13},0.08>\}))$,
$(\{o_6\},(\{<a_1,0.31>,<a_7,0.08>,<a_{13},0.18>\},\{<a_1,0.69>,<a_7,0.92>,<a_{13},0.82>\}))$,
$(\{o_7\},(\{<a_1,0.43>,<a_7,0.24>,<a_{13},0.56>\},\{<a_1,0.57>,<a_7,0.76>,<a_{13},0.44>\}))$,
$(\{o_8\},(\{<a_1,0.87>,<a_7,0.06>,<a_{13},0.08>\},\{<a_1,0.13>,<a_7,0.94>,<a_{13},0.92>\}))$,
$(\{o_9\},(\{<a_1,0.42>,<a_7,0.32>,<a_{13},0.02>\},\{<a_1,0.58>,<a_7,0.68>,<a_{13},0.98>\}))$,
$(\{o_{11},o_{12},o_{13}\},(\{<a_1,0.04>,<a_7,0.31>,<0.49>\},\{<a_1,0.92>,<a_7,0.65>,<a_{13},0.34>\}))$,
$(\{o_{10}\},(\{<a_1,0.01>,<a_7,0.10>,<a_{13},0.23>\},\{<a_1,0.99>,<a_7,0.90>,<a_{13},0.77>\}))$.

The $(S_u,(\widetilde{T}_u(S_u),\widetilde{T}_u^{-}(S_u)))$ is a fuzzy 3W-concept fusion, and the corresponding fuzzy 3W-concept space is $\widetilde{\mathcal{G}}_i^F = \{(S_u,(\widetilde{T}_u(S_u),\widetilde{T}_u^{-}(S_u)))|u=1,2,\dots,u_t\}$, where $i=1,2,\dots,k$. In the fusion process of fuzzy 3W-concept, we set the weight of the sub-concept mainly based on its corresponding extent's size. Note that the weight of all fuzzy 3W-concepts adds up to 1, ensuring that the sum of the total effects is 1. Compared with the original concept, the concept fusion retains the original information based on the concept space and reduces the redundant concept, which could enhance the effectiveness of cognitive learning for concept recognition.

Example 4. According to Example 3, we can further learn the fuzzy 3W-concept fusion, and then there are 3, 4 and 2 fuzzy 3W-concepts fusion in $\widetilde{\mathcal{G}}_1^F$, $\widetilde{\mathcal{G}}_2^F$ and $\widetilde{\mathcal{G}}_3^F$, which are shown in Table 4.

4.2. Tumor diagnosis process

In the process of tumor diagnosis, a vital link is to analyze and make decisions on the gene data of patients, that is, to identify the class label. In this subsection, we design a recognition indicator of the fuzzy 3W-concept used for tumor diagnosis and then present a diagnosis mechanism based on the fuzzy 3W-concept fusion for gene data.

Definition 11. According to the fuzzy 3W-concept fusion space $\widetilde{\mathcal{G}}^F = \{\widetilde{\mathcal{G}}_1^F,\widetilde{\mathcal{G}}_2^F,\dots,\widetilde{\mathcal{G}}_k^F\}$ learning in subsection 4.1. For the object o, the membership degree and non-membership degree to R are $\widetilde{T}$ and $\widetilde{T}^{-}$, respectively. Then, the recognition degree between o and $(S_u,(\widetilde{T}_u(S_u),\widetilde{T}_u^{-}(S_u)))\in\widetilde{\mathcal{G}}_i^F$ can be reformulated as follows:

$$Rec(o,\widetilde{\mathcal{G}}_i^F) = argmin_{(S_u,(\widetilde{T}_u(S_u),\widetilde{T}_u^{-}(S_u)))\in\widetilde{\mathcal{G}}_i^F}\sqrt{\|\widetilde{T}-\widetilde{T}_u(S_u)\|^2+\|\widetilde{T}^{-}-\widetilde{T}_u^{-}(S_u)\|^2}.$$

It should be pointed out that the more substantial the similarity, the minor recognition degree. Hence, the patients can be diagnosed according to the following definition.

Definition 12. A patient o was diagnosed as D_{k^*}, if $Rec(o,\widetilde{\mathcal{G}}_{k^*}^F)$ is global minimum recognition degree, that is,

$$D_{k^*} = argmin_{D_k} Rec(o,\widetilde{\mathcal{G}}_k^F).$$

According to the above analysis, we can easily discover that the tumor diagnosis process is a recognition process in our method. Hence, we need to obtain the result with a global minimum recognition degree. The detailed processes of the diagnosis process are shown in Algorithm 3.

It should be pointed out that the construct of Algorithm 2 and Algorithm 3 is according to Algorithm 1. The main task of Algorithm 2 and Algorithm 3 is to construct a fuzzy 3W-concept space and fusion fuzzy 3W-concept space. Hence, the time complexity of these two algorithms mainly focuses on the construction and fusion of fuzzy 3W-concept, and it is easy to verify that their time complexity is significantly lower than that of Algorithm 1. In addition, these algorithms need to learn two parameters (δ,δ'). Hence, it is easy to know that the overall time complexity of our method takes $O(|\delta||\delta'||\Lambda||\Omega|^2)$. However, this paper mainly focuses on analyzing tumor gene data, i.e., the number of samples is much smaller than the feature dimension. Thus, the time complexity of the CCL3S method is linear order.

Example 5. Given an unlabeled object x_0 with the membership degree $(<a_1,0.74>,<a_7,0.09>,<a_{13},0.18>)$ of three core attributes, we could identify its class label according to the Definition 11. The recognition degree between x_0 and other existing fuzzy 3W-concept fusion in Example 4 are as follows:

$$Rec(x_0,\widetilde{\mathcal{G}}_1^F(S_u)) = 1.4206,\qquad Rec(x_0,\widetilde{\mathcal{G}}_2^F(S_u)) = 0.3335,\qquad Rec(x_0,\widetilde{\mathcal{G}}_3^F(S_u)) = 1.4636.$$

According to Definition 12, we have $D_2 = argmin_{D_k} Rec(x_0,\widetilde{\mathcal{G}}_k^F)$. Thus, x_0 can be classed to the second class.

Algorithm 3 Diagnosis process based fusion fuzzy 3W-concept space.

Input: Fuzzy three-way concept space $\widetilde{\mathcal{G}} = \{\widetilde{\mathcal{G}}_1, \widetilde{\mathcal{G}}_2, \ldots, \widetilde{\mathcal{G}}_k\}$;
Output: Diagnosis k^*;
Initial $\widetilde{\mathcal{G}}_i$;
for all $\widetilde{\mathcal{G}}_i \in \widetilde{\mathcal{G}}$ **do**
  Set supremum fuzzy 3W-concept $(S_u, (\widetilde{T}_u(S_u), \widetilde{T}_u^-(S_u)))$;
  for all $(S_j, (\widetilde{T}_j(S_j), \widetilde{T}_j^-(S_j))) \in \widetilde{\mathcal{G}}_i$ **do**
    if $(S_j, (\widetilde{T}_j(S_j), \widetilde{T}_j^-(S_j))) \subseteq (S_u, (\widetilde{T}_u(S_u), \widetilde{T}_u^-(S_u))) \in \widetilde{\mathcal{G}}_i^F$ **then**
      Get $(S_u, (\widetilde{T}_u(S_u), \widetilde{T}_u^-(S_u)))$ by Definition 10;
      $\widetilde{\mathcal{G}}_i^F \leftarrow \widetilde{\mathcal{G}}_i^F \cup (S_u, (\widetilde{T}_u(S_u), \widetilde{T}_u^-(S_u)))$;
    end if
  end for
end for
Let $\widetilde{\mathcal{G}}^F \leftarrow \widetilde{\mathcal{G}}_i^F$;
for all $(S_u, (\widetilde{T}_u(S_u), \widetilde{T}_u^-(S_u))) \in \widetilde{\mathcal{G}}^F$ **do**
  Get $Rec(o, \widetilde{\mathcal{G}}_i^F(S_u))$ by Definition 11;
  Let $k^* \leftarrow argmin_i Rec(o, \widetilde{\mathcal{G}}_i^F(S_u))$;
end for
return k^*.

Table 5
Detailed information of 9 selected datasets.

No.s	Tumor name	Samples	Gene attribute	Classes	Continuous
1	Allaml	77	7129	2	Yes
2	Colon	62	2000	2	No
3	Glioma	50	4434	4	Yes
4	Leukemia	72	7070	2	No
5	Lung	203	3312	5	Yes
6	Lung_Discrete	73	325	7	No
7	Lymphoma	96	4026	9	No
8	Prostate_Ge	102	5966	2	Yes
9	Tox_171	171	5748	4	Yes

5. Experiments

In this section, we validate the effectiveness of CCL3S for tumor gene data analysis in the fuzzy context. Specifically, our framework is compared with several fuzzy-based methods on public tumor gene datasets (see https://jundongl.github.io/scikit-feature/datasets.html), whose characteristics are summarized in Table 5. The experimental computing program on a personal computer, and its specific configuration is OS: Microsoft Win10; Processor: Intel(R) Core(TM) i7-10750H CPU 2.60 GHz; Memory: 32GB; Programming language: MATLAB 2020a.

Since they could not evaluate the proposed approaches, some pre-processing data methods were applied to the source data. The source data have been transformed into values ranging from 0 to 1 according to [46], which can be considered as the membership degree.

$$\widetilde{I}(o_i, a_j) = \frac{s(x_i, a_j) - \min(s(a_j))}{\max(s(a_j)) - \min(s(a_j))},$$

where $s(x_i, a_j)$ denotes the value of o_i in a_j, the $\max(s(a_j))$ and $\min(s(a_j))$ denote the maximum and minimum value of objects o_i in a_j.

5.1. Performance evaluation

We demonstrate the performance of CCL3S for tumor diagnosis, and the primary task is to verify the classification accuracy of the various methods. This subsection compares CCL3S with other classification methods, including the classic and fuzzy-based classification methods. The following experiment comparisons for tumor classification on the selected datasets are adapted with 10-fold cross-validations to evaluate various methods. The detailed flowchart of the CCL3S is shown in Fig. 2.

In order to illustrate the efficiency of CCL3S, we mainly compare the outcome of CCL3S with some popular classification methods on classification performance in this subsection. Consider that CCL3S is constructed based on the fusion fuzzy 3W-concept via core gene attribute, a classification method based on concept distance. Thus, we compare it with some popular classification methods, including several classic machine learning methods [47,48]: KNN(K = 3), SVM, MNB, LR, RNN, and Forest_PA; and several fuzzy-based methods [30,49]: FENN, IF_KNN, PFRNN, FRNN_FRS, CFKNN, and ILMPFTC.

Tables 6 and 7 record the classification performance of selected classification methods on various gene datasets under the optimal (δ, δ'). The mean (M) and standard (SD) of classification accuracy are shown in the table. Then we can find it easy that our CCL3S method has the highest accuracy and most minor standard in most cases. Specifically, for the six classic classification methods, Table 2 indicates that CCL3S performs much better than other methods on gene datasets 2-3 and gene datasets 5-9, and achieves the best performance on datasets 1 and 4. Moreover, for the fuzzy-based classification methods, Table 3 shows that the classification

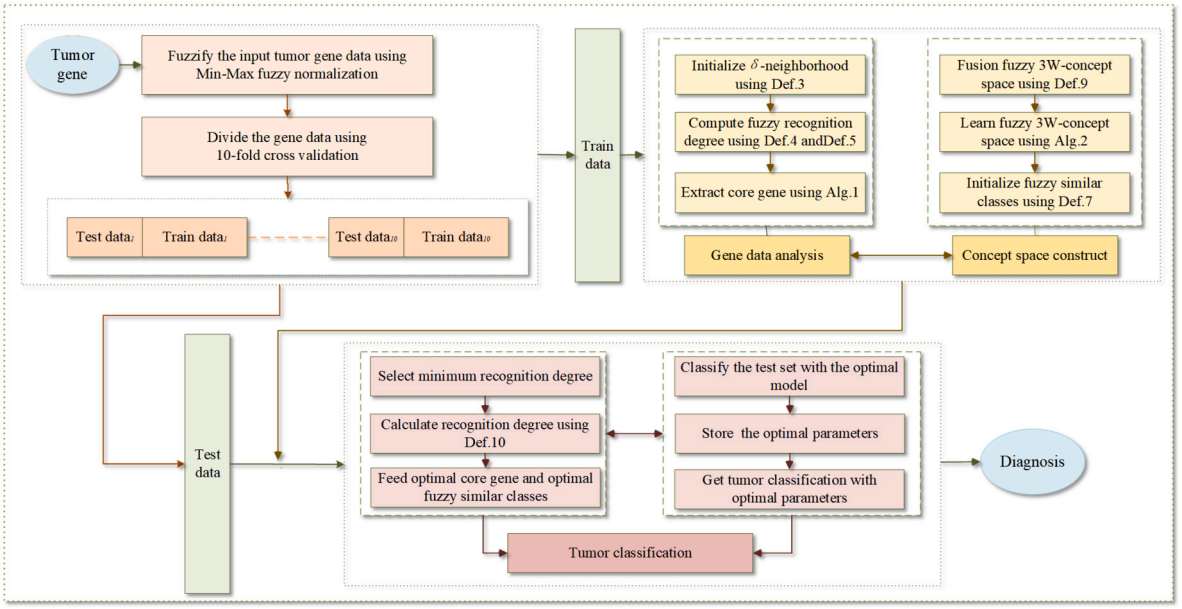


Fig. 2. Detailed flowchart of CCL3S.

Table 6
Classification performance (M ± SD) of CCL3S and six classic classification methods.

No.s	(δ,δ')	CCL3S	KNN	SVM	GNB	LR	RNN	Forest_PA
1	(0.4,0.0)	**1.0000±0.0000**	0.7464±0.2456	0.9571±0.0915	0.8607±0.1242	0.9286±0.1720	0.6429±0.4392	0.9444±0.0985
2	(0.0,0.1)	**0.9357±0.1145**	0.8357±0.1973	0.8381±0.1494	0.8690±0.1630	0.8548±0.1382	0.6500±0.1920	0.7903±0.1614
3	(0.0,0.0)	**0.8950±0.1462**	0.6800±0.1327	0.7200±0.2400	0.4000±0.2366	0.6600±0.2973	0.1000±0.1612	0.6600±0.1944
4	(0.4,0.0)	**1.0000±0.0000**	0.7893±0.1450	0.9714±0.0857	0.8482±0.1400	0.9429±0.1309	0.6429±0.4392	0.9167±0.0738
5	(0.8,0.1)	**0.9505±0.0408**	0.7400±0.3923	0.7455±0.3898	0.7007±0.3659	0.7355±0.3946	0.6800±0.4490	0.9163±0.0461
6	(0.7,0.0)	**0.9054±0.0883**	0.8768±0.0996	0.8750±0.0997	0.9036±0.1104	0.8625±0.1110	0.2839±0.1794	0.7397±0.1012
7	(0.5,0.0)	**0.9133±0.0871**	0.4956±0.2897	0.6378±0.2845	0.7489±0.1375	0.6589±0.2631	0.4633±0.4050	0.8889±0.0998
8	(0.3,0.0)	0.9118±0.0709	0.6982±0.2161	0.8727±0.0770	0.5645±0.2935	0.8636±0.0876	0.0200±0.0600	**0.9216±0.0717**
9	(0.7,0.0)	**0.9765±0.0568**	0.3111±0.1773	0.4176±0.3162	0.3350±0.2712	0.3882±0.3002	0.0000±0.0000	0.7251±0.1151

Table 7
Classification performance (M ± SD) of CCL3S and six fuzzy-based classification methods.

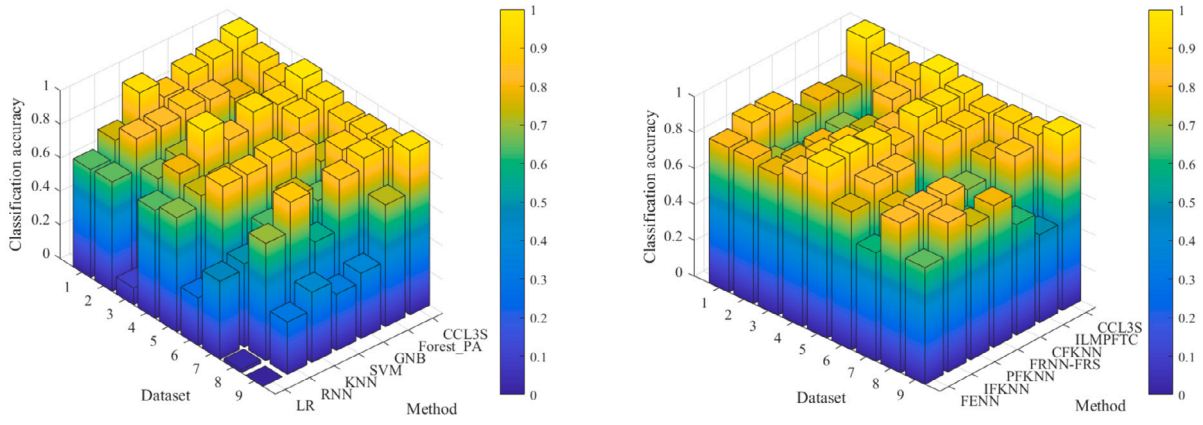
No.s	(δ,δ')	CCL3S	FENN	IFKNN	PFKNN	FRNN-FRS	CFKNN	ILMPFTC
1	(0.4,0.0)	**1.0000±0.0000**	0.8054±0.1520	0.8750±0.1143	0.8750±0.1143	0.7393±0.1235	0.7911±0.1460	0.7619±0.0338$
2	(0.0,0.1)	**0.9357±0.1145**	0.8054±0.1520	0.7071±0.1881	0.6595±0.1872	0.6476±0.0381	0.6881±0.2036	0.5294±0.0322
3	(0.0,0.0)	**0.8950±0.1462**	0.7800±0.1661	0.7800±0.1661	0.8000±0.1265	0.3400±0.1281	0.7400±0.1562	0.8571±0.0312
4	(0.4,0.0)	**1.0000±0.0000**	0.8482±0.0962	0.8768±0.1142	0.8768±0.0946	0.6536±0.0635	0.8196±0.1096	0.8095±0.0346
5	(0.8,0.1)	0.9505±0.0408	0.9507±0.0381	**0.9605±0.0373**	0.9410±0.0478	0.8669±0.0550	0.9560±0.0403	0.9483±0.0082
6	(0.7,0.0)	**0.9054±0.0883**	0.7679±0.1041	0.8536±0.1371	0.8518±0.1250	0.1357±0.0853	0.8946±0.0953	0.8889±0.0329
7	(0.5,0.0)	**0.9133±0.0871**	0.6044±0.1521	0.7744±0.0961	0.5433±0.0939	0.4778±0.0272	0.6811±0.1515	0.7826±0.0309
8	(0.3,0.0)	**0.9118±0.0709**	0.8336±0.1326	0.8427±0.1281	0.8518±0.1367	0.6209±0.1131	0.5673±0.1511	0.8621±0.0175
9	(0.7,0.0)	**0.9765±0.0568**	0.6500±0.1039	0.8314±0.0851	0.7431±0.0731	0.7895±0.0953	0.6147±0.0749	0.4898±0.0206

performance of CCL3S is almost more significant than that of the other methods, except dataset 5. Meanwhile, the more intuitive remarkable comparison is shown in Fig. 3 and Fig. 4. It can be found clearly that the mean classification accuracy of CCL3S is significantly higher than others in most gene datasets.

To observe a significant difference between CCL3S and other classification methods, we adopt the Wilcoxon pairwise test to compare this experiment and set the P-value threshold to 0.01. From the compassion Table 8, we know all the test P-values on accuracy are smaller than 0.05, indicating that CCL3S is more efficient and robust than other classification methods in classification performance. In conclusion, the proposed CCL3S mechanism is an excellent diagnostic mechanism.

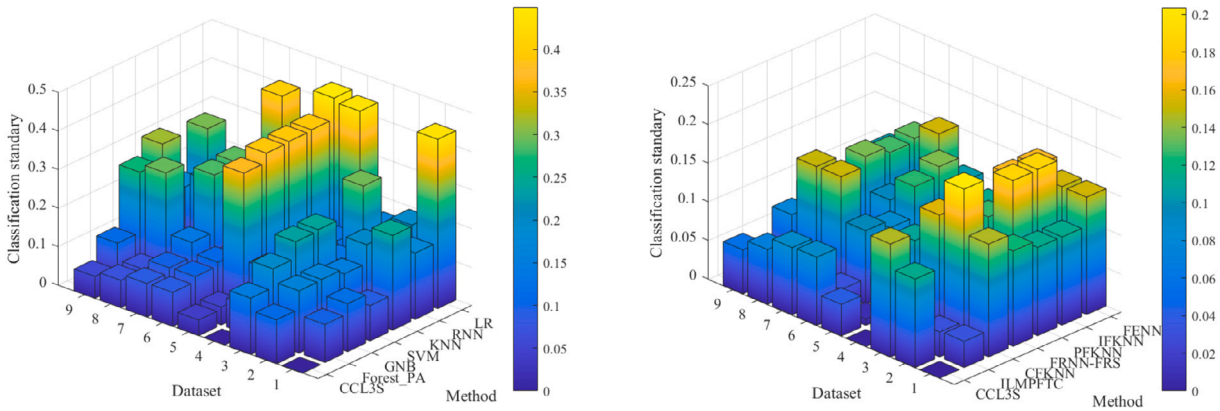
5.2. Robustness analysis

Based on the above experiments, we analyze the robustness of the proposed CCL3S method as follows. In this part, we further compare their classification robustness to evaluate the performance of CCL3S and other compared algorithms on different datasets. Firstly, we have the definition of robustness [50] as follows.



(a) classic classification (b) fuzzy-based classification

Fig. 3. The comparison of classification accuracy on 9 selected gene datasets.



(a) classic classification (b) fuzzy-based classification

Fig. 4. The comparison of classification standard on 9 selected gene datasets.

Table 8
The comparison of average classification and Wilcoxon test result of several methods on 9 selected gene datasets.

Classic classification			Fuzzy-based classification		
Method	Average accuracy	P-value	Method	Average accuracy	P-value
CCL3S	0.9431	–	CCL3S	0.9431	–
KNN	0.6859	0.0039	FENN	0.7828	0.0078
SVM	0.7817	0.0039	IFKNN	0.8335	0.0078
GNB	0.6923	0.0039	PFKNN	0.7936	0.0039
LR	0.7661	0.0039	FRNN-FRS	0.5857	0.0039
RNN	0.3870	0.0039	CFKNN	0.7503	0.0078
Forest_PA	0.8337	0.0078	ILMPFTC	0.7700	0.0039

$$R_{M_i}(D_j) = \frac{Acc_{M_i}(D_j)}{min_{M_i \in M} Acc_{M_i}(D_j)},$$

where $R_{M_i}(D_j)$ denotes the classification accuracy of algorithm M_i on dataset D_j and $min_{M_i \in M} Acc_{M_i}(D_j)$ represents the minimum classification accuracy of all methods on dataset D_j. The whole robustness of $M_i = \sum_{j=1}^{s} R_{M_i}(D_j)$ (where s represents the number of datasets), the higher the value of robustness, the better the performance of the method.

Note that the RNN method showed the worst performance in all datasets, which also reflects that RNN is unsuitable for high-dimensional data classification. Thus, in this part, we only compare the robustness of CCL3S with other methods except for the RNN

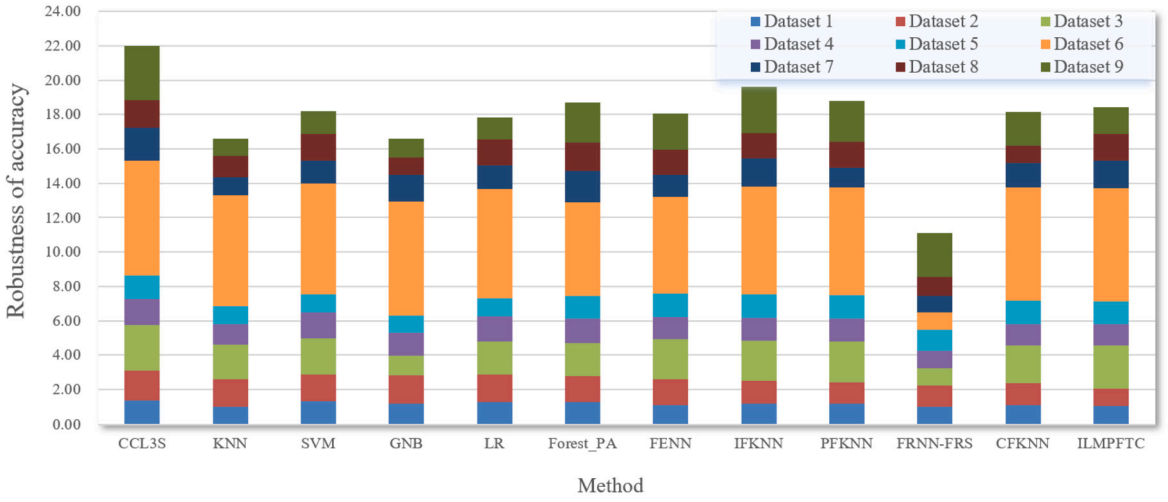


Fig. 5. Robustness analysis.

Table 9
Classification accuracy of different parameters on Allaml gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.8196	0.6196	0.3821	0.4500	0.3089	0.7464	0.7768	0.7464	0.7179	0.6893	0.6893
0.1	0.9286	0.9286	0.8875	0.8464	0.9018	0.9571	0.7232	0.7232	0.9286	0.8768	0.7786
0.2	0.9286	0.9286	0.9143	0.9000	0.8857	0.9286	0.8571	0.8571	0.8429	0.8143	0.8143
0.3	0.9304	0.9304	0.9304	0.9161	0.9446	0.8911	0.9304	0.9018	0.8321	0.7893	0.8054
0.4	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.9714	0.9429	0.9143	0.9714	0.9589
0.5	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9857	0.9857	0.9286	0.9000
0.6	0.9018	0.9018	0.9018	0.9018	0.9018	0.9143	0.9286	0.9429	0.9571	0.9571	0.8571
0.7	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9143	0.9429	0.9571	0.9429
0.8	0.9196	0.9196	0.9196	0.9196	0.9196	0.9196	0.9196	0.9196	0.9196	0.9196	0.9339
0.9	0.9429	0.9429	0.9429	0.9429	0.9429	0.9429	0.9429	0.9429	0.9429	0.9429	0.9429
1.0	0.6446	0.6446	0.6446	0.6446	0.6446	0.6446	0.6446	0.6446	0.6446	0.6446	0.6446

method, as shown in Fig. 5. From Fig. 5, we intuitively observe that the height of CCL3S is higher than that of other algorithms, which can illustrate the robustness and stability of our method.

After the above discussion on classification performance and hypothesis testing, it is not difficult to find that CCL3S still has a satisfactory classification performance compared with many popular classifiers. In addition, different from neural network learning, classification results obtained through concepts are causal knowledge and have strong interpretability. Meanwhile, CCL3S is still a machine-learning method, so parameters play a significant role in the system. In the following subsection, it is necessary to analyze the influence of parameters on the CCL3S system.

5.3. Parameters analysis

In the previous subsection, we demonstrated the efficacy of CCL3S in classification by comparing it with several popular classification methods. It should be pointed out that the parameter (δ, δ') greatly influences the fuzzy three-way concept space construction of the core gene. Therefore, it is necessary to analyze the influence of parameter (δ, δ') changes on the performance of CCL3S. Then, we set the step size to 0.1 for all gene datasets in our method, namely, $(\delta, \delta') \in \{0, 0.1, 0.2, \ldots, 1\} \times \{0, 0.1, 0.2, \ldots, 1\}$.

For the same parameter (δ, δ'), we conducted ten-fold cross-validations on the same gene datasets, and the classification accuracy was calculated. Fig. 6 illustrates the changing trend of the mean accuracy of CCL3S along with the parameter differences. More details can be found in Tables 9-17. From these tables, we find that the classification accuracy of algorithms varies greatly with δ at a given δ', but does not change much with δ' when δ set in most cases. These two parameters affect the final classification performance and must be selected on different datasets.

6. Conclusions

The two emerging studies of artificial intelligence and cognitive computing, namely, cognitive learning and concept learning, can achieve the same result by different methods. While cognitive learning explores the learning law of the learning theory of the human cognitive process, concept learning reveals the systematic law of the human brain learning concepts from given clues through specific cognitive models. Based on the unified viewpoint, many scholars began to research concept cognitive learning, which simulates the human cognitive procedure by integrating concept learning and concept learning. Although concept-cognitive learning has made considerable achievements in theoretical promotion and model construction, its application research is still in its infancy.

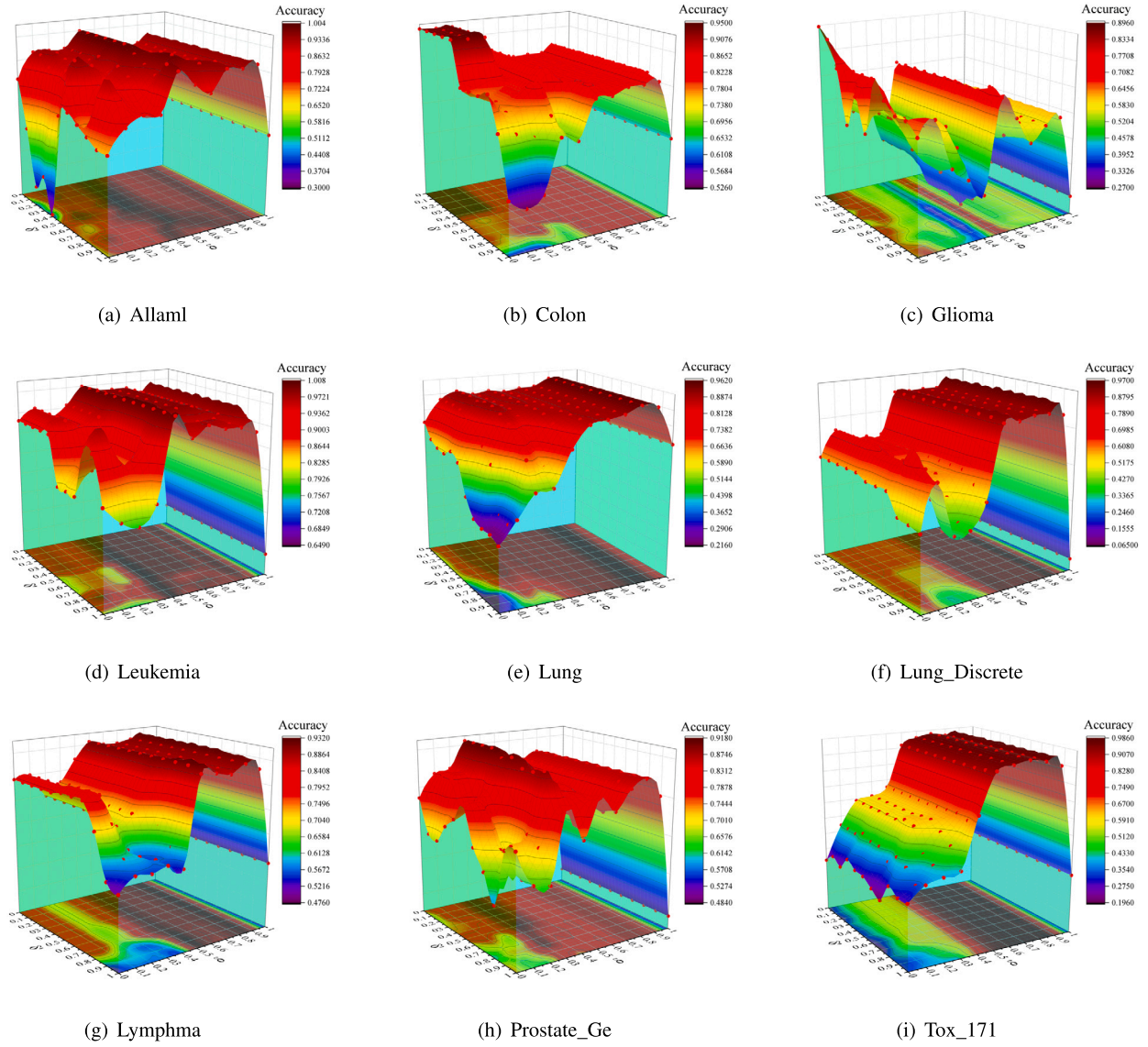


Fig. 6. Relationship between the parameters (δ, δ') and accuracy of CCL3S on 9 selected gene datasets.

Table 10
Classification accuracy of different parameters on Colon gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.9357	0.9357	0.9357	0.9357	0.9357	0.8071	0.8071	0.8071	0.8238	0.7286	0.5595
0.1	0.9333	0.9333	0.9333	0.9333	0.9333	0.7833	0.7833	0.7833	0.7667	0.7190	0.5262
0.2	0.9333	0.9333	0.9333	0.9333	0.9333	0.8024	0.8024	0.8024	0.8024	0.7024	0.5548
0.3	0.8024	0.8024	0.8024	0.8024	0.8024	0.8024	0.8024	0.8024	0.8357	0.7548	0.7071
0.4	0.8571	0.8571	0.8571	0.8571	0.8571	0.8524	0.8524	0.8524	0.7071	0.6905	0.6881
0.5	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8000
0.6	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8167	0.8000
0.7	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190
0.8	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190	0.8190
0.9	0.8381	0.8381	0.8381	0.8381	0.8381	0.8381	0.8381	0.8381	0.8381	0.8381	0.8214
1.0	0.6429	0.6429	0.6429	0.6429	0.6429	0.6429	0.6429	0.6429	0.6429	0.6429	0.6429

This work aims to concentrate on an application problem of concept-cognitive learning for medical decision-making, especially in tumor gene data analysis, from an interpretability viewpoint. Hence, it is worth mentioning that, different from neural network learning, the result of concept-cognitive learning is generally causal knowledge, which has strong interpretability. Moreover, this

Table 11
Classification accuracy of different parameters on Glioma gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.8950	0.8550	0.7550	0.5500	0.6750	0.5500	0.7650	0.7050	0.6650	0.6650	0.6250
0.1	0.7350	0.7350	0.7350	0.7350	0.7350	0.6950	0.6150	0.6150	0.5350	0.6400	0.6750
0.2	0.5350	0.5350	0.5550	0.5750	0.5750	0.5700	0.5300	0.5550	0.4750	0.4600	0.4900
0.3	0.5600	0.5600	0.5600	0.5600	0.5600	0.5400	0.5400	0.6000	0.5950	0.5350	0.4350
0.4	0.3900	0.3900	0.3900	0.3900	0.3650	0.3050	0.3050	0.3050	0.2850	0.3300	0.3650
0.5	0.7150	0.7150	0.7150	0.7150	0.7150	0.7150	0.7150	0.7100	0.7100	0.7350	0.7100
0.6	0.5250	0.5250	0.5250	0.5250	0.5250	0.5250	0.5250	0.5250	0.5250	0.5450	0.6250
0.7	0.5400	0.5400	0.5400	0.5400	0.5400	0.5400	0.5400	0.5400	0.5400	0.5800	0.5200
0.8	0.5750	0.5750	0.5750	0.5750	0.5750	0.5750	0.5750	0.5750	0.5750	0.5750	0.5750
0.9	0.5950	0.5950	0.5950	0.5950	0.5950	0.5950	0.5950	0.5950	0.5950	0.5950	0.5950
1.0	0.2700	0.2700	0.2700	0.2700	0.2700	0.2700	0.2700	0.2700	0.2700	0.2700	0.2700

Table 12
Classification accuracy of different parameters on Leukemia gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.9304	0.9304	0.9304	0.9304	0.9304	0.8196	0.8196	0.8196	0.9304	0.9321	0.8304
0.1	0.9571	0.9571	0.9571	0.9571	0.9571	0.8714	0.8714	0.8714	0.9714	0.9286	0.7911
0.2	0.9321	0.9321	0.9321	0.9321	0.9321	0.8750	0.8750	0.8750	0.8750	0.8875	0.7750
0.3	0.9571	0.9571	0.9571	0.9571	0.9571	0.8429	0.8429	0.8429	0.9143	0.9286	0.8179
0.4	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
0.5	0.9875	0.9875	0.9875	0.9875	0.9875	0.9875	0.9875	0.9875	0.9750	0.9750	0.9482
0.6	0.9857	0.9857	0.9857	0.9857	0.9857	0.9857	0.9857	0.9857	0.9446	0.9714	0.9714
0.7	0.9857	0.9857	0.9857	0.9857	0.9857	0.9857	0.9857	0.9857	0.9589	0.9732	0.9589
0.8	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9571	0.9571
0.9	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9714	0.9429
1.0	0.6500	0.6500	0.6500	0.6500	0.6500	0.6500	0.6500	0.6500	0.6500	0.6500	0.6500

Table 13
Classification accuracy of different parameters on Lung gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.7136	0.6186	0.5840	0.5743	0.6143	0.5690	0.3800	0.2726	0.2471	0.2476	0.2179
0.1	0.8610	0.8610	0.8610	0.8510	0.8162	0.7817	0.6874	0.5986	0.3157	0.2919	0.3569
0.2	0.9105	0.9105	0.9105	0.8955	0.9105	0.9052	0.8757	0.8362	0.7671	0.6686	0.5000
0.3	0.8810	0.8810	0.8810	0.8810	0.8757	0.8757	0.8507	0.7967	0.7093	0.6102	0.5119
0.4	0.8964	0.8964	0.8964	0.8964	0.8914	0.8864	0.8862	0.8762	0.8367	0.8021	0.7324
0.5	0.8812	0.8812	0.8812	0.8812	0.8812	0.8812	0.8812	0.8812	0.8812	0.8762	0.8664
0.6	0.8960	0.8960	0.8960	0.8960	0.8960	0.8960	0.8960	0.8960	0.8960	0.8910	0.8860
0.7	0.9017	0.9017	0.9017	0.9017	0.9017	0.9017	0.9017	0.9017	0.9017	0.9017	0.9064
0.8	0.9505	0.9505	0.9505	0.9505	0.9505	0.9505	0.9505	0.9505	0.9505	0.9505	0.9505
0.9	0.9305	0.9305	0.9305	0.9305	0.9305	0.9305	0.9305	0.9305	0.9305	0.9305	0.9305
1.0	0.6840	0.6840	0.6840	0.6840	0.6840	0.6840	0.6840	0.6840	0.6840	0.6840	0.6840

Table 14
Classification accuracy of different parameters on Lung-Discrete gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.5821	0.5821	0.5821	0.5821	0.5821	0.5554	0.5554	0.5554	0.4446	0.4339	0.4179
0.1	0.7250	0.7250	0.7250	0.7250	0.7250	0.6964	0.6964	0.6964	0.7804	0.6964	0.6536
0.2	0.6625	0.6625	0.6625	0.6625	0.6625	0.5946	0.5946	0.5946	0.5000	0.3625	0.3643
0.3	0.6643	0.6643	0.6643	0.6643	0.6643	0.5964	0.5964	0.5964	0.4946	0.3857	0.3732
0.4	0.6643	0.6643	0.6643	0.6643	0.6643	0.6268	0.6268	0.6268	0.6250	0.5679	0.5018
0.5	0.9036	0.9036	0.9036	0.9036	0.9036	0.9036	0.9036	0.9036	0.9036	0.9036	0.8893
0.6	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.8875
0.7	0.9054	0.9054	0.9054	0.9054	0.9054	0.9054	0.9054	0.9054	0.9054	0.9054	0.9054
0.8	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018	0.9018
0.9	0.9000	0.9000	0.9000	0.9000	0.9000	0.9000	0.9000	0.9000	0.9000	0.9000	0.8857
1.0	0.0661	0.0661	0.0661	0.0661	0.0661	0.0661	0.0661	0.0661	0.0661	0.0661	0.0661

paper also provides a new thought of tumor diagnosis based on gene data analysis via the selected core gene for data classification and builds a classifier model from a cognitive viewpoint.

Our work studies the fuzzy 3W-concept fusion on the basis of the core gene for tumor diagnosis. This idea does not focus on researching feature selection and classification mechanisms but provides a new perspective for gene data analysis in medical decision-making. Hence, some important and interesting problems still exist to be a concern, such as how to transfer learned reasonable concepts to practical problem-solving. In addition, a concept-cognitive learning system for dynamic data also deserves to be explored.

Table 15
Classification accuracy of different parameters on Lymphoma gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.7889	0.7889	0.7889	0.7889	0.7889	0.8011	0.8011	0.8011	0.7000	0.5289	0.5022
0.1	0.8000	0.8000	0.8000	0.8000	0.8000	0.8089	0.8089	0.8089	0.7156	0.5989	0.5567
0.2	0.7000	0.7000	0.7000	0.7000	0.7000	0.6789	0.6789	0.6789	0.6033	0.5956	0.5500
0.3	0.7511	0.7511	0.7511	0.7511	0.7511	0.7178	0.7178	0.7178	0.5611	0.5700	0.5667
0.4	0.8433	0.8433	0.8433	0.8433	0.8433	0.8433	0.8433	0.8433	0.6756	0.6067	0.5400
0.5	0.9133	0.9133	0.9133	0.9133	0.9133	0.9133	0.9133	0.9133	0.9133	0.9133	0.8922
0.6	0.8956	0.8956	0.8956	0.8956	0.8956	0.8956	0.8956	0.8956	0.8956	0.8956	0.8856
0.7	0.8933	0.8933	0.8933	0.8933	0.8933	0.8933	0.8933	0.8933	0.8833	0.8833	0.8722
0.8	0.9044	0.9044	0.9044	0.9044	0.9044	0.9044	0.9044	0.9044	0.9044	0.9044	0.9044
0.9	0.8956	0.8956	0.8956	0.8956	0.8956	0.8956	0.8956	0.8956	0.8856	0.8856	0.8756
1.0	0.4767	0.4767	0.4767	0.4767	0.4767	0.4767	0.4767	0.4767	0.4767	0.4767	0.4767

Table 16
Classification accuracy of different parameters on Prostate-GE gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.7709	0.6818	0.6745	0.7236	0.7527	0.8000	0.7036	0.6545	0.5855	0.7318	0.7418
0.1	0.8318	0.8318	0.8318	0.7618	0.7718	0.8027	0.7736	0.7018	0.7218	0.6527	0.6527
0.2	0.8409	0.8409	0.8409	0.7809	0.8218	0.7818	0.6836	0.6936	0.7436	0.7218	0.6427
0.3	0.9118	0.9118	0.9118	0.9118	0.8927	0.9018	0.8809	0.8809	0.8909	0.8109	0.8218
0.4	0.8836	0.8836	0.8836	0.8836	0.8836	0.8836	0.8545	0.8345	0.8255	0.8127	0.7364
0.5	0.8309	0.8309	0.8309	0.8309	0.8309	0.8309	0.8309	0.8409	0.8318	0.8218	0.8327
0.6	0.8027	0.8027	0.8027	0.8027	0.8027	0.8027	0.7827	0.7827	0.7918	0.7818	0.7918
0.7	0.8418	0.8418	0.8418	0.8418	0.8418	0.8418	0.8418	0.8418	0.8418	0.8518	0.8418
0.8	0.8609	0.8609	0.8609	0.8609	0.8609	0.8609	0.8609	0.8609	0.8609	0.8609	0.8609
0.9	0.8118	0.8118	0.8118	0.8118	0.8118	0.8118	0.8118	0.8118	0.8118	0.8118	0.8118
1.0	0.4845	0.4845	0.4845	0.4845	0.4845	0.4845	0.4845	0.4845	0.4845	0.4845	0.4845

Table 17
Classification accuracy of different parameters on Tox-171 gene data.

δ, δ'	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
0.0	0.2235	0.2765	0.2412	0.3176	0.2824	0.2765	0.2353	0.2000	0.3176	0.2824	0.2882
0.1	0.4412	0.4412	0.4353	0.4647	0.4412	0.4412	0.3765	0.4353	0.4059	0.3353	0.3706
0.2	0.5882	0.5882	0.5882	0.5882	0.5941	0.5882	0.6118	0.6000	0.4647	0.4294	0.3941
0.3	0.6059	0.6059	0.6059	0.6059	0.6059	0.6059	0.6176	0.6235	0.5765	0.5235	0.4118
0.4	0.6529	0.6529	0.6529	0.6529	0.6529	0.6529	0.6588	0.6647	0.6706	0.6529	0.7059
0.5	0.9176	0.9176	0.9176	0.9176	0.9176	0.9176	0.9176	0.9176	0.9176	0.9235	0.9353
0.6	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588
0.7	0.9765	0.9765	0.9765	0.9765	0.9765	0.9765	0.9765	0.9765	0.9765	0.9765	0.9765
0.8	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588	0.9588
0.9	0.9235	0.9235	0.9235	0.9235	0.9235	0.9235	0.9235	0.9235	0.9235	0.9235	0.9235
1.0	0.2588	0.2588	0.2588	0.2588	0.2588	0.2588	0.2588	0.2588	0.2588	0.2588	0.2588

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

No data was used for the research described in the article.

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