Abstract

Processing of spatial queries has been studied extensively in the literature. In most cases, it is accomplished by indexing spatial data using spatial access methods. Spatial indexes, such as those based on the Quadtree, are important in spatial databases for efficient execution of queries involving spatial constraints and objects. In this paper, we study a recent balanced disk-based index structure for point data, called xBR*-tree, that belongs to the Quadtree family and hierarchically decomposes space in a regular manner. For the most common spatial queries, like Point Location, Window, Distance Range, Nearest Neighbor and Distance-based Join, the R-tree family is a very popular choice of spatial index, due to its excellent query performance. For this reason, we compare the performance of the xBR*-tree with respect to the R*-tree and the R+*-tree for tree building and processing the most studied spatial queries. To perform this comparison, we utilize existing algorithms and present new ones. We demonstrate through extensive experimental performance results (I/O efficiency and execution time), based on medium and large real and synthetic datasets, that the xBR*-tree is a big winner in execution time in all cases and a winner in I/O in most cases.

Keywords: Spatial Databases, Spatial Access Methods, Quadtrees, xBR-trees, R-trees, Query Processing, Performance Evaluation

1. Introduction

Due to the demanding need for efficient spatial access methods in many spatial database applications [1, 2], significant research effort has been devoted to the development of new spatial index structures [3, 4, 5]. However, as shown in several previous comparative studies [6, 7, 8, 9], there is no unique index structure that works efficiently, in all cases. These performance studies were executed taking into account a great variety of modern applications, where a variety of Spatial Queries arise.

The most common spatial queries where points are involved are Point Location, Window, Distance Range, Nearest Neighbor and Distance-based Join Queries. Moreover, such queries have been also used as the basis of many complex operations in advanced applications (e.g. multimedia databases [10], medical images databases [11], geometric databases [12], CAD [13], Geographical Information Systems (GIS) [14], etc).

Hierarchical index structures are useful because of their ability to focus on the interesting subsets of data [3, 4]. This focusing results in an efficient representation and improved execution times on query processing and is, thus, particularly useful for performing spatial operations [5]. Important advantages of these structures...
are their conceptual clarity and their great capability for query processing. The Quadtree is a well known hierarchical index structure, which has been applied successfully on GIS, image processing, spatial information analysis, computer graphics, digital databases, etc. [4, 5]. It was introduced in the early 1970s [6]. It is based on the principle of recursive decomposition of space and has become an important access method for spatial data [6].

The External Balanced Regular (xBR)-tree [7] is a secondary memory structure that belongs to the Quadtree family (widely used in GIS applications [4]), which is suitable for storing and indexing multidimensional points (and, in extended versions, line segments, or other spatial objects). We utilize an improved version of xBR-tree, called xBR"-tree [8], which is also a disk-resident structure. The xBR"-tree improves the xBR-tree in the node structure and in the splitting process. The node structure of the xBR"-tree stores information which process query processing more efficiently.

In this paper, we compare the xBR"-tree with popular R-tree indexes, regarding storage requirements, time needed for the tree construction and spatial query performances. The family of R-trees has been populated with lots of assorted variations. Each variation tries to optimize a particular aspect (splitting, deletion, etc). However, we concentrate on the R"-tree [9], because it is the most commonly employed spatial indexing structure in the spatial database community [4,2], and to the R"-tree, because it is an index structure based on disjoint decomposition of space like the xBR"-tree.

This paper substantially extends our previous work [20] (where xBR-trees were compared to R"-trees using single dataset queries and datasets of medium size and it was shown that the two structures are comparable) and [18] (where a new tree, the xBR"-tree, was presented and compared to the xBR-tree using single dataset queries and datasets of medium size and it was shown that the two structures are comparable in building, while the xBR"-tree is a winner in query processing) and its contributions include the following:

- The presentation of a new alternative Depth-First (DF) algorithm for Distance Range Queries (DRQs), K Nearest Neighbor Queries (KNNQs) and Constrained K Nearest Neighbor Queries (CKNNQs), utilizing a minimum binary heap (minHeap) instead of sorting, on R"-trees and R"-trees,
- A detailed performance comparison (I/O and execution time) of xBR"-trees (non-overlapping trees of the quadtree family) against R"-trees (non-overlapping trees of the R"-family) and R"-trees (industry standard belonging to the R"-family) on tree building, single dataset queries (Point Location Queries -PLQs-, Window Queries -WQs-, DRQs, KNNQs and CKNNQs) and dual dataset (distance-based join) queries (KCPQs, eDJQs).

Note that, in this paper we utilize large spatial datasets (where the quantifier “large” designates several tens of millions of spatial objects) since we believe that such datasets can be effectively processed in centralized systems, if efficient methods are used. Even larger (huge) datasets would require the utilization of methods on parallel and distributed environments (e.g. http://spatialhadoop.cs.umn.edu).

This paper is organized as follows. In Section 2 we review related work on comparing spatial access methods, regarding spatial query processing and provide the motivation for this work. In Section 3 we briefly review the main characteristics of the R-trees (highlighting the R"-tree and R"-tree). In Section 4 we describe the xBR"-tree. In Section 5 we present the algorithms for processing spatial queries, where one or two datasets are involved, over R-trees and the xBR"-tree. In Section 6 we show results of the extensive experimentation performed, using real and synthetic datasets, for comparing the performance of the two R-trees index structures (R"-tree and R"-tree) and the xBR"-tree. Finally, in Section 7 we provide the conclusions arising from this research work and discuss related future work directions.

2. Related Work and Motivation

The Quadtree belongs to a class of hierarchical data structures whose common property is that they are based on the principle of recursive regular decomposition of space. These structures are characterized as space-driven access methods according to [11]. It is most often used to partition a 2d space by recursively subdividing it into four quadrants or regions: NW (North West), NE (North East), SW (South West) and SE (South East). According to [21], Quadtrees can be classified by following three principles: (1) the type of data
that they are used to represent (points, regions, curves, surfaces and volumes), (2) the principle guiding the decomposition process, and (3) the resolution (variable or not).

In order to represent Quadtrees, there are two approaches: the pointer-based and pointerless approaches. In general, the pointer-based Quadtree representation is one of the most natural ways to represent a Quadtree structure. In this method, every node of the Quadtree will be represented as a record with pointers to its four sons. Sometimes, in order to process specific operations, an extra pointer from a node to its father could also be included. The xBR*+tree belongs to the category of pointer-based Quadtrees. On the other hand, the pointerless representation of a Quadtree defines each node of the tree as a unique locational code [14]. By using the regular subdivision of space, it is possible to compute the locational code of each node in the tree. The linear Quadtree is an example of pointerless Quadtree. We refer the reader to [14, 3, 5, 22] for further details.

The xBR*+tree [18] belongs to the category of pointer-based Quadtrees and it is an extension of the xBR-tree [17, 20]. The xBR*+tree has similarities with other well-known multidimensional access methods [16]. For example, the form of nodes in xBR*+trees has similarities to the form of nodes of Generalized B-trees (GBD-trees) [23]. GBD-trees are based on ktree-like decomposition of space, while xBR*+trees on Quadtree-like decomposition. Moreover, the splitting of internal nodes in xBR*-trees is handled in a more sophisticated way than in GBD-trees. The xBR*+tree has also similarities to the hB-tree [24], where space is also partitioned according to kd-tree-like decomposition. Unlike the hB-tree, in the xBR*+tree, each internal node has only one pointer to a child node and the entries of an internal node are region-pointer pairs and not tree structures (kd-trees), as in the hB-tree. Finally, we refer the reader to [14, 3, 16, 5, 22] for further details on multidimensional access methods.

Regarding the performance comparison of spatial query algorithms using the most cited spatial access methods (R-trees and Quadtrees), several previous research efforts have been published. In [6] a qualitative comparative study was performed taking into account three popular spatial indexes (R*-tree [19], R*-tree [25] and PMR Quadtree [26]), in the context of processing spatial queries (point query, nearest line segment, window query, etc.) in large line segment databases. The conclusion reached was that the R*+tree and PMR Quadtree were the best when the operations involve search, since they result in a disjoint decomposition of space. On the other hand, the R*+-tree was more compact than the R*+-tree (and the PMR Quadtree) but its performance was not as good as the R*+-tree, due to the non-disjointness of the decomposition induced by it.

In [7], various R-tree variants (R-tree [27], R*-tree and R*+-tree) and the PMR Quadtree have been compared for the traditional spatial overlap join operation. They showed that the R*-tree and PMR Quadtree outperform the R-tree and R*+-tree using 2d GIS spatial data. That is, with respect to the overlap join, the spatial data structures based on a disjoint decomposition of space (like the R*+-tree and PMR Quadtree) outperformed spatial data structures based on a non-disjoint decomposition such as the numerous variants of the R-tree including the R*+-tree. Moreover, as the size of the output of the spatial join increases with respect to the larger of the two inputs, methods based on a disjoint regular decomposition (like the PMR Quadtree) performed significantly better. Due to the good performance results of the R*+-tree for overlap join, in this research work, we have compared this structure to the xBR*+-tree for spatial queries.

Another interesting comparison was presented in [9], where the R-tree and the Quadtree have been contrasted in the context of Oracle Spatial, using a variety of range and Nearest Neighbor (NN) queries on spatial data arising in 2d Geographical Information Systems (GISs). It was shown that, in general, the R-tree outperforms the Quadtree. From this experimental comparison, Oracle, in general, recommends using R-trees over Quadtrees, due to higher tiling levels in the Quadtree that cause very expensive preprocessing and storage costs.

In [28], the R*-tree and a Quadtree index enhanced with Minimum Bounding Rectangle (MBR) keys for the internal nodes (MBRQuadtree) have been compared with respect to the All-Nearest Neighbor (ANN) query. The ANN query takes as input two datasets of multidimensional points and computes for each point in the first dataset the NN in the second one. Experimentally, the authors showed that for ANN queries, the MBRQuadtree is a much more efficient indexing structure than the R*+tree index.

In [8], the authors have compared the performance of R-trees and Quadtrees index structures for evaluating the KNN and the K Distance Join (using the algorithms described in [29]) query operations and the index construction methods (dynamic insertion for the R*-tree and bucket Quadtree) and bulk-loading algorithm (Sort-Tile-Recursive, STR, for the R-tree [30] and bulk-loading for the Quadtree). It was shown that the query
processing performance of the $R^*$-tree was significantly affected by the index construction methods, while the Quadtree was relatively less affected by the index construction method. The regular and disjoint partitioning method used by the Quadtree has an inherent structural advantage over the $R^*$-tree in performing KNN and $K$ Distance Join queries. The Quadtree-based index structure could be a better choice than the widely used $R^*$-tree for spatial queries when indices are constructed dynamically. Moreover, it was shown that when data are static (i.e. when a bulk-loading operation is used for an index construction) and $KNNQ$s / $K$ Distance Join Queries are executed, the STR built R-tree showed the best performance. However, when data are dynamic (i.e. there are frequent updates), a bucket Quadtree begins to outperform the $R^*$-tree. This is due to overlap among MBRs that increases with increasing dataset sizes (once the dynamic $R^*$-tree algorithm is used), and the $R^*$-tree performance is degraded.

In the context of performance studies, in [18], an interesting performance comparison (with respect to number of disk read accesses, response time and memory requirements) of distance-based query (Distance Range, $K$-Nearest Neighbors, $K$-Closest Pairs and $e$Distance Join) algorithms (Depth-First Search -DFS-, Best-First Search -BFS- and Recursive Best-First Search -RBFS-) on $R^*$-trees was presented. The main conclusion was that BFS was the best for all studied distance-based queries, but it may consume many main memory resources. DFS was slightly worse than BFS (except for the case where an LRU-buffer is included), but it consumed less memory resources, since it needs linear space with respect to the height of the $R^*$-trees. RBFS was the worst alternative (although it uses recursion and it needs linear space) since it revisits internal nodes to follow a best-first order.

In [20], the performance of $R^*$-trees and xBR-trees was compared for the most usual spatial queries, like Point Location, Window, Distance Range, $K$ Nearest Neighbor and Constraint KNN queries. The conclusions arising from this comparison showed that the two indexes were competitive. The xBR-tree is more compact and it is built faster than the $R^*$-tree. The performance of the xBR-tree was higher for PLQs, DRQs and WQs, while the $R^*$-tree was slightly better for $KNNQ$s and needed less disk accesses for $CKNNQ$s.

Finally, in [18] improvements of the xBR-tree (modified internal node structure and tree building process) were presented, leading to the xBR$^+$-tree. An extensive performance studio (I/O efficiency and execution time) based on real and synthetic datasets was also presented, taking into account the tree building process and the processing of single dataset queries, using the two Quadtrees-based structures. These results showed that the two trees are comparable regarding their building performance, however, the xBR$^+$-tree was an overall winner regarding spatial query processing.

The main objective of this paper is to compare the xBR$^+$-tree performance [18] (the best index structure of the xBR-tree family) against the performance of the most popular spatial access method of the R-tree family, the $R^*$-tree and a non-overlapping member of this family, the $R^*$-tree, considering the most representative spatial queries, where one or two indexes are involved and to highlight the performance winner, considering the characteristics of each query. Our contribution differs from [5] in the following aspects:

- We utilized a new dynamic, disk-resident, balanced Quadtree-based index structure (called xBR$^+$-tree). In [5], a simple bucket Quadtree, a partially RAM-resident, unbalanced structure was utilized.
- The performance comparison is carried out for more spatial queries when one dataset is involved (PLQ, WQ, DRQ and $KNNQ$s) and when two datasets are involved ($e$DJQ), not only for the $KNNQ$ and $KCPQ$ (called $K$ Distance Join Query in [8]).
- We have compared the xBR$^+$-tree with the $R^*$-tree also (an R-tree index based on disjoint decomposition of space), not only with the $R^*$-tree as in [5].
- We have used in our experiments two large real datasets from OpenStreetMap [4] with 5.8 and 11.5 million of 2d points, whereas in [5], the authors used artificial data from Palomar Observatory Sky Survey [5] choosing for their experiments just the first 2 million of records from the original data (from around 90 millions) and for creating 2d points, the first two attributes of the 39 stored.

3. The R-tree Family

R-trees [27] are hierarchical, height balanced data structures, derived from B-trees [32] and designed to be used in secondary storage. R-trees are considered as excellent choices for indexing various kinds of spatial data (points, rectangles, line-segments, polygons, etc.) and

\[\text{http://spatialhadoop.cs.umn.edu/datasets.html}\]
\[\text{http://astronomy.mnstate.edu/cabanela/MAPS_Database/}\]
have been adopted in known commercial systems (e.g. Informix [33], Oracle Spatial [34] 35, MySQL [36], PostGIS [37, 38], etc.). They are used for the dynamic organization of a set of spatial objects represented by their Minimum Bounding Rectangles (MBRs). The MBR represents the smallest axes-aligned rectangle in which the spatial objects are contained. A 2d MBR is determined by two 2d points that belong to its faces, one that has the minimum and one that has the maximum coordinates (these are the endpoints of one of the diagonals of the MBR). Using the MBR instead of the exact geometrical representation of the object, its representational complexity is reduced to two points where the most important features of the spatial object (position and extension) are maintained. Consequently, the MBR is an approximation widely employed, and the R-trees belong to the category of data-driven access methods [1], since their structure adapts itself to the MBRs distribution in the space (the partitioning adapts to the object distribution in the embedding space).

The rules obeyed by the R-tree are as follows.

1. All leaves reside on the same level.
2. Each leaf node contains entries, \( E \), of the form \((\text{MBR}, \text{Oid})\), such that \( \text{MBR} \) is the minimum bounding rectangle that encloses the object determined by the identifier \( \text{Oid} \).
3. Internal nodes contain entries, \( E \), of the form \((\text{MBR}, \text{Addr})\), where \( \text{Addr} \) is the address of the child node and \( \text{MBR} \) is the minimum bounding rectangle that encloses MBRs of all entries in that child node (it is also called directory MBR).
4. Nodes (except possibly for the root) of an R-tree of class \((m, M)\) contain between \( m \) and \( M \) entries, where \( m \leq \lfloor M/2 \rfloor \) (\( M \) and \( m \) are called maximum and minimum branching factor, or fan-out).
5. The root contains at least two entries, if it is not a leaf.

For more details about the R-tree structure, see [1].

Like other spatial tree-like index structures, an R-tree partitions the multidimensional space by grouping objects in a hierarchical manner. A subspace occupied by a tree node in an R-tree is always contained in the subspace of its parent node, i.e. the MBR enclosure property. According to this property, an MBR of an R-tree node (at any level, except at the leaf level) always encloses the MBRs of its descendant R-tree nodes. This property of spatial containment between MBRs stored in R-tree nodes is commonly used by spatial queries as the \( WQ \) and spatial join. Another important property of the R-trees that store spatial objects in a spatial database is the MBR face property. This property says that every face of any MBR of an R-tree node (at any level) touches at least one point of some spatial object in the spatial database. Distance-based queries, like the \( \text{KNNQ}, \text{DRQ}, \text{KCPQ} \) and \( \text{sDJQ} \), use this last property.

3.1. The \( R^* \)-tree

Many variations of R-trees have appeared in the literature (exhaustive surveys can be found in [16] [4]). One of the most popular and efficient variations is the \( R^* \)-tree [19]. The \( R^* \)-tree is a variant of the R-tree that provides several improvements to the insertion algorithm. Essentially, these improvements aim at optimizing the following parameters: (1) node overlapping, (2) area covered by a node, and (3) perimeter of an MBR of internal node. The latter is representative of the shape of the rectangles because, given a fixed area, the shape that minimizes the rectangle perimeter is the square.

The \( R^* \)-tree added two major enhancements to the R-tree, in case a node overflows. First, rather than just considering the area, the node-splitting algorithm in the \( R^* \)-tree also minimized the perimeter and overlap enlargement of the MBRs. It tends to reduce the number of subtrees to follow for search operations. Second, the \( R^* \)-tree introduced the notion of forced reinsertion to make the tree shape less dependent to the insertion order. When a node overflows, it is not split immediately, but a portion of entries of the node is reinserted from the tree root. The forced reinsertion provides two important improvements. First, it may reduce the number of splits and, second it is a dynamic technique for tree reorganization. With these two enhancements, the improved split algorithm and the reinsertion strategy, the \( R^* \)-tree results in a much better organization with respect to the original R-tree.

It is worth remembering that the data structures for the R-tree and \( R^* \)-tree are the same. Hence, the data retrieval operations defined for the R-tree remain valid for the \( R^* \)-tree. Due to the better organization of the \( R^* \)-tree, the performance of the spatial queries is likely to be significantly improved. For this reason, the \( R^* \)-tree generally outperforms R-tree and it is commonly accepted that the \( R^* \)-tree is one of the most efficient R-tree variants [1].

Figure [1] depicts a collection of points representing 16 capital cities and the corresponding \( R^* \)-tree (assuming \( M = 4 \) and \( m = 2 \)), where the tree nodes correspond to disk pages. Observe that the index structure, while keeping the tree balanced, adapts to the skewness of data distribution. Solid lines denote the MBRs of the subtrees that are rooted in inner nodes (dotted rectangles). In this figure, the leaves are represented by \( L_i \) (1 \( i \leq 6 \)), the MBRs enclosing points are denoted as...
3.2. The $R^+$-tree

To overcome the problems associated with overlapping of regions in the R-trees, in [23] an access method called the $R^+$-tree was introduced. The main motivation for the $R^+$-tree is to avoid overlap among the MBRs. Unlike the R-tree, the $R^+$-tree uses clipping; that is, there is no overlap between MBRs at the same level. MBRs that intersect more than one MBRs have to be stored on several different nodes. The result of this data structure is that there may be several paths, starting at the root to the same rectangle. As a result of this policy and taking into account its structure, the $R^+$-tree will lead to an increase of the height of the tree. However, considering the retrieval time, point searches in $R^+$-trees correspond to single-path tree traversals from the root to one of the leaves (and therefore, it tends to be faster than the corresponding R-tree operation). On the other hand, range searches usually lead to the traversal of multiple paths in both index structures.

The $R^+$-tree can be characterized as follows [1]:

1. The root has at least two entries, except when it is a leaf.
2. The MBRs of two internal nodes at the same level cannot overlap.
3. If node $N$ is not a leaf (internal node), its MBR contains all rectangles in the subtree rooted at $N$.
4. A rectangle of the collection to be indexed is as signed to all leaf nodes the MBRs of which it overlaps. A rectangle assigned to a leaf node $N$ is either overlapping $N.MBR$ or is fully contained in $N.MBR$. This duplication of objects into several neighbor leaves is similar to what we encountered earlier in other space-driven structures (they are based on partitioning the embedding space into rectangular cells, independently of the distribution of the spatial objects).

Figure 2 presents an $R^+$-tree for the same collection of points. Note also that both at the leaf level and at internal levels, node MBRs are not overlapping (different organization of the nodes with respect to Figure [1]). The notation of internal nodes and leaves are the same as in the $R^+$-tree of Figure [1].

The structure of an $R^+$-tree node is the same as that of the R-tree. However, because we cannot guarantee a minimal storage utilization $m$ (as for the R-tree), and because rectangles are duplicated, an $R^+$-tree can be significantly larger (in terms of height) than the R-tree built for the same dataset. The construction and maintenance of the $R^+$-tree are rather more complex than with the other variants of the R-tree.

As examples of spatial query processing using $R^+$-trees, the point location query performance benefits from the non-overlapping of nodes. As for space-driven structures [1], a single path down the tree is followed, and fewer nodes are visited than with the R-tree. The gain for window query is less obviously assessed. Object duplication not only increases the tree size, but potentially leads to expensive post-processing of the result (sorting for duplication removal).

4. The xBR$^+$-tree

The xBR$^+$-tree [13] (an extension of the xBR-tree [17, 20]) is a hierarchical, pointer-based, disk-resident index structure, built utilizing a regular decomposition of space (space-driven access method), suitable for indexing multidimensional points. For 2D the hierarchical decomposition of space in the xBR$^+$-tree is that of Quadtrees (the space is recursively subdivided in 4
The nodes of the tree are disk pages of two kinds: leaves, which store the actual multidimensional data themselves and internal nodes, which provide a multiway indexing mechanism.

4.1. Internal Nodes

Internal node entries in xBR+-trees contain entries of the form (Shape, qside, DBR, Pointer). Each entry corresponds to a child-node pointed by Pointer. The region of this child-node is related to a subquadrant of the original space. Shape is a flag that determines if the region of the child-node is a complete or non-complete square (the area remaining, after one or more splits; explained later in this subsection). This field is heavily used in queries. DBR (Data Bounding Rectangle) stores the coordinates of the rectangular subregion of the child-node that contains point data (at least two points must reside on the sides of the DBR), while qside (not stored in xBR+-tree internal node entries) is the side length of the subquadrant of the original space that corresponds to the child-node.

The subquadrant of the original space related to the child-node is expressed by an Address. This Address (which has a variable size) is not explicitly stored in the xBR+-tree (unike the xBR-tree), although it is uniquely determined and can be easily calculated using qside and DBR (in fact, the coordinates of the subquadrant expressed by Address are calculated by query processing algorithms using qside and DBR). Each Address represents a subquadrant which has been produced by Quadtree-like hierarchical subdivision of the current space (of the subquadrant of the original space related to the current node). It consists of a number of directional digits that make up this subdivision. The NW, NE, SW and SE subquadrants of a quadrant are distinguished by the directional digits 0, 1, 2 and 3, respectively. For 2d space, we use two directional bits, one for each dimension. The lower bit represents the subdivision on the horizontal (X-axis) dimension, while the higher bit represents the subdivision on the vertical (Y-axis) dimension [17, 20]. It is easy to extend this representation to three or more dimensions by using a number of directional bits equal to the number of dimensions. For example, the Address 1 represents the NE quadrant of the current space, while the Address 10 the NW subquadrant of the NE quadrant of the current space. The address of the left child is * (has zero digits), since the region of the left child is the whole space minus the region of the right child.

However, the actual region of the child-node is, in general, the subquadrant of its Address minus a number of smaller subquadrants, the subquadrants corresponding to the next entries of the internal node (the entries in an internal node are saved sequentially, in preorder traversal of the Quadtree that corresponds to the internal node). For example, in Figure 3 an internal node (a root) that points to 2 internal nodes that point to 7 leaves is depicted. The region of the root is the original space, which is assumed to have a quadrangular shape. The region of the right child is the NW quadrant of the original space. The region of the left child is the whole space minus the region of the NW quadrant, a non-complete square. The * symbol is used to denote the end of a variable size address. The Address of the right child is 0*, since the region of this child is the NW quadrant of the original space. The Address of the left child is * (has zero directional digits), since the region of this child refers to the remaining space. Each of these Ad-
dresses is expressed relatively to the minimal quadrant that covers the internal node (each Address determines a subquadrant of this minimal quadrant). For example, in Figure 3 the Address 3* is the SE subquadrant of the NW subquadrant of whole space (absolute Address 03*). During a search, or an insertion of a data element with specified coordinates, the appropriate leaf and its region is determined by descending the tree from the root.

Figure 3: The same collection of points, the corresponding grouping to xBR+-tree nodes and the xBR+-tree structure.

Note that all the fields of an xBR+-tree internal node entry have a fixed size. By avoiding storing the variable-sized field Address (unlike the xBR-tree), processing of internal nodes is simplified, since their capacity is fixed. Moreover, the use of the DBR field (not stored in xBR-tree internal node entries) makes processing of spatial queries more efficient, since it signifies the subregion of the child-node that actually contains data, which is (in general) different to and smaller than the region of this child-node, leading to higher selectivity of the paths that have to be followed downwards when descending the tree and deciding the parts of the tree that may contain (part of) the query answer.

4.2. Leaf Nodes

External nodes (leaves) of the xBR+-tree simply contain the data elements and have a predetermined capacity C. When C is exceeded, due to an insertion in a leaf, the region of this leaf is partitioned in two subregions. The one (new) of these subregions is a subquadrant of the region of the leaf which is created by partitioning the region of the leaf according to hierarchical (Quadtree like) decomposition, as many times as needed so that the most populated subquadrant (that corresponds to this new subregion) has a cardinality that is smaller than or equal to C. The other one (old) of these subregions is the region of the leaf minus the new subregion. In [18], the criterion of choosing the new subregion was the cardinality of this subregion to be smaller or equal to xC, where 0.5 < x < 1, however the criterion we use in this paper was more effective and simple. Note also that in the xBR+-tree, data elements are stored in leaves in X-order (the elements are sorted in ascending order of their X-axis coordinate). This order permits us to use the plane sweep technique (when appropriate) during processing of the data elements of a leaf, in the process of answering certain query types.

4.3. Splitting Process of Nodes

When an internal node of the xBR+-tree overflows, it is split in two. The goal of this split is to achieve the best possible balance between the space use in the two nodes.

4.3.1. Splitting of internal nodes

The split in the xBR+-tree is either based on existing quadrants or in ancestors of existing quadrants. First, a Quadtree is built that has as nodes the quadrants specified in the internal node [17]. This tree is used for determining the best possible split of the internal node in two nodes that have almost equal number of bits, as proposed in [17], or entries (a simpler and equally effective criterion, according to experimentation).

4.3.2. Splitting of leaves

Splitting of a leaf creates a new entry that must be hosted by an internal node of the parent level. This can cause backtracking to the upper levels of the tree and may even cause an increase of its height. More details appear in [17].
5. Spatial Query Processing

In this section, we outline algorithms for processing PLQs, WQs, DRQs, KNNQs, CKNNQs, KCPQs, and εDJQs on the R-tree family (query processing in R*-trees, R+-trees and R-trees, in general, is similar) and xBR*-trees. In general terms, the definitions of these spatial queries are as follows:

- Given an index \( I_p \) and a query point \( q \), the PLQ returns true if \( q \) belongs to \( I_p \), false otherwise.
- Given an index \( I_p \) and a query rectangle \( r \), the result of the WQ is the set of all points in \( I_p \) that are completely inside \( r \).
- Given an index \( I_p \), a query point \( q \) and a distance threshold \( \varepsilon \geq 0 \), the DRQ returns all points of \( I_p \), that are within the specified distance \( \varepsilon \) from \( q \) (according to a distance function).
- Given an index \( I_p \), a query point \( q \), and a value \( K > 0 \), the KNNQ returns \( K \) points of \( I_p \) which are closest to \( q \) based on a distance function.
- Given an index \( I_p \), a query point \( q \), a value \( K > 0 \) and a distance threshold \( \varepsilon \geq 0 \), the CKNNQ returns \( K \) closest points of \( I_p \) which are within the distance \( \varepsilon \) from \( q \).
- Given two indexes \( I_p \) and \( I_q \), and an integer value \( K > 0 \), the KCPQ \([39][40]\) returns a set of \( K \) different pairs of points \( (p_i, p_j) \in I_p \times I_q \), such that \( p_i \in I_p \), \( p_i \in I_q \), with the \( K \) smallest distances between all possible pairs of points that can be formed by choosing one point of \( I_p \) and one point of \( I_q \), based on a distance function.
- Given two indexes \( I_p \) and \( I_q \), and a real value \( \varepsilon \geq 0 \), εDJQ \([51]\) returns all the possible different pairs of points \( (p_i, p_j) \in I_p \times I_q \) that can be formed by choosing one point \( p_i \in I_p \) and one point \( p_j \in I_q \), having a distance smaller than or equal to \( \varepsilon \) of each other, based on a distance function.

To answer the aforementioned spatial queries using members of the R-tree family, or xBR*-trees a two-step procedure is followed \([41]\). Filter step: the collection of all spatial objects whose MBRs/DBRs satisfy the given spatial query is found. These spatial objects constitute the candidate set. Refinement step: the actual exact geometry of each member of the candidate set is examined to eliminate false hits and find the final answer to the spatial query. In the following, we will describe in more detail the query processing techniques that have developed for each spatial query type. Since the Refinement step is orthogonal to the Filtering step, the developed techniques have mainly focused on the latter.

5.1. Algorithmic techniques used

All the single dataset queries above can be processed in a top-down manner beginning from the root of the tree. There are two, well known, basic techniques that can be applied.

The first one is processing the nodes of the tree in Depth-First (DF) mode: By examining the relation of an entry of the current internal node to the query object, point or area, we decide on recursively applying the same procedure on the child node pointed by this entry. When this recursive call returns, another entry of this internal node may be examined, depending on the query being processed and the result calculated so far.

When a recursive call reaches a leaf node, the Refinement step is applied.

The second one is processing the nodes of the tree in Best-First (BF) mode: By examining the relation of each entry of the current internal node to the query object, point or area, we decide about inserting this entry in a global priority queue, where there may already exist entries inserted during earlier stages of the algorithm. After all entries of the current node have been examined, the entry with top priority is extracted from the queue and processing continues with the node pointed by this entry.

We applied four versions of DF algorithms.

- The first one, named Normal Depth First (N-DF) algorithm, is the simplest of all. The query object is tested first against each entry of the current node, in the order that the entries are stored. The criterion for such a test depends on the query being processed and the result calculated so far and its result is boolean (true / false). If the result for the entry tested is true, then the algorithm is applied recursively on the child node pointed by this entry.

- The second one is named Depth First (DF) algorithm. For each entry of the current node (in the order that the entries are stored), the minimum distance, mindist, between the query object and the region of the entry is calculated. If the (non-boolean) value of this metric for the entry examined satisfies the criterion corresponding to the query being processed and the result calculated so far, then the algorithm is applied recursively on the node pointed by this entry.
• The third one, named Sorted Depth First (S-DF) algorithm, is a fairly used and efficient DF technique. There is an initial step that must be implemented when an internal node is visited, so as to select the entry of this node that best satisfies the criterion corresponding to the query being processed and the result calculated so far. In this step, for all entries of the current node, \( \text{mindist}(q, M) \) values are calculated, inserted in an array and sorted. Then the algorithm is applied recursively on the node pointed by the entry corresponding to the lowest \( \text{mindist} \) value. When this recursive call returns, recursion is possibly (depending on the query being processed and the result calculated so far) applied on the entry with the next \( \text{mindist} \) value.

• The fourth one, named Heap Depth First (H-DF) algorithm, is a new technique that utilizes one local (to the current node) minimum Heap \( \text{minHeap} \) prioritized by the \( \text{mindist} \) metric. The \( \text{minHeap} \) replaces the sorted array of S-DF and this is expected to speed up the selection process of the next best entry for applying recursion. In fact, the fewer the entries of the current node that will be eventually used for recursive calls, the more the algorithm will accelerate (since extracting from \( \text{minHeap} \) part and not all of its entries corresponds to a partial application of HeapSort, in contrast to always completely sorting the respective array of S-DF).

We also applied one BF algorithm.

• In the following, this is called BF algorithm and it is iterative. It keeps a global (to the whole tree) minimum binary heap, \( \text{minHeap} \), holding (part of) the entries of the nodes visited so far, prioritized by their \( \text{mindist} \) to the query object. Initially, \( \text{minHeap} \) contains the tree root. Iteratively, the entry at the root of \( \text{minHeap} \) is removed from the heap and the node pointed by this entry is visited; its entries are potentially added to the heap, according to the relation of \( \text{mindist} \) of each entry to the criterion of the query being processed and the result calculated so far. The algorithm continues by visiting the node pointed by the entry with the minimum \( \text{mindist} \) in \( \text{minHeap} \) until the heap becomes empty or the \( \text{mindist} \) value of the entry located in the root of the heap does not satisfy the criterion corresponding to the query being processed and the result calculated so far. When the algorithm reaches a leaf node, the Refinement step is applied.

All the dual dataset queries above can be processed in a top-down manner by synchronous tree traversals, beginning from the roots of the two trees. Again, the basic ideas of processing the nodes of the trees in DF and BF mode are utilized.

We applied three versions of DF algorithms for dual dataset queries. N-DF cannot be applied, due to its boolean criterion. We did not apply a version analogous to DF, since, when the entries of two nodes (one from each tree representing a different dataset) are combined, the number of combinations that should be examined is large, unless a technique that reduces the number these combinations is applied. Thus, we applied versions analogous to S-DF and H-DF, only.

• The first one is named Sorted Depth First for 2 datasets (S-DF-2) algorithm. We start at the roots of the two trees (current pair of nodes). For each pair of entries formed by combining the entries of the current pair of nodes, the minimum distances, \( \text{mindist} \) values, between the regions of the elements of the pair are calculated (these are distances between rectangular regions), inserted in an array and sorted. Then the order of this array is used for recursive application of the algorithm. If \( \text{mindist} \) of the next array entry (a pair of nodes) satisfies the criterion corresponding to the query being processed and the result calculated so far, then the algorithm is applied recursively on the nodes pointed by the elements of this pair. In case a recursive call reaches a pair of nodes where one of its elements is a leaf, then the pairs of entries are formed by the region of this leaf and the entries of the node pointed by the other element of the pair (which is an internal node). In case a recursive call reaches a pair of nodes where both of its elements are leaves, the Refinement step is applied.

• The second one is named Heap Depth First for 2 datasets (H-DF-2) algorithm, is a new technique that utilizes one local (to the current pair of nodes) minimum Heap \( \text{minHeap} \) prioritized by the \( \text{mindist} \) metric that replaces the sorted array of S-DF-2. For the reasons described above, this algorithm is expected to speed up the selection process of the next best entry for applying recursion.

• The third one is named Classic Plane Sweep Depth First for 2 datasets (C-DF-2) algorithm. In this algorithm, when a pair of nodes is visited, for each node of this pair, the starting coordinate of one of the axes, w.l.o.g. let’s assume this is \( x \)-axis, of the rectangular regions of this node entries are sorted and Classic Place Sweep is applied between the two sorted coordinate sequences. If \( x \)-
We also applied one BF algorithm for dual dataset queries.

- This is called Classic Plane Sweep Best First for 2 datasets (C-BF-2) algorithm and also utilizes Classic Place Sweep [42]. This algorithm is iterative. It keeps a global (to the whole pair of trees) minimum binary heap, minHeap, holding (part of) the pairs of entries of the pairs of nodes visited so far, prioritized by their mindist values. Note that in C-DF-2, when a recursive call reaches a pair of nodes where one of its elements is a leaf, plane sweep is not applied (plane sweep makes sense when two sets of rectangular regions are combined), but the region of this leaf is combined with all the entries of the other node.

We also applied one BF algorithm for dual dataset queries.

5.2. Point Location and Window Queries

PLQs and WQs can be processed using N-DF algorithm on both the R-tree and xBR+-tree families. The query object in the case of PLQs is the query point and the testing criterion is whether there is overlapping between the query point and the the MBR/DBR of the current entry of the R-tree/xBR+-tree. The query object in the case of WQs is the query window (rectangle) and the testing criterion is whether there is intersection between the query window and the the MBR/DBR of the current entry. Since the criterion can only get one of two possible values TRUE/FALSE, there is no way or reason the values of the criterion to be compared between entries. When the node pointed by the Addr is a leaf then Refinement step is applied. For PLQs, the query point is searched between the points of the leaf and if it is found the result is returned in the calling procedure in order the searching process to be terminated. For WQs, the set of points of the current leaf within the query window are found and this set of points is returned. The searching process will be terminated when all entries of the root node have been tested.

Especially for the xBR+-tree, as noted in Subsection 5.1, the entries in an internal node are saved in preorder traversal of the Quadtree that corresponds to the internal node and are examined in reverse sequential order (this means that first a subregion is examined before any enclosing region of this subregion, and in this way, multiple examinations of overlapping regions are avoided). So the last entry of the current internal node is examined first. Moreover, for the xBR+-tree, in WQs a termination condition can be applied and the searching process can be terminated before all entries of the current node have been tested: whenever the query window is contained within the REG of the current entry of the node processing stops. This is due to no overlapping between regions of the nodes.

5.3. Distance Range Queries

DRQs can be performed with all variants of DF and BF algorithms that were described above in Subsection 5.1 on both the R-tree and xBR+-tree families. The query object is a circle centered on the query point with radius a given value e. Since in N-DF algorithm the testing criterion is whether there is intersection between the query circle and the MBR/DBR of the current entry, in order to simplify processing, the query circle is replaced by its MBR in the Filter step, while in the Refinement step the points inside the actual query circle are selected. Especially for the xBR+-tree, the same termination condition noted in Subsection 5.2 can be applied in the N-DF algorithm.
For the other four algorithms (DF, H-DF, S-DF and BF) the query object is the circle described above and mindist is the distance between the center of the query circle and the MBR/DBR of the current entry. The testing criterion is whether this mindist value is smaller than or equal to ε. The special termination condition of the xBR⁺-tree for the DF algorithm can be applied just like the N-DF one, while for the other three algorithms (S-DF, H-DF and BF) it must be partially changed, since the examination of the entries is not in the reverse order in which they are saved in the node. Thus, if the query circle is contained in the REG and the region of the entry is a complete square then the termination condition is applied.

5.4. Nearest Neighbor Queries

Based on the branch-and-bound paradigm, the K Nearest Neighbor Query algorithms use several metrics to prune the search space [43]. The most important metric is mindist, the minimum distance between the query object and the region of the entry under examination. Another metric, minmaxdist, refers to the minimum distance from the query object within which a point in the region of the entry under examination is guaranteed to be found. Finally, maxdist is the maximum distance between the query object and any point in the region of the entry under examination.

The first Nearest Neighbor Query (NNQ) algorithm for R-trees, proposed in [43], traverses the tree recursively in a DF manner. Starting from the root, all entries are sorted according to their mindist from the query object, and the entry with the smallest mindist is visited first. The process is repeated recursively until the leaf level is reached, where a potential NN is found. During backtracking to the upper levels, the algorithm only visits entries whose mindist is smaller than or equal to the distance of the NN found so far. This algorithm was enhanced in [44], proving that any node can be pruned by using minmaxdist distance function. A BF algorithm for NNQ was proposed in [45] for Quadtrees and in [46] for R-trees. BF keeps a minimum binary heap, minHeap, with the entries of the nodes visited so far, prioritized according to their mindist. Initially, minHeap contains the entries of the tree root. When the root of minHeap is chosen for processing, it is removed from the heap and the entries of its tree node are added to the heap. The algorithm continues visiting the entry with the minimum mindist in minHeap, until the heap becomes empty or the mindist value of the node entry located in the root of heap is larger than the distance value of the nearest neighbor that has been found so far (i.e. the pruning distance). BF is I/O optimal because it only visits the nodes necessary for obtaining the NN. The generalization to find the K Nearest Neighbor (KNN) is straightforward. An additional data structure is just needed, a maximum binary heap, maxKHeap (prioritized by the distance from the query point), holding the K nearest points encountered so far.

It is obvious that the four algorithms (DF, S-DF, H-DF and BF) described in Subsection 5.1 can be adapted to KNNQs on both the R-tree and xBR⁺-tree families. The query object is the circle centered at the query point and having radius equal to the key of the root of the full maxKHeap; otherwise (not full maxKHeap) this circle covers the whole space. The testing criterion (Filter step) is whether there is an intersection between the query circle and the MBR/DBR of the current entry; in the Refinement step the points inside the actual query circle are selected.

Especially for the xBR⁺-tree, the same termination condition noted in Subsection 5.3 can be applied in the algorithms for KNNQs; when the region of the current entry is square and contains the query circle then the process is terminated. More details about this algorithm appear in [20, 47].

The CKNNQ is a combination of the KNNQ and DRQ; for this query, we can adapt the DF, S-DF, H-DF or BF algorithms for NNQ on both the R-tree and xBR⁺-tree families. The query object is the circle with center the query point and radius the given maximum value for the case of not full maxKHeap, otherwise the radius is the key of the root of the full maxKHeap. The testing criterion (Filter step) is whether there is intersection between the query circle and the MBR/DBR of the current entry in the Filter step; in the Refinement step the points inside the actual query circle are selected. Especially for the xBR⁺-tree, the same termination condition can be applied as in the the NNQ algorithms.

5.5. Distance Join Queries

Be reminded that the KCPQ asks for the K closest pairs of spatial objects in the Cartesian Product of two datasets. If both datasets are indexed by R-trees, the concept of synchronous tree traversal and DF or BF traversal order can be combined for query processing [20, 48, 49, 50]. Details on such DF and BF algorithms on two R⁺-trees, from the non-incremental point of view, using several optimization techniques (i.e. plane-sweep, distance functions like minmaxdist and maxdist) appear in [20]. In the following, we outline the distance join algorithms we applied on all the three trees.
• For KCPQs, we applied all the four algorithms S-DF-2, H-DF-2, C-DF-2 and C-BF-2 described in Subsection 5.1. The testing criterion is based on the distance threshold which is, either equal to the key of the root of the maxKHeap, in case of a full maxKHeap, or to an infinite length, in case of a non-full maxKHeap. The testing criterion is whether the distance of the pair objects (MBR/DBR) under examination is smaller than the distance threshold. In the Refinement step (when the algorithm visits a pair of leaves), Classic Plane Sweep is applied between the points of the two leaves. If a pair of points consists of points with a distance smaller than or equal to the distance threshold, this pair is inserted in maxKHeap.

• For the sDJQ ($\varepsilon \geq 0$), the above DF or BF algorithms for KCPQ (for all trees) are adapted in a straightforward way. There is no maxKHeap, or limit on the cardinality of the result and the distance threshold always equals $\varepsilon$. Starting from the root nodes, tree nodes are traversed down to the leaves, depending on the result of whether minlist of the pair of entries under examination is less than or equal to $\varepsilon$. When the algorithm reaches a pair of leaves, Classic Plane Sweep is applied between the points of the two leaves. All the pairs of points with a distance smaller than or equal to $\varepsilon$ are added to the answer set.

These algorithms (except for H-DF-2, which is new) have been proposed in the past for the R-tree family. However, algorithms for the KCPQ and the sDJQ have not been presented for the xBR* -tree before. In this work, we adapted the existing R-tree algorithms and applied the H-DF-2 technique on the specific structure of xBR*-tree.

6. Experimentation

We designed and run a large set of experiments to compare xBR* -trees with respect to R-tree variants (R*-tree and R*-tree).

6.1. Experimental Settings

We used 6 real spatial datasets of North America, representing cultural landmarks (NAclN with 9203 points) and populated places (NAppN with 24491 points), roads (NArdN with 569082 line-segments) and rail-roads (NArrN with 191558 line-segments). To create sets of 2d points, we have transformed the MBRs of line-segments from NArdN and NArrN into points by taking the center of each MBR (i.e. |NArdN| = 569082 points, |NArrN| = 191558 points). Moreover, in order to get the double amount of points from NArrN and NArdN, we chose the two points with min and max coordinates of the MBR of each line-segment (i.e. |NArdND| = 1138164 points, |NArrND| = 383116 points). The data of these 6 files were normalized in the range [0, 1].

We have also created synthetic clustered datasets of 125000, 250000, 500000 and 1000000 points, with 125 clusters in each dataset (uniformly distributed in the range [0, 1]), where for a set having N points, N/125 points were gathered around the center of each cluster, according to Gaussian distribution. We have also used two large real spatial datasets (retrieved from http://spatialhadoop.cs.umn.edu/datasets.html [49]) to justify the use of spatial query algorithms on disk-resident data instead of using them in-memory. They represent water resources of North America (Water) consisting of 5836360 line-segments and parks or green areas of all world (Park) consisting of 11504035 polygons. To create sets of points, we have transformed the MBRs of line-segments from Water into points by taking the center of each MBR and we have considered the centroid of polygons from Park.

The experiments were run on a Ubuntu Linux v. 14.04 machine with Intel core duo 2x2.8 GHz processor, 4 GB of RAM and a Seagate Barracuda 3TB SATA 3 hard disk, using the GNU C/C++ compiler (gcc).

For page (node) sizes of 1KB, 2KB, 4KB, 8KB and 16KB we run experiments for tree building, counting tree characteristics and creation time and experiments for all spatial queries studied here (PLQ, WQ, DRQ, KNNQ, CKNNQ, KCPQ and sDJQ), counting disk read accesses (I/O) and total execution time (I/O and CPU).

6.2. Experiments for comparing index structures

In these experiments, we built the xBR*-tree, the R*-tree and the R*-tree. We constructed each tree, using LRU-buffer of 1024 pages. For each dataset, the insertion order of the data was the same for all trees. In Table 1 construction characteristics of the three trees, for a representative set of dataset and node size combinations (for the sake of presentation length), are depicted.

Regarding tree heights, studying the complete set of construction characteristics of the three trees (for all dataset and node size combinations), we conclude that:

• The xBR*-tree and R*-tree have similar tree heights.

1The improvement of the creation times of the xBR*-tree in relation to the respective creation times in [13] is due to the use of the LRU-buffer.
Table 1: Tree construction characteristics.

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Num Elem (x10^3)</th>
<th>Node size (KB)</th>
<th>Tree height</th>
<th>Tree size (MBytes)</th>
<th>Creation time (secs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAcIN</td>
<td>9.203</td>
<td>1</td>
<td>xBR⁺ R⁺ R⁺</td>
<td>xBR⁺ R⁺ R⁺</td>
<td>xBR⁺ R⁺ R⁺</td>
</tr>
<tr>
<td>NAppN</td>
<td>24.491</td>
<td>1</td>
<td>4 4 4</td>
<td>0.615 0.669 0.652</td>
<td>0.0511 0.3119 0.1252</td>
</tr>
<tr>
<td>NArrN</td>
<td>191.558</td>
<td>2</td>
<td>4 4 4</td>
<td>1.600 0.820 1.718</td>
<td>0.2286 1.0239 0.2663</td>
</tr>
<tr>
<td>NArrND</td>
<td>383.180</td>
<td>4</td>
<td>4 4 3 3</td>
<td>11.61 13.47 12.39</td>
<td>2.5324 15.385 2.8480</td>
</tr>
<tr>
<td>NAdN</td>
<td>569.082</td>
<td>8</td>
<td>3 3 3 3</td>
<td>22.78 26.82 24.03</td>
<td>6.5064 86.771 8.0914</td>
</tr>
<tr>
<td>NAdND</td>
<td>1138.19</td>
<td>16</td>
<td>3 3 3 3</td>
<td>34.73 40.67 34.97</td>
<td>12.112 461.78 19.558</td>
</tr>
<tr>
<td>125KCN</td>
<td>125.000</td>
<td>2</td>
<td>4 4 4 4</td>
<td>69.31 82.10 67.95</td>
<td>39.606 3450.7 66.697</td>
</tr>
<tr>
<td>250KCN</td>
<td>250.000</td>
<td>4</td>
<td>3 3 3 3</td>
<td>7.578 7.984 7.242</td>
<td>1.0643 8.6246 1.5947</td>
</tr>
<tr>
<td>500KCN</td>
<td>500.000</td>
<td>8</td>
<td>3 3 3 3</td>
<td>15.09 15.90 14.23</td>
<td>2.9603 46.682 4.5291</td>
</tr>
<tr>
<td>1000KCN</td>
<td>1,000.00</td>
<td>16</td>
<td>3 3 3 3</td>
<td>30.02 31.83 28.06</td>
<td>8.5643 339.39 15.969</td>
</tr>
<tr>
<td>Water</td>
<td>5,836.36</td>
<td>2</td>
<td>5 5 5 11</td>
<td>359.2 438.1 395.4</td>
<td>114.97 358.23 286.98</td>
</tr>
<tr>
<td>Water</td>
<td>5,836.36</td>
<td>4</td>
<td>4 4 4 5</td>
<td>352.9 443.6 382.3</td>
<td>139.92 1638.6 262.23</td>
</tr>
<tr>
<td>Park</td>
<td>11,504.0</td>
<td>8</td>
<td>4 4 4 4</td>
<td>684.0 839.7 731.6</td>
<td>402.91 9460.3 947.12</td>
</tr>
<tr>
<td>Park</td>
<td>11,504.0</td>
<td>16</td>
<td>3 3 3 3</td>
<td>682.7 855.5 719.0</td>
<td>565.42 37174 1240</td>
</tr>
</tbody>
</table>

- The R⁺-tree for the large real spatial datasets and the smaller node sizes (1KB and 2KB) is significantly higher.

This is due to the fact that the R⁺-tree, to avoid overlapping, in many cases, splits internal nodes and several of their descendants at subsequent levels, creating nodes with limited occupancy. For a smaller node size, an internal node is more likely to be split unevenly and the new node with the smaller occupancy may not increase significantly its occupancy in the future, if there are not enough new data within its region. This shows the sensitivity of the R⁺-tree to the order of insertion of the data.

Regarding tree sizes, the three trees have similar sizes, since the largest part of each tree consists of leaves and the leaves exhibit similar occupancy in all trees (average leaf occupancy of the xBR⁺-tree, the R⁺-tree and the R⁺-tree is 65.14%, 68.24% and 65.14%, respectively). In conclusion:

- For real datasets the xBR⁺-tree needs less space in disk (i.e. it is more compact).
- For synthetic datasets the R⁺-tree has the smallest disk size.

Regarding creation times:

- The xBR⁺-tree is always the fastest.

This is due to the regular way that the xBR⁺-tree divides the space. Moreover, node splitting follows a single path, starting from the leaf level and ending, on the worst case, at the root level. On the contrary, in the R⁺-tree splits may be propagated to parent, as well as, to children nodes [25].

- The R⁺-tree is always the slowest.

This is due to forced reinsertion and the multiple paths while searching for the appropriate leaf that will host the new point [19].

6.3. Creation of input for queries on single datasets

We split the whole space into $2^{4}$, $2^{6}$, $2^{8}$, $2^{10}$ equal rectangular windows, in a row-order mapping manner. These windows were used as query windows for WQs. The centroids of these windows were used as query points PLQs, K-NNQs and CK-NNQs. The incircles of these windows were used as query ranges for DRQs (the centroid of each of these windows was used as the center of a query range and the extend of this range, $\varepsilon$, was equal to the half of the side length of this window). For K-NNQs and CK-NNQs, we used the set of $K$ values {1, 10, 100, 1000}.

6.4. Experiments for non distance-based queries on single datasets (PLQs and WQs)

As the number of experiments performed was huge, we show only representative results, since they were analogous for each query category. For PLQs we executed two sets of experiments using the N-DF algorithm. In the first set we used as query points the original datasets and in the second one we used as query points...
points the centroids of the query windows. Indicative results for the Water dataset are shown in Figures 4a (I/O) and 4b (execution time) and for the 1000KCN dataset are shown in Figures 4c (I/O) and 4d (execution time).

These figures show that the results are different for the two cases of experiments. For the case of the query shown in Figures 4a and 4b (Water), when searching for an existing point into the spatial dataset, the number of disk read accesses needed by the R*-tree and the xBR+-tree is equal to the tree height. On the other hand, the number of disk read accesses for the R*-tree is a little larger than the height of the tree. The execution time of R*-tree is smaller than the one of the R’+-tree and a little larger than the one of the xBR+-tree.

Studying the complete set of results of PLQs using as query points the original datasets, we find out that the same situation appears. Regarding I/O, we conclude that:

- For both the xBR+-tree and the R’+-tree, the number of disk read accesses is equal to the height of the tree for every query point, if this point exists in the dataset, because of the single path that has to be followed until this point is found.
- For the R’+-tree, the number of disk read accesses is a little larger than the height of the tree because of the multiple paths that are possibly needed to be followed until the point is found.

Summarizing the results for the execution time:

- The xBR+-tree was faster than the R’+-tree in all cases (60/60) and faster than the R’*-tree in most cases (56/60).
- The R’*-tree was faster than the R’+-tree in all cases, for all datasets and node sizes.
- Especially, for the node size of 16KB, the xBR+-tree needed fewer disk read accesses for all datasets, with an average relative difference of 5.75% to the R’+-tree.
- Moreover, it was faster for all datasets (12/12) with an average relative difference of 70.9% to the R’+-tree.

For the case of the experiment shown in Figures 4c and 4d (1000KCN dataset), the number of disk read accesses needed by the R’+-tree when searching for a point non-existing in the spatial dataset is equal to the tree height. Note that for this dataset, the tree height of the R’+-tree, the R’*-tree and the xBR’+-tree equals 6, 5, 6 for 1KB nodes, 4, 4, 5 for 2KB nodes, 4, 4, 4 for 4KB nodes and 3, 3, 3 for 8KB and 16KB nodes, respectively. In the case of the xBR’+-tree, the number of disk read accesses needed is less than the tree height for most query points. In the case of R’+-tree, the number of disk read accesses depends on the size of the empty space in relation to the occupied space (inside MBRs) and is larger than the tree height for all node sizes. Studying the results for the execution time, we note that there is a fairly constant difference in favor of the xBR’+-tree against the other two trees. This query (PLQ) is related to the tree height and the size of MBRs that enclose the data points. So it seems easier for the R’+-tree to decide that the query point does not exist in the dataset, than for the xBR’+-tree. But this fact is not enough to make the R’+-tree faster than the xBR’+-tree, since CPU processing of the tree structure is lighter for the xBR’+-tree.

Studying the complete set of results of PLQs using as query points the centroids of the query windows, we find out that for R’+-trees, the number of disk read accesses is smaller than the height of the tree for all real datasets, while for synthetic datasets this number is larger than the height of the tree. For R’*-trees, the number of disk read accesses is always equal to the height of the tree because there is no overlapping between its leaves. For xBR’+-trees, the number of disk read accesses is always smaller than the tree height. Summarizing I/O results, we find out that:

- The R’+-tree needed the smallest number of disk read accesses in most cases (41/60).
- The xBR’+-tree needed the smallest number of disk read accesses in 18/60 cases.
- Only in one case the R’*-tree needed the smallest number of disk read accesses.

The results for the execution time showed that:

- The xBR’+-tree is faster for all datasets and node sizes (60/60).

The WQ was executed using the N-DF algorithm, for all datasets (12) and all node sizes (5), searching for the points residing inside the query windows of various sizes (6). The results of the WQ for the NArND dataset, using 212 windows that cover the whole data space, regarding the number of disk read accesses per query (Table 2) and the execution time vs. the node size (Table 2 and Figure 5a) are shown as a representative case. The use of the table is preferred due to the large difference of values between R’+-tree and the other two
trees, especially for the cases of small node sizes (1KB, 2KB).

In Table 2, it is shown that the xBR+-tree needed fewer disk read accesses (Acc) than the other two trees. As the node size increases, the absolute I/O difference between the trees becomes smaller, but the relative difference \((Acc_{R} - Acc_{xBR})/Acc_{R}\) has values (0.83, 0.80, 0.75, 0.72, 0.71) that are all in favor of R+-tree, while the relative difference \((Acc_{xBR} - Acc_{BR})/Acc_{xBR}\) has values (0.11, 0.15, 0.22, 0.28, 0.26) that are all in favor of xBR+-tree. Note the reduction of the difference from the smallest node size (1KB) to the largest size (16KB). This is due to the reduction of tree height, as the node size increases. In Table 2 and in Figure 5a, it is shown that the xBR+-tree is the fastest and the R+-tree is faster than the R*-tree, for all node sizes. All three trees needed less total execution time (I/O and CPU) for the node size equal to 4KB, even though larger node sizes needed fewer disk read accesses.

The results of the WQ on the large dataset Park in-

<table>
<thead>
<tr>
<th>Node Size</th>
<th>Disk Read Accesses</th>
<th>Execution Time (µs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>144.4</td>
<td>24.60</td>
</tr>
<tr>
<td>2</td>
<td>69.05</td>
<td>13.82</td>
</tr>
<tr>
<td>4</td>
<td>36.33</td>
<td>9.049</td>
</tr>
<tr>
<td>8</td>
<td>20.75</td>
<td>5.714</td>
</tr>
<tr>
<td>16</td>
<td>14.71</td>
<td>4.267</td>
</tr>
</tbody>
</table>

Table 2: WQ: disk read accesses and exec. time per query on NAndND (2^12 query windows) vs. node size.

Figure 5: WQ: exec. time vs. (a) node size (NAndND, 2^12, query windows) and (b) number of query windows (Park with node size=4K).

Figure 4: PLQ: disk read accesses (a) and exec. time (b) vs. node size (Water) with query points all dataset points and disk read accesses (c) and exec. time (d) vs. node size (1000KCN) with query points the centroids of the query windows.

Table 3: WQ: disk read accesses and exec. time per query on Park (node size=4KB) vs. number of Query Windows.

<table>
<thead>
<tr>
<th>Number</th>
<th>Disk Read Accesses</th>
<th>Execution Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wins</td>
<td>R^+</td>
<td>R^-</td>
</tr>
<tr>
<td>2^6</td>
<td>26.18</td>
<td>11.38</td>
</tr>
<tr>
<td>2^8</td>
<td>10.71</td>
<td>2.865</td>
</tr>
<tr>
<td>2^10</td>
<td>4.869</td>
<td>0.726</td>
</tr>
<tr>
<td>2^12</td>
<td>2.312</td>
<td>0.188</td>
</tr>
<tr>
<td>2^14</td>
<td>1.122</td>
<td>0.051</td>
</tr>
<tr>
<td>2^16</td>
<td>0.555</td>
<td>0.015</td>
</tr>
</tbody>
</table>

The average relative difference of execution time performance between the R+-tree and the xBR+-tree is between 49.6% and 64.7%, increasing with the enlargement of the node size.

In all trees, the execution time is reduced as the node size is increased. It is minimized for node

- The number of disk read accesses per query window for the xBR+-tree was the smallest for the most experiments (323/360).
- For the R+-tree, it was smallest for the remainder of the experiments (37/360).

Regarding the execution time metric:
- The xBR+-tree had the best performance in all cases (360/360).
- The average relative difference of execution time performance between the R+-tree and the xBR+-tree is between 49.6% and 64.7%, increasing with the enlargement of the node size.
size equal to 4KB, or 8KB. This is due to a tradeoff between I/O cost and CPU processing.

This behavior holds for the experiments of all datasets and all query windows.

6.5. Experiments for distance-based queries on single datasets (DRQs)

The DRQ was executed for all datasets (12) and all node sizes (5), searching for the points inside the incircle of the query windows, for various radius sizes (6 ε-values). Five Algorithms, N-DF, DF, S-DF, H-DF and BF, were tested for all (360) experiments. The number of disk read accesses is the same for the algorithms DF, S-DF, H-DF and BF because they all use the mindist metric and the query object is fixed. The R+-tree responded best with the algorithms using the mindist in all cases (360/360) in disk read accesses and faster with the DF algorithm (216/360 in execution time). The R*-tree responded best with the algorithms using the mindist in most cases (360/360) and faster with the BF algorithm in most cases (350/360 in execution time). The xBR+-tree responded best with the algorithms using the mindist in most cases (327/360) and faster with the DF algorithm (191/360 in execution time). So the performance comparison for the DRQ was performed among the R+-tree with the DF, the R*-tree with the BF and the xBR+-tree with the DF algorithm. The results of the DRQ executed on the NArrND dataset for the 2^{12} ranges (with $\varepsilon \leq \frac{1}{2} \times \frac{1}{\sqrt{256}}$) scanning the data space are shown as a representative case. The number of disk read accesses per query (Table 4 and the execution time (Table 5) and Figure 6a) vs. node size, are depicted. The use of a table is preferred because of the large difference of values between R+-tree and the other two trees, especially for the cases of small node sizes (1KB, 2KB, 4KB).

In this table, it is shown that the xBR+-tree needed fewer disk read accesses (Acc) than the other two trees. As the node size increases, the I/O difference between the trees remains almost stable. The relative difference

$$\frac{\text{Acc}_{R^+} - \text{Acc}_{xBR^+}}{\text{Acc}_{R^+}}$$

has values (0.82, 0.78, 0.70, 0.72, 0.55) that are all in favor of the R+-tree, while the relative difference $\frac{\text{Acc}_{xBR^+}}{\text{Acc}_{xBR^+}} - \frac{\text{Acc}_{xBR^+}}{\text{Acc}_{R^+}}$ has values (0.04, 0.12, -0.09, 0.15, 0.13) that are all (except the negative one) in favor of the xBR+-tree. Note the reduction of the difference from the smallest node size (1KB) to the largest one (16KB). This is due to the reduction of the tree height as the node size increases. In Table 4 and Figure 6a, it is shown that the xBR+-tree is the fastest and the R*-tree is faster than the R+-tree, for all node sizes. The R*-tree needed less total execution time (I/O and CPU) with node size equal to 4KB, while the other two trees needed less execution time with node size equal to 2KB, even though larger node sizes needed fewer disk read accesses.

The results of the DRQ on the synthetic dataset 500KCN indexed by trees with node size=4KB, for various ε sizes, regarding the number of disk read accesses (Table 5 and the execution time (Table 5 and Figure 6a) vs. the number of query ranges are shown. The xBR+-tree has the best performance regarding disk read accesses in most of the cases (except the one for node size=4KB) and the R*-tree has the worst, while the xBR+-tree has always the best execution time performance and the R+-tree the worst.

Studying the complete set of results (360 experiments) of DRQs, we validate the above performance behavior. Regarding I/O:

- The xBR+-tree had the best performance in most experiments (292/360).
- The R*-tree had the best performance in the re-
Regarding the execution time metric:

- The xBR⁺-tree had the best performance in all cases (360/360).
- The average relative difference of execution time performance between the R⁺-tree and the xBR⁺-tree is between 49.3% and 68.4%, increasing with the enlargement of node size.

### 6.6. Experiments for neighboring queries on single datasets (K-NNQs and CK-NNQs)

The \( KNNQ \) was executed for all datasets (12) and all node sizes (5), searching for the points near the centroids of the \( (2^{12}) \) query windows, for various values of \( K \) (4). Four Algorithms, DF, S-DF, H-DF and BF, were tested for all (240) experiments. The R⁺-tree responded best with the BF algorithm (222/240 in disk read accesses and 201/240 in execution time). The R⁺-tree responded best with the BF algorithm (224/240 in disk read accesses and 239/240 in execution time). The xBR⁺-tree responded best with the BF algorithm in disk read accesses in most cases (166/240) and was faster with H-DF algorithm in 161/240 cases. We considered as most important criterion the execution time and selected the BF algorithm for both R-trees and the H-DF algorithm for the xBR⁺-tree to continue the performance comparison for \( KNNQs \). In Figures 7a and 7b, we can see the results of the \( KNNQ \) with \( K=100 \) executed on the NArDn dataset for the \( 2^{12} \) query points, distributed evenly in data space, as one representative case. The number of disk read accesses per query point and the execution time vs. the node size are shown. Because of the large difference of values between R⁺-tree and the other two trees, it is not easy to distinguish the differences between xBR⁺-tree and R⁺-tree. Therefore, Table 6 has been included.

<table>
<thead>
<tr>
<th>Node Size</th>
<th>Disk Read Accesses</th>
<th>Execution Time (µs)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>R⁺ (BF)</td>
<td>R⁺ (H-DF)</td>
</tr>
<tr>
<td>1</td>
<td>268.1</td>
<td>16.92</td>
</tr>
<tr>
<td>2</td>
<td>125.7</td>
<td>12.23</td>
</tr>
<tr>
<td>4</td>
<td>89.92</td>
<td>9.022</td>
</tr>
<tr>
<td>8</td>
<td>43.91</td>
<td>5.979</td>
</tr>
<tr>
<td>16</td>
<td>26.92</td>
<td>2.527</td>
</tr>
</tbody>
</table>

Table 6: \( K=100 \) \( KNNQ \); disk read accesses per query on NArDn \( (2^{12} \) query points) vs. node size.

The average relative difference \( \mu \) of execution time with the R⁺-tree has values \((-0.55, -0.24, -0.07, -0.28, -0.12) \) that are all in favor of the R⁺-tree and the relative difference \( \Delta Acc_R^+ - \Delta Acc_{BR^+} / \Delta Acc_R^+ \) has values \((-0.55, -0.24, -0.07, -0.28, -0.12) \) that are also all in favor of the R⁺-tree. As the node size is increased exponentially, the number disk read accesses is reduced but not with the same ratio. For the R⁺-tree the ratio of the numbers of disk read accesses between two consecutive node sizes varies from 0.47 up to 0.72. For the R⁺-tree the ratio of the numbers of disk read accesses between two consecutive node sizes presents smaller variation (from 0.66 up to 0.87) while for the xBR⁺-tree this ratio presents an intermediate level of variation (from 0.58 up to 0.79). In Table 6 and in Figure 7b, it is shown that the xBR⁺-tree is faster than R⁺-tree for node sizes larger than 1KB, and the R⁺-tree is faster than the R⁺-tree, for all node sizes. All three trees have different behavior in total execution time (I/O and CPU). For the R⁺-tree, the total execution time varies without any monotony. For the R⁺-tree the execution time has monotonous enlargement with node size. Contrary to the previous behaviors, the xBR⁺-tree needed less total execution time for a node size equal to 4KB, even though larger node sizes needed fewer disk read accesses.

In Figures 7c and 7d, we can see the results of the \( KNNQ \) on the synthetic dataset 250KCN indexed by trees with node size=4KB, for \( 2^{12} \) query points, regarding the number of disk read accesses and the execution time vs. the value of \( K \). The xBR⁺-tree has the best performance regarding disk read accesses looking for the 1 or 10 NNs, while R⁺-tree has best performance for the 10² or 10³ NNs. The R⁺-tree needed the most disk read accesses for all values of \( K \). The xBR⁺-tree has always the best execution time performance and the R⁺-tree has the worst.

Studying the complete set of results (240 experiments for each tree) of the \( KNNQ \) we validate the above performance behavior:

- The number of disk read accesses per query point was the smallest for the R⁺-tree in most experiments (173/240).
- It was the smallest for the xBR⁺-tree in the rest of the experiments (67/240).
- Regarding the execution time metric, the xBR⁺-tree had the best performance in most cases (209/240).
- The xBR⁺-tree has the minimum number of best performance cases in execution time with the smallest node size (26/48) and has the maximum number of best performance cases with the biggest node size (48/48).
The average relative difference of execution time performance between the R*-tree and the xBR*-tree in the node size of 16KB is 49.2%.

The CKNNQ was executed for all datasets (12) and all node sizes (5), searching for the points inside the incircles of the (2D) query windows (with \( \epsilon \leq \frac{1}{2} \times \frac{1}{2^K} \)), for various values of \( K \) (4). Four Algorithms, DF, S-DF, H-DF and BF, were tested for all (240) experiments. All the three structures responded best with the BF algorithm. In detail, the R*-tree responded best in 197/240 experiments in disk read accesses and in 191/240 in execution time. The xBR*-tree responded best 202/240 in disk read accesses and in 132/240 in execution time. Finally, xBR*-tree responded best 144/240 in disk read accesses and in 190/240 in execution time. In Figures 8a and 8b, we can see the results of the CKNNQ executed on the NArrN dataset for the 2D query points, distributed evenly in data space, as one representative case. The number of disk read accesses per query point and the execution time vs. the node size are shown. Because of the large difference of values between R*-tree and the other two trees, it is not easy to distinguish the differences between xBR*-tree and R*-tree. Therefore, Table 7 is depicted.

In this table and in Figure 8a, it is shown that the R*-tree and xBR*-tree needed an almost equal number of disk read accesses (Acc). As the node size increases, the I/O difference between the trees decreases. The relative difference (AccBF - AccBR) has values (0.80, 0.75, 0.73, 0.58, 0.54) that are all in favor of the R*-tree and the relative difference (AccBF - AccBR) has values (-0.04, -0.05, 0.00, 0.02, -0.01), the 3 negative ones being in favor of the R*-tree. For the R*-tree the ratio of the numbers of disk read accesses between two consecutive node sizes varies widely (from 0.59 up to 0.91). For the xBR*-tree this ratio presents a smaller variation (from 0.73 up to 0.98) and for the xBR*-tree it presents a similar variation (from 0.73 up to 1.01). In Table 7 and in Figure 8b, it is shown that the xBR*-tree is the fastest and the R*-tree is faster than the R*-tree, for all node sizes. All three trees have similar behavior in total execution time (I/O and CPU). The total execution time has monotonous increment with node size. In Figures 8c and 8d, we can see the results of the CKNNQ on the large real dataset Water indexed by the three trees with node size=4KB, for 2D query points, regarding the number of disk read accesses and execution time vs. the value of K. Because of the large number of nodes in this dataset the number of disk read accesses is quite stable for all trees. It is most stable for the R*-tree while for the other two trees varies between 1.4 and 1.8 for R*-tree and 1.8 and 2.2 for the xBR*-tree. The R*-tree has the best performance regarding disk read accesses and the R*-tree the worst, while the xBR*-tree has always the best execution time performance and the R*-tree has the worst.

Studying the complete set of results (240 experiments for each tree) of the CKNNQ, we validate the above performance behavior.

- The number of disk accesses per query point for the xBR*-tree was the smallest in most experiments (138/240) and for the R*-tree it was the smallest in the rest of the experiments (102/240).
- Regarding the execution time metric, the xBR*-tree has the best performance in all the experiments (240/240).
- The average relative difference of execution time performance between the R*-tree and the xBR*-
tree is between 39.6% and 60.5%, increasing with the enlargement of the node size.

6.7. Creation of input for queries on dual datasets

In the experiments performed, the effect of LRU-buffer has also been studied, because a node of the one tree can be paired with several nodes of the other tree, in successive or not time points. Moreover, both trees corresponding to a combination of datasets were of equal node size.

6.8. Experiments for join (dual dataset) queries (KCPQs and eDJQs)

In the experiments performed, the lowest execution time value is with a buffer size of $2^{10}$ pages (nodes) for all algorithms and the minimum execution time value, 72,450 ms (72 sec), with the C-DF-2 algorithm.

Considering the complete set of 45/50 experiments for the 5 buffer sizes (the biggest of the 10 dataset combinations, Water x Park, was not tested for all node sizes because of the big execution time values it required), we collected the minimum execution time values for each combination and these results are shown in Table 8. It is shown that there is not a single best buffer size, neither a single best node size. We conclude that for combinations between small real datasets it is better to have no buffering, while for combinations of small synthetic and larger real datasets it is better to have buffering larger than $2^8$ pages (nodes).

Before we present the results on the combination of synthetic datasets with real datasets, it is important to check whether there was a difference between the versions of the algorithm. The execution time value is with a buffer size of $2^{10}$ pages (nodes) for all algorithms and the minimum execution time value, 72,450 ms (72 sec), with the C-DF-2 algorithm.

By considering the combinations of datasets, the difference between the versions of the algorithm is not significant, the C-BF-2 algorithm is better only in a few cases (less than 2% of the total execution time value).

In the experiments performed, the effect of LRU-buffer has also been studied, because a node of the one tree can be paired with several nodes of the other tree, in successive or not time points. Moreover, both trees corresponding to a combination of datasets were of equal node size.

6.8.1. Selection of buffer size and algorithms for the KCPQ

All combinations of datasets (10) and all node sizes (5), for various values of $K$ (5) and with several values of LRU-buffer size (5) were used. In this series of experiments the target was to find out for which buffer size and with which algorithm among S-DF-2, H-DF-2, C-DF-2 and C-BF-2 each tree responded better. It is obvious that as the size of the LRU-buffer increases, the number of disk read accesses decreases and the related results will be omitted. So for the above target, only the execution time per query will be studied.

In Figure 8a, we can see the results of the KCPQ on the combination of synthetic datasets $1000K_{C1N} \times 1000K_{C2N}$, both indexed by $R^2$-trees with node size of 2KB, searching for the $K=1000$ closest pairs with all four algorithms, using LRU-buffer sizes of $0, 2^6, 2^8, 2^{10}, 2^{12}$ pages, as one representative case. It is shown that with the C-DF-2 and C-BF-2 algorithms the $R^2$-tree is approximately 3 times faster than with the other algorithms for all buffer sizes. The lowest execution time value is with a buffer size of $2^{10}$ pages (nodes) for all algorithms and the minimum execution time value, 72,450 ms (72 sec), with the C-DF-2 algorithm.

In Figure 8b, we can see the results of the KCPQ on the combination of real datasets NArdN x Water, both indexed by $R^2$-trees with node size=2KB, searching for the $K=1000$ closest pairs with all four algorithms, using LRU-buffer sizes of $0, 2^6, 2^8, 2^{10}, 2^{12}$, as one representative case. It is shown that with the C-BF-2 algorithm the $R^2$-tree is from 1.6 up to 2 times faster than the best of the other tree algorithms for all buffer sizes. The smallest execution time value was achieved with buffer size of 0 pages (nodes) for all algorithms and the minimum execution time value, 42.418 ms, was achieved with the

<table>
<thead>
<tr>
<th>Node Size (KB)</th>
<th>Time per Query (µs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1555</td>
</tr>
<tr>
<td>2</td>
<td>1570</td>
</tr>
<tr>
<td>4</td>
<td>1540</td>
</tr>
<tr>
<td>8</td>
<td>1560</td>
</tr>
<tr>
<td>16</td>
<td>1545</td>
</tr>
<tr>
<td>32</td>
<td>1550</td>
</tr>
<tr>
<td>64</td>
<td>1565</td>
</tr>
<tr>
<td>128</td>
<td>1580</td>
</tr>
<tr>
<td>256</td>
<td>1600</td>
</tr>
<tr>
<td>512</td>
<td>1605</td>
</tr>
</tbody>
</table>

6.8.2. Selection of buffer size and algorithms for the eDJQ

All combinations of datasets (10) and all node sizes (5), for various values of $K$ (5) and with several values of LRU-buffer size (5) were used. In this series of experiments the target was to find out for which buffer size and with which algorithm among S-DF-2, H-DF-2, C-DF-2 and C-BF-2 each tree responded better. It is obvious that as the size of the LRU-buffer increases, the number of disk read accesses decreases and the related results will be omitted. So for the above target, only the execution time per query will be studied.

In Figure 8c, we can see the results of the KCPQ on the combination of synthetic datasets $1000K_{C1N} \times 1000K_{C2N}$, both indexed by $R^2$-trees with node size of 2KB, searching for the $K=1000$ closest pairs with all four algorithms, using LRU-buffer sizes of $0, 2^6, 2^8, 2^{10}, 2^{12}$ pages, as one representative case. It is shown that with the C-DF-2 and C-BF-2 algorithms the $R^2$-tree is approximately 3 times faster than with the other algorithms for all buffer sizes. The lowest execution time value is with a buffer size of $2^{10}$ pages (nodes) for all algorithms and the minimum execution time value, 72,450 ms (72 sec), with the C-DF-2 algorithm.
The table below shows the execution time per query for different algorithms and datasets:

<table>
<thead>
<tr>
<th>Combination of datasets</th>
<th>Exec. time (ms)</th>
<th>Node size (KB)</th>
<th>Buffer size (pages)</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAppN × NArdN</td>
<td>0.1725</td>
<td>1</td>
<td>2</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NAppN × NArdN</td>
<td>0.4091</td>
<td>1</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArrN × NArdN</td>
<td>1.0496</td>
<td>8</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArrND × NArdND</td>
<td>1.8803</td>
<td>8</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>250KCl1 × 250KCl2</td>
<td>1.7793</td>
<td>8</td>
<td>2^10</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>500KCl1 × 500KCl2</td>
<td>5.6271</td>
<td>16</td>
<td>2^8</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>500KCl2 × 1000KCl1</td>
<td>12.112</td>
<td>16</td>
<td>2^12</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>1000KCl1 × 1000KCl2</td>
<td>28.515</td>
<td>16</td>
<td>2^12</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArdND × Water</td>
<td>342.64</td>
<td>16</td>
<td>2^12</td>
<td>C-BF-2</td>
</tr>
</tbody>
</table>

Table 8: \( K = 10^3 \) CPQ with R*-tree: Min Exec Time per query for all combinations of datasets.

The table below shows the execution time per query for different algorithms and datasets:

<table>
<thead>
<tr>
<th>Combination of datasets</th>
<th>Exec. time (ms)</th>
<th>Node size (KB)</th>
<th>Buffer size (pages)</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAppN × NArdN</td>
<td>36.640</td>
<td>2</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NAppN × NArdN</td>
<td>136.46</td>
<td>4</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArrN × NArdN</td>
<td>157.64</td>
<td>1</td>
<td>2^8</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArrND × NArdND</td>
<td>310.96</td>
<td>1</td>
<td>2^8</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>250KCl1 × 250KCl2</td>
<td>206.93</td>
<td>4</td>
<td>2^6</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>500KCl1 × 500KCl2</td>
<td>405.03</td>
<td>4</td>
<td>2^6</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>500KCl2 × 1000KCl1</td>
<td>599.60</td>
<td>8</td>
<td>2^6</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>1000KCl1 × 1000KCl2</td>
<td>845.10</td>
<td>16</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArdND × Water</td>
<td>30.255</td>
<td>1</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>Water × Park</td>
<td>1,031.9</td>
<td>4</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
</tbody>
</table>

Table 9: \( K = 10^3 \) CPQ with R*-tree: Min Exec Time per query for all combinations of datasets.

with all four algorithms, using LRU-buffer sizes of 0, 2^6, 2^8, 2^10, 2^12, as one representative case. It is shown that with the C-BF-2 algorithm the xBR*-tree is from 3.0 up to 3.3 times faster than the best of the S-DF-2 and C-DF-2 algorithms and from 1.1 up to 1.2 faster than the H-DF-2 algorithm for all buffer sizes. The lowest execution time value was achieved with buffer size of 0 pages (nodes) for all algorithms and the minimum execution time value, 30.706 ms, was achieved with the C-BF-2 algorithm.

Considering the complete set of all (50) experiments for the 10 dataset combinations and 5 buffer sizes, we collected the minimum execution time values for each combination and these results are shown in Table 10. It is shown that xBR*-tree responded best in all the cases (10/10) without buffering. The best algorithm for xBR*-trees executing the KCPQ was the C-BF-2 (in 8/10 cases).

In conclusion, we note that:

- There is no meaning for a comparison between the R*-tree and the other two trees because of the very large difference in execution times observed (the R*-tree was mainly designed for PLQs and WQs).
- Based on the above results, we continue the performance comparison between the R*-tree and xBR*-tree, using the C-BF-2 algorithm for both trees.

![Figure 9: KCPQ with (a) R*-tree on 1000KC1N × 1000KC2N; (b) R*-tree on NArdND × Water; (c) xBR*-tree on NArdND × Water: exec. time vs. buffer size per Algorithm with K=10^3 and node size=2KB.](image-url)
without LRU-buffer (0 pages) for all node sizes, for various values of \( K \) (1, 10, 10^2, 10^3 and 10^4) and for both performance metrics (i.e. the number of disk read accesses and the execution time).

### 6.8.2. Performance study of the KCPQ

In Figures 10a and 10b, we can see the results of the KCPQ with \( K = 10^4 \), executed on the combination of large real datasets Water × Park, as one representative case. The number of disk read accesses per query point and the execution time vs. the node size are shown. The \( xBR^+ \)-tree needed fewer disk read accesses (Acc) than the \( R^+ \)-trees having node sizes between 2KB and 8KB. As the node size increases, the ratio of the I/O difference between the two trees varies. The relative difference (Acc$_{BR} - $Acc$_{xBR} / $Acc$_{BR}$) has values (-1.59, 0.22, 0.20, 0.12, -0.23), the 3 positive one being in favor of the \( xBR^+ \)-tree. For the \( R^+ \)-tree, the ratio of the numbers of disk read accesses between two consecutive node sizes presents a small variation (from 0.5 up to 0.6) and is always decreased. For the \( xBR^+ \)-tree, this ratio presents a similar variation from 0.6 up to 0.8 (except the first case from 1 to 2 KB where it is 0.2). In Figure 10b, it is shown that the \( xBR^+ \)-tree is faster than \( R^+ \)-tree for all node sizes bigger than 1KB. For both trees the execution time has a minimum value with a node size of 4KB, even though larger node sizes needed fewer disk read accesses. In Figures 10c and 10d, we can see the results of the KCPQ on the same combination of large real datasets indexed by trees with node size of 4KB, regarding the number of disk read accesses and the execution time vs. the value of \( K \). The number of disk read accesses needed by both trees remains stable although the number of \( K \) is increased exponentially. The \( xBR^+ \)-tree has the best performance regarding disk read accesses in all the cases.

Studying the complete set of results (250 experiments) for each tree) for the KCPQ, we validate the above performance behavior.

- The number of disk accesses per query for the \( xBR^+ \)-tree was the smallest for most experiments (224/250).
- The \( xBR^+ \)-tree was faster than the \( R^+ \)-tree in all experiments with node sizes of 2KB and 16KB, in 46/50 cases with node size of 4KB, while, in total, it was faster in 231/250 cases.
- The average relative difference of execution time performance between the \( R^+ \)-tree and the \( xBR^+ \)-tree is between 62.7% and 71.9%.

<table>
<thead>
<tr>
<th>Combination of datasets</th>
<th>Exec time (ms)</th>
<th>Node size (KB)</th>
<th>Buffer size (pages)</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAppN × NArrN</td>
<td>0.146</td>
<td>1</td>
<td>2^10</td>
<td>H-DF-2</td>
</tr>
<tr>
<td>NAppN × NArrN</td>
<td>0.347</td>
<td>1</td>
<td>0</td>
<td>H-DF-2</td>
</tr>
<tr>
<td>NArrN × NArrN</td>
<td>0.837</td>
<td>1</td>
<td>2^10</td>
<td>H-DF-2</td>
</tr>
<tr>
<td>NArrND × NArrND</td>
<td>2.085</td>
<td>1</td>
<td>2^10</td>
<td>H-DF-2</td>
</tr>
<tr>
<td>250KIC1N × 250KIC2N</td>
<td>5.994</td>
<td>1</td>
<td>2^4</td>
<td>H-DF-2</td>
</tr>
<tr>
<td>500KIC1N × 500KIC2N</td>
<td>25.16</td>
<td>1</td>
<td>2^8</td>
<td>H-DF-2</td>
</tr>
<tr>
<td>500KIC2N × 1000KIC1N</td>
<td>29.98</td>
<td>1</td>
<td>2^10</td>
<td>H-DF-2</td>
</tr>
<tr>
<td>1000KIC1N × 1000KIC2N</td>
<td>55.97</td>
<td>1</td>
<td>2^8</td>
<td>H-DF-2</td>
</tr>
<tr>
<td>NArrND × Water</td>
<td>2.202</td>
<td>4</td>
<td>2^10</td>
<td>C-BF-2</td>
</tr>
</tbody>
</table>

Table 11: \( eDIQ \) (\( \epsilon = 1.25 \times 10^{-3} \)) with \( R^+ \)-tree: Min Exec Time per query for all combinations of datasets.

### 6.8.3. Selection of buffer size and algorithms for the \( eDIQ \)

For the \( eDIQ \) the same scenario of experiments to the one of KCPQ was performed to find out for which buffer size and with which algorithm among S-DF-2, H-DF-2, C-DF-2 and C-BF-2 each tree responded better, regarding the execution time metric.

In Figure 11a, we can see the results of the \( eDIQ \) on the combination of synthetic datasets 1000KC1N × 1000KC2N, both indexed by \( R^+ \)-trees, with node size of 4KB, searching for the pairs with distance \( \leq 1.25 \times 10^{-5} \) with all four algorithms, using LRU-buffer sizes of 0, 2^6, 2^8, 2^10, 2^12 pages, as one representative case. We chose to present the same dataset combinations to the previous query (KCPQ) because of the similarity which exists between the two types of queries. It is shown that with the C-DF-2 algorithm the \( R^+ \)-tree is slightly faster than with the other algorithms for all buffer sizes. The lowest execution time value is achieved with buffer size of 2^10 pages (nodes) for all algorithms and the minimum execution time value, 152,541 ms (152 sec), is achieved with the C-DF-2 algorithm.

Considering the complete set of 45/50 experiments for the 5 buffer sizes (the biggest combination Water × Park was not tested for all node sizes because of the big execution time values) we collected the minimum execution time values for each combination and these results are shown in Table 11. It is shown that there is not a single best buffer size, while 9/10 best execution times were achieved with node size equal to 1KB. We conclude that for combinations between small real datasets it is better to have 2^10 pages in LRU-buffer, while for combinations of small synthetic and large real datasets it is better to have 2^9 buffer pages (nodes). The best algorithm for \( R^+ \)-trees executing the \( eDIQ \) is the H-DF-2 (in 9/10 cases).

In Figure 11b, we can see the results of the \( eDIQ \) on the combination of real datasets NArrND × Water, both
indexed by R*-trees with node size of 4KB, searching for the pairs with distance \( \leq 1.25 \times 10^{-5} \) with the four algorithms, using LRU-buffer sizes of 0, 2\(^6\), 2\(^8\), 2\(^{10}\), 2\(^{12}\) pages, as one representative case. It is shown that with the C-BF-2 algorithm the R*-tree is from 1.1 up to 1.4 times faster than the best of the other tree algorithms for all buffer sizes. The lowest execution time value is achieved with buffer size of 0 pages (nodes) for all algorithms and the minimum execution time value, 37.837 ms, is achieved with the C-BF-2 algorithm.

Considering the complete set of all (50) experiments for the 10 dataset combinations and 5 buffer sizes, we collected the minimum execution time values for each combination and these results are shown in Table 12. It is shown that R*-tree responded best in half cases (5/10), including the combinations between large real datasets, without buffering, while in the 4 combinations between synthetic datasets it responded best with 2\(^6\) pages in LRU-buffer (3/4 cases). The best algorithm for R*-trees executing the eDJQ is the C-BF-2.

Finally, in Figure 11c, we can see the results of the eDJQ on the combination of real datasets NArdND × Water, both indexed by xBR*-trees with node size of 4KB, searching for the pairs with distance \( \leq 1.25 \times 10^{-5} \) with all four algorithms, using LRU-buffer sizes of 0, 2\(^6\), 2\(^8\), 2\(^{10}\), 2\(^{12}\) pages, as one representative case. It is shown that with the C-BF-2 algorithm the xBR*-tree is from 2.8 up to 3.5 times faster than the best among the S-DF-2 and C-DF-2 algorithms and from 1.03 up to 1.13 faster than the H-DF-2 algorithm for all buffer sizes. The lowest execution time value was achieved with buffer size of 2\(^6\) pages (nodes) for all algorithms and the minimum execution time value, 33.437 ms, was achieved with the C-BF-2 algorithm.

Considering the complete set of all (50) experiments, we collected the minimum execution time values for each combination of datasets and these results are shown in Table 13. It is shown that xBR*-tree responded best without buffering in all combinations of datasets. The best algorithm for xBR*-trees executing the eDJQ is the H-DF-2 (8/10 cases).

In conclusion, we note that:

- There is no meaning for a comparison between the R*-tree and the other two trees for eDJQ, because

<table>
<thead>
<tr>
<th>Combination of datasets</th>
<th>Exec. time (ms)</th>
<th>Node size (KB)</th>
<th>Buffer size (pages)</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAppN × NArdN</td>
<td>50.619</td>
<td>4</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NAppN × NArdN</td>
<td>129.48</td>
<td>4</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NAppN × NArdN</td>
<td>157.00</td>
<td>1</td>
<td>2(^6)</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArdN × NArdND</td>
<td>319.55</td>
<td>4</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArdND × NArdND</td>
<td>250KC1N × 250KC2N</td>
<td>176.06</td>
<td>8</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArdND × NArdND</td>
<td>500KC1N × 500KC2N</td>
<td>356.79</td>
<td>16</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArdND × NArdND</td>
<td>500KC2N × 1000KC1N</td>
<td>532.82</td>
<td>16</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>NArdND × NArdND</td>
<td>1000KC1N × 1000KC2N</td>
<td>782.53</td>
<td>16</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>Water × NArdND</td>
<td>25.698</td>
<td>1</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>Water × Park</td>
<td>1212.5</td>
<td>4</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
</tbody>
</table>

Table 12: eDJQ (\( e = 1.25 \times 10^{-5} \)) with R*-tree: Min Exec Time per query for all combinations of datasets.
of the very big difference in execution times observed (the $R$-tree was mainly designed for PLQs and WQs).

- We continue the performance comparison between the $R$-tree and xBR$^+$-tree, using the C-BF-2 algorithm for the first one and the H-DF-2 algorithm for the second one, without LRU-buffer (0 pages) for all node sizes, for various values of $\varepsilon(0, 1.25 \times 10^{-5}, 2.5 \times 10^{-5}, 5 \times 10^{-5}, 10 \times 10^{-5})$ and for both performance metrics (i.e. the number of disk read accesses and the execution time).

### 6.8.4. Performance study of the $eDJQ$

In Figures 12a and 12b, we can see the results of the $eDJQ$ with $\varepsilon = 1.25 \times 10^{-5}$ executed on the combination of large real datasets Water $\times$ Park, as one representative case. The number of disk read accesses per query and the execution time vs. the node size are shown. The xBR$^+$-tree needed fewer disk read accesses (Acc) than the $R$-tree for all node sizes. As the node size increases, the ratio of the I/O difference between the two trees varies. The relation between I/O performance and the node size is quite stable (almost linear). The relative difference ($\text{Acc}_R - \text{Acc}_{xBR^+}$)/$\text{Acc}_R$ has values (0.76, 0.71, 0.66, 0.61, 0.49), all in favor of the xBR$^+$-tree.

For the $R$-tree, the ratio of the numbers of disk read accesses between two consecutive node sizes presents a small variation (from 0.42 up to 0.49 and always is decreased) and for the xBR$^+$-tree this ratio presents a similar level of variation, from 0.51 up to 0.60. In Figure 12b, it is shown that the xBR$^+$-tree is faster than the $R$-tree for all node sizes. For both trees the execution time has minimum value with node size of 4KB, even though larger node sizes needed fewer disk read accesses. In Figures 12c and 12d, we can see the results of the $eDJQ$ on the same combination of large real datasets indexed by trees with node size of 4KB, regarding the number of disk read accesses and the execution time vs. the value of $\varepsilon$. The number of disk read accesses needed by xBR$^+$-tree remains very stable although the value of $\varepsilon$ is increased exponentially. The xBR$^+$-tree has the best performance regarding disk read accesses in the most cases (3/5), while in the execution time it was the best in all cases.

Studying the complete set of results (250 experiments for each tree) for the $eDJQ$, we validate the above performance behavior.

- The number of disk accesses per query for the xBR$^+$-tree was the smallest for most experiments (216/250).
- The xBR$^+$-tree was faster than the $R$-tree in all experiments with node sizes 2KB and 4KB, in 49/50 cases with node size of 16KB, while in total it was faster in 235/250 case.
- The average relative difference of execution time performance between the $R$-tree and the xBR$^+$-tree is between 66.2% and 68.2%.

### 6.9. Summary and conclusions of experimental results

The experimental results of tree building are summarized in the following.

- The xBR$^+$-tree needs a little less space (in most cases) and is built in a smaller time than the two $R$-trees.
- The xBR$^+$-tree building is faster than the $R$-tree and the $R$-tree is faster than $R$-tree for all datasets and node sizes.
- This difference is increasing as the node size increases and becomes bigger for the large real datasets.

The fractions of cases where the xBR$^+$-tree is an execution time and I/O performance winner, for each (single, or dual dataset) query, is depicted in Table 14. The second and third columns refer to the aggregate results for all page sizes, while the fourth and sixth columns refer to results when using a page size of 16KB. The fifth column refers to the xBR$^+$-tree gain in execution time, ($R$-tree exec. time $-$ xBR$^+$-tree exec. time) / $R$-tree exec. time, for the page size of 16KB (e.g. a gain value equal to 66.67% for a query means that the xBR$^+$-tree needs 1/3 of the execution time of the $R$-tree to answer this query). By studying these results, we conclude that the xBR$^+$-tree is a clear performance winner, in relation to the $R$-tree (the best among $R$-trees). More specifically:

<table>
<thead>
<tr>
<th>Combination of datasets</th>
<th>Exec Time (sec)</th>
<th>Node size</th>
<th>Buffer size</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAppN x NArnN</td>
<td>11.094</td>
<td>16</td>
<td>0</td>
<td>H-BF-2</td>
</tr>
<tr>
<td>NAppN x NArnN</td>
<td>27.156</td>
<td>4</td>
<td>0</td>
<td>H-BF-2</td>
</tr>
<tr>
<td>NArnN x NArnN</td>
<td>46.244</td>
<td>4</td>
<td>0</td>
<td>H-BF-2</td>
</tr>
<tr>
<td>NJyN x NJyN</td>
<td>119.86</td>
<td>2</td>
<td>0</td>
<td>H-BF-2</td>
</tr>
<tr>
<td>250KC1N x 250KC2N</td>
<td>21.346</td>
<td>16</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>500KC1N x 500KC2N</td>
<td>47.708</td>
<td>8</td>
<td>0</td>
<td>H-BF-2</td>
</tr>
<tr>
<td>500KC2N x 1000KC1N</td>
<td>73.090</td>
<td>8</td>
<td>0</td>
<td>H-BF-2</td>
</tr>
<tr>
<td>1000KC1N x 1000KC2N</td>
<td>102.57</td>
<td>8</td>
<td>0</td>
<td>H-BF-2</td>
</tr>
<tr>
<td>NArnND x Water</td>
<td>23.360</td>
<td>2</td>
<td>0</td>
<td>C-BF-2</td>
</tr>
<tr>
<td>Water x Park</td>
<td>682.02</td>
<td>4</td>
<td>0</td>
<td>H-BF-2</td>
</tr>
</tbody>
</table>

Table 13: $eDJQ$ ($\varepsilon = 1.25 \times 10^{-5}$) with xBR$^+$-tree: Min Exec Time per query for all combinations of datasets.
The building time of an xBR*-tree in queries can be credited to the following:

1. The xBR*-tree is a big winner in execution time in all cases and a winner in I/O in all cases except of the I/O of the KNNQ.

2. The xBR*-tree is an almost absolute winner when the page size equals 16KB (for this page size the xBR*-tree is a relative winner in the I/O of the KNNQ, too). Note the high percentages of gain for this page size.

Note that the R*-tree was designed specifically for PLQs and WQs and not for other ones, like DRQs, KNNQs, KCPQs, eDJQs, etc.

The regular subdivision of space, the additional representation of the minimum rectangles bounding the actual data objects (DBRs), the extra termination condition applicable in certain queries and the storage order of the entries of internal nodes gave the ability to the xBR*-tree to be a more efficient structure than R-trees and even than the R*-tree. More specifically, the building performance of the xBR*-tree can be credited to the following:

1. Due to the regular subdivision of space, the calculations needed are much fewer and simpler than those of the R*-tree.

The building time of an xBR*-tree is smaller even than the one needed for building the respective, very simple, R*-tree. The very good performance of the xBR*-tree in queries can be credited to the following:

1. The regular subdivision of space leads to laying the (sub)quadrants, created by the data distribution, in the corners of the embedding (sub)space. In this way, the distances between them are maximized and pruning during join query processing is increased.

2. Due to the quadrangular shape of the (sub)quadrants, the dimensions of the contained DBRs are minimized. The minimal dimensions of DBRs in conjunction with their laying in the corners of the embedding (sub)space allows the high exploitation of metrics like mindist (the R*-trees, due to their structure, do not utilize efficiently such pruning techniques).

3. In xBR*-trees, DBRs are exploited as an extra tool of delimiting the subspace containing data objects.

4. By examining the entries of an xBR*-tree internal node in reverse preorder traversal of the Quadtree that corresponds to this internal node (a subregion is examined before any enclosing region of this subregion), multiple examinations of overlapping regions are avoided (at least in point location and window queries).

5. The disjointness between regions and the combination of the region of each node with the Shape property of this node gives the ability of an extra termination condition in window and range queries (this condition cannot be applied in R-trees, due to their structure).

The conclusions arising from the performance results of the alternative DF/BF algorithms for processing queries are summarized in the following:

- For PLQs and WQs, N-DF algorithms are the only applicable, since the criterion for such queries is boolean (true/false).

Table 14: Synopsis of efficiency of xBR*-tree in all queries vs. R*-tree

<table>
<thead>
<tr>
<th>Query name</th>
<th>all node sizes</th>
<th>node size=16KB</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Time</td>
<td>I/O</td>
</tr>
<tr>
<td>Single-dataset queries:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>WQ</td>
<td>360/360</td>
<td>323/360</td>
</tr>
<tr>
<td>DRQ</td>
<td>360/360</td>
<td>292/360</td>
</tr>
<tr>
<td>KNNQ</td>
<td>209/240</td>
<td>67/240</td>
</tr>
<tr>
<td>CKNNQ</td>
<td>240/240</td>
<td>138/240</td>
</tr>
<tr>
<td>Dual-dataset queries:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>KCPQ</td>
<td>231/250</td>
<td>224/250</td>
</tr>
<tr>
<td>eDJQ</td>
<td>235/250</td>
<td>216/250</td>
</tr>
</tbody>
</table>

Figure 12: eDJQ on large real datasets Water-Park: disk read accesses (a) and exec. time (b) vs. node size (ε = 1.25 × 10^-5) and disk read accesses (c) and exec. time (d) vs. ε values (node size=4KB).
7. Conclusions and Future Work

In [13], the xBR*+-tree was compared to the xBR-tree for single dataset queries and datasets of medium size and “a detailed relative performance study of the xBR*+-tree against the R+-tree and/or R*-tree for single dataset and multi-dataset queries” was mentioned as the main future work target, since these structures had never been compared in the literature.

In this paper, we accomplished this target based on single, as well as, on dual dataset queries, utilizing existing and new algorithms and performing experiments on medium, as well as, large datasets. More specifically, in this paper, we presented algorithms for PLQs and WQs used in the above three structures. We also presented for these structures N-DF, S-DF and BF existing algorithms and the new H-DF algorithm for DRQs, KNNQs and CKNNQs. Moreover, we presented the first algorithms for KCPQs and eDJQs on the xBR*+-tree and a new alternative DF algorithm (H-DF-2) for KCPQs and eDJQs for all the three trees. We also highlighted the differences between alternative algorithms.

Moreover, by a detailed performance comparison (I/O and execution time) of xBR*+-trees (non-overlapping trees of the quadtree family), R*+-trees (non-overlapping trees of the R-tree family) and R*-trees (industry standard belonging to the R-tree family) for tree building, processing single point dataset queries (PLQs, WQs, DRQs, KNNQs and CKNNQs) and distance-based join queries (KNNQs, eDJQs), using medium and large spatial (real and synthetic) datasets, we showed that the xBR*+-tree is a clear winner in tree building, a big winner in execution time in all cases and a winner in I/O in all cases, except for the I/O of the KNNQ (it is an almost absolute winner when the page size equals 16KB).

The building performance of the xBR*+-tree is due to the regular subdivision of space that leads to much fewer and simpler calculations. The higher query performance of the xBR*+-tree is due to the combination of the regular subdivision of space, the additional representation of the minimum rectangles bounding the actual data objects (DBRs) and the extra termination condition applicable in certain queries and the storage order of the entries of internal nodes gave

In the future we plan to:

- Compare the three trees for data of dimensionality larger than 2,
- Create extensions of the xBR*+-tree for non-point data objects and algorithms for processing queries on them and compare to competitive structures,
- Create extensions of the xBR*+-tree for parallel and distributed environments,
- Create algorithms to bulk-load xBR*+-trees.

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