

# GeDual-DBSCAN: A Generalized Dual-tree Algorithm for the DBSCAN problem

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## ABSTRACT

In this paper a novel approach to the classical DBSCAN problem is proposed which is based on two-fold innovative ideas. On the one hand, several fine-grained sub-problems of the DBSCAN problem are identified for the first time, which address certain sub-cases of the DBSCAN problem with less distance computations. On the other hand, the DBSCAN problem is considered from the perspective of a *dual-set* problem, and for the first time a delicate dual-tree algorithm surpassing the trivial dual-tree range search algorithm is proposed. The GeDual-DBSCAN algorithm proposed in this paper, named after Generalized Dual-tree algorithm, links the two new ideas using the new concept of *intermediate cases*. When the tree traversal encounters an intermediate case, the algorithm will be switched to a different sub-traversal to solve the sub-problem corresponding to this case, which is exactly one of the new sub-problems defined in this paper. This paper uses three variants to introduce the GeDual-DBSCAN algorithm, where the first one establishes the traversal order, the second one integrates the intermediate cases into the basic traversal, and the third one involves a new idea of *state transitions* to employ the power of intermediate cases to the full extent. In addition to providing correctness and time complexity analysis of these algorithms, substantial experimental results are presented to evaluate their performance. It is shown that the final variant, named GeDual-DBSCAN-Transitions, outperforms the state-of-the-art DBSCAN algorithm under almost all the parameter settings on all datasets tested. In summary, the new GeDual-DBSCAN algorithm brings not only conceptual advancements for both the DBSCAN problem and dual-tree algorithms, and also efficiency improvement against existing DBSCAN algorithms.

## CCS CONCEPTS

- Information systems → Clustering

## KEYWORDS

DBSCAN, dual-tree algorithm, intermediate cases.

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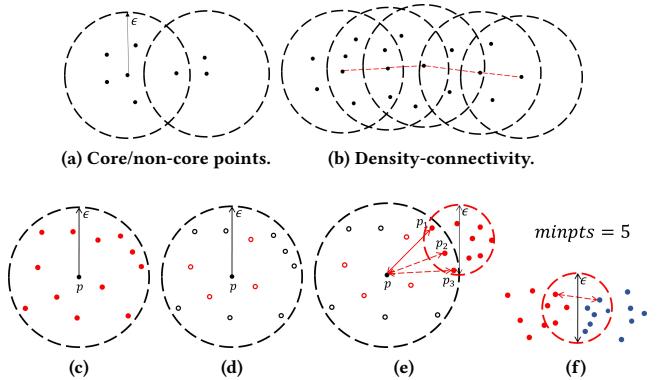


Figure 1: (a)(b) Demonstrates DBSCAN concepts ( $\text{minpts} = 5$ ). (c) Points visited by range search. In contrast with: minimal points needed to (d) identify a core point, (e) merge a core point with a cluster, and (f) merge two clusters.

## 1 INTRODUCTION

DBSCAN [11] is a well-acknowledged density-based clustering approach with long research history [4, 5, 15, 17, 21, 23, 26, 32, 38] and wide application [9, 10, 34]. It was included in various textbooks as a classical clustering method [20, 35], and inspired many other density-based methods such as OPTICS [1] and HDBSCAN [25].

The DBSCAN problem involves two parameters,  $\text{minpts}$  which is the threshold for number of neighboring points, and  $\epsilon$  which is the neighborhood radius. Let  $\text{Ball}(p, \epsilon)$  be the  $d$ -dimensional ball centered at  $p$  with radius  $\epsilon$ , and let  $P$  be the point set to be clustered. A point  $p \in P$  is called core point if  $|\text{Ball}(p, \epsilon) \cap P| \geq \text{minpts}$ , and non-core point otherwise. Note that  $p$  itself is included. The points are clustered based on the concept of density-connectivity. It is said that two points  $p$  and  $q$  are density-connected, if there exists a chain of core points, each within a distance of  $\epsilon$  to the next one, that can connect  $p$  and  $q$ . Figure 1a and 1b demonstrates the idea of core/non-core points and density-connectivity, respectively.

It is well known that the DBSCAN problem can be divided into three critical components [33], i.e., *identifying core/non-core points*, *clustering core points*, and *assigning non-core points*. The three parts of tasks can be trivially solved by executing a *range search* for each point  $p \in P$ , i.e., find  $\text{Ball}(p, \epsilon) \cap P$  for  $\forall p \in P$ . This is also the initial method adopted by the seminal paper [11].

It has been long recognized that the original solution based on range search will incur a lot of unnecessary distance computations and lead to sub-optimal algorithms. Many efforts have been taken to develop more efficient DBSCAN algorithms in almost 30 years' research history. See a brief survey in Section 2.

Different with all the existing works, in this paper, the way to reduce unnecessary distance computations and improve algorithmic efficiency originates from a careful conceptual inspection

of the DBSCAN problem. For the first time, several fine-grained sub-problems of the DBSCAN problem are identified, which solve specific sub-cases of the three critical components mentioned above with less distance computations. Let us introduce the idea of these sub-problems using the following examples shown in Figure 1.

**Example 1.** In Figure 1c, a range search is executed on the black-colored point  $p$ , incurring distance computation between  $p$  and all the red points. However, as Figure 1d shows, knowing  $\text{minpts} = 5$ , it only needs to compute the distance from  $p$  to the four red-circled points to know  $p$  is a core point. Thus, a lot of distance computations can be spared during the procedure of identifying core points.

**Example 2.** In Figure 1e, assume that  $p$  is known to be a core point, and the red points are known to be a density-connected cluster of core points. Then, it only needs to compute the distance between  $p_1$  and  $p$  to know  $p$  is density connected to the red cluster. Compared with the range search in Figure 1c, the distance computation between  $p_2, p_3$  and  $p$  can be spared.

**Example 3.** In Figure 1f, assume that the red points and blue points are known to be two density-connected clusters of core points. To further know the two clusters are density-connected, it only needs to know the distance between one pair of points. The distance computation between the other pairs of points in these two clusters can all be avoided, saving a lot of time.

Summarizing the above examples, the central idea to avoid unnecessary distance computations is that, different procedures with less distance computations should be carried out for points known to be core point and point sets known to be one density-connected cluster. This insight has not been clearly stated in former research works as far as we know. We then define several new problems to represent the idea of the above examples. The problems in Figure 1d, 1e and 1f are called the  $\epsilon$ -minpts,  $\epsilon$ -connect-single,  $\epsilon$ -connect-dual problems, respectively. This is the first time these sub-problems are defined for solving the DBSCAN problem, and the formal definitions will be given in Section 3.2.

With these new sub-problems defined, there comes new questions to answer, i.e., how to solve these new sub-problems, and how these new sub-problems contribute to solving the DBSCAN problem. Our second part of main contribution gives answer to these questions, that is the DBSCAN problem can be solved elegantly by a *generalized dual-tree* algorithm that integrates all these sub-problems in a one-pass tree traversal. Generalizing the dual-tree algorithm described by Curtin et al. [8] which includes four parts of logic split, the tree index structure, the traversal rule, the point-to-point base case, and the pruning rule, our proposed *generalized dual-tree* algorithm introduces a new logic part which is called the *intermediate cases*. When the traversal encounters an intermediate case which is specified by the information of the current visiting node, it will switch to a new traversal where different traversal rules would be applied on the sub-tree below the current node. In terms of the DBSCAN problem, the intermediate cases exactly correspond to the sub-problems newly identified in this paper. Thus, the proposed generalized dual-tree algorithm is a conceptual advancement not only against the existing DBSCAN approaches, and also against the original dual-tree algorithm.

The concrete contributions of this paper are listed below.

First, a novel algorithm for the DBSCAN problem is proposed named as GeDual-DBSCAN. This algorithm incorporates the newly

defined DBSCAN sub-problems with the new idea of generalizing dual-tree algorithms by the so-called *intermediate cases*. The name comes from the Generalized Dual-tree algorithm, and it is introduced using three variants, each established based on the former one. The three variants are postfixed by Basic, InterCases and Transitions, respectively. The Basic invariant establishes the overall traversal order. The InterCases variant is a generalized dual-tree algorithm which integrates the intermediate cases with the basic traversal. The Transitions variant involves a novel idea of *state transitions* for the tree nodes, and reduces the number of distance computations as much as possible. The correctness and complexity of these algorithms are also provided.

Second, substantial experimental results are presented to evaluate the performance of the GeDual-DBSCAN algorithms. It is shown that the final variant, GeDual-DBSCAN-Transitions, outperforms the state-of-the-art DBSCAN algorithm in almost all parameter settings on all datasets tested.

The rest of this paper is organized as follows. Section 2 overviews the related works. Section 3 introduces the preliminary knowledge, as well as the new DBSCAN sub-problems. Section 4 proposes the GeDual-DBSCAN algorithms progressively using the Basic, InterCases and Transitions variants. The experimental results are presented in Section 5. Finally Section 6 concludes this paper.

## 2 RELATED WORKS

### 2.1 Existing approaches for solving DBSCAN

There is vast literature on the DBSCAN problem due to many years of research efforts, among which the ball-based and grid-based algorithms form two main categories. They have a similar idea that first divide the input point set into smaller subsets, then try to utilize the intra-subset and inter-subset properties to reduce the number of distance computations. They differ, obviously, in the way to divide the subsets using balls or grids. For ball-based algorithms, the  $k$ -nearest-neighbors balls are used in [5], the  $\epsilon/2$ -balls are used in [4], and the  $\delta$ -relaxed balls are used in [18]. For grid-based algorithms, the well-known baseline algorithm was proposed by Gan and Tao [13], and recently a grid-tree data structure was introduced in [19]. The brief discussion of related works ends here due to space limitation against abundant existing works on DBSCAN problem.

### 2.2 Dual-tree algorithm and dual-set problems

A dual-tree algorithm [8, 16] is given two tree structures called query tree  $\mathcal{T}_Q$  and reference tree  $\mathcal{T}_R$ , respectively (it is allowed that  $\mathcal{T}_Q = \mathcal{T}_R$ ), to traverse the node combinations  $N_q \in \mathcal{T}_Q$  and  $N_r \in \mathcal{T}_R$  to solve a specific problem. It is an algorithm framework parameterized by the problem specific BaseCase and Score functions. The BaseCase function describes the action to take on a combination of points, and the Score function describes the pruning rule.

Dual-tree algorithms are naturally suitable for *dual-set* problems, that is, given two points sets  $Q$  and  $R$ , where  $Q$  is called the query set and  $R$  is called the reference set, find a problem-specific subset  $R_{pq} \subset R$  for each  $pq \in Q$ . Lots of problems can be characterized as a dual-set problem. For example, the All-Nearest-Neighbors problem [37], is to find the nearest neighbor of  $pq$  in  $R$  for each  $pq \in Q$ . The All-range-search problem, is to find  $B(pq, r) \cap R$  for each  $pq \in Q$

given a distance range  $r$ . The seminal approach for DBSCAN [11] actually solves the All-Range-Search problem.

Surprisingly, there are some problems that implicitly possesses dual-set problem characteristics. The most notable example is the Euclidean minimum spanning tree (EMST) problem. In a dual-set problem point of view, EMST is given one point set  $P$  (the query and reference set is the same in this case), to find the neighborhood points  $R_p \in P$  for each  $p$  such that any shortest path from  $p$  to other points in  $P$  must be via  $R_p$ , and the EMST is constructed by adding edges between  $p$  and points in such  $R_p$ . Finding EMST can be elegantly solved by a dual-tree Boruvka algorithm [24].

The DBSCAN problem can also be regarded as a dual-set problem, but unfortunately there are no existing dual-tree algorithms designed. It is partially because any algorithm for All-Range-Search problem trivially solves the DBSCAN problem, but this approach is actually redundant. With the new sub-problems identified, the newly proposed dual-tree traversal algorithm for the DBSCAN problem performs much better than All-Range-Search algorithms.

### 3 PRELIMINARIES

#### 3.1 Terminologies and notations

**3.1.1 Metric space.** This paper adopts the Euclidean distance, i.e.,  $D(x, y) = \sqrt{\sum_{i=1}^d (x_{(i)} - y_{(i)})^2}$  where  $x = (x_{(1)}, \dots, x_{(d)})$  and  $y = (y_{(1)}, \dots, y_{(d)})$  are  $d$ -dimensional points. Note that the capital  $D(\cdot, \cdot)$  is used to denote the Euclidean distance function, and  $d$  is used to denote the number of dimension. Let  $\text{Ball}(p, r)$  be the  $d$ -dimensional ball centered at  $p$  with radius  $r$ , i.e.  $\text{Ball}(p, r) = \{x \in \mathbb{R}^d \mid D(x, p) \leq r\}$ . The minimum bounding rectangle (MBR) of a point set  $P$ , is the  $d$ -dimensional axis-parallel rectangle with minimum length in each dimension that contains all points in  $P$ .

**3.1.2 DBSCAN terminologies.** From now on the input point set of the DBSCAN problem is denoted as  $P$ . The DBSCAN problem involves the following well-known terminologies based on two input parameters  $\epsilon$  and  $\text{minpts}$ .

(**Core and non-core points**). A point  $p$  is called core point if  $|\text{Ball}(p, \epsilon) \cap P| \geq \text{minpts}$ , and non-core point otherwise.

(**Density-connectivity**). A point  $q \in P$  is said to be density-reachable from  $p \in P$ , or equivalently,  $p, q$  are density-connected, if there is a sequence of core points  $p_1, p_2, \dots, p_k \in P$  such that (1)  $p = p_1, p_{k+1} = q$ , and (2)  $D(p_i, p_{i+1}) \leq \epsilon$  for all  $1 \leq i \leq k$ .

(**Noise and border points**). A non-core point  $p \in P$  is called a border point, if there exists at least one  $q \in \text{B}(p, \epsilon)$  that is a core point. Otherwise it is called a noise point.

(**DBSCAN clusters**). A cluster  $C$  generated by DBSCAN satisfies the following two properties. (1) Connectivity. Any two points  $p, q \in C$  are density-connected. (2) Maximality. There is no  $p^* \in P \setminus C$  such that  $p^*$  is density-reachable from any point in  $C$ .

The following extra denotations are used in this paper.

(**Dense point sets**). A set of points  $S$  is called *dense*, if  $\forall p \in S$  is a core point and  $\forall p_1, p_2 \in S$  are density-connected.

( **$\epsilon$ -neighbors**). If  $D(q, p) \leq \epsilon$  then  $p$  and  $q$  are called  $\epsilon$ -neighbors of each other. It is also said that  $(p, q)$  is an  $\epsilon$ -neighbor pair.

**3.1.3 Union-find set.** The union-find set is a very efficient data structure to represent a set of disjoint sets [6] and has been used for

solving DBSCAN long ago [27]. Given a set  $S$  of elements, the union-find set stores a representative element  $\text{rep}(p)$  for each element  $p \in S$ . There are two operations, Union and Find, where  $\text{Union}(p, q)$  sets the representative for  $p$  and  $q$  as the same, and  $\text{Find}(p)$  returns the representative  $\text{rep}(p)$ . By known results [36], the Union and Find operations can be executed in amortized  $O(1)$  time.

Slightly abusing notations, in this paper the Union and Find operations are allowed to be applied on a set of points  $S$ , but only when it is known that all points in  $S$  have the same representative, i.e.,  $\text{Find}(p) = \text{Find}(p')$  for all  $p, p' \in S$ . Under such constraints,  $\text{Find}(S)$  returns the single representative of the points in  $S$ .  $\text{Union}(p, S)$  is equivalent to  $\text{Union}(p, p')$  where  $p' \in S$ .  $\text{Union}(S_1, S_2)$  is equivalent to  $\text{Union}(p_1, p_2)$  where  $p_1 \in S_1$  and  $p_2 \in S_2$ .

**3.1.4 KDTTree.** KDTTree [3] is a well-known classical space partition tree, and is adopted in this paper as the index structure for traversal. Given a point set  $P$ , each KDTTree node is associated with a subset of  $P$  together with the minimal bounding box (MBR) of this subset. KDTTree is a balanced binary tree, where the two children nodes are obtained by splitting the MBR of parent node at the middle point in one dimension, and the splitting dimension is circularly chosen as the tree is descended. In the following, a KDTTree node will be denoted as  $N$ . For convenience,  $N$  will sometimes be used to refer to the point set contained in this node if no ambiguity is involved.

There are several well-known properties for the KDTTree.

(**KDTTree for range search**). It is well known that the range search on KDTTree takes  $O(n^{1-1/d})$  time in worst case [22].

(**MBR for distance bounds**). Since each KDTTree node is associated with an MBR, point-to-node and node-to-node distance bounds are available by regarding the MBR as a boundary of the node. Let  $D_{\max}(p, N)$ ,  $D_{\min}(p, N)$  be the maximum and minimum distance from point  $p$  to a KDTTree node  $N$ , and let  $D_{\max}(N_1, N_2)$ ,  $D_{\min}(N_1, N_2)$  be the maximum and minimum distance between the two nodes, respectively. The four distance bounds can all be computed in  $O(d)$  time based on the MBR.

In this paper some new notations related to the KDTTree are used.

(**KDTTree node as a compound data structure**). In algorithmic point of view, a KDTTree node can be regarded as a compound data structure storing various information. Table 1 lists the notations.

(**Dense nodes**). A KDTTree node is called dense, if it contains no less than  $\text{minpts}$  points and the longest diagonal of its MBR is no more than  $\epsilon$ , i.e.,  $N.\text{count} \geq \text{minpts}$  and  $N.\text{diag} \leq \epsilon$ . Defining dense KDTTree node follows the idea of defining dense point sets.

(**Left-to-right node ordering**). Based on the notation of left and right children, a left-to-right relationship can be defined across the KDTTree nodes. A node  $N_1$  is said to be on the left to another node  $N_2$ , intuitively, if  $N_1$  appears left to  $N_2$  in the tree, and formally, if  $N_{A1}$  is one ancestor of  $N$ ,  $N_{A2}$  is one ancestor of  $N_2$ , such that  $N_{A1} \neq N_{A2}$ ,  $N_{A1}$  and  $N_{A2}$  have the same parent,  $N_{A1}$  is the left child, and  $N_{A2}$  is the right child.

**3.1.5 Dual-tree algorithm terminologies.** The following terminologies are used to refer to different kinds of node combinations visited in a dual-tree algorithm. The phrase *node combination* may be abbreviated to *combination* if the context is clear, and expanded to *query-reference* combination for emphasizing. If both nodes in the combination are leaves, it will be called a *leaf combination*. If the two

**Table 1: Summary of notations**

Notation	Meaning
KDTree node information	
$N$	a KDTree node
$N.\text{left}$	left child of node $N$
$N.\text{right}$	right child of node $N$
$N.\text{diag}$	the longest diagonal of the MBR of $N$
$N.\text{count}$	the number of points contained in $N$
algorithmic notations	
$\epsilon, \text{minpts}$	the two DBSCAN parameters
$N_q, N_r$	the query and reference node
$p_q, p_r$	the query and reference point
$Nbrs(p)$	the $\epsilon$ -neighbors found so far for point $p$
$ufset$	a union-find set maintaining clustering information

nodes in the combination are the same, it is called a *self combination*. The special combination where both nodes are the root is called the *root combination*. Note that the root combination will always be firstly visited at the beginning of the traversal. For a specific combination  $(N_q, N_r)$ , the term *sub-combination* is used to refer to any combination  $(N'_q, N'_r)$  where  $N'_q$  and  $N'_r$  are descendant nodes of  $N_q$  and  $N_r$ , respectively.

### 3.2 The newly defined DBSCAN sub-problems

Four new sub-problems of the DBSCAN problem are defined here. Besides the classical **Input** and **Output** statement for problem definitions, the definitions given below additionally have **Early Termination** and **Side Effect** statements. The **Early Termination** statement forces any algorithm for this problem to stop once the stated condition is satisfied, incurring less distance computations. The **Side Effect** statement describes some additional actions executed on the inputs after the algorithm is terminated, which may help other procedures and reflects the essence that they are sub-procedures of the DBSCAN problem.

*Definition 3.1.* The  $\epsilon$ -minpts problem.

**Input:** query point  $p_q$ , reference set  $R$ .

**Output:** answer YES if  $|B(p_q, \epsilon) \cap R| \geq \text{minpts}$ , and NO otherwise.

**Early Termination:** terminate once  $\text{minpts}$  number of  $\epsilon$ -neighbors have been found.

**Side Effect:** (1) record the  $\epsilon$ -neighbors of  $p_q$  encountered in the set  $Nbrs(p_q)$ ; (2) mark  $p_q$  as core point if the answer is YES.

The  $\epsilon$ -minpts problem is the initial problem to be solved for each point. For a core point  $p$ , the early termination rule should be applied after the algorithm discovers that  $p$  is core point. For a non-core point  $p$ , the side effect ensures that all its  $\epsilon$ -neighbors are recorded, and the final process to decide whether it is border/noise is feasible by examining whether  $Nbrs(p)$  contains a core point.

*Definition 3.2.* The  $\epsilon$ -minpts-in-dense problem.

**Input:** query point  $p_q$ , the recorded  $\epsilon$ -neighbors  $Nbrs(p_q)$ , reference set  $R$  which is dense.

**Output:** answer YES if  $|Nbrs(p_q)| + |B(p_q, \epsilon) \cap R| \geq \text{minpts}$ , and NO otherwise.

**Early Termination:** terminate once  $\text{minpts}$  number of  $\epsilon$ -neighbors have been found.

**Side Effect:** (1) put the newly found  $\epsilon$ -neighbors for  $p_q$  into  $Nbrs(p_q)$ ; (2) mark  $p_q$  as core point if the answer is YES; (3) add  $p_q$  into  $R$  if the answer is YES.

The  $\epsilon$ -minpts-in-dense problem is the only one that is not illustrated in Section 1. Compared with the  $\epsilon$ -minpts problem above, it utilizes the fact that the reference set  $R$  is dense, and involves an extra side effect that expands the cluster of  $R$  by adding  $p_q$  into it if the query points  $p_q$  is identified as a core point.

*Definition 3.3.* The  $\epsilon$ -connected-single problem.

**Input:** core point  $p_q$ , reference set  $R$  which is dense.

**Output:** answer YES if  $\exists p_r \in R$  such that  $D(p_q, p_r) \leq \epsilon$ , and NO otherwise.

**Early Termination:** terminate once such  $p_r$  is found.

**Side Effect:** add  $p_q$  to  $R$  if the answer is YES.

$\epsilon$ -connected-single deals with the relationship between a core point and a dense set. If it is found that  $p_q$  and  $R$  are density-connected via some point  $r \in R$ ,  $p_q$  will be added into  $R$ .

*Definition 3.4.* The  $\epsilon$ -connected-dual problem.

**Input:** query set  $Q$ , reference set  $R$ , which are both dense.

**Output:** answer YES if  $\exists p_q \in Q, p_r \in R$  such that  $D(p_q, p_r) \leq \epsilon$ , and NO otherwise.

**Early Termination:** terminate once such pair is found.

**Side Effect:** union  $Q$  and  $R$  if the answer is YES.

$\epsilon$ -connected-dual deals with the relationship between two dense sets, and union the two dense sets if they are density-connected, expanding the cluster of dense sets.

## 4 THE GEDUAL-DBSCAN ALGORITHMS

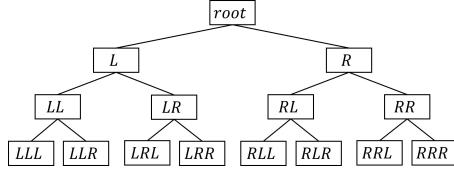
The following auxiliary data structures are available for the algorithms introduced in this section. A KDTree  $\mathcal{T}$  is built on the input set  $P$ , and root node is denoted as *root*. A priority queue  $\mathcal{PQ}$  is used to ensure the traversal order. A union-find set  $ufset$  is used to store the information of clusters. A set  $Nbrs(p)$  is used to record the  $\epsilon$ -neighbors encountered during the search for each point  $p \in P$ . See the second part of Table 1 for algorithmic notations.

The GeDual-DBSCAN algorithm is introduced using three variants, each enhancing the former one with some new ideas. The first variant mainly describes the order of tree traversal and how to implement the desired traversal order. The second variant introduces the *intermediate cases* corresponding to the sub-problems defined above, and describes how to solve these intermediate cases and how they are integrated in the overall traversal. The third variant, which is the most powerful, considers the fact that a node may be discovered as dense during the traversal and explains how to utilize this information on-the-fly using *state transition* functions.

### 4.1 GeDual-DBSCAN variant 1: basic traversal

The basic traversal algorithm is introduced in three parts, the traversal order, the BaseCase function, and the Score function.

**4.1.1 Traversal order.** Let us first consider the basic dual-tree traversal on KDTree without any pruning, where each leaf combination should be visited once and only once. The basic traversal is established on the following simple idea of avoiding duplicate distance computations. (1) If  $D(p_q, p_r)$  is computed, then  $D(p_r, p_q)$  can be avoided to compute. (2) If the combination  $(N_q, N_r)$  is visited, then the combination  $(N_r, N_q)$  can be avoided to visit.

**Figure 2: An example of KDTree node notations.**

A straightforward idea to avoid duplicate visit is to label the nodes in numbers  $1, 2, \dots, n$ , and visit the combinations in an ordered way like  $(1, 2), (1, 3), \dots, (2, 3), (2, 4), \dots, (n-1, n), (n, n)$ . For KDTree nodes, the numbering is unnecessary since an left-to-right order has already been defined. Using the KDTree in Figure 2 as an example, the traversal order should be as follows. First using  $LLL$  as the query node, visit reference nodes in the following order:  $LLL, LLR, LRL, \dots, RRR$ . Then, using  $LLR$  as the query node, visit reference nodes in the following order:  $LLR, LRL, \dots, RRR$ . So forth, until the last leaf combination ( $RRR, RRR$ ) is visited.

To realize the above order to visit the combinations, the algorithm uses a priority queue  $\mathcal{PQ}$  to guide the traversal where the elements in it are the query-reference node combinations. Two parts of traversal rules are used to make a correct traversal order, which are the descending rules and priority rules.

**Descending rules.** The descending rules apply to a visited combination  $(N_q, N_r)$  which are not both leaves, to decide subsequent node combinations to be pushed into the priority queue for further traversal. The descending rules include the following three terms.

- (*Self descending*) If  $N_q = N_r$ , push the following combinations into  $\mathcal{PQ}$ :  $(N_q.\text{left}, N_q.\text{left}), (N_q.\text{left}, N_q.\text{right}), (N_q.\text{right}, N_q.\text{right})$ .
- (*Query descending*) If  $N_q \neq N_r$  and  $N_q$  is not leaf, push  $(N_q.\text{left}, N_r)$  and  $(N_q.\text{right}, N_r)$  into  $\mathcal{PQ}$ .
- (*Reference descending*) If  $N_q$  is leaf, push  $(N_q, N_r.\text{right})$  and  $(N_q, N_r.\text{right})$  into  $\mathcal{PQ}$ .

The idea of query descending and reference descending rules is to first descend the query node down to the leaf, then start to descend the reference node using a leaf node as the query node. The self descending rule is to visit the node combinations recursively and ensure the traversal indeed visits all possible combinations.

**Priority rules.** The priority rules determine the order of visiting the node combinations stored in the priority queue. For two combinations  $(N_{q1}, N_{r1})$  and  $(N_{q2}, N_{r2})$ ,  $(N_{q1}, N_{r1})$  should be visited before  $(N_{q2}, N_{r2})$  if one of the following conditions happen:

- (*Ancestor query first*)  $N_{q1}$  is an ancestor of  $N_{q2}$ ;
- (*Left query first*)  $N_{q1}$  is left to  $N_{q2}$ ;
- (*Left reference first*)  $N_{q1} = N_{q2}$  but  $N_{r1}$  is left to  $N_{r2}$ .

The basic traversal works by integrating the descending rules and priority rules. An example traversal on the KDTree shown in Figure 2 is given in Table 2. The first column in the table is the number of steps. The second column shows the contents in the priority queue  $\mathcal{PQ}$ , and the priority order is shown using ' $\prec$ '. The third column is the current combination to be visited and it will be popped out of  $\mathcal{PQ}$  after visited. The fourth column is the subsequent combinations to be pushed into  $\mathcal{PQ}$ . At the beginning of the algorithm the root combination  $(\text{root}, \text{root})$  is pushed into  $\mathcal{PQ}$ , and then the traversal goes as follows.

(1)  $(\text{root}, \text{root})$  is the top combination which is popped out. By *Self*

**Table 2: Part of traversal on KDTree in Figure 2.**

Step	Contents and order	Selection	Descend
1	$(\text{root}, \text{root})$	$(\text{root}, \text{root})$	$(L, L), (L, R), (R, R)$
2	$(L, L) \prec (L, R) \prec (R, R)$	$(L, L)$	$(LL, LL), (LL, LR), (LR, LR)$
3	$(L, R) \prec (LL, LL) \prec (LL, LR) \prec (R, R)$	$(L, R)$	$(LL, R), (LR, R)$
4	$(LL, LL) \prec (LL, LR) \prec (LL, R) \prec (R, R)$	$(LL, LL)$	$(LLL, LLL), (LLL, LLR), (LLR, LLR)$
5	$(LL, LR) \prec (LL, R) \prec (LLL, LLL) \prec (LLL, LLR) \prec (LLR, LLR) \prec (R, R)$	$(LL, LR)$	$(LLL, LR), (LLR, LR)$
6	$(LLL, LLL) \prec (LLL, LLR) \prec (LLL, LR) \prec (LLR, LLL) \prec (LLR, LR) \prec (R, R)$	$(LL, R)$	$(LLL, R), (LLR, R)$
7	$(LLL, LLL) \prec (LLL, LLR) \prec (LLL, LR) \prec (LLR, LLL) \prec (LLR, LLR) \prec (LLR, LR) \prec (R, R)$	$(LLL, LLL)$	Leaf combination reached. Invoke BaseCase.
...	...	...	...

descending rule,  $(L, L), (L, R), (R, R)$  are pushed into  $\mathcal{PQ}$ .

(2)  $(L, L)$  is of highest priority, which is popped out. By *Self descending* rule,  $(LL, LL), (LL, LR), (LR, LR)$  are pushed into  $\mathcal{PQ}$ .

...

(6)  $(LL, R)$  should be visited by the *Ancestor query first* rule. By *Query descending* rule,  $(LLL, R), (LLR, R)$  are pushed in to  $\mathcal{PQ}$ .

(7) Now a leaf combination  $(LLL, LLL)$  is of highest priority where descending is not applicable. The *BaseCase* function should be invoked on leaf combinations, which will be introduced next.

It can be noticed that the first leaf combination visited is the left-most leaf  $LLL$ . Also, before the next leaf  $LLR$  is visited as query node, all combinations using  $LLL$  as query node will be traversed since the combinations with  $LLL$  as query node all have a higher priority. Thus, it is true that the desired traversal order is ensured.

**4.1.2 BaseCase function.** The *BaseCase* function is invoked on a leaf combination  $(N_q, N_r)$ . It is responsible to solve the DBSCAN problem partially on  $(N_q, N_r)$ , so that the DBSCAN problem will be solved after *BaseCase* is invoked on each leaf combination once. Specified to a single query point  $p_q \in N_q$ , after the *BaseCase* function is invoked on all leaf combinations using  $N_q$  as query node, all its  $\epsilon$ -neighbors should be found, and  $p_q$  should be joined with the core points in  $Nbrs(p_q)$  if  $p_q$  is a core point.

This goal is divided into two stages. In the first stage, the  $\epsilon$ -minpts problem is executed on  $p_q$  and the  $\epsilon$ -neighbors are gradually added into  $Nbrs(p_q)$  as the *BaseCase* function is invoked left-to-right across the leaf nodes. This stage is terminated once  $|Nbrs(p_q)|$  exceeds  $minpts$ , and the *PointTurnToCore* function is invoked to join  $p_q$  with the core points in  $Nbrs(p_q)$ . Then it begins the second stage, where  $\epsilon$ -neighbors newly found this stage will be joined with  $p_q$  into one cluster if the neighbor point is also a core point.

There are several important notes. First, if two points are already known in the same cluster, there is no need to compute the distance between them. Second, if  $D(p_q, p_r) \leq \epsilon$  and the reference point  $p_r$  is a non-core point,  $p_q$  should be added to  $Nbrs(p_r)$  since  $p_q$  is also an  $\epsilon$ -neighbor of  $p_r$ . In such way, although the *BaseCase* function is invoked in a left-to-right order on the leaf combinations, a point  $p_r \in N_r$  may be discovered as a core point before  $N_r$  is visited as query node. It needs to prove that such unordered discovery of core points still manages to find the correct DBSCAN clusters.

**LEMMA 4.1.** *For each pair of core points  $p_1, p_2$  s.t.  $D(p_1, p_2) \leq \epsilon$ , they have the same representative in the union-find set after the *BaseCase* function is invoked on all leaf combinations.*

---

```

1 Function BaseCase_BothLeaves( $N_q, N_r$ ):
2   foreach  $p_q \in N_q, p_r \in N_r$  do
3     if  $|Nbrs(p_q)| \geq minpts$  then
4       if  $ufset.Find(p_q) = uiset.Find(p_r)$  then
5         continue;
6       Compute  $D(p_q, p_r)$ ;
7       if  $D(p_q, p_r) \leq \epsilon$  then
8         if  $|Nbrs(p_r)| < minpts$  then AddNbr( $p_r, p_q$ );
9         else  $ufset.Union(p_q, p_r)$ ;
10    else
11      Compute  $D(p_q, p_r)$ ;
12      if  $D(p_q, p_r) \leq \epsilon$  then
13        AddNbr( $p_q, p_r$ );
14        if  $|Nbrs(p_r)| < minpts$  then AddNbr( $p_r, p_q$ );
15  Function AddNbr( $p, nbr$ ):
16    Add  $nbr$  into  $Nbrs(p)$ ;
17    if  $|Nbr(p)| \geq minpts$  then PointTurnToCore( $a$ );
18  Function PointTurnToCore( $p$ ):
19    foreach  $p' \in Nbrs(p)$  do
20      if  $|Nbrs(p')| \geq minpts$  then  $ufset.Union(p, p')$ ;

```

---

**4.1.3 Score function.** By combining the traversal rules with the BaseCase function, a naive traversal which invokes the BaseCase function on each possible leaf combination can be established. However, an efficient tree traversal algorithm must have the ability to prune nodes unnecessary to be visited, which is the reason to introduce the Score function.

The Score function used here is invoked on a query-reference combination  $(N_q, N_r)$ , to test whether it is valid for further traversal. The return value of Score function is a non-negative real number  $score$ . If  $score = 0$ , it means that  $N_q$  and  $N_r$  are close enough that all points in  $N_q$  are  $\epsilon$ -neighbors of all points in  $N_r$ . If the  $score$  is a large enough number, which is supposed to be  $\infty$ , it means that  $N_q$  and  $N_r$  are so far that it is impossible to find  $\epsilon$ -neighbor pairs between the two nodes. For both cases there is no need to traverse the sub-combinations of  $(N_q, N_r)$ . If none of the two cases happen, the combination  $(N_q, N_r)$  should be pushed into the priority queue  $\mathcal{P}Q$  for further traversal.

Intuitively, the Score function must utilize upper and lower bounds on the pairwise distances between  $p_q \in N_q$  and  $p_r \in N_r$ . Recall that  $Dmax(N_q, N_r)$  and  $Dmin(N_q, N_r)$ , which are the maximum and minimum distances between the MBR of the two nodes, can well serve this goal. Thus, the Score function works by compare these two values against the DBSCAN parameter  $\epsilon$ .

The Score function cooperates with Decide and BaseCase\_NearNodes functions. The Decide function is invoked during the traversal when it needs to decide whether a combination  $(N_q, N_r)$  should be pushed into the priority queue for further traversal. It invokes the Score function to make the decision. The BaseCase\_NearNodes function is invoked when  $score = 0$  to deal with the case that all points in  $N_q$  are  $\epsilon$ -neighbors of all points in  $N_r$ .

**4.1.4 Overall algorithm.** Now we are ready to present the overall GeDual-DBSCAN-Basic algorithm, which is given in Algorithm 1. The correctness of the algorithm follows by Lemma 4.1 and the fact that the pruning rule never throws out any possible  $\epsilon$ -neighbor

---

```

1 Function Decide( $N_q, N_r, \mathcal{P}Q$ ):
2    $score \leftarrow Score(N_q, N_r)$ ;
3   if  $score = 0$  then BaseCase_NearNodes( $N_q, N_r$ );
4   else if  $score < \infty$  then push  $(N_q, N_r)$  into  $\mathcal{P}Q$ ;
5 Function Score( $N_q, N_r$ ):
6   Compute  $Dmax(N_q, N_r)$  and  $Dmin(N_q, N_r)$ ;
7   if  $Dmax(N_q, N_r) \leq minpts$  then return 0;
8   else if  $Dmin(N_q, N_r) > \epsilon$  then return  $\infty$ ;
9   else return  $Dmin(N_q, N_r)$ ;
10 Function BaseCase_NearNodes( $N_q, N_r$ ):
11   foreach  $p_q \in N_q$  do
12     if  $|Nbrs(p_q)| \leq minpts$  then
13       foreach  $p_r \in N_r$  do AddNbr( $p_q, p_r$ );
14   foreach  $p_r \in N_r$  do
15     if  $|Nbrs(p_r)| \leq minpts$  then
16       foreach  $p_q \in N_q$  do AddNbr( $p_r, p_q$ );
17   foreach  $p_q \in N_q, p_r \in N_r$  that are both core do
18      $ufset.Union(p_q, p_r)$ ;

```

---

**Algorithm 1:** GeDual-DBSCAN-Basic

---

```

1 Push  $(root, root)$  into  $\mathcal{P}Q$ ;
2 while  $\mathcal{P}Q$  is not empty do
3    $(N_q, N_r) \leftarrow \mathcal{P}Q.pop()$ ; // gets the top element
4   if  $N_q$  is leaf then
5     if  $N_r$  is leaf then
6       BaseCase_BothLeaves( $N_q, N_r$ );
7     else // Apply Reference descending rule
8       Decide( $N_q, N_r.left, \mathcal{P}Q$ ); Decide( $N_q, N_r.right, \mathcal{P}Q$ );
9   else
10    if  $N_q = N_r$  then // Apply Self descending rule
11      Push( $N_q.left, N_q.left$ ) and  $(N_q.right, N_q.right)$  into  $\mathcal{P}Q$ ;
12      Decide( $N_q.left, N_q.right, \mathcal{P}Q$ );
13    else // Apply Query descending rule
14      Decide( $N_q.left, N_r, \mathcal{P}Q$ ); Decide( $N_q.right, N_r, \mathcal{P}Q$ );
15 AssignNonCorePoints();
16 Function AssignNonCorePoints():
17   foreach  $p$  s.t.  $|Nbrs(p)| \leq minpts$  do
18     if  $\exists p' \in Nbrs(p)$  s.t.  $|Nbrs(p')| \geq minpts$  then
19        $ufset.Union(p, p')$  and continue;

```

---

pair. The complexity of the algorithm is shown in Theorem 4.2, and the proof is omitted due to space limitation.

**THEOREM 4.2.** *The time complexity of GeDual-DBSCAN-Basic algorithm is  $O(n^{2-1/d}) + O(n \log n) = O(n^{2-1/d})$ .*

## 4.2 GeDual-DBSCAN variant 2: intermediate cases

The GeDual-DBSCAN-Basic algorithm establishes the framework of traversal order, but did not concern the sub-problems introduced in Section 3.2, i.e., the  $\epsilon$ -minpts-in-dense,  $\epsilon$ -connect-single and  $\epsilon$ -connect-dual problems. The GeDual-DBSCAN-InterCases algorithm to be introduced in this section works by integrating these sub-problems into the traversal framework of the basic algorithm, which further reduces the number of distance computations.

**Algorithm 2:** GeDual-DBSCAN-InterCases

---

```

1 Push (root, root) into  $\mathcal{PQ}$ ;
2 FindInitialDenseNodes();
3 while  $\mathcal{PQ}$  is not empty do
4    $(\mathcal{N}_q, \mathcal{N}_r) \leftarrow \mathcal{PQ}.pop()$ ;
5   if  $\mathcal{N}_q$  is leaf or dense then
6     if  $\mathcal{N}_r$  is leaf or dense then
7       if  $\mathcal{N}_q = \mathcal{N}_r$  and  $\mathcal{N}_q$  is dense then continue;
8       if  $\mathcal{N}_q$  is dense and  $\mathcal{N}_r$  is dense then
9         | InterCase_BothDense( $\mathcal{N}_q, \mathcal{N}_r$ );
10      else if  $\mathcal{N}_q$  is leaf and  $\mathcal{N}_r$  is dense then
11        | InterCase_LeafDense( $\mathcal{N}_q, \mathcal{N}_r$ );
12      else if  $\mathcal{N}_q$  is dense and  $\mathcal{N}_r$  is leaf then
13        | InterCase_LeafDense( $\mathcal{N}_r, \mathcal{N}_q$ );
14      else if  $\mathcal{N}_q$  is leaf and  $\mathcal{N}_r$  is leaf then
15        | BaseCase_BothLeaves( $\mathcal{N}_q, \mathcal{N}_r$ );
16      else
17        | Decide ( $\mathcal{N}_q, \mathcal{N}_r.left$ ); Decide ( $\mathcal{N}_q, \mathcal{N}_r.right$ );
18    else
19      if  $\mathcal{N}_q = \mathcal{N}_r$  and  $\mathcal{N}_q$  is not dense then
20        | Push( $\mathcal{N}_q.left, \mathcal{N}_q.left$ ) and ( $\mathcal{N}_q.right, \mathcal{N}_q.right$ ) into  $\mathcal{PQ}$ ;
21        | Decide ( $\mathcal{N}_q.left, \mathcal{N}_q.right$ );
22      else
23        | Decide ( $\mathcal{N}_q.left, \mathcal{N}_r$ ); Decide ( $\mathcal{N}_q.right, \mathcal{N}_r$ );
24 AssignNonCorePoints();
25 Function FindInitialDenseNodes():
26   foreach  $\mathcal{N}$  in KDTTree  $\mathcal{T}$  do
27     if  $\mathcal{N}.diag \leq \epsilon$  and  $\mathcal{N}.count \geq minpts$  then mark  $\mathcal{N}$  as dense;
```

---

Recall that the sub-problems defined in Section 3.2 require the input point set is known to be dense. To produce such information so that these sub-problems are applicable, an extra sub-procedure `FindInitialDenseNodes` is executed at the beginning of the algorithm. It is to check all the nodes in the KDTTree to find the *dense* nodes, i.e., the nodes satisfying  $\mathcal{N}.diag \leq \epsilon$  and  $\mathcal{N}.count \geq minpts$ . It is easy to see points in such node forms a density-connected cluster of core points, meeting the definition of dense point sets.

The traversal begins after the dense nodes are identified. The priority rules, `Decide` and `Score` functions of the former Basic variant still completely apply for this `InterCases` variant, but they differ in descending rules. The Basic variant descends until leaf combinations, but in the `InterCases` variant, if a combination containing dense nodes is encountered during the traversal, it is said that an intermediate case is met, and the subsequent traversal will be substituted by what is defined by the `InterCase` functions. If both nodes in the combination are dense, the `InterCase_BothDense` function will be invoked. The other case is one node in the combination is leaf and the other is dense, which resorts to the `InterCase_LeafDense` function. A special case is that if a self combination of dense node is visited, there is no need for further descending. Before diving into the details of the intermediate cases, keep in mind that to ensure the correctness of the traversal algorithm, the intermediate cases should also solve the partial DBSCAN problem on the visited combination, so that the DBSCAN problem would be solved after all possible base cases and intermediate cases are visited.

**Intermediate Cases 1: both dense**


---

```

1 Procedure InterCase_BothDense( $\mathcal{N}_q, \mathcal{N}_r$ ):
2   if Score( $\mathcal{N}_q, \mathcal{N}_r$ ) = 0 then
3     |  $ufset.Union(\mathcal{N}_q, \mathcal{N}_r)$ ;
4   else if Score( $\mathcal{N}_q, \mathcal{N}_r$ ) <  $\infty$  then
5     |  $found \leftarrow false$ ;
6     | EpsConnect_Dual( $\mathcal{N}_q, \mathcal{N}_r, found$ );
7   if  $found = true$  then  $ufset.Union(\mathcal{N}_q, \mathcal{N}_r)$ ;
```

---

**4.2.1 InterCase\_BothDense.** If a combination  $(\mathcal{N}_q, \mathcal{N}_r)$  with two dense nodes is visited, to produce the correct DBSCAN clusters it needs to test whether the two nodes are density-connected. Recall that it is exactly the functionality of the  $\epsilon$ -connect-dual problem. Thus, the `InterCase_BothDense` function will change the traversal beneath  $(\mathcal{N}_q, \mathcal{N}_r)$  so as to solve the  $\epsilon$ -connect-dual problem.

Using a way similar with introducing the GeDual-DBSCAN-Basic algorithm, the traversal algorithm for  $\epsilon$ -connect-dual problem is split into the following parts including the descending and priority rules, as well as the `BaseCase`, `Decide` and `Score` functions. Additionally, a *termination rule* should be involved to meet the Early Termination statement in the problem definition.

**Descending rule.** The descending rule is simple which only ensures all the possible leaf combinations are visited. Specifically, when a non-leaf combination is visited, descend to the four children combinations. If a combination with one leaf and one non-leaf is visited, descend the non-leaf node.

**Priority rule.** Unlike the GeDual-DBSCAN-Basic algorithm where the priority rule applies to all the combinations in a global priority queue, the priority rule of  $\epsilon$ -connect-dual problem applies locally only to the sibling combinations obtained by the descending rule. It simply asks to visit the local sibling combinations in ascending order of the *score*.

**Termination rule.** A boolean value *found* is maintained indicating whether a  $\epsilon$ -neighbor pair is found. The algorithm will be terminated once *found* turns true.

**BaseCase.** The `BaseCase` function simply iterates through all pairs of points to find an  $\epsilon$ -neighbor pair, and terminate the iteration once such pair is found. It indeed solves the  $\epsilon$ -connect-dual problem on the leaf combination as `BaseCase` functions should do.

**Decide.** There are three cases for the `Decide` function. The near case is that all points in  $\mathcal{N}_q$  are within distance  $\epsilon$  to all points in  $\mathcal{N}_r$ . In such a case the algorithm should be early terminated by setting *found* to be true. The far case is that the points between the two nodes are at least  $\epsilon$  apart, and this combination is pruned. Beside the two cases is the normal case, where the combination is put into the local traversal list for descending.

**Score.** The `Score` function used in GeDual-DBSCAN-Basic is reused, since the near and far case in the above `Decide` function can be successfully identified by that `Score` function.

The cooperation of priority rule, termination rule and `Score` function makes it possible to find an  $\epsilon$ -neighbor pair earlier in combinations with lower score, resulting in earlier termination and less distance computations.

**4.2.2 InterCase\_LeafDense.** The `InterCase_LeafDense` function deals with the combinations containing one leaf and one dense node. This intermediate case is separated into two sub-cases.

The first sub-case is that query node  $N_q$  is leaf and reference node  $N_r$  is dense. To solve the partial DBSCAN problem on  $(N_q, N_r)$  knowing  $N_r$  is dense, further consider whether  $p_q \in N_q$  is a core point. For core point  $p_q$ , it exactly needs to solve the  $\epsilon$ -connect-single problem, i.e., find but one  $\epsilon$ -neighbor of  $p_q$  in  $N_r$  to know  $p_q$  and  $N_r$  are density-connected. If  $p_q$  is not known to be a core point yet, the  $\epsilon$ -minpts-in-dense problem should be solved. Namely, first find enough  $\epsilon$ -neighbors of  $p_q$  in  $N_r$  to know it is a core point, and it is immediately known that  $p_q$  and  $N_r$  are density-connected.

The second sub-case is that  $N_q$  is dense and  $N_r$  is leaf. To solve the partial DBSCAN problem on  $(N_q, N_r)$ , the following actions should be executed for each  $p_q \in N_q$ . First find all the  $\epsilon$ -neighbors of  $p_q$  in  $N_r$ . If the neighbor point  $p_r$  is already a core point, join  $p_q$  and  $p_r$  into one cluster. Otherwise, add  $p_q$  into  $Nbrs(p_r)$ . Note that these actions are initiated by query points and the reference point are passively visited, but it can be equivalently rephrased using actions initiated by the reference points. For each  $p_r \in N_r$ , if  $p_r$  is a core point, then if there exist  $p_q \in N_q$  such that  $D(p_r, p_q) \leq \epsilon$ ,  $p_r$  will be joined with  $N_q$ . If  $p_r$  is not known to be a core point yet, find enough  $\epsilon$ -neighbors of  $p_r$  in  $N_q$  to discover it is a core point, and then join  $p_r$  with  $N_q$  into one cluster. Thus, it is equivalent to solve  $\epsilon$ -connect-single problem for core points in  $N_r$  and solve  $\epsilon$ -minpts-in-dense problem for the other points.

In both sub-cases,  $\epsilon$ -connect-single and  $\epsilon$ -minpts-in-dense problems should be solved, using points in the leaf node as query point and using the dense node as the reference node. The traversal algorithm for these two problems are introduced below.

### Intermediate Cases 2: one leaf and one dense

```

1 Procedure InterCase_LeafDense( $N_{leaf}, N_{dense}$ ):
2   foreach  $p \in N_{leaf}$  do
3     if  $|Nbrs(p)| \geq minpts$  then
4        $found \leftarrow false$ ;
5       EpsConnect_Single( $p, N_{dense}, found$ );
6       if  $found = true$  then  $ufset.Union(p, N_{dense})$ ;
7     else
8       EpsMinptsInDense( $p, N_{dense}$ );
9       if  $|Nbr(p)| \geq minpts$  then  $ufset.Union(p, N_{dense})$ ;
```

$\epsilon$ -connect-single. The algorithm is similar to but simpler than that for  $\epsilon$ -connect-dual problem since there is only one tree to descend for  $\epsilon$ -connect-single problem.

**Descending rule.** Simply descend the reference node to the two children nodes, until leaf node is reached.

**Priority rule.** Locally visit the child node with lower score first.

**Termination rule.** The algorithm should be terminated once the boolean indicator  $found$  turns true.

**BaseCase.** Iterates all points in the reference node, and terminate once an  $\epsilon$ -neighbor is found.

**Decide.** Similar with the Decide function of  $\epsilon$ -connect-dual problem, the near case is that all points in  $N_r$  are within  $\epsilon$  distance to  $p_q$ , the far case is that all points in  $N_r$  are  $\epsilon$  far away from  $p_q$ , and excepting the near and far case is the normal case.

**Score.** The Score function is based on the point-to-node distance bound of KDTREE nodes, i.e.,  $Dmax(p_q, N_r)$  and  $Dmin(p_q, N_r)$ . The near and far cases are identified by comparing these two values with  $\epsilon$ . For normal case  $Dmin(p_q, N_r)$  is used as the score value.

### Sub-problem 2: $\epsilon$ -connect-single

```

1 Procedure EpsConnect_Single( $p_q, N_r, found$ ):
2   if  $N_r$  is leaf then
3     BaseCase_EpsConnect_Single( $p_q, N_r, found$ );
4   else
5     Make an empty local traversal list  $LTL$ ;
6     Decide_EpsConnect_Single( $p_q, N_r.left, found, LTL$ );
7     Decide_EpsConnect_Single( $p_q, N_r.right, found, LTL$ );
8     foreach refNode in  $LTL$  do
9       if  $found = true$  then terminate;
10      EpsConnect_Single( $p_q, refNode, found$ );
11 Function BaseCase_EpsConnect_Single( $p_q, N_r, found$ ):
12   foreach  $p_r \in N_r$  do
13     if  $D(p_q, p_r) \leq \epsilon$  then
14        $found \leftarrow true$  and terminate;
15 Function Decide_EpsConnect_Single( $p_q, N_r, found, LTL$ ):
16    $score \leftarrow Score\_Single(p_q, N_r)$ ;
17   if  $score = 0$  then
18      $found \leftarrow true$  and terminate;
19   else if  $score < \infty$  then
20     Add  $N_r$  into  $LTL$ , and sort in ascending order of  $score$ ;
21 Function Score_Single( $p_q, N_r$ ):
22   Compute  $Dmax(p_q, N_r)$  and  $Dmin(p_q, N_r)$ ;
23   if  $Dmax(p_q, N_r) \leq \epsilon$  then return 0;
24   else if  $Dmin(p_q, N_r) > \epsilon$  return  $\infty$ ;
25   else return  $Dmin(p_q, N_r) > \epsilon$ ;
```

$\epsilon$ -minpts-in-dense. The algorithm has a similar base case with the GeDual-DBSCAN-Basic algorithm since they both solve the  $\epsilon$ -minpts problem for query point  $p_q$ , but traversal body is simpler since there is only one tree to descend.

**Descending rule.** Descend the reference node to the two children nodes until leaf node.

**Priority rule.** Locally visit the child node with lower score first.

**Termination rule.** Terminate once  $|Nbrs(p_q)|$  exceeds  $minpts$ .

**BaseCase.** Iterate all points in the reference node to find the  $\epsilon$ -neighbors. Terminate once  $|Nbrs(p_q)| \geq minpts$ .

**Decide.** The Decide function is similar with that of the GeDual-DBSCAN-Basic algorithm. The near case is dealt by the BaseCase\_EpsMinptsInDense\_NearNode function where all points in  $N_r$  are  $\epsilon$ -neighbor of  $p_q$ . The far case is pruned since it is impossible to find an  $\epsilon$ -neighbor of  $p_q$  in  $N_r$ .

**Score.** The Score\_Single function in  $\epsilon$ -connect-single algorithm is reused, since it suffices to separate the near and far cases for the  $\epsilon$ -minpts-in-dense problem.

The correctness of the overall GeDual-DBSCAN-InterCases algorithm follows by each intermediate case being able to successfully solve the partial DBSCAN problem on the visited combination, and every possible combination being ensured to be visited. The complexity of the algorithm is given in the following theorem.

**LEMMA 4.3.** *The time complexity of  $\epsilon$ -minpts-in-dense is  $O(n^{1-1/d} + minpts)$ , the expected time complexity of  $\epsilon$ -connect-single is  $O(\sqrt{mn})$ , and the time expected complexity of  $\epsilon$ -connect-single is  $O(\sqrt{n})$ .*

**THEOREM 4.4.** *Suppose all the dense nodes contain  $n_0$  points. The time complexity of GeDual-DBSCAN-InterCases is  $O((n-n_0)n^{1-1/d})$ .*

**Sub-problem 3:  $\epsilon$ -minpts-in-dense**


---

```

Procedure EpsMinptsInDense( $p_q, N_r$ ):
  if  $N_r$  is leaf then
    | BaseCase_EpsMinptsInDense( $p_q, N_r$ );
  else
    | Make an empty local traversal list  $LTL$ ;
    | Decide_EpsMinptsInDense( $p_q, N_r.left, LTL$ );
    | Decide_EpsMinptsInDense( $p_q, N_r.right, LTL$ );
    | foreach refNode in  $LTL$  do
      | | if  $p_q$  becomes core then terminate;
      | | EpsMinptsInDense( $p_q, refNode$ );
  Function BaseCase_EpsMinptsInDense( $p_q, N_r$ ):
    foreach  $p_r \in N_r$  do
      | | if  $D(p_q, p_r) \leq \epsilon$  then AddNbr( $p_q, p_r$ );
      | | if  $|Nbrs(p_q)| \geq minpts$  then terminate;
  Function Decide_EpsMinptsInDense( $p_q, N_r, LTL$ ):
    score  $\leftarrow$  Score_Single( $p_q, N_r$ );
    if score = 0 then
      | BaseCase_EpsMinptsInDense_NearNodes( $p_q, N_r$ );
    else if score <  $\infty$  then
      | Add  $N_r$  into  $LTL$ , and sort in ascending order on score;
  Function BaseCase_EpsMinptsInDense_NearNodes( $p_q, N_r$ ):
    foreach  $p_r \in N_r$  do
      | AddNbr( $p_q, p_r$ );
      | if  $|Nbrs(p_q)| \geq minpts$  then terminate;

```

---

**4.3 GeDual-DBSCAN variant 3: state transitions**

The GeDual-DBSCAN-InterCases algorithm uses the information of dense nodes but not to the maximum extent. The dense nodes are identified at the beginning and the whole algorithm depends only on this initial knowledge. However, a node initially not dense may become dense as the algorithm proceeds, since points in the node are continuously discovered to be core points and neighboring core points are joined into a cluster. To utilize the information of dense nodes on-the-fly, the final variant of our algorithm is proposed which is called GeDual-DBSCAN-Transitions.

The core idea of GeDual-DBSCAN-Transitions is to attach some boolean *state indicators* the nodes showing certain information. Specifically, each node is associated with three indicators named *AllCore*, *OneCluster*, and *Dense*. The *AllCore* indicator is to show whether all points in this node are core points. The *OneCluster* indicator is to show whether all points in this node are in the same cluster. The *Dense* indicator is, by the definition of dense nodes, the conjunction of the *OneCluster* and *AllCore* indicators.

All indicators are false at the beginning of the algorithm. Then the *InitialCheck* function is invoked on each node  $N$  to set the initial states of the nodes. If  $N.\text{diag} \leq \epsilon$  then the *OneCluster* indicator is set to be true. If further  $N.\text{count} \geq minpts$  then *AllCore* and *Dense* indicators are set to be true. The *InitialCheck* function should replace the *FindInitialDenseNodes* function in the InterCases variant. Next the transition functions for these three state indicators are introduced respectively.

**AllCore indicator.** An auxiliary function *IncNumCore* operating a counter  $N.\text{numCores}$  helps to set the *AllCore* indicator of

*AllCore* indicator related functions.

---

```

Function InitialCheck():
  foreach KDT tree node  $N$  do
    | | if  $N.\text{diag} \leq \epsilon$  then
    | | |  $N.\text{OneCluster} \leftarrow true$ ;
    | | | if  $N.\text{count} \geq minpts$  then
    | | | |  $N.\text{AllCore} \leftarrow true$  and  $N.\text{Dense} \leftarrow true$ ;
  Function IncNumCore( $N, N_q$ ):
    Increase  $N.\text{numCores}$  by 1;
    if  $N.\text{numCores} = N.\text{count}$  then
      | NodeTurnTo_AllCore( $N, N_q$ );
  Function NodeTurnTo_AllCore( $N, N_q$ ):
     $N.\text{AllCore} \leftarrow true$ ;
    if  $N = N_q$  then flag  $\leftarrow$  CheckOneCluster( $N$ );
    else flag  $\leftarrow$  CheckOneCluster_BruteForce( $N$ );
    if flag = true then NodeTurnTo_Dense( $N, N_q$ );

```

---

each node  $N$ . The *PointTurnToCore* function invoked on point  $p$  triggers the *IncNumCore* function on the node  $N$  containing  $p$  to increase the  $N.\text{numCores}$  counter. When  $N.\text{numCores}$  reaches  $N.\text{count}$ , the transition function *NodeTurnTo\_AllCore* will be invoked to set the *AllCore* indicator. It further triggers the checking process for the *OneCluster* indicator, and invokes the transition function for *Dense* indicator if *OneCluster* is set to be true.

**OneCluster indicator.** The checking process is triggered by the *NodeTurnTo\_AllCore* function to test whether the *OneCluster* indicator should be set, and there are two different processes for query nodes and reference nodes respectively. For query nodes, a cheaper method based on union-find set is used. The other function for reference nodes computes all the pairwise distances among the points in  $N$ . The reason to use two difference functions is as follows. For a query node  $N_q$ , by that time *CheckOneCluster* is triggered by *NodeTurnTo\_AllCore*, all the pairwise distances among points in  $N_q$  must have been computed since the self combination of  $N_q$  must have been visited. But it is not the case for a reference node  $N_r$ . To know whether the reference node is of one cluster as early as possible, it is better to compute the pairwise distances among points in  $N_r$  at this time before  $N_r$  is visited as query node.

*OneCluster* indicator related functions.

---

```

Function CheckOneCluster( $N$ ):
   $p_1 \leftarrow$  an arbitrary points in  $N$ ;
  foreach  $p \in N$  do
    | | if  $ufset.\text{Find}(p) \neq ufset.\text{Find}(p_1)$  then return false;
    | |  $N.\text{OneCluster} \leftarrow true$ ;
  return true;
Function CheckOneCluster_BruteForce( $N$ ):
  foreach  $p_1, p_2 \in N$  do
    | | if  $ufset.\text{Find}(p_1) = ufset.\text{Find}(p_2)$  then continue;
    | | if  $D(p_1, p_2) \leq \epsilon$  then  $ufset.\text{Union}(p_1, p_2)$ ;
  return CheckOneCluster( $N$ );

```

---

**Dense indicator.** The transition function for the *Dense* indicator tries to propagate the *Dense* state to the ancestors so that subsequent traversal could switch to the less expensive intermediate cases earlier. The propagation starts from the  $N_p$  which is the parent node of  $N_r$ . When the two children nodes of  $N_p$  are

---

Dense indicator related functions.

---

```

1 Function NodeTurnTo_Dense( $\mathcal{N}, \mathcal{N}_q$ ):
2    $\mathcal{N}.\text{Dense} \leftarrow \text{true}$  and  $\mathcal{N}_p \leftarrow$  the parent of  $\mathcal{N}$ ;
3   while  $\mathcal{N}_p$  is not null and is not ancestor of  $\mathcal{N}_q$  do
4     if the children of  $\mathcal{N}_p$  are both dense then
5       if  $ufset.\text{Find}(\mathcal{N}_p.\text{left}) = ufset.\text{Find}(\mathcal{N}_p.\text{right})$  then
6          $\mathcal{N}_p.\text{Dense} \leftarrow \text{true}$ , and  $\mathcal{N}_p \leftarrow$  the parent of  $\mathcal{N}_p$ ;
7         continue;
8       else
9          $found \leftarrow \text{true}$ ;
10        EpsConnect_Dual( $\mathcal{N}.\text{left}, \mathcal{N}.\text{right}, found$ );
11        if  $found$  then
12           $ufset.\text{Union}(\mathcal{N}_p.\text{left}, \mathcal{N}_p.\text{right})$ ;
13           $\mathcal{N}_p.\text{Dense} \leftarrow \text{true}$ , and  $\mathcal{N}_p \leftarrow$  the parent of  $\mathcal{N}_p$ ;
14          continue;
15        else break;
16      else break;

```

---

both dense, the  $\epsilon$ -connect-dual algorithm will be used to check whether they are density-connected. If so,  $\mathcal{N}_p$  is set to *Dense* and the procedure recursively ascends in the tree. The propagation must stop when  $\mathcal{N}_p$  is an ancestor of  $\mathcal{N}_q$  to avoid duplicate distance computations between  $\mathcal{N}_p$  and  $\mathcal{N}_r$ .

Finally, the overall traversal body of GeDual-DBSCAN-Transitions is given in Algorithm 3. The algorithm cooperates with the state transition functions via the AddNbr function invoked in the base case functions, since it triggers the IncNumCore function which is the single entrance point for all the state transition functions.

There are several new skipping conditions in Algorithm 3. If a self combination is visited and one of the *OneCluster* or *AllCore* indicators is true, this node will not be recursed into. The rational is that, if a query node is *AllCore* or *OneCluster*, it must be set by the InitialCheck function, and there is no need to compute the distances among the points. If a reference node is *AllCore*, NodeTurnTo\_AllCore must have been invoked and the pairwise distances among points in this node have already been computed.

The correctness of GeDual-DBSCAN-Transitions comes from the following argument. Any time a state transition happens on node  $\mathcal{N}$  when combination  $(\mathcal{N}_q, \mathcal{N}_r)$  is being visited, there does not exist a combination  $(\mathcal{N}'_q, \mathcal{N}'_r)$  in the priority queue  $\mathcal{PQ}$  such that  $\mathcal{N}_q \neq \mathcal{N}'_q$  and  $\mathcal{N}'_r$  is a descendant of  $\mathcal{N}$ . This claim can be proved by the descending rules and priority rules of the basic traversal, and the proof is omitted due to space limitation. Thus, any state transition will not affect the following traversal. All subsequent combinations will be visited in a fresh new correct state.

The time complexity of GeDual-DBSCAN-Transitions is given in Theorem 4.5, and the proof is omitted due to space limitation.

**THEOREM 4.5.** Suppose there are  $n_1$  points that are identified as core point before it is visited as a query point, then the time complexity of GeDual-DBSCAN-Transitions is  $O((n - n_1)n^{1-1/d})$ .

## 5 EXPERIMENTS

### 5.1 Preparations

*Our methods.* The three algorithm variants proposed in this paper will be referred as *Basic*, *InterCases* and *Transitions*, respectively.

---

### Algorithm 3: GeDual-DBSCAN-Transitions

---

```

1 Push ( $root, root$ ) into  $\mathcal{PQ}$ ;
2 InitialCheck();
3 while  $\mathcal{PQ}$  is not empty do
4    $(\mathcal{N}_q, \mathcal{N}_r) \leftarrow \mathcal{PQ}.\text{pop}()$ ;
5   if  $\mathcal{N}_q$  is leaf or dense then
6     if  $\mathcal{N}_r$  is leaf or dense then
7       if  $\mathcal{N}_q = \mathcal{N}_r$  and  $\mathcal{N}_q$  is OneCluster or AllCore then
8         continue;
9       if  $\mathcal{N}_q$  is dense and  $\mathcal{N}_r$  is dense then
10         InterCase_BothDense( $\mathcal{N}_q, \mathcal{N}_r$ );
11       else if  $\mathcal{N}_q$  is leaf and  $\mathcal{N}_r$  is dense then
12         InterCase_LeafDense( $\mathcal{N}_q, \mathcal{N}_r$ );
13       else if  $\mathcal{N}_q$  is dense and  $\mathcal{N}_r$  is leaf then
14         InterCase_LeafDense( $\mathcal{N}_r, \mathcal{N}_q$ );
15       else if  $\mathcal{N}_q$  is leaf and  $\mathcal{N}_r$  is leaf then
16         BaseCase_BothLeaves( $\mathcal{N}_q, \mathcal{N}_r$ );
17     else
18       Decide ( $\mathcal{N}_q, \mathcal{N}_r.\text{left}$ ); Decide ( $\mathcal{N}_q, \mathcal{N}_r.\text{right}$ );
19   else
20     if  $\mathcal{N}_q = \mathcal{N}_r$  and  $\mathcal{N}_q$  is not OneCluster nor AllCore then
21       Push( $\mathcal{N}_q.\text{left}, \mathcal{N}_q.\text{left}$ ) and ( $\mathcal{N}_q.\text{right}, \mathcal{N}_q.\text{right}$ ) into  $\mathcal{PQ}$ ;
22       Decide ( $\mathcal{N}_q.\text{left}, \mathcal{N}_q.\text{right}$ );
23     else
24       Decide ( $\mathcal{N}_q.\text{left}, \mathcal{N}_r$ ); Decide ( $\mathcal{N}_q.\text{right}, \mathcal{N}_r$ );
25 AssignNonCorePoints();

```

---

*Methods compared.* The following four methods are considered. *GanTao* is a baseline DBSCAN algorithm provided by Gan and Tao [14], and the binary executable is available at [12]. *mlpack* [7] implements the dual-tree range search algorithm for solving DBSCAN, and it is used as a baseline to compare with our generalized dual-tree algorithms. *GAP* [18] and *GrIT* [19] are the most recent implementations and the state-of-the-art DBSCAN algorithms.

*Datasets.* Both synthetic and real-world datasets are used. The synthetic datasets are generated by the seed spreader generator provided by Gan and Tao [14] which is widely used in related works. The generator can only produce integral data in range  $[1, 10^5]$ . It generates data in a random walk manner and can generate data with similar or varied density across clusters, which produces the **GTGen\_Var**, **GTGen\_Sim** datasets, respectively. For datasets generated with different dimensionality, the notation of its name further adds a postfix **\_dx**, e.g., **GTGen\_Var\_d9** refers to the synthetic dataset with varied density and the dimensionality is 9.

Four real-world datasets all from the UCI dataset repository [2] are used. **Bitcoin** contains address features on the heterogeneous Bitcoin network used for outlier detection to identify ransomware payments [31]. **Household** is a measurement of electric power consumption in one household [28]. **GasSensor** contains the acquired time series from 16 chemical sensors exposed to gas mixtures [30]. **PAMAP2** is a dataset for human physical activity monitoring containing data collected by different monitors [29]. The information of number and dimension of the datasets are listed in Table 3.

Since the *GanTao* method only receives integer input in range  $[1, 10^5]$  and it indeed runs significantly slower on the synthetic

datasets than *GAP* method, it is not compared with the other methods on the real-world datasets. Thus, unlike many other works where the real-world datasets are scaled and rounded to the integer domain  $[1, 10^5]$ , we do not do such manipulation to distort the original distribution of the datasets.

*Environment setup.* All the experiments ran on a machine with Intel Core i7-10700 CPU and 128GB RAM running Ubuntu 20.04 operating system. Except for *GanTao* which is provided in binary executable, all the other codes are written in C++ and compiled using g++ with -O3 optimization.

*Parameter settings.* The parameter settings adopted in this paper are aimed to make a clear comparison with the state-of-the-art method *GAP* [18]. For the synthetic datasets **GTGen\_Var** and **GTGen\_Sim**, exactly the same settings with the *GAP* paper [18] are adopted. Specifically, the *minpts* parameter is varied from 20 to 70 with gap 10, and the default value is 50. The  $\epsilon$  parameter is varied from 1000 to 7000 with gap 1000, and the default value varies for different dimensionality (see Figure 4 for the specific values). For the datasets containing different number of points, the one containing 2 million points is used by default. For the real-world datasets, since the authors of *GAP* method normalized the datasets to integer domain  $[1, 10^5]$  but we use the original data, the parameters are set so that the *GAP* method exhibits similar performance with the experimental results given in their paper [18].

## 5.2 Self evaluation

By comparing the performance of three algorithm variants proposed in this paper, the following observations can be summarized.

First, the *Basic* variant which does not utilize the information of core points and dense nodes, indeed runs orders of magnitudes slower than the other two variants.

Second, although the *Transitions* variant always runs faster than the *InterCases* variant, the gap between the running time of them is usually small. Such phenomenon is supported by the theoretical complexity analysis. By comparing Theorem 4.4 and Theorem 4.5, the complexity difference of the two variants originates from the number of points that are identified as core points during the traversal but not by finding initial dense KDTrees nodes. For most parameter settings tested, most of the core points can be identified by examining dense KDTrees nodes, resulting in marginal difference of the two variants. However, the *Transitions* variant is still reasonable and essential, since otherwise the GeDual-DBSCAN algorithms will show no improved efficiency against the state-of-the-art. The most notable example is on the **GasSensor** dataset by varying *minpts* (Figure 3f), where the *InterCases* variant is beaten by *GAP* method but the *Transitions* variant still performs the best.

## 5.3 Comparison

*Explanation for missing points.* First, as mentioned before, the *GanTao* method is not run on the real-world datasets since it only receives integral value in range  $[1, 10^5]$ . Second, the *mlpack* method runs out of memory ( $> 128\text{GB}$ ) under many parameter settings, resulting in many missing points in its curves. Third, the *GriT* method reports segmentation fault on *Bitcoin* dataset when  $\epsilon < 60000$  due to unknown bug in their customized codes for KDTree construction,

resulting in a partial curve for *GriT* in Figure 3a. Also, the curve for *GriT* completely vanishes in Figure 3e since  $\epsilon$  is set to 20000.

*Overall comparison.* In an overview, the most powerful variant *Transitions* algorithm provides the best efficiency than all the other methods under almost all the parameter settings on all the datasets.

There is only a few exceptions where our *Transition* algorithm shows inferior performance than *GAP* method, that are on the **GTGen\_Var** datasets and on **GasSensor** dataset when  $\epsilon$  is small (see the left part of Figure 3b, 4d, 4e and 4f) or *minpts* is large (see the right part of Figure 3f, 4j and 4k). The reason is that the advantage of our method lies in the utilization of core points, and the theoretical complexity decrease as number of core points increases. When  $\epsilon$  is small or *minpts* is large, there will be less core points, and the theoretical complexity and also experimental running time would increase. In comparison, the *GAP* method employs geometric methods to prune points more efficiently, which works also well when there are less core points.

However, there are two arguments. First, when there are less core points, it is usually the case that the  $\epsilon$  and *minpts* parameter are inappropriately set to produce meaningful clusters. Second, the *generalized dual-tree* algorithm framework is an orthogonal contribution with how the intermediate cases are implemented. Actually, the traversal algorithms for the intermediate cases solving the  $\epsilon$ -connect dual,  $\epsilon$ -connect-single and  $\epsilon$ -minpts-in-dense problems, are the most basic implementation that only uses the pruning function based on MBR of the KDTrees nodes, and the pruning function of *GAP* method can also be integrated into our algorithm framework for further efficiency improvement.

*Influence of number.* By a vertical comparison in each figure of the bottom row in Figure 4, it can be noticed that the increasing trend of our methods is the same with the state-of-the-art *GAP* method. But the performance is also affected by the dimensionality and the varied density phenomenon. See the analysis below.

*Influence of dimensionality.* By a horizontal comparison between the columns of Figure 4, it can be noticed that the advantage of our methods enlarges as the dimensionality grows. It indicates that our methods is more suitable in higher dimensions.

*Influence of  $\epsilon$  and minpts.* Observing the first row in Figure 4, the running time of the *Basic* variant increases as  $\epsilon$  gets larger, since less nodes are pruned and more nodes combinations are visited when  $\epsilon$  is large. For the other two variants, varying these two parameters indirectly influence the number of core points which in turn affects the performance. It can be noticed that the running time of *InterCases* and *Transitions* variant typically drop as  $\epsilon$  gets larger but increases as *minpts* gets larger. Exceptions exist on the **Household** dataset, where the varied density phenomenon is dominant.

*Varyed density.* In Figure 3g, the strongly varied density of **Household** dataset leads to unstable running time variation as  $\epsilon$  increases. However, the performance of our methods are not much affected by varied density, which is another advantage of our methods.

## 6 CONCLUSION

This paper proposes the GeDual-DBSCAN algorithms, which bring not only conceptual novelty but also efficiency improvement against existing DBSCAN algorithms. The novel idea of *intermediate cases* elegantly integrates the DBSCAN sub-problems newly defined in

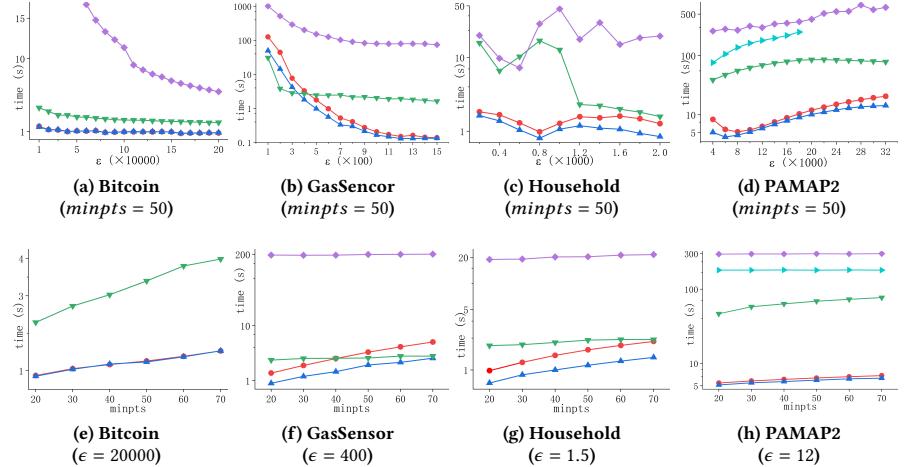
this paper into the dual-tree algorithm framework. The power of avoiding unnecessary distance computations possessed by these intermediate cases are fully employed by the new idea of *state transitions* for tree nodes during the tree traversal. The resulted GeDual-DBSCAN-Transitions algorithm performs better than the state-of-the-art DBSCAN algorithm under almost all parameter

settings on all the datasets tested. It must be noted that the generalized dual-tree algorithm framework proposed in this paper is orthogonal with the geometric approaches of other works for improving algorithmic efficiency. More efficient algorithms can be obtained by using more efficient implementations for the DBSCAN sub-problems newly defined in this paper.

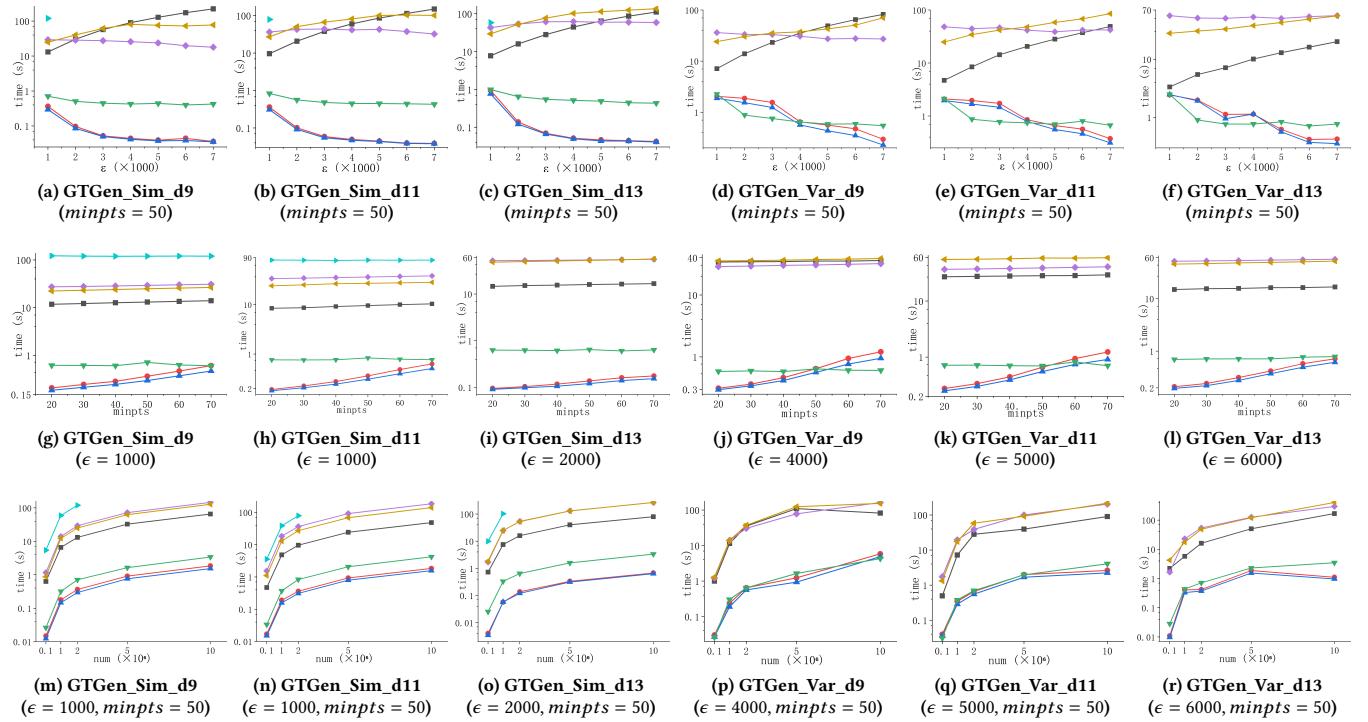
**Table 3: datasets information**

synthetic datasets		
dataset	GTGen_Vary	GTGen_Sim
number	0.1m, 0.5m, 1m, 2m, 5m, 10m	
dimension	9, 11, 13	
real-world datasets		
dataset	Bitcoin	Household
number	2916697	2075259
dimension	5	7
dataset	GasSensor	PAMAP2
number	4208261	961049
dimension	16	39

—■— Basic; —●— InterCases; —▲— Transitions;  
 —▼— GAP-DBC; —○— GritT; —◆— GanTao; —◆— mlpack;



**Figure 3: Running time results on real-world datasets.  
Upper row: varying  $\epsilon$ . Lower row: varying  $minpts$ .**



**Figure 4: Running time results on synthetic datasets GTGen.  
Top row: varying  $\epsilon$ . Middle row: varying  $minpts$ . Bottom row: varying  $num$ .**

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