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Online Unsupervised Heterogeneous Group Streaming Feature Selection

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Abstract

Online streaming feature selection emerges as a preeminent technique for extracting optimal feature subsets from high-dimensional datasets, while traditional feature selection methods are inefficient for vast volumes of data. In practical applications, there is a large amount of unlabeled data, and features may be heterogeneous and be generated in streaming groups. Besides, since streaming features arrive randomly, predicting feature type information for the following arriving streaming features in advance is impractical. Most existing supervised streaming feature selection methods need labeled data for training. Meanwhile, existing unsupervised streaming feature selection techniques have the presumption of feature homogeneity and an inability to accommodate unknown feature types. To solve this practical problem, we propose a new online unsupervised heterogeneous group streaming feature selection method named UHGSFS. Based on maximum information coefficient and adaptive clustering techniques, UHGSFS does not require parameter setting for streaming feature clustering and utilizes feature redundancy minimization to select the most representative features. Extensive experimentation was conducted on 14 benchmark datasets, complemented by comparative analyses against state-of-the-art supervised and unsupervised streaming feature selection algorithms. Experimental results demonstrate the effectiveness and practicality of our new method.

Keywords: Unsupervised Feature Selection, Streaming Feature, Unknown Feature Type, Maximal Information Coefficient

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1. Introduction

The primary objective of feature selection is to discern optimal subsets from the original feature set, thereby enhancing model performance [1]. In the contemporary era of big data, the exponential proliferation of data has precipitated the advent of expansive feature space, thereby engendering what is commonly referred to as the "dimensionality disaster" [2]. Feature selection emerges as a pivotal instrument to address this predicament. Through the choosing and curation of pertinent features and the discarding of extraneous ones, feature selection not only refines learning performance but also engenders heightened computational efficiency and diminished memory storage requirements [3, 4].

Figure 1: Illustration of a real-world scenario for unsupervised heterogeneous group streaming feature selection. When a new patient enters the hospital, several inspection items are required to determine the cause of the illness. The results (features) of these different inspection items arrived randomly over time, resulting in groups of heterogeneous streaming features. How to deal with the heterogeneous streaming feature groups without labeling information is the problem we want to investigate.

With the increase in data volume and dimensionality, traditional feature selection methods can no longer meet the demand in terms of efficiency [2]. Meanwhile, traditional feature selection methods assume that all instances and features in the target dataset can be required before learning [5]. However, in real application scenarios, e.g., in image analysis [6], Mars exploration [7], and healthcare [8], we are often confronted with streaming features. As shown in Fig.1, a patient needs to be examined by different items, and different features are constantly generated by different examination items. The task of online streaming feature selection is to dynamically process features that keep arriving over time while the number of instances remains fixed [9]. Online streaming feature selection faces two challenges: 1) The size of the entire feature space is unknown or even infinite; 2) The algorithm needs to decide whether to keep or discard newly arrived features since

storing all these streaming features is impossible [10].

In recent years, many techniques for supervised streaming feature selection have been proposed, such as Fast-OSFS [9], OFS-Density [11], OFS-3WD [10], OMSFSLC [12] and LOSSA [13]. They mainly contain these four steps: 1) Require new streaming features (single/group); 2) Determine the new features to be added to the selected subset or discarded directly by analyzing the feature relevance; 3) Update the selected feature subset by redundancy analysis; 4. Repeat steps 1 to 3 until all the features have been examined. Although considerable progress has been made in supervised streaming feature selection, the reliance on data labeling makes these algorithms unsuitable for realistic scenarios with large amounts of unlabeled data.

On the other hand, unsupervised streaming feature selection needs to be studied more. In [14], an unsupervised streaming feature selection approach (named USFS) has been introduced for analyzing social media data using link information. USFS is only applicable to isomorphic data and has high computational complexity. In [15], Unsupervised Feature Selection for Dynamic Features (named UFSSF) extends k-means clustering by clustering continuous streaming features at the individual level. However, the performance of k-means clustering is sensitive to noise and is not applicable to handle discrete features. [16] proposed an online unsupervised streaming feature selection framework based on dynamic density feature clustering, but it needs to know the type of streaming features (discrete or continuous) in advance. [17] proposed a new feature selection method for feature streaming, which introduces a dynamic similarity graph to evaluate irrelevant features adaptively and utilizes similarity graph diffusion to eliminate those irrelevant features in the feature streams. The current state-of-the-art unsupervised streaming feature selection methods exhibit significant computational complexity, are constrained to isomorphic features, and cannot effectively handle heterogeneous streaming features. Besides, the order of arrival of streaming features is random in practical. Therefore, it is unrealistic to know the feature type of the next arriving streaming features in advance.

For example, in a real-world application scenario (shown in Fig.1), a new patient needs various medical diagnostic procedures in sequence to determine the cause of the disease. Over time, these inspection items will continue to generate various streaming data, such as image data from X-rays, signal data from ECGs, and text data from electronic case reports. The influx of large amounts of streaming data makes applying feature selection imperative. This issue has three challenges: 1) Due to the lack of labeled information related to new patients, supervised streaming feature selection

methods that rely on labeled data become inapplicable; 2) Streaming features are continuously generated, and the feature selection process should be applied on the fly; 3) The feature types of each group streaming features are heterogeneous. Moreover, the arrival of the next streaming group is random. In other words, we cannot know the feature type of the next streaming group in advance. Most existing unsupervised feature selection methods, which rely on the prerequisites of feature isomorphism and feature type prediction, are insufficient to cope with this intricate situation.

Motivated by this, we investigate a new unsupervised online heterogeneous streaming feature selection method where the streaming features are heterogeneous and dynamically generated in groups. Besides, we assume that the feature types of streaming features are unknown in advance for practical situations. Specifically, we use MIC (Maximum Information Coefficient) [18], which can discover nonlinear relationships and complex correlation structures to measure the relationship between heterogeneous features. Then, we utilize feature streaming density analysis to compute the density of each feature. Based on this, we propose a new adaptive feature clustering to group features with high redundancy. Finally, we perform the feature selection by selecting the feature with the highest density for the streaming feature selection. Our new method satisfies feature relevance maximization and feature redundancy minimization. The main contributions of this paper are as follows:

- We first focus on the practical issue of online unsupervised heterogeneous streaming feature selection where streaming features are generated dynamically in groups without the information of feature types in advance.
- We propose a new unsupervised heterogeneous group streaming feature selection method based on density-based streaming feature clustering. Specifically, we first evaluate the density of arriving features through MIC and feature streaming density formulas. We then employ a novel adaptive feature clustering method that does not require parameter setting for feature clustering and utilizes feature redundancy minimization to select the most representative subset of features.
- Extensive experiments were conducted on 14 datasets, involving a meticulous examination and comparison with eight online supervised streaming feature selection methods and one online unsupervised streaming feature selection algorithm. The experimental results, coupled with

rigorous statistical analyses, conclusively indicate that, in the absence of labeling information and under the circumstance of unknown streaming feature types, the performance of our new method is tantamount to that of supervised streaming feature selection algorithms or even better.

The rest of this article is organized as follows. In Section 2, we describe related work. In Section 3, the formal definition of the problem, the technology involved, and a new approach to unsupervised heterogeneous streaming Feature Selection is proposed. Section 4 gives the experimental analysis. Finally, Section 5 gives a brief conclusion.

2. Related Work

Research on feature selection has been conducted for many years, and a large number of excellent algorithms have been proposed [5]. According to different types of data generation, we can classify feature selection into two categories: traditional feature selection for static data and online feature selection for streaming data [2].

2.1. Traditional Feature Selection Methods

Depending on how the labeling information is used, traditional feature selection algorithms can be classified as supervised algorithms, unsupervised, and semi-supervised algorithms.

Supervised feature selection assumes we can require all the label information for the training data. More specifically, Fisher Score [19] achieved the same eigenvalues in the same class and different eigenvalues in different classes by calculating the ratio of interclass separation and intraclass variance for each feature. ReliefF [20] was a feature selection method based on the distance between samples, which performs feature selection by calculating the importance of each feature for sample classification. Mutual Information can measure the correlation between each feature and the target variable, and [21] discussed the practical implementation of mutual information (MI) in feature selection.

Without the labeling information, unsupervised feature selection cannot use the label to measure the importance of each feature. For example, Laplacian Score [22] evaluated the importance of features by their variance and power of locality preserving and matches similar features by constructing a nearest neighbor graph. FSFS [23] introduced the Maximum Information Compression

Index (MICI) to reduce feature redundancy by using clustering features with high similarity and selecting the most compact feature in each cluster (determined by the distance between features). MCFS [24] processed feature selection by exploring the clustering structure of the data and then using regularized regression to measure the importance of the features and ultimately selecting the features with the most informative value. SPLR [25] was an unsupervised feature selection method that combines self-paced learning into a subspace learning framework. SPLR preserved global data reconstruction information while effectively reducing the adverse effects of outliers. SDFS [26] was a multi-view unsupervised feature selection based on structural regularisation. SDFS calculated the similarity matrix of sample space from different views and automatically weighted each view-specific graph to learn a consensus similarity graph.

Besides, Semi-supervised feature selection assumes that we have a small amount of labeled data and a large amount of unlabelled data. For instance, SRFS [27] was a semi-supervised feature selection method that treats unlabelled data in a Markov blanket as labeled data through relevance gain. A-SFS [28] was a semi-supervised feature selection based on multi-task self-supervision, which innovatively introduces a self-supervision mechanism based on deep learning into the feature selection problem.

In summary, traditional feature selection methods necessitate full knowledge of the feature space before learning, rendering them unsuitable for online scenarios. Moreover, the substantial volume of data often results in computational overhead and time complexity that traditional feature selection methods, when applied to large-scale datasets, frequently fail to meet real-time requirements.

2.2. Online Streaming Feature Selection Methods

2.2.1. Supervised Streaming Feature Selection

With the advent of the big data era, online streaming feature selection has been a research hotspot dealing with high-dimensional datasets. In general, online supervised streaming feature selection can be divided into individual streaming feature selection and group streaming feature selection.

Individual streaming feature selection assumes features arrive one by one over time. For example, Grafting [29], which employs a stagewise gradient descent approach, represented the first individual-level streaming feature selection (SFS) method. Grafting considered feature selection as an integral part of learning a predictor within a regularized framework. Zhou et al. [30] pro-

posed the Alpha-investing algorithm, which leverages streamwise regression for online streaming feature selection. Specifically, Alpha-investing is utilized as penalized likelihood ratios in streamwise regression for streaming feature selection (SFS). Based on the redundancy minimization and relevance maximization processes, the online streaming feature selection (OSFS) framework and its named Fast-OSFS [9] were proposed. The Scalable and Accurate Online Feature Selection Approach (SAOLA) [31] maintained a parsimonious model by using a pairwise comparison method based on mutual information theory. OMSFSLC [12] investigated multi-label streaming feature selection in real-life scenarios where labels are interdependent and interrelated, and the method evaluates the relevance of features to labels through mutual information and correlation between features and labels. OFS-3WD [10] was a new online scalable streaming feature selection framework from a dynamic decision-making perspective, which dynamically classifies input features as selected, discarded, or delayed to minimize decision risk. OCFSSFs [32] was an online feature selection method based on causal discovery by mining and identifying relationships in Markov blankets about parents and children (PCs) and spouses. LOSSA [13] was an online sparse flow feature selection algorithm based on latent factor analysis, which uses latent factor analysis to solve the problem of missing data in sparse flow features. Meanwhile, some Rough Set-based SFS methods were proposed recently, including K-OFSD [33], OFS-A3M [34], OFS-density [11], and ASFS [35].

Existing supervised methods have achieved good performance in different aspects. However, these methods cannot be applied to unsupervised application scenarios since they require labeled data for training.

2.2.2. Unsupervised Streaming Feature Selection

In practice, data is mostly unlabelled. Online unsupervised streaming feature selection methods were proposed to handle online feature selection without label information.

Specifically, in [14], the authors performed unsupervised streaming feature selection against social media data by identifying link information. This method is only applicable to social media data. Meanwhile, it can only handle isomorphic feature streaming and requires stable link information with high computational complexity. In [15], the method implemented unsupervised streaming feature selection based on k-means for continuous individual feature streams, which cannot handle discrete features because k-means is sensitive to noise. In [16], the authors developed a feature density formulation adapted to streaming features and achieved feature correlation maximization and

redundancy minimization based on density clustering. However, it can not handle feature selection for mixed streaming data and artificially sets a parameter for clustering, which is not in line with real-world applications' unsupervised and unparameterized nature. [17] proposed a new feature selection method for feature streaming, which introduces dynamic similarity graphs to adaptively evaluate irrelevant features and uses similarity graph diffusion to eliminate those irrelevant features in the feature streaming.

In sum, most existing streaming feature selection approaches are constructed upon supervised information, which overlook the scarcity of labels in practical applications. While some researchers have introduced unsupervised streaming feature selection methods, their high computational complexity, restriction to isomorphic features, and incapacity to handle unknown features render these methods unsuitable for addressing unsupervised heterogeneous streaming feature selection challenges.

3. The Proposed Framework

This section describes the definition of the problem and the concrete implementation of the proposed method. We summarize some of the notations used in this paper in Table 1.

3.1. Notations, Assumptions, and Definitions

Let $\mathbb{F} = \{G_1, G_2, ..., G_T\}$ representes the entire streaming features, where $G_t = \{f^1_{G_t}, f^2_{G_t}, ..., f^m_{G_t}\}$ denotes the streaming feature group arriving at timestamp t. For each streaming group G_t, it is heterogeneous, and we cannot know the feature type information for each streaming feature $f^i_{G_t}$ in it. At each timestamp t, FS_t denotes the selected feature subset by the algorithm. Online unsupervised streaming feature selection aims to obtain an optimal feature subset FS_t from $\mathbb{F}$ under the following assumptions:

- The quantities of samples and classes are fixed;
- Streaming features arrive as groups over time;
- The label and feature type information for each streaming group are unknown.

Since feature space changes over time, we cannot store all features for online streaming feature selection. Meanwhile, since there is no labeling information, we have no basis for judging the importance of features. Therefore, unsupervised streaming feature selection often requires discovering

Table 1: Summary on Mathematical Notations

Notations	Definition
t	the timestamp
n	total number of samples
G_t	a group of streaming features arrive at timestamp t
T	the total number of streaming feature groups
m	the number of the features in the group G_t
f_i^i	the i^{th} streaming feature in G_t
FS_t	the selected feature subset after timestamp t
D_{f_i}	the density value of streaming feature f_i
FC_t	the extracted streaming feature cluster set at timestamp t
C	a cluster of streaming features in FC_t
r_C	the radius of the cluster C
$\|FC_t\|$	the number of feature clusters in FC_t
$d(f_a, f_b)$	the distance from the feature f_a to the feature f_b

relationships between features to select or discard features. In addition, we need an effective metric to explore the relationships between heterogeneous streaming features.

To solve this problem, we apply density-based streaming feature clustering to select the representative features and discard the redundant features. Suppose the streaming features are clustered into multiple clusters FC_t at timestamp t, and C is one of cluster in FC_t.

Definition 1. **[Representative feature]** The representative feature in streaming feature cluster C is defined as the feature with the maximal density as: $f_R = \underset{f \in C}{max}\{D_f\}$, where D_f is the density value of streaming feature f.

For the new arriving streaming group G_t, we calculate the density of each streaming feature in it and cluster them into multiple clusters. We designate the feature by the local maximum density value as the cluster center and the representative feature.

Definition 2. **[Redundant features]** For the features in the same cluster C, features other than representative features are considered redundant.

Based on steaming feature clustering, highly correlated features are clustered in the same cluster. According to **Definition 1**, we selectively choose the most representative feature from each cluster and consider the other features redundant. This approach can effectively reduce feature redundancy.

Based on these two definitions, our online unsupervised streaming feature selection method can effectively implement a strategy of maximizing relevance and minimizing redundancy.

3.2. Our New Framework

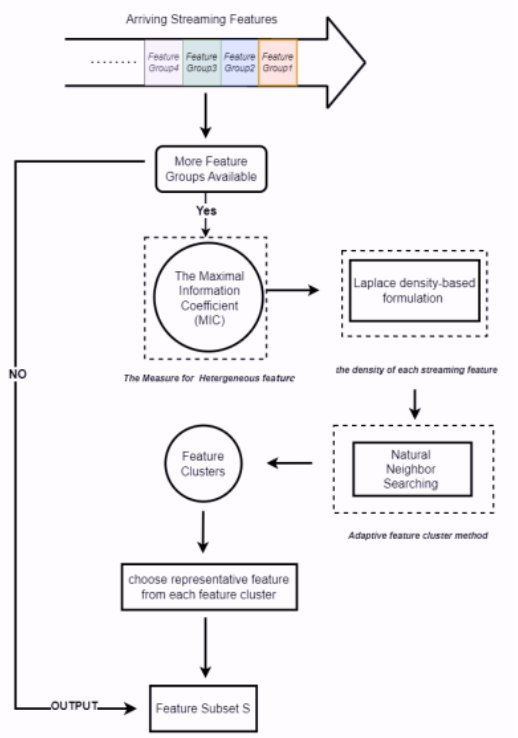


Figure 2: An overview of the Unsupervised Heterogeneous Group Streaming Feature Selection framework.

The depicted framework of our proposed Unsupervised Heterogeneous Group Streaming Feature Selection (UHGSFS) is illustrated in Fig.2. Specifically, we first apply the Maximum Information Coefficient (MIC) to measure the information between heterogeneous streaming features, which can discover complex linear relationships for a distance evaluation. Then, we calculate the density of each streaming feature. We select the feature with the current highest density to perform adaptive feature clustering to cluster the features into different clusters. Finally, we obtain the optimal feature subset by selecting the most relevant features and discarding redundant features.

3.2.1. The Measure for Unknown Type and Heterogeneous Feature

The generated streaming features in practical applications often exhibit heterogeneity. Meanwhile, each streaming feature arrives randomly, and we cannot know their feature types in advance. Previous streaming feature selection methods, supervised or unsupervised, have predominantly been designed to handle a single feature type (discrete or continuous). Therefore, there is an urgent need to develop novel metrics that can effectively address the challenges posed by heterogeneous streaming features of unknown types.

MIC (maximal information coefficient) is a data analysis algorithm that evaluates variable relationships without assuming data distribution [18]. MIC partitions a scatter plot into grids and computes dissimilarity using mutual information. The highest mutual information value represents the Maximum Information Coefficient (MIC). MIC has been proven to effectively measure the dependence of two variables and can capture a wide range of functional and unfunctional associations.

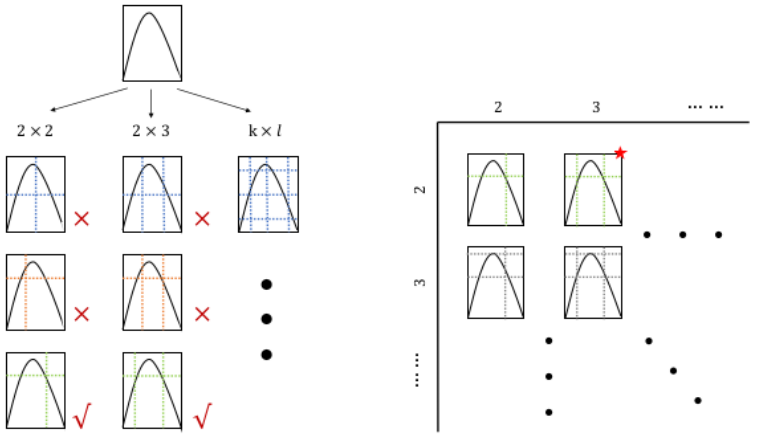
In Fig.3, MIC employs dynamic axis division, enabling the calculation of mutual information for both numerical and categorical data, rendering it highly versatile across diverse applications. For a two-dimensional variable dataset $D = \{(x_1, y_1), (x_2, y_2), ..., (x_n, y_n)\}$, the parameters (k, l) may assume any valid pair. The calculation of the MIC(D) is as follows:

$$MIC(D) = max\{M(D)_{k,l}\} \tag{1}$$

$$M(D)_{k,l} = \frac{maxMI(D)_{(k,l)}}{log(min\{k, l\})} \tag{2}$$

Where $MI(D)_{(k,l)}$ denotes the mutual information value divided according to the integers (k, l) on the two-dimensional variable dataset D. The size of k and l when the party mutual information is the maximum value can be obtained by the exhaustive method. $k \times l \leq B(n)$, B is a function of the sample size n expressed as $B(n) = n^{0.6}$.

For online heterogeneous streaming feature selection, the inherent uncertainty lies in the inability to ascertain the feature type of the next streaming feature preemptively. The Maximum Information Coefficient (MIC) uniquely quantifies correlations across various types of variables. In light of our objective to compute feature distances, we leverage the concept that higher correlations result in shorter distances. Therefore, we incorporate the complementary metric of $1 - MIC$ to effectively measure and represent the distances between these heterogeneous streaming features within our



(a) original instances distribution

(b) new spatial instancesdistribution aftertransductive warping

Figure 3: Taking a parabola as an example, a schematic diagram of calculating MIC.

novel information metric framework.

3.2.2. The Density of Streaming Feature

Before we cluster these arriving streaming features in groups, we need to calculate the density of each feature. In [16], the authors introduced a pioneering two-phase streaming clustering methodology referred to as **dpps-clustering**. This approach treats the critical data processing task as an optimization process, demonstrating superior efficacy even when substantial prior knowledge is lacking. [16] derived a multilevel lower bound function using the Laplacian density formula and replaced it with clusters. The density distribution in the input feature group is calculated, and the derived Laplacian density lower bound effectively solves the problem of noise features in the streaming. The lower bound density function of each streaming feature is calculated as follows:

$$D_{f_i} = \sum_{f_j \in G_t} e^{-(\frac{d(f_i,f_j)}{\beta_t})^{\gamma_t}} + \sum_{f_k \in FC_{t-1}} e^{-(\frac{d(f_i,f_k)}{\beta_t})^{\gamma_t}} \times D_{f_k} \tag{3}$$

where f_i is the streaming feature in group G_t, $d(f_i, f_j)$ is the feature distance between features f_i and f_j. Besides, for each selected candidate feature f_k in FC_{t-1}, we calculate the distance between f_i and f_k. D_{f_k} is the density value of f_k. β_t and γ_t are the normalization parameters and stabilization parameters at timestamp t, respectively. We employ the identical parameter estimation procedure

outlined in [36] to derive β_t and γ_t. Meanwhile, we define $d(f_i, f_j) = 1 - MIC(f_i, f_j)$ as the distance function in this paper.

By applying this formula, we can effectively estimate feature density within the current feature group by leveraging the selected candidate features and the current streaming feature group. Significantly, the recursive lower bound derived from this formula relies exclusively on the retention of clustering historical data (selected features), eliminating the need to store the entirety of the historical streaming data.

3.2.3. Adaptive Feature Cluster Method

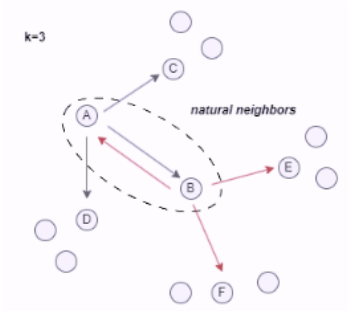


Figure 4: Natural neighborhood search. Suppose we are looking for k nearest neighbors (k=3). It can be observed that node A is closest to nodes B, C, and D. Meanwhile, node B is closest to nodes A, E, and F. Based on the natural neighbors search, it can be inferred that nodes A and B are neighbors.

"Natural Neighbors" introduces a novel paradigm of proximity akin to human social interactions: Take, for instance, a trio of individuals denoted as A, B, and C. If A lacks amicability towards B, while B reciprocates with friendliness towards A, one may infer that A's affinity towards B is unidirectional rather than a reciprocal friendship. Conversely, if A and C both display mutual animosity, it establishes that they do not share a close bond. In contrast, the amicability between B and C suggests a genuine friendship. Unlike traditional k-nearest neighbors search, Fig.4 illustrates the natural neighbor search process.

Diverging from the conventional k-nearest neighbor (KNN) approach, the natural nearest neighbor method leverages the intrinsic structure of the dataset to discern the closest neighbors for each data instance. Noteworthy is its unique capacity to dynamically ascertain the optimal number of nearest neighbors for each data point, obviating the need for a priori parameter specification.

Motivated by the notion of natural neighborhoods, we extend this concept to devise an adaptive feature clustering method tailored for feature streaming data.

Given a data set $\mathbb{X}$, we define $d(p,q)$ as the distance between data points p and q in $\mathbb{X}$. Let data point k be the k^{th} nearest neighbors of data point p. The interpretations of k-nearest neighbors, reversed k-nearest neighbors, natural stable state, and natural search neighbor are given as follows.

Definition 3. [**K-Nearest Neighbors**] **KNN**: For data point p, its k-Nearest Neighbors set can be expressed as:

$$KNN_k(p) = Find_{knn}(p,k) \tag{4}$$

where $Find_{knn}(p,k)$ represents the searching function of KNN which searches for the k^{th} nearest neighbors of p. Here, a KD tree can be utilized to accelerate the KNN searching process.

Definition 4. [**Stable Searching State**]: Suppose the searching round r increases from 1 to n. The natural neighbor searching becomes stable when the following condition is satisfied:

$$(\forall p \in \mathbb{X}) \wedge (\exists q \in \mathbb{X}) \wedge (p \neq q) \longrightarrow p \in KNN_r(q) \wedge q \in KNN_r(p) \tag{5}$$

When the stable searching state is reached, the maximal search round r is called the natural neighbor eigenvalue.

Definition 5. [**Natural Search Neighbors**]: When the natural neighbor searching process keeps a stable searching state, the data point p and data point q are natural neighbors if $p \in KNN_r(q)$ and $q \in KNN_r(p)$.

Motivated by the concept of natural neighbor search, we have formulated an algorithm for adaptive feature clustering, drawing upon the definition and analysis outlined above. A comprehensive exposition of the clustering process employing natural feature neighbor search is presented in Algorithm 1.

Specifically, for the target feature f, we aim to find its maximal natural neighbors as the cluster of f. Step 1 initializes $r = 1$. Then, we continuous search the r^{th} neighbor of f as q in Step 3. Steps 4-7 check whether f belongs to the r nearest neighbors of q. If it does, then r is incremented by 1. Otherwise, it means that feature f reaches the **STABLE SEARCHING STATE** and we end the searching.

After we have assigned all the features to the possible clusters by Algorithm 1, we determine whether there is a high degree of overlap between the clusters by the presence of a density valley

Algorithm 1 Natural Neighbor Clustering

Input:

F: Feature set;

f: Feature f;

Output:

C_f: The cluster of feature f;

Initialization: $r = 1$;
Repeat
    Find the r^{th} nearest neighbors of f as q
    If $f \in KNN_r(q)$
        $C_f = C_f \cup \{q\}$;
        r=r+1;
    End If
Until f reaches stable searching state
Return C_f

between the two clusters. Density valley [37] refers to a point between two cluster cores as follows:

Definition 6. [Density Valley]: Suppose f_B represents the boundary feature of cluster $C1$, f_{C1} and f_{C2} represent the cluster centers of the two clusters nearby, if $D_{f_B} < MIN(D_{f_{C1}}, D_{f_{C2}})$, it means that there exists a valley of density between these two clusters.

In other words, there is a density valley if the density of the boundary feature f_B is lower than the minimum of these two cluster cores. There is no need to merge if there is a density valley between these clusters. In contrast, if there is no density valley between the clusters, the two clusters highly overlap, so merging is required.

3.2.4. The Proposed Framework.

Since the online streaming feature selection operates unsupervised, it necessitates consideration of feature correlation and redundancy. Without data labels for measuring feature importance and relevance, we rely on the representation within each feature cluster to assess feature significance. In the context of density-based clustering methods, it is customary for the cluster center to exhibit the highest local density value, thus establishing the feature cluster center as the most pertinent feature within the cluster. Moreover, given that features with greater similarity are typically chosen within

feature clusters, it is reasonable to infer that features of the same cluster exhibit redundancy. By exclusively selecting feature centers, we can effectively minimize redundancy. Employing these two strategies enables the extraction of crucial feature subsets from a feature streaming while maintaining low redundancy and high correlation among them. Drawing from the preceding solution, we introduce UHGSFS, an unsupervised method designed to select heterogeneous streaming features, as shown in 2.

Algorithm 2 Unsupervised Heterogeneous Group Streaming Feature Selection(UHGSFS)

Input:

G_t: a group of streaming features arrive at timestamp t;

Output:

FS_t: the selected feature subset;

Repeat
  $D_{G_t} = \{\}$: the density values of each feature in G_t;
  For each feature $f^i_{G_t} \in G_t$
    Calculate $D_{f^i_{G_t}}$ using Eq.3 with MIC;
    $D_{G_t} = D_{G_t} \bigcup \{D_{f^i_{G_t}}\}$;
  End For
  Rank all features in G_t based on their density values;
  $FC_t = \{\}$: the extracted streaming feature cluster set;
  Repeat
    Select the feature f in G_t with the maximal density value
    Generate the cluster C_f by Algorithm 1;
    $FC_t = FC_t \cup C_f$;
    G_t=G_t-C_f;
  Until no more features in G_t
  Update FC_t by merging clusters based on possible density valleys;
  If FS_{t-1} in not empty
    Merge FC_t with historical feature clusters in FC_{t-1};
  End If
  FS_t=select representative feature from each cluster in FC_t;
Until no more streaming feature groups
Return FS_t

Specifically, suppose UHGSFS gets a new streaming feature group G_t at timestamp t. Steps 3-6 calculate the density values of each feature in G_t in terms of Eq.3 and the maximum information coefficient (MIC). In step 7, we sort all the features by their density values. Steps 9-14, we select feature f with the highest density in G_t at each time and apply Algorithm1 to generate the cluster of f until all the features are assigned to the clusters. Step 15 determines whether merging is required by the presence of density valleys between the two clusters. In steps 16-18, we check the possible merging of current clusters FC_t and historical clusters in FC_{t-1}. Finally, we select the representative feature from each cluster as the selected feature subset.

3.3. Time Complexity

In our algorithm, the computation of the feature distance matrix for the unknown heterogeneous feature streaming necessitates $O(m^2)$ distance calculations. The search for feature clusters through our natural neighbor search method incurs $O(nlogn)$ computational complexity. Likewise, the merging process involving historical feature clustering and new feature clustering entails $O(|FC_t||FC_{t-1}|)$ calculations. As a result, the worst-case time complexity of our algorithm is expressed as $O(m^2 + nlogn + |FC_t||FC_{t-1}|)$.

4. Experiments

In this section, we conduct experiments on several benchmark datasets and comparative studies with state-of-the-art supervised and unsupervised streaming feature selection methods to demonstrate the effectiveness of our new framework.

4.1. Experiment Setup

4.1.1. Datasets

To verify the effectiveness of our proposed new method, we conducted extensive experiments on 14 real-world datasets, including four discrete datasets and ten consecutive datasets. We can find these datasets from the ASU feature selection repository[1]. Table 2 summarizes the properties of these datasets in terms of sample size, feature size, class size, application domain, and type.

[1] Public available at https://jundongl.github.io/scikit-feature/datasets.html

Table 2: Real-world Datasets

Data Set	instances	Features	Classes	Domain	Type
Arcene	200	10000	2	Medical	continuous
AllMall	72	7129	2	Medical	continuous
LUNG	73	325	7	Medical	discrete
Lymphoma	96	4026	9	Medical	discrete
Carcinom	174	9182	11	Biological	continuous
Colon	62	2000	2	Biological	discrete
GLI-85	85	22283	2	Biological	continuous
GLIMA	50	4434	4	Biological	continuous
Nci-9	60	9712	9	Biological	discrete
SMK-CAN-187	187	19993	2	Biological	continuous
Coil20	1440	1024	40	Image	continuous
Orlraws10P	100	10304	10	Image	continuous
Pixraw10P	100	10000	10	Image	continuous
WarpPIE10P	210	1024	15	Image	continuous

4.1.2. Comparing Algorithms

We compare our new method with nine state-of-the-art streaming feature selection methods [1], including Alpha-investing [30], SAOLA [31], Fast-OSFS [9], OFS-Density [11], OFS-A3M [34], OFS-3WD [10], Group-SAOLA [31], OGSFS-FI [38] and OUFSDFC [16]. The first eight algorithms are supervised, and OUFSDFC is an unsupervised method. Meanwhile, the first six algorithms are individual streaming feature selection methods, while the last three are group-based approaches. According to [38], the α value of Fast-OSFS, SAOLA, and Group-SAOLA is set to 0.01. For Alpha-investing, OFS-density, OFS-A3M, and OGSFS-FI, the default parameter settings in [11, 34] are used to obtain the final selected feature subset.

4.1.3. Evaluation Metrics

Classification performance is used to show the effectiveness of these competing algorithms. Fundamental classifiers were employed, including KNN (k = 5), SVM (with the linear kernel), and DT(decision tree), to evaluate the feature subset selected in the experiment. For each dataset, we use a 5-fold cross-validation method, dividing the dataset into five equal parts, with four parts

[1] Public available at https://github.com/kuiy/LOFS, and https://github.com/doodzhou/OSFS.

for training and one part for testing each time. We utilize the same training and testing set division for each competing algorithm.

Two well-known evaluation metrics, including Accuracy (Acc) and f-score (F_{mac}), are used as performance evaluation metrics. To account for imbalances in class distribution, we use the macro-average of f-score, which is expressed as follows:

$$F_{mac} = \frac{1}{n_c} \sum_{i=1}^{n_c} F_i \tag{6}$$

where F_i and n_c denote the F-measure for the i^{th} class and the number of classes, respectively.

Besides, we conducted the statistical test using Friedman's test at a significance level of 95%, assuming the null hypothesis [39]. If the null hypothesis is rejected, we conduct the Nemenyi test as a post-hoc test and construct critical distance (CD) graphs [40].

4.1.4. Computational Device

All experiments were conducted on a computer running Windows 10, AMD Ryzen 7 3700X 8-core processor 3.6 GHz, 16 GB RAM.

4.2. Results and Discussions

Tables 3-8 present a comprehensive summary of the accuracy (ACC) and F_{mac} achieved by these competing algorithms, utilizing KNN, SVM, and DT classifiers. Additionally, Table 9 provides insights into each algorithm's average number of selected features.

UHGSFS and FOUFSDFC are implemented in Python, while the other eight algorithms are implemented in Matlab. Thus, we can only compare the running time between UHGSFS and OUFSDFC. Fig.6 compares the running times between UHGSFS and OUFSDFC algorithms.

For the accuracy metric (ACC), the p-values obtained from the Friedman test for KNN, SVM, and DT(decision tree) classifiers are 3.04E-04, 3.00E-03, and 1.03E-01, respectively. Similarly, for the F_{mac}, the p-values for KNN, SVM, and DT classifiers are 3.84E-04, 2.91E-02, and 1.69E-02, respectively. These p-values indicate significant differences exist in both accuracy and F_{mac} among these competing algorithms. Therefore, Fig.5 illustrates the statistical analysis conducted to evaluate the prediction accuracy and F_{mac} of these competing algorithms in the context of KNN, SVM, and DT(decision tree) classifiers.

From Tables 3-8 and Fig.5-6, we can observe:

Table 3: Predictive Accuracy Using KNN as the Classifier

Data Set	Alpha-investing	SAOLA	Fast-OSFS	OFS-Density	OFS-A3M	Group-SAOLA	OFS-3WD	OGSFS-FI	OUFSDFC	UHGSFS
Arcene	0.74	0.59	0.69	**0.815**	0.755	0.62	0.555	0.675	0.72	**0.815**
ALLAML	0.8429	0.9286	0.9143	0.9286	0.8714	0.8571	0.9286	0.9	0.9028	**0.9304**
Carcinom	0.684	0.7526	0.684	0.5978	0.6951	**0.8965**	0.6835	0.7408	0.7647	0.862
COIL20	0.9611	0.6056	0.7729	**0.9854**	0.9597	0.9799	0.4583	0.5667	0.8625	0.6944
Colon	0.4833	0.7667	0.7833	0.8	0.75	0.7333	**0.8667**	0.8167	0.7756	0.7923
GLI-85	0.8353	0.7647	**0.8471**	0.8353	0.8118	0.7294	0.8118	0.6706	0.7764	0.8352
GILMO	0.62	0.6	0.62	**0.78**	0.74	0.42	0.4	0.74	0.6799	0.7599
Lung	0.7272	0.6318	0.4523	0.5477	0.641	0.7805	0.4544	0.6472	**0.7942**	0.6857
Lymphomas	0.5263	0.6737	0.5684	0.7263	0.7789	0.8947	0.5474	0.7158	0.8957	**0.9057**
Nci-9	0.1333	0.1667	0.1667	0.2667	0.3667	0.4	0.2	0.1167	0.2666	**0.4833**
Orlraws10P	0.59	0.56	0.52	0.6	0.9	**0.93**	0.67	0.65	0.9	0.9099
Pixraw10P	0.86	0.81	0.66	**0.97**	0.92	0.95	0.63	0.82	0.94	0.95
SMK-CAN-187	0.6108	0.6541	0.6054	0.5676	0.6595	0.5027	0.6162	0.6541	0.6362	**0.6957**
WarpPIE100	0.881	0.5905	0.7524	0.9143	0.8857	**0.9714**	0.8286	0.6286	0.8571	0.8095
AVG.	0.6782	0.6496	0.6455	0.7382	0.7668	0.7618	0.6179	0.6673	0.7694	**0.7949**
AVG. RANKS	6.4643	7.0714	6.9643	4.1429	4.6071	4.8929	7.1071	6.4286	4.4643	**2.8571**

Table 4: Predictive Accuracy Using SVM as the Classifier

Data Set	Alpha-investing	SAOLA	Fast-OSFS	OFS-Density	OFS-A3M	Group-SAOLA	OFS-3WD	OGSFS-FI	OUFSDFC	UHGSFS
Arcene	0.7	0.59	0.68	0.76	**0.79**	0.575	0.575	0.705	0.65	0.7299
ALLAML	0.8857	0.9286	0.9286	0.9286	0.8571	0.8286	0.8714	0.9286	0.9438	**0.9714**
Carcinom	0.7067	0.7812	0.6439	0.5916	0.7185	**0.8966**	0.7245	0.8106	0.7932	0.8043
COIL20	0.9896	0.4701	0.6722	0.9931	0.9688	**0.9958**	0.3632	0.4951	0.934	0.7173
Colon	0.7333	0.7167	**0.7833**	0.7333	0.7333	0.7333	0.7167	0.7667	0.7448	0.7435
GLI-85	0.8235	0.7882	0.8118	**0.8588**	0.8235	0.7294	0.8235	0.6706	0.6352	0.7294
GILMO	0.52	0.54	0.6	**0.76**	0.62	0.42	0.36	0.66	0.64	0.72
Lung	0.7026	0.5477	0.4831	0.5118	0.5764	**0.84**	0.4718	0.5918	0.8085	0.7266
Lymphomas	0.4737	0.6211	0.6105	0.7053	0.8	**0.8632**	0.5474	0.7053	0.7926	0.8031
Nci-9	0.1	0.1833	0.1167	0.2667	**0.3833**	0.3333	0.2333	0.0667	0.25	0.2833
Orlraws10P	0.73	0.68	0.47	0.52	0.88	0.95	0.68	0.77	**0.97**	**0.97**
Pixraw10P	0.92	0.92	0.73	0.95	0.96	0.89	0.76	0.84	0.9199	**0.97**
SMK-CAN-187	0.6486	0.6486	0.5784	0.5892	0.6378	0.6108	**0.6595**	0.6432	0.6469	0.6524
WarpPIE100	0.9571	0.5524	0.7	0.9571	0.9333	**0.9762**	0.9048	0.6714	0.9047	0.9095
AVG.	0.7065	0.6406	0.6292	0.7233	0.7630	0.7602	0.6208	0.6661	0.7595	**0.7665**
AVG. RANKS	5.7143	6.8214	7.25	4.8571	4.4643	4.8214	7.4643	5.7857	4.6786	**3.1429**

- UHGSFS *vs.* Alpha-investing: According to the average ranks of statistical tests, UHGSFS outperforms Alpha-investing regarding prediction accuracy and F_{mac} with KNN, SVM, and DT classifiers. Alpha-investing tends to select fewer features than UHGSFS, except for the COIL-20 dataset. Alpha-investing selects only the first few features for some datasets, resulting in the poor prediction accuracy among all competing algorithms. This indicates that Alpha-investing may not be suitable for handling diverse datasets. In contrast, UHGSFS addresses this issue by selecting an appropriate number of features based on the feature clus-

Table 5: Predictive Accuracy Using DT as the Classifier

Data Set	Alpha-investing	SAOLA	Fast-OSFS	OFS-Density	OFS-A3M	Group-SAOLA	OFS-3WD	OGSFS-FI	OUFSDFC	UHGSFS
Arcene	0.69	0.515	0.66	**0.735**	0.715	0.63	0.525	0.64	0.68	0.725
ALLAML	0.7571	0.8857	**0.9286**	**0.9286**	0.8714	0.8571	0.9	0.8429	0.8733	0.8342
Carcinom	0.5339	0.575	0.5061	0.5746	**0.6556**	0.5464	0.5002	0.5516	0.6097	0.6379
COIL20	0.8931	0.5993	0.734	**0.8993**	0.8736	0.8799	0.4299	0.5375	0.7493	0.7201
Colon	0.5833	0.75	0.7167	0.75	0.5667	0.6667	**0.7833**	0.7667	0.7282	0.7089
GLI-85	0.7647	0.6353	0.8	**0.8471**	0.7765	0.7529	0.7529	0.6235	0.7294	0.7294
GILMO	0.54	0.4	0.56	**0.58**	0.52	0.46	0.42	0.56	0.4599	0.5599
Lung	0.519	0.4256	0.4256	0.4544	0.3723	0.4523	0.4985	0.4564	0.4666	**0.5628**
Lymphomas	0.3684	0.5158	0.5684	0.5684	0.5053	0.5684	0.4632	**0.5895**	0.5647	0.5742
Nci-9	0.05	0.1667	0.1167	0.2833	0.2833	0.2667	0.1833	0.1	0.3166	**0.3666**
Orlraws10P	0.73	0.67	0.5	0.54	0.74	0.57	0.66	0.76	0.73	**0.8**
Pixraw10P	0.95	0.91	0.68	**0.96**	0.93	0.58	0.78	0.85	0.9199	0.9099
SMK-CAN-187	0.5514	0.5946	0.573	0.5568	0.5892	0.5784	**0.6324**	0.5784	0.5513	0.6044
WarpPIE100	0.7429	0.5762	0.6714	0.7619	**0.7857**	0.6952	0.6571	0.519	0.6238	0.7333
AVG.	0.6196	0.5871	0.6029	0.6742	0.6560	0.6074	0.5847	0.5983	0.6431	**0.6762**
AVG. RANKS	5.8929	6.7143	6.1071	**3.3929**	4.6786	6.4286	6.3214	6	5.5	3.9643

Table 6: F_{mac} Using KNN as the Classifier

Data Set	Alpha-investing	SAOLA	Fast-OSFS	OFS-Density	OFS-A3M	Group-SAOLA	OFS-3WD	OGSFS-FI	OUFSDFC	UHGSFS
Arcene	0.7386	0.58	0.6867	**0.8141**	0.7543	0.6078	0.5331	0.668	0.7154	0.8129
ALLAML	0.76	0.8986	0.8951	0.9132	0.8303	0.8367	0.9228	0.8794	0.8852	**0.9252**
Carcinom	0.5768	0.6528	0.5848	0.4909	0.6222	**0.8481**	0.5888	0.6246	0.6678	0.8059
COIL20	0.9593	0.5869	0.7628	**0.9849**	0.9591	0.9815	0.429	0.5508	0.8522	0.6768
Colon	0.4134	0.7252	0.7543	0.7656	0.7315	0.7177	**0.8512**	0.7728	0.7081	0.7493
GLI-85	0.7878	0.726	0.7975	0.7551	0.788	0.6809	0.7421	0.5239	0.7283	**0.8045**
GILMO	0.5228	0.4985	0.5614	**0.7222**	0.6993	0.3829	0.3326	0.7074	0.5817	0.7159
Lung	0.6624	0.5365	0.2799	0.4599	0.5422	**0.7945**	0.279	0.5186	0.7566	0.5705
Lymphomas	0.3306	0.4522	0.3255	0.5567	0.6418	**0.838**	0.2928	0.5774	0.7707	0.7925
Nci-9	0.111	0.1426	0.1787	0.293	0.4022	**0.409**	0.2063	0.1049	0.1992	0.3638
Orlraws10P	0.5884	0.5205	0.4622	0.5738	0.8778	**0.9353**	0.6083	0.6435	0.8853	0.9
Pixraw10P	0.8237	0.8166	0.6141	0.9335	0.922	**0.9597**	0.5952	0.7811	0.9306	0.938
SMK-CAN-187	0.6053	0.6459	0.5969	0.5629	0.6535	0.4435	0.6101	0.6464	0.6191	**0.6805**
WarpPIE100	0.8495	0.5686	0.6921	0.9089	0.8681	**0.9724**	0.835	0.631	0.8497	0.8008
AVG.	0.6235	0.5965	0.5851	0.6953	0.7352	0.7434	0.5590	0.6164	0.7250	**0.7526**
AVG. RANKS	6.5714	7.0714	6.9286	4.5714	4.2857	4.3571	7.0714	6.4286	4.7857	**2.9286**

tering of the target dataset. This strategy ensures performance stability and enhances the UHGSFS's ability to handle various datasets.

- UHGSFS *vs.* SAOLA: Based on the Nmenyi test, UHGSFS significantly performs better than SAOLA in terms of ACC-KNN, F_{mac}-KNN, and F_{mac}-DT. On the other classifiers, UHGSFS achieves lower average ranks than SAOLA. SAOLA employs an innovative online pairwise comparison technique that exclusively considers the relationship between two features. Meanwhile, SAOLA exhibits a lower average number of selected features compared to

Table 7: F_{mac} Using SVM as the Classifier

Data Set	Alpha-investing	SAOLA	Fast-OSFS	OFS-Density	OFS-A3M	Group-SAOLA	OFS-3WD	OGSFS-FI	OUFSDFC	UHGSFS
Arcene	0.6978	0.5799	0.6762	0.7582	**0.7873**	0.5665	0.4909	0.6992	0.6426	0.7271
ALLAML	0.8025	0.8962	0.9101	0.9132	0.8265	0.8056	0.8363	0.9151	0.9342	**0.9672**
Carcinom	0.6604	0.6956	0.5415	0.4684	0.6424	**0.8761**	0.6438	0.768	0.6889	0.6625
COIL20	0.9888	0.4291	0.661	0.9936	0.9681	**0.995**	0.3241	0.4372	0.9282	0.6923
Colon	0.497	0.6796	**0.7543**	0.6942	0.7034	0.7152	0.6661	0.717	0.6317	0.6692
GLI-85	0.7685	0.7327	0.7639	**0.8007**	0.7756	0.6673	0.7651	0.5049	0.5976	0.5364
GILMO	0.4633	0.4819	0.5047	**0.6606**	0.5672	0.3763	0.2912	0.6123	0.4963	0.612
Lung	0.6894	0.4377	0.3314	0.4173	0.515	**0.8053**	0.2567	0.5144	0.6854	0.5604
Lymphomas	0.3725	0.4356	0.4306	0.5639	0.6939	**0.7782**	0.393	0.5706	0.5373	0.5467
Nci-9	0.0948	0.1691	0.1244	0.3003	**0.4113**	0.4089	0.262	0.0468	0.1514	0.2064
Orlraws10P	0.7324	0.6392	0.4245	0.4893	0.8639	0.9589	0.6705	0.7745	**0.9686**	0.968
Pixraw10P	0.9277	0.9291	0.6963	**0.9672**	0.9571	0.8962	0.7283	0.8017	0.9039	0.9647
SMK-CAN-187	0.6442	0.6448	0.5738	0.5823	0.6327	0.6079	**0.6559**	0.634	0.6029	0.63491
WarpPIE100	0.9495	0.5331	0.6664	0.9533	0.9159	**0.9743**	0.9044	0.6674	0.8997	0.9069
AVG.	0.6635	0.5917	0.5757	0.6830	0.7329	**0.7451**	0.5635	0.6188	0.6906	0.6896
AVG. RANKS	5.9286	6.3571	7.2857	4.3571	**4.0000**	4.3571	7.2857	5.4286	5.6429	4.3571

Table 8: F_{mac} Using DT as the Classifier

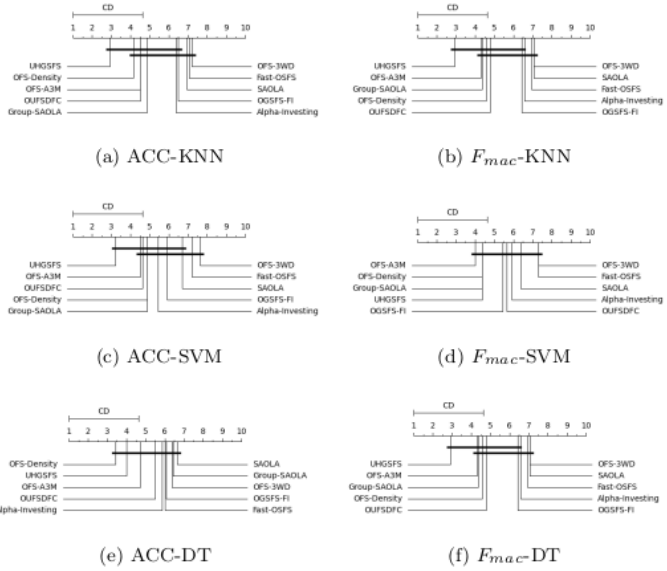
Data Set	Alpha-investing	SAOLA	Fast-OSFS	OFS-Density	OFS-A3M	Group-SAOLA	OFS-3WD	OGSFS-FI	OUFSDFC	UHGSFS
Arcene	0.6846	0.501	0.6586	**0.7318**	0.7091	0.6216	0.5134	0.6343	0.6772	0.7184
ALLAML	0.7302	0.8684	0.9195	**0.9207**	0.8479	0.8367	0.8816	0.8152	0.8608	0.8189
Carcinom	0.4485	0.5441	0.4137	0.4702	**0.5876**	0.4682	0.3985	0.4743	0.5005	0.4873
COIL20	0.8903	0.5904	0.726	**0.8965**	0.8722	0.8779	0.4139	0.5289	0.7439	0.7122
Colon	0.4601	0.6936	0.6609	0.7213	0.5147	0.6347	**0.7452**	0.7131	0.6316	0.6821
GLI-85	0.679	0.5467	0.699	**0.7868**	0.7001	0.6896	0.6873	0.5423	0.5536	0.6518
GILMO	0.4579	0.3227	0.4211	0.5133	0.4552	0.409	0.3386	**0.5658**	0.4276	0.4901
Lung	**0.5063**	0.3152	0.2662	0.375	0.3125	0.3579	0.3146	0.3946	0.3894	0.4626
Lymphomas	0.1315	0.2994	0.2872	0.4065	0.391	**0.455**	0.2486	0.3967	0.3871	0.3877
Nci-9	0.0452	0.2106	0.1317	0.3071	0.2676	0.2399	0.1747	0.0758	0.2621	**0.3379**
Orlraws10P	0.7363	0.6319	0.4555	0.5244	0.7525	0.5729	0.656	0.7425	0.702	**0.784**
Pixraw10P	**0.9553**	0.9171	0.618	0.9479	0.9449	0.5492	0.7491	0.8197	0.9146	0.9053
SMK-CAN-187	0.548	0.5932	0.5696	0.5498	0.5819	0.5755	**0.6229**	0.5742	0.5382	0.5924
WarpPIE100	0.7292	0.5603	0.6471	0.7151	**0.785**	0.6824	0.6507	0.4899	0.6183	0.7336
AVG.	0.5716	0.5425	0.5339	**0.6333**	0.6230	0.5693	0.5282	0.5548	0.5862	0.6260
AVG. RANKS	5.8571	6.3571	7	**3.2857**	4	6.0000	6.5714	6.0714	5.8571	4

UHGSFS. However, it is worth noting that SAOLA can not handle mixed type of streaming features.

- UHGSFS *vs.* Fast-OSFS: Based on the Nmenyi test, UHGSFS performs significantly better than SAOLA regarding ACC-KNN, F_{mac}-KNN, ACC-SVM, F_{mac}-DT. Judging from the average number of selected features, Fast-OSFS selects much fewer features than UHGSFS. However, it is worth noting that among all competing algorithms, Fast-OSFS selects the fewest features, which may lead to the loss of important information and thus reduce predic-

Table 9: The mean number of selected features

Data Set	Alpha-Investing	SAOLA	Fast-OSFS	OFS-Density	OFS-A3M	Group-SAOLA	OFS-3WD	OGSFS-FI	OUFSDFC	UHGSFS
Arcene	9.2	26.4	5.2	37.2	31.4	8	3.4	6.2	61	535.8
ALLAML	11.6	30.8	4.4	3.6	12.6	1	11.8	20	120	252.8
Carcinom	30.8	47.4	8.6	5.8	35.4	1337.6	19.6	72.8	91.4	398.6
COIL20	193.4	3.4	7	119.6	17.2	74.4	13.2	3.2	172.2	16.2
Colon	1.8	5.4	2.2	5.6	18.4	5.4	21.8	15	236.8	77.4
GLI-85	16	33.6	5.2	7	14.8	1	12.4	5	227.6	377.2
GILMO	6.2	15	3.4	8.6	21	2.4	2	16.2	144.2	118.6
Lung	13.8	8.2	3	4	8.6	93.8	2	10.6	99.8	14.6
Lymphomas	9.8	21.4	4.6	7.4	15	715.2	6.4	32.2	241.6	319.6
Nci-9	5.4	17.6	3.6	7.2	24	215	26.8	10.2	274.4	287.6
Orlraws10P	9.8	5.6	3.2	2.6	13.2	279.6	25.2	4.8	776.0	438.4
Pixraw10P	10.4	7.6	4.2	166.2	7.4	287	20.6	2.6	96.4	359.2
SMK-CAN-187	14.8	11.2	5	15	31.6	1	26.4	28.2	96.6	607.8
WarpPIE100	45	3.6	4.6	28.8	29.4	27	24.2	6.2	139.4	94.0
AVG.	27.0	16.9	4.6	29.9	20.0	217.7	15.4	16.7	198.4	278.4
AVG. RANKS	5.00	4.75	2.14	4.43	6.07	5.61	4.29	4.57	9.07	9.07



(a) ACC-KNN (b) F_{mac}-KNN

(c) ACC-SVM (d) F_{mac}-SVM

(e) ACC-DT (f) F_{mac}-DT

Figure 5: The statistical test graph of these competing algorithms

tion accuracy.

- UHGSFS *vs*. OFS-Density: UHGSFS and OFS-Density exhibit comparable prediction accuracy. Specifically, on average predictive accuracy and F_{mac}, UHGSFS demonstrates superior

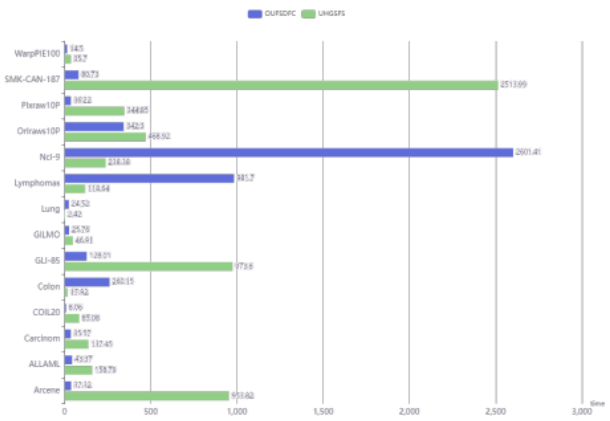


Figure 6: Running time (seconds).

to OFS-Density in most cases of KNN, SVM, and DT algorithms. Regarding the number of selected features, OFS-Density selects more features than UHGSFS on the COIL20 dataset. In contrast, OFS-Density selects significantly fewer features than UHGSFS for other datasets. OFS-Density is a neighborhood rough set-based method, which exhibits high time complexity for large sample datasets. Furthermore, OFS-Density utilizes neighborhood density information for feature selection and may not handle unevenly distributed datasets effectively.

- UHGSFS *vs*. OFS-A3M: There is no significant difference between UHGSFS and OFS-A3M on prediction accuracy. On average predictive accuracy and F_{mac}, UHGSFS performs better than OFS-A3M in the cases of KNN, SVM, and DT. Like OFS-Density, OFS-A3M is a neighborhood rough set-based method with high time complexity for large sample datasets. Regarding the number of selected features, OFS-A3M selects significantly fewer features than UHGSFS. OFS-A3M utilizes neighborhood information for feature selection, which is greatly influenced by the distribution of samples.

- UHGSFS *vs*. OFS-3WD: Based on the Nmenyi test, UHGSFS outperforms significantly better than OFS-3WD in terms of accuracy for KNN and SVM algorithms. Meanwhile, UHGSFS demonstrates significantly superior performance over OFS-3WD in terms of F_{mac} for KNN and DT algorithms. Regarding the average number of selected features, OFS-3WD selects fewer features than UHGSFS. OFS-3WD utilizes global dynamics and three-way decision-making

techniques for feature selection. However, it is essential to note that OFS-3WD cannot handle heterogeneous streaming features, limiting its applicability in such scenarios.

- UHGSFS *vs*. Group-SAOLA: There is no statistically significant difference in prediction accuracy and F_{mac} between UHGSFS and Group-SAOLA. However, on average, UHGSFS outperforms Group-SAOLA in most cases. Regarding the average number of selected features, Group-SAOLA selects much more features than UHGSFS on datasets Carcinom, COIL20, and Lymphomas, while it selects much fewer features on the remaining datasets. Group-SAOLA is an online streaming group feature selection method that exhibits fast execution on ultra-high-dimensional datasets. However, it does not consider feature relationships between streaming groups. Group-SAOLA selects a significantly smaller number of features (just one feature) on some datasets, potentially losing important information.

- UHGSFS *vs*. OGSFS-FI: Regarding accuracy (ACC) and F_{mac}, UHGSFS exhibits higher average prediction accuracy and lower average ranks than OGSFS-FI for KNN, SVM, and DT classifiers. Additionally, OGSFS-FI selects fewer features on average than UHGSFS. OGSFS-FI is an online group streaming feature selection method that employs mutual information for feature selection, but it cannot handle heterogeneous streaming features.

- UHGSFS *vs*. OUFSDFC: Both UHGSFS and OUFSDFC are unsupervised online streaming feature selection algorithms. Regarding accuracy (ACC) and F_{mac}, UHGSFS demonstrates higher average prediction accuracy and lower average ranks than OUFSDFC. On the average number of selected features, UHGSFS and OUFSDFC select about the same. Analyzing the running times depicted in Fig.6, it is observed that UHGSFS exhibits shorter running times for discrete datasets (e.g., lung, NCI-9) compared to OUFSDFC. Conversely, for continuous datasets (e.g., COIL20), OUFSDFC requires less time than UHGSFS. OUFSDFC requires more time to discover the relationship between two features when processing continuous streaming features. It is important to note that OUFSDFC employs separate metrics for processing continuous and discrete datasets, making it incapable of handling scenarios where the feature streaming type is unknown.

In sum, UHGSFS performs excellently on average accuracy (ACC) and F_{mac} in cases of KNN, SVM, and DT classifiers. Even without label information, UHGSFS exhibits statistically better or

equivalent performance compared to supervised streaming feature selection methods. Furthermore, compared to competing algorithms, UHGSFS indicates enhanced scalability regarding running time and the number of selected features. Importantly, UHGSFS can effectively handle heterogeneous streaming features without knowing the information about feature types in advance.

4.3. The Effectiveness of UHGSFS in Handling Heterogeneous Streaming Features

Since the data sets in Table 2 are continuous or discrete feature datasets. To verify the effectiveness of our UHGSFS algorithm in handling heterogeneous streaming features, we take the continuous datasets in Table 2, randomly select 50% features, and discretize these features into ten equal parts. Then, we conduct experiments on these two types of datasets (original and mixed). The experimental results on prediction accuracy and F_{mac} are shown in Tables 10 and 11, where KNN-ACC-MIX, SVM-ACC-MIX, and DT-ACC-MIX denote the prediction accuracy of UHGSFS on mixed streaming features.

Table 10: ACC of Heterogeneous Streaming Features

Data Set	KNN-ACC	KNN-ACC-MIX	SVM-ACC	SVM-ACC-MIX	DT-ACC	DT-ACC-MIX
Arcene	0.8150	0.8350	0.7299	0.7250	0.7250	0.7750
ALLAML	0.9304	0.9314	0.9714	0.9038	0.8342	0.9171
Carcinom	0.8620	0.8213	0.8043	0.8042	0.6379	0.5916
COIL20	0.6944	0.7840	0.7173	0.8146	0.7201	0.7576
GLI-85	0.8352	0.7882	0.7294	0.7529	0.7294	0.8118
GILMO	0.7599	0.7400	0.7200	0.6600	0.5599	0.6000
Orlraws10P	0.9099	0.9100	0.9700	0.9600	0.8000	0.7700
Pixraw10P	0.9500	0.9300	0.9700	0.9700	0.9099	0.8800
SMK-CAN-187	0.6957	0.6209	0.6524	0.6633	0.6044	0.5192
WarpPIE100	0.8095	0.8286	0.9095	0.8619	0.7333	0.7000
AVG.	0.8262	0.8190	0.8174	0.8116	0.7254	0.7322

From Tables 10 and 11, we can observe that for some datasets, the selected features on mixed version and the final classification ACC and F_{mac} do not perform as well as when using the original dataset. Meanwhile, features selected on the mixed dataset outperform the original dataset on some other datasets. This fluctuation is slight, and the root cause is the instability of the feature selection algorithm. Overall, our new algorithm performs essentially equally well on both two kinds of datasets. These results demonstrate our method's capability when dealing with heterogeneous streaming features.

Table 11: F_{mac} of Heterogeneous Streaming Features

Data Set	KNN-F_{mac}	KNN-F_{mac}-MIX	SVM-F_{mac}	SVM-F_{mac}-MIX	DT-F_{mac}	DT-F_{mac}-MIX
Arcene	0.8129	0.8321	0.7271	0.7221	0.7184	0.7708
ALLAML	0.9252	0.9166	0.9672	0.8881	0.8189	0.9047
Carcinom	0.8059	0.8213	0.6625	0.6848	0.4873	0.4859
COIL20	0.6768	0.7709	0.6923	0.8055	0.7122	0.7513
GLI-85	0.8045	0.7504	0.5364	0.5795	0.6518	0.7777
GILMO	0.7159	0.7033	0.6120	0.5060	0.4901	0.5535
Orlraws10P	0.9000	0.9060	0.9680	0.9533	0.7840	0.7567
Pixraw10P	0.9380	0.9168	0.9647	0.9627	0.9053	0.8707
SMK-CAN-187	0.6805	0.5922	0.6349	0.6433	0.5924	0.4994
WarpPIE100	0.8008	0.8125	0.9069	0.8592	0.7336	0.6900
AVG.	0.8061	0.8022	0.7672	0.7604	0.6894	0.7061

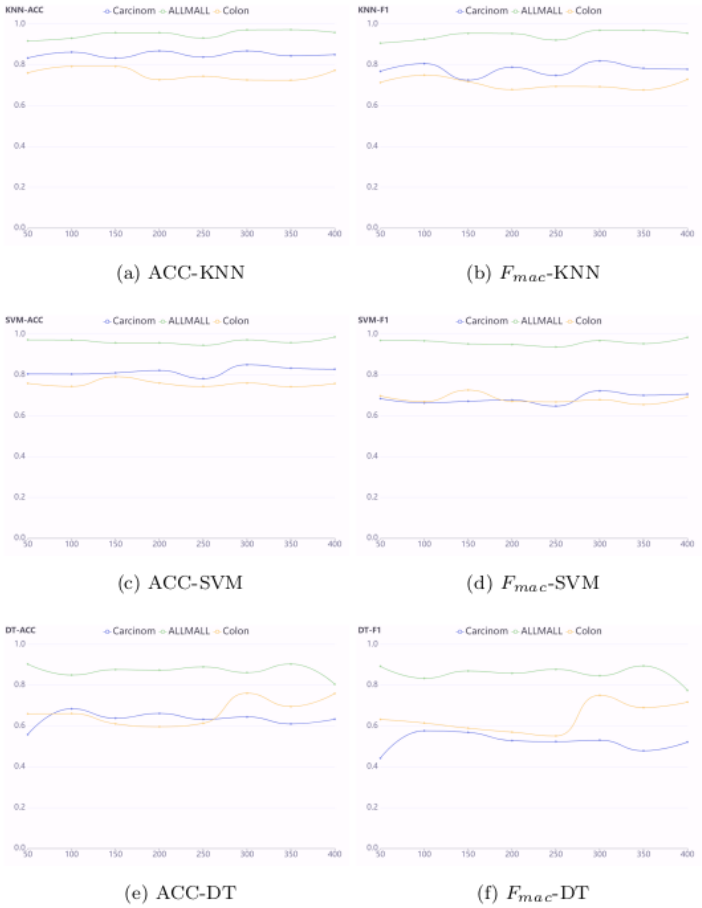
4.4. Analysis of Streaming Group Size

In order to investigate the effect of different group sizes on the UHGSFS, we chose three representative datasets, Carcinom, ALLAML, and Colon, for parameter analysis. Carcinom and ALLAML are continuous datasets, while Colon is a discrete dataset. We set the group size to increase from 50 to 400, and the interval between each increase was 50. Fig.7 shows the accuracy and F_{mac} curves for KNN, SVM, and DT classifiers varying with different group sizes, respectively.

By observing the experimental results, we can find that ACC and F_{mac} performance on these three datasets presents little change regardless of different group sizes regarding KNN, SVM, and DT classifiers. This indicates that group size does not significantly affect the results of UHGSFS.

5. Conclusion

In this paper, we have developed an unsupervised online streaming feature selection method to handle heterogeneous unknown-type streaming features. Specifically, we employ MIC to calculate the relationship between heterogeneous streaming features. Then, we design an adaptive feature clustering algorithm to reduce redundancy among features. Representative features from each feature cluster are selected by maximizing feature relevance and minimizing redundancy. Experimental results and comparative studies demonstrate that, without label information, the UHGSFS method statistically outperforms or performs equally well as state-of-the-art supervised streaming feature selection methods. However, due to the computational demands of MIC, UHGSFS exhibits higher



(a) ACC-KNN (b) F_{mac}-KNN

(c) ACC-SVM (d) F_{mac}-SVM

(e) ACC-DT (f) F_{mac}-DT

Figure 7: Accuracy and F_{mac} curves of UHGSFS varying in different sizes of the group.

time complexity. In the future, we will focus on distributed methods to address the time complexity issue of UHGSFS.

Acknowledgment

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