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An efficient sampling algorithm for uncertain abnormal data detection in biomedical image processing and disease prediction

Fei Liu [a,*], Xi Zhang [b] and Yan Jia [a]
[a] *School of computer, National University of Defense Technology. 410073, Changsha, Hunan, China*
[b] *School of Biomedical Engineering, Fourth Military Medical University. 710032, Xian, Shaanxi, China*

Abstract. In this paper, we propose a computer information processing algorithm that can be used for biomedical image processing and disease prediction. A biomedical image is considered a data object in a multi-dimensional space. Each dimension is a feature that can be used for disease diagnosis. We introduce a new concept of the top (k_1, k_2) outlier. It can be used to detect abnormal data objects in the multi-dimensional space. This technique focuses on uncertain space, where each data object has several possible instances with distinct probabilities. We design an efficient sampling algorithm for the top (k_1, k_2) outlier in uncertain space. Some improvement techniques are used for acceleration. Experiments show our methods' high accuracy and high efficiency.

Keywords: Biomedical image, disease diagnosis, computer information processing, abnormal detection, outlier, uncertain

1. Introduction

Biomedical image processing is an important tool for disease diagnosis and predication. Data processing using computers is the basic technique in this field. For example, urinary bladder cancer has become the fourth most common cancer among males [1]. The early detection of bladder cancer is extremely important. With recent advances in imaging and visualization techniques, virtual cystoscopy (VCy), which is based on volumetric computed tomography (CT) or magnetic resonance (MR) imaging data, has revealed its potentials for detecting bladder abnormalities [2]. As reported in [3], bladder cancerous tissue invades gradually from the mucosa into the wall muscles, inducing morphological changes and texture changes in the bladder wall. Therefore, the bladder image (MR or CT) contains some important clinical information for bladder cancer prediction. such as bladder wall thickness (BWT) [4], textural grey-level intensity, and many other features. Figure 1 show an MR bladder image acquired from a patient. The red and yellow contours represent the inner and outer borders of a bladder wall, respectively. Naturally, the BWT of the abnormal region is larger than the normal wall tissue. After we collect these abstract

*Address for correspondence: Fei Liu, Team 7, School of Computer, National University of Defense Technology, Changsha, Hunan, 410073, China. Tel: +86 15873192183; Fax: +86 0731 84574614; E-mail:1986figo@163.com.

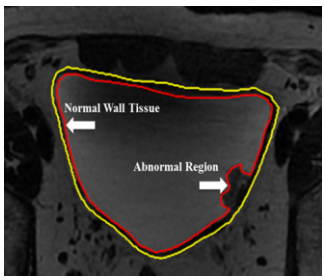


Fig. 1. MR bladder images.

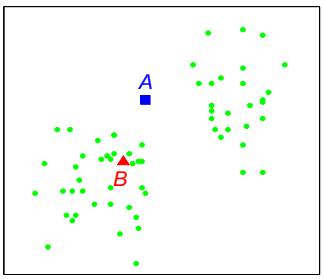


Fig. 2. A two-dimensional deterministic space.

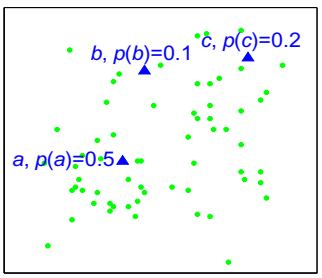


Fig. 3. A two-dimensional uncertain space.

features together, we can construct a multi-dimensional space. Each dimension is a feature, and each biomedical image is a data object in the space. In a set of many biomedical images, the data objects far away from their neighbor objects can be considered abnormal, because some of their features' values are very different from the others'. The difference could be caused by pathological changes. For example, in the two-dimensional space in Figure 2, A is considered 'abnormal', because its feature values depart from the majority. B is considered 'normal' because it is similar to many of the surrounding data objects.

At the same time, uncertainty is inherent in real application due to various factors, like noise, device imprecision, incompleteness of data, delay in data transfer, or even manual misplay [5–7]. In this case, the feature values of a data object in some dimensions would be uncertain. For example, in Figure 3, data object A could be represented by three different instances: a, b, or c. It's difficult to obtain A's distance from its neighbors and compare A with other objects. Our research in this paper focuses on this problem and attempts to detect abnormal data objects, denoted as outliers, in uncertain space.

An outlier is an observation that deviates so much from the other observations that it arouses suspicion that it was generated by a different mechanism [8]. Outlier detection is a basic technique in data analysis and is widely used in many applications. Many kinds of outlier have been proposed, such as the Distribution-based outlier, the Distance-based outlier, the Density-based outlier, and so on. In this paper, we use the concept of a Distance-based outlier, where the distance between a data object and its neighbors are used as the measurement for outlier detection.

We use the classic x-tuple model [9] and possible world semantics [10] to describe uncertain data. An uncertain data object (abbreviated as object) is noted as an x-tuple, containing several tuples. Each tuple belonging to an x-tuple is a possible data instance (abbreviated as instance) of the corresponding object. Each instance has an appearance probability. Instances belonging to the same object are exclusive. The sum of these instances' probabilities is no more than 1. For example, in Table 1, t_{11} and t_{12} are two tuples of x-tuple T_1, and t_{11} and t_{12} cannot both appear at the same time. t_{21} with probability p_{21} is the unique tuple of x-tuple T_2. If p_{11}+p_{12}<1, T_1 would not appear with a probability 1-p_{11}-p_{12}.

Based on the x-tuple model, a possible world is a subset of tuples from different x-tuples. There would be no more than one tuple of the same x-tuple appearing in a possible world. Table 2 shows six possible worlds produced from the x-tuples in Table 1. $\{t_{11}\}$ is the second possible world with a probability $p_{11}(1\text{-}p_{21})$. It contains only one tuple, t_{11}.

The remainder of this paper is organized as follows. In section 2, some preliminary definitions are introduced. A naive sampling method is described in section 3. Section 4 proposes an efficient sampling algorithm to accelerate the naive sampling method. We experimentally evaluate our algorithms in section 5. We introduce some existing research related to our work in section 6 and conclude our contribution in section 7.

Table 1
x-tuple Model

x-tuple	tuple	probability
T_1	t_{11}	p_{11}
	t_{12}	p_{12}
T_2	t_{21}	p_{21}

Table 2
Possible Worlds

possible world	probability
{}	(1-p_{11}-p_{12})(1-p_{21})
{t_{11}}	p_{11}(1-p_{21})
{t_{12}}	p_{12}(1-p_{21})
{t_{21}}	(1-p_{11}-p_{12})p_{21}
{t_{11},t_{21}}	$p_{11}p_{21}$
{t_{12},t_{21}}	$p_{12}p_{21}$

2. Preliminary

An uncertain dataset is constituted by many x-tuples. A large number of possible worlds would be produced as instances of the uncertain dataset. Let D be an uncertain dataset, t be a tuple and $T(t)$ be the x-tuple containing t. $P(t)$ is t's appearance probability and $P(T)$=$\sum_{t\in T} P(t)$. Let W be the set of all possible worlds produced from D. For a possible world $w \in W$, $t \in w$ means tuple t appears in w, and $T \in w$ means that a tuple of T appears in w. Let $P(w)$ be the probability of w, and $P(w)$=$\prod_{t\in w} P(t)\prod_{T\notin w}$(1-$P(T)$). For each tuple t, we assign it an outlier score $s(w,t)$ in possible world w, which is the average distance between t an its n nearest neighbors in w. Based on the above assumptions, we propose following definitions.

Definition 1 Top k_1 outliers in a possible world: In a possible world w, the top k_1 outliers are the k_1 tuples with the largest outlier scores.

Definition 2 P_{k_1} probability: For an x-tuple T, its P_{k_1} probability, $P_{k_1}(T)$, is the probability sum of all possible worlds where one of T's tuples is a top k_1 outlier. Formally, $P_{k_1}(T)$=$\sum_{w\in W(T)} P(w)$. $W(T)$ is the set of possible worlds, where there is a tuple $t \in T$ and t is a top k_1 outlier.

Definition 3 Top (k_1,k_2) outliers in an uncertain dataset: In an uncertain dataset D, the top (k_1,k_2) outliers are the k_2 x-tuples with the highest P_{k_1} probabilities.

The straightforward calculation of an x-tuple's P_{k_1} probability according to definition 2 needs to traverse all possible worlds. It is a #p-complete [11,12] problem leading to a time cost that is too high. Therefore, we propose an approximate method based on sampling to detect the top (k_1,k_2) outliers with high accuracy and efficiency.

3. Naive sampling method

To avoid enumerating all possible worlds, we sample x-tuples one by one to produce samples of possible worlds. In each sampled possible world, the top k_1 outliers can be detected in a deterministic situation. For each x-tuple T, let $F_{k_1}(T)$ be T's frequency of being a top k_1 outlier in M sampled possible worlds. Based on the law of large numbers [13,14], $F_{k_1}(T)$ converges to $P_{k_1}(T)$ in a large sampling frequency. We use $F_{k_1}(T)$ as the approximation of $P_{k_1}(T)$ and sort all x-tuples according to $F_{k_1}(T)$ in descending order. The first k_2 x-tuples are output as the top (k_1,k_2) outliers. We call this process the naive sampling algorithm, whose details are shown in algorithm 1. The classic RBRP [15] algorithm is used to detect the top k_1 outliers in a possible world.

Algorithm 1 Naive sampling algorithm

Input: M, D, k_1, k_2, F, $F[i]$=0, 0<i≤|D|, m=0.
Step 1: sample each x-tuple in D to construct a possible world w.
Step 2: calculate outlier score for each tuple t using $RBRP$.
Step 3: detect top k_1 outliers in w.
Step 4: for each x-tuple T_i and each tuple $t \in T_i$, if t is a top k_1 outlier, $F[i]$=$F[i]$+1.
Step 5: if $m<M$, go to step 1.
Output: k_2 x-tuples with largest values $F[i]/M$.

4. Efficient sampling algorithm

Although the naive sampling algorithm can detect the top (k_1, k_2) outliers successfully, a high frequency of sampling is needed to get high accuracy. RBRP algorithm must be repeated in each sampled possible world. Clustering and detecting the n nearest neighbors' in the RBRP algorithm leads to a high time cost. In order to overcome this problem, we propose an efficient sampling algorithm.

We find that the n nearest neighbors of a tuple always exist nearby. We maintain a local region for a tuple, where most of its possible neighbors are located; then we can detect its n nearest neighbors just in the local region in each possible world. For tuple t, let $L_N(t)$ be t's nearest neighbors list. For any tuple t_i in L, $T(t_i)\neq T(t)$. All tuples in $L_N(t)$ are sorted in ascending order according to their distance from t. The RBRP algorithm can be used to construct $L_N(t)$. Let μ be the sum of all tuple's probability in $L_N(t)$. When μ is large enough, the n nearest neighbors of t in a possible world will always appear in $L_N(t)$. In order to detect t's n nearest neighbors in a sampled possible world, we can just search $L_N(t)$ in order to get the first n appearing tuples. The outlier score can then be calculated easily. This procedure is in linear time cost and much more efficient than the naive sampling algorithm. The steps of the efficient sampling algorithm are shown in algorithm 2. In this way, the clustering operation of the RBRP algorithm is executed once before sampling, and the detection of the n nearest neighbors for each tuple is greatly accelerated.

4.1. Improvement

Although the efficient sampling algorithm avoids repeating clustering and improves the efficiency of detecting the n nearest neighbors, it's also redundant. Because k_1 is always much smaller than |D| and n is always much smaller than |$L_N(t)$|, it's unnecessary to sample all x-tuples to produce a possible

Algorithm 2 Efficient sampling algorithm

Input: M, D, k_1, k_2, F, $F[i]$=0, 0<i≤|D|, m=0.
Step 1: detect |$L_N(t)$| possible n nearest neighbors for each tuple t and construct $L_N(t)$.
Step 2: sample each x-tuple in D to construct a possible world w.
Step 3: calculate outlier score for each tuple t using $L_N(t)$.
Step 4: detect top k_1 outlier in the possible world.
Step 5: if $t \in T_i$ is a top k_1 outlier, $F[i]$=$F[i]$+1.
Step 6: if $m<M$, go to step 2.
Output: k_2 x-tuples with largest values $F[i]/M$.

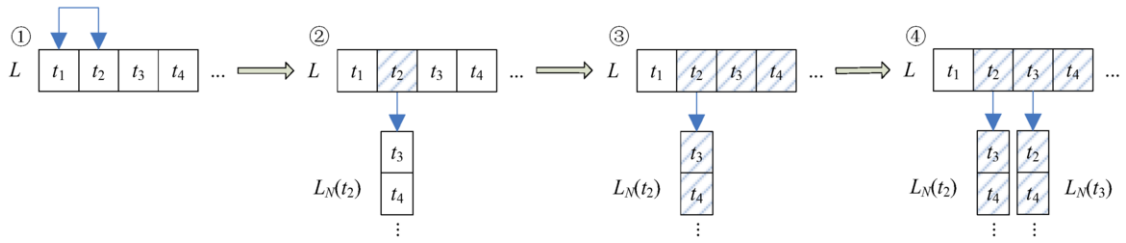


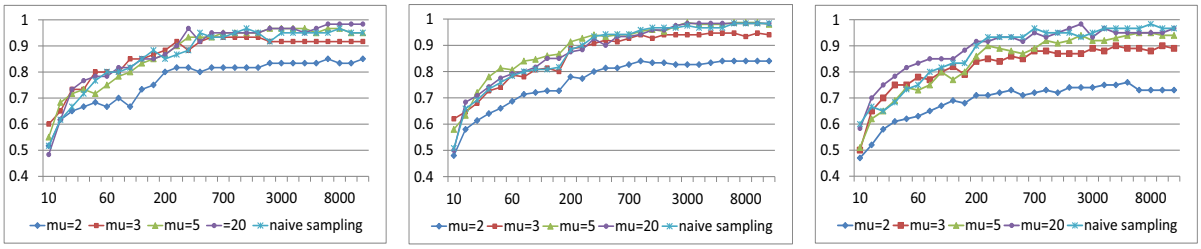
Fig. 4. An example of improved sampling process.

world. If we can sample tuples with large outlier scores early on, many other x-tuples can be pruned without sampling. In this way, we propose an improved efficient sampling algorithm. Step 2 and step 3 in the efficient sampling algorithm are substituted by following process. All tuples are sorted in a list L according to their expected outlier score in descending order before sampling, because tuples with larger expected outlier scores are more likely to be a top k_1 outlier in a possible world. The expected outlier score can be calculated using dynamic algorithm, whose details are neglected due to space limitation. Then the tuples in L are processed one by one for sampling. Suppose t_i is sorted in front of t_j and $T(t_i) \neq T(t_j)$. We sample x-tuple $T(t_i)$ first. If t_i is not selected, then we sample x-tuple $T(t_j)$. If t_i is selected, then we search the tuples in $L_N(t_i)$ to get t_i's n nearest neighbors. Suppose the first tuple in $L_N(t_i)$ is t_k, and $T(t_k)$ has been sampled, but t_k is not selected. Then t_k is jumped over, and the next tuple in $L_N(t_i)$ is checked. If t_k is selected, t_k is added to t_i's n nearest neighbors in this possible world. Then we check the nest tuple in $L_N(t_i)$ until the n nearest neighbors of t_i are detected. Then, t_i's outlier score in the possible world is calculated. After that, t_j is processed similarly. If no less than k_1 tuples in L have been processed, the k_1th largest outlier score can be a threshold h. For any following tuple t_x, if the upper bound of t_x's outlier score is smaller than h, t_x can be pruned. The upper bound of tuple t can be calculated using function $\sum_{1 \leq i \leq n'} d(t, t'_i) + \sum_{|L_N(t)|-n+n'+1 \leq k \leq |L_N(t)|} d(t, L_N(t)[k])$, where t'_i is one of t's n nearest neighbors that have been detected and $L_N(t)[k]$ is the kth tuple in $L_N(t)$. For example in Figure 4, let L=<t_1, t_2, t_3, t_4...>, $T(t_1)$=$T(t_2)$. t_1 is the first tuple and $T(t_1)$ is sampled. Suppose t_2 is selected. Then t_1 is jumped over, and the tuples in $L_N(t_2)$ are checked. Suppose $L_N(t_2)$ = <t_3, t_4...>. Then t_3, t_4 ... are checked one by one until the n neighbors of t_2 are detected. Then t_2's outlier score can be calculated. Suppose both t_3 and t_4 are selected. Then the tuples in $L_N(t_3)$ are checked to detect t_3's n nearest neighbors. Suppose $L_N(t_3)$=<t_2, t_4...>. Because $T(t_2)$ and $T(t_4)$ have been processed, they will not be redundantly sampled.

5. Experiments

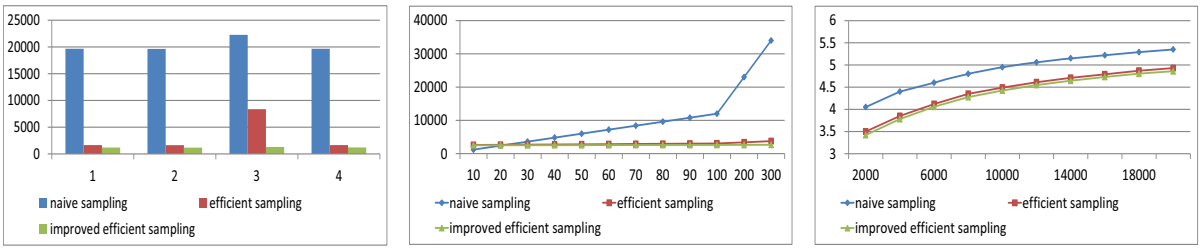
In this section, we conduct an empirical study on a PC with a2 2.5 GHz intel Core i5 CPUs, 8.0 GB main memory, running on the Microsoft Windows 7 operating system. Because our research is based on the novel proposed definitions, we compare the three algorithms we proposed in this paper, the naive sampling algorithm, the efficient sampling algorithm, and the improved efficient sampling algorithm. We construct a synthetic dataset to simulate data objects with the features of biomedical images. In the synthetic dataset, every object contains no more than 10 instances. The number of instances of a data object is decided randomly. For each feature, the value is in region (0,1), satisfying normal distribution with both the expectation and variance randomly produced in (0,1).

We first test the accuracy of our algorithms. We compare the efficient sampling algorithm with the different parameter values of μ and the naive sampling algorithm. We use the result of the naive sampling



(a) (b) (c)

Fig. 5. Accuracy of algorithms.



(a) (b) (c)

Fig. 6. Efficiency and scalability of algorithms.

algorithm with a sampling frequency 10^5 as the real outliers. In Figure 5(a), n=5, k_1=10, and k_2=20. The x-axis shows the sampling frequency. The y-axis shows the accuracy of outlier detection. In Figure 5(b), n=5, k_1=10, and k_2=30. In Figure 5(c), n=5, k_1=20 and k_2=20. A larger μ means a larger $L_N(t)$ and higher memory cost, but it also means higher accuracy. As shown in these figures, when μ is larger than 5, the accuracy of the efficient sampling algorithm is no less than 90% of the naive sampling algorithm's accuracy.

We then test the efficiency of our algorithms. Figure 6(a) shows the time cost of the three algorithms. The x-axis shows four groups of histograms. The first groups corresponds to the parameter set {μ=5, n=5, k_1=10, k_2=20}. The second one corresponds to the parameter set {μ=5, n=5, k_1=10, k_2=30}. The third one corresponds to the parameter set {μ=5, n=10, k_1=10, k_2=20}. The y-axis shows the time cost (millisecond). It is obvious that the efficient sampling algorithm greatly increases efficiency, and the improvement method leads to further acceleration.

Finally, we show the scalability of the algorithms. Figure 6(b) shows the time cost of the three algorithms with increasing sampling frequencies. The x-axis shows the changing sampling frequency, and the y-axis shows the time cost (millisecond). The results show that the naive sampling algorithm costs much more time than the other algorithms, and the improved efficient sampling algorithm saves the most time. Figure 6(c) shows the time cost of the three algorithms with a sampling frequency of 100 at different dataset sizes. The x-axis shows the changing dataset sizes. The y-axis is the logarithmic value of the time cost (millisecond). We can find that the efficient sampling algorithm, especially the improved one performs much better than the naive sampling algorithm.

6. Related work

In order to detect outliers in uncertain space, [16] proposes an outlier model and the detection method on uncertain data. However, they do not consider the diversity of a data object where a data object is only

represented by a single instance, so they cannot be used for uncertain biomedical images processing with many possible instances. In their research, grid-based pruning is used to improve efficiency. The grid is only discussed in two dimensions and is not suitable for high-dimension space.

7. Contribution

We propose a new definition of outliers in uncertain space and offer the naive sampling algorithm. We design an efficient sampling algorithm to avoid redundant clustering operations and accelerate the detection of n nearest neighbors. Then we further improve its efficiency using sorting and pruning strategies. Experiments show the effectiveness of our methods.

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