R-trees Have Grown Everywhere

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Spatial data management has been an active area of intensive research for more than two decades. In order to support spatial objects in a database system several issues should be taken into consideration such as: spatial data models, indexing mechanisms, efficient query processing, cost models. One of the most influential access methods in the area is the R-tree structure proposed by Guttman in 1984 as an effective and efficient solution to index rectangular objects in VLSI design applications. Since then, several variations of the original structure have been proposed towards: providing more efficient access, handling objects in high-dimensional spaces, supporting concurrent accesses, supporting I/O and CPU parallelism, efficient bulk-loading. It seems that due to the modern demanding applications and after the academia has paved the way, recently the industry recognized the use and necessity of R-trees. The simplicity of the structure and its resemblance to the B-tree, allowed developers to easily incorporate the structure into existing database management systems in order to support spatial query processing. In this paper we provide an extensive survey of the R-tree evolution, studying the applicability of the structure and its variations to efficient query processing, accurate proposed cost models, and implementation issues like concurrency control and parallelism. Based on the observation that 'space is everywhere', we anticipate that we are in the beginning of the era of the 'ubiquitous R-tree' in an analogous manner as B-trees were considered 25 years ago.

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1. INTRODUCTION

The paper entitled 'The ubiquitous B-tree' by Comer was published in ACM Computing Surveys in 1979 [36]. Actually, the keyword 'B-tree' was standing as a generic term for a whole family of variations, namely the B*-trees , the B^+-trees and several other minor variants [78]. The title of the paper might seem provocative at that time. However, it represented a big truth, which is still valid in our days, since all textbooks on databases or data structures devote a considerable number of pages to explain definitions, characteristics and basic procedures for searches, inserts and deletes on B-trees. Moreover, B^+-trees are not just a theoretical notion. On the contrary, for years they remain the de facto standard access method in all prototype and commercial relational systems for typical transaction processing applications, although one could observe that some quite more elegant and efficient structures have appeared in the literature.

While the 80s were the period of the wide acceptance of relational systems in the market, at the same time it became apparent that the relational model was not adequate to host new emerging applications. To name a few of them: multimedia, CAD/CAM, geographical, medical and scientific applications are just some examples, where the relational model had been proven to behave poorly. Thus, the object-oriented model and the object-relational model were proposed in the sequel. One of the reasons for the shortcoming of the relational systems was their inability to handle the new kind of data with B-trees. More specifically, B-trees were designed to handle alphanumeric (i.e., one-dimensional) data, like integers, characters and strings, where an ordering relation can be defined. A number of new B-tree variations have appeared in the literature to handle object-oriented data (see [17] for a comparative study). Mainly, these structures were aiming at hosting data of object hierarchies of data in a single structure. However, these efforts had limited applicability and could not cover the requirements of the so many new application areas.

In light of this evolution, entirely novel access methods were proposed, evaluated, compared and established. One of these structures, the R-tree, was proposed by Guttman in 1984 aiming at handling geometrical data, such as points, line segments, surfaces, volumes and hyper-volumes in high-dimensional spaces [57]. R-trees were treated in the literature in much the same way as B-trees. In particular, many improving variations have been proposed for various instances and environments, several novel operations have been developed for them and new cost models have been suggested. It seems that due to the modern demanding applications and after the academia has paved the way, recently the industry recognized the use and necessity of R-trees. Thus, R-trees are adopted as an additional access method to handle multidimensional data. Based on the observation that 'space is everywhere' [153], we anticipate that we are in the beginning of the era of the 'ubiquitous R-tree' in an analogous manner as B-trees were considered 25 years ago. Nowadays, spatial databases and geographical information systems have been established as a mature field, spatiotemporal databases and manipulation of moving points and trajectories are being studied extensively, and finally image and multimedia databases able to handle new kinds of data, such as images, voice, music, or video, are being designed and developed. An application in all these cases should rely to R-trees as

a necessary tool for data storage and retrieval.

R-tree applications cover a wide spectrum, from spatial and temporal to image and video (multimedia) databases. The initial application that motivated Guttman to his pioneering research was VLSI design (i.e., how to efficiently answer whether a space is already covered by a chip or not). Of course, handling rectangles quickly found application in geographical and, in general, spatial data, including GIS (buildings, rivers, cities etc.), image or video/audio retrieval systems (similarity of objects either in original space or in high-dimensional feature space), time series and chronological databases (time intervals are just 1D objects), and so on. Therefore, we argue that R-trees are found everywhere.

This survey aims at summarizing the literature relevant to R-trees. The structure of the paper is as follows. In Section 2, we present the original R-tree structure and its variants. The number of the R-tree variants is quite large and, therefore, we examine them in several subsections, having in mind the special characteristics of the assumed environment or application. In Section 3, query processing issues are presented by focusing on new types of queries, such as topological, directional and distance operators. Section 4 presents work on query optimization, including analytical cost models and histogram-based optimization techniques. The next section describes implementation issues concerning R-trees, such as parallelism and concurrency control, and summarizes what is known from the literature about prototype and commercial systems that have implemented them. The last section concludes the survey.

2. THE FAMILY TREE OF R-TREES

The survey by Gaede and Guenther [47] annotates a vast list of citations related to multidimensional access methods and, in particular, refers to R-trees to a significant extent. In the present survey, we are further focusing in the family of R-trees by enlightening the similarities and differences, the advantages and disadvantages of the various variations in a more exhaustive manner. Since the numbers of variants that have appeared in the literature is large, we group them according to the special characteristics of the assumed environment or application and examine the members of each group in chronological order.

2.1 Dynamic Versions of R-trees

In this subsection, we present dynamic versions of the R-tree, where the objects are inserted on a one-by-one basis, as opposed to the case where a special packing technique can be applied to insert an apriori known static set of objects into the structure by optimizing the storage overhead and the retrieval performance. The latter case will be examined in the next subsection. In simple words, here we focus in the way that dynamic insertions and splits are performed in assorted R-tree variants.

2.1.1 *The Original R-tree.* Although, nowadays the original R-tree is being described in many standard textbooks and monographs on databases [88; 101; 146; 147], we briefly recall its basic properties. R-trees are hierarchical data structures based on B^+-trees. They are used for the dynamic organization of a set of d-dimensional geometric objects representing them by the minimum bounding

d-dimensional rectangles (for simplicity, MBRs in the sequel). Each node of the R-tree corresponds to the minimum MBR that bounds its children. The leaves of the tree contain pointers to the database objects, instead of pointers to children nodes. The nodes are implemented as disk pages.

It must be noted that the MBRs that surround different nodes may be overlapping. Besides, an MBR can be included (in the geometrical sense) in many nodes, but can be associated to only one of them. This means that a spatial search may visit many nodes, before confirming the existence or not of a given MBR.

The rules obeyed by the R-tree are as follows. Leaves reside on the same level. Each leaf contains pairs of the form (R, O), such that R is the MBR that contains spatially object O. Every other node contains pairs of the form (R, P), where P is a pointer to a child of the node and R is the MBR that contains spatially the MBRs contained in this child. Every node (with the possible exception of the root) of an R-tree of class (m, M) contains between m and M pairs, where $m \leq \lceil M/2 \rceil$. The root contains at least two pairs, if it is not a leaf. Figure 1 depicts some objects on the left and the corresponding R-tree on the right. Data rectangles R_1 through R_9 are stored in leaf nodes, whereas MBRs R_a, R_b and R_c are hosted in intermediate nodes.

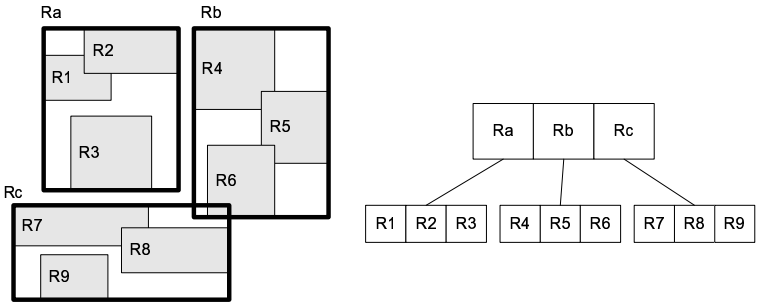


Fig. 1. An R-tree example.

Insertions of new objects are directed to leaf nodes. At each level, the node that will be least enlarged is chosen. Thus, finally the object is inserted in an existing leaf if there is adequate space, otherwise a split takes place. The minimization of the sum of the areas of the two resulting nodes being the driving criterion, Guttman proposed three alternative algorithms to handle splits, which are of linear, quadratic and exponential complexity:

Linear. Choose two objects as seeds for the two nodes, where these objects are as furthest as possible. Then, consider each remaining object in a random order and assign it to the node requiring the smaller enlargement of its respective MBR.

Quadratic. Choose two objects as seeds for the two nodes, where these objects if put together create as much dead space as possible (dead space is the space that remains from the MBR if the areas of the two objects are ignored). Then, until there are no remaining objects, choose for insertion the object for which the difference of dead space if assigned to each of the two nodes is maximized, and insert it in the node that requires smaller enlargement of its respective MBR.

Exponential. All possible groupings are exhaustively tested and the best is chosen with respect to the minimization of the MBR enlargement.

Guttman suggested using the quadratic algorithm as a good compromise to achieve reasonable retrieval performance.

In all R-tree variants that have appeared in the literature, tree traversals for any kind of operations are executed in exactly the same way as in the original R-tree (see next section). Basically, the variations of R-trees differ in the way they perform splits during insertions by considering different minimization criteria instead of the sum of the areas of the two resulting nodes. Therefore, in the sequel, we present and annotate them according to their chronological order of appearance.

2.1.2 *The R^+-tree.* R^+-trees were proposed as a structure that avoids visiting multiple paths during point queries and, thus, the retrieval performance could be improved [160; 152]. This is achieved by using the clipping technique. In simple words, R^+-trees do not allow overlapping of MBRS at the same tree level. In turn, to achieve this, inserted objects have to be divided in two or more MBRs, which means that a specific object's entries may be duplicated and redundantly stored in various nodes. Therefore, this redundancy works in the opposite direction of decreasing the retrieval performance in case of window queries. At the same time, another side effect of clipping is that during insertions, an MBR augmentation may lead to a series of update operations in a chain-reaction type. Also, under certain circumstances, the structure may lead to a deadlock, as, for example, when a split has to take place at a node with $M+1$ rectangles, where every rectangle encloses a smaller one. An R^+-tree for the same dataset illustrated in Figure 1, is presented in Figure 2.

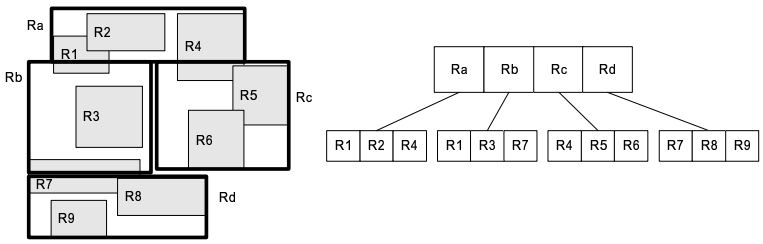


Fig. 2. An R^+-tree example.

2.1.3 *The R^*-tree.* Although proposed in 1990 [12], R^*-trees are still very well received and widely accepted in the literature as a prevailing performance-wise structure that is often used as a basis for performance comparisons. The R^*-tree does not obey the limitation for the number of pairs per node and follows a sophisticated node split technique. More specifically, the technique of 'forced reinsertion' is applied, according to which, when a node overflows, p entries are extracted and reinserted in the tree (p being a parameter, with 30% a suggested optimal value). Other novel features of R^*-trees is that it takes into account additional criteria except the minimization of the sum of the areas of the produced MBRs. The benefit from involving these criteria will be made clear later, in Section 4, where the

performance of the R*-tree will be analyzed. These criteria are the minimization of the overlapping between MBRs at the same level, as well as the minimization of the perimeter of the produced MBRs. The benefits from considering these criteria will be made clear in Section 4, where the R*-tree performance will be analyzed. Conclusively, the R*-tree insertion algorithm is quite improving in comparison to that of the original R-tree and, thus, improves the latter structure considerable as far as retrievals are concerned (up to 50%). Evidently, the insertion operation is not for free as it is CPU demanding since it applies a plane-sweep algorithm.

2.1.4 *Hilbert R-tree.* The Hilbert R-tree is a hybrid structure based on R-trees and B^+-trees [77]. Actually, it is a B^+-tree with geometrical objects being characterized by the Hilbert value of their centroid. Thus, leaves and internal nodes are augmented by the largest Hilbert value of their contained objects or their descendants, respectively. For an insertion of a new object, at each level the Hilbert values of the alternative nodes are checked and the smallest one that is larger than the Hilbert value of the object under insertion is followed. In addition, another heuristic used in case of overflow by Hilbert R-trees is the redistribution of objects in sibling nodes. In other words, in such a case up to s siblings are checked in order to find available space and absorb the new object. A split takes place only if all s siblings are full and, thus, $s+1$ nodes are produced. This heuristic is similar to that applied in B*-trees, where redistribution and 2-to-3 splits are performed during node overflows [78]. According to the authors' experimentation, Hilbert R-trees were proven to be the best dynamic version of R-trees as of the time of publication. However, this variant is vulnerable performance-wise to large objects.

2.1.5 *Linear Node Splitting.* Ang and Tan in [7] have proposed a linear algorithm to distribute the objects of an overflowing node in two sets. The primary criterion of this algorithm is to distribute the objects between the two nodes as evenly as possible, whereas the second criterion is the minimization of the overlapping between them. Finally, the third criterion is the minimization of the total coverage. Experiments using this algorithm have shown that it results in R-trees with better characteristics and better performance for window queries in comparison with the quadratic algorithm of the original R-tree.

2.1.6 *Optimal Node Splitting.* Garcia, Lopez and Leutenegger elaborated the optimal exponential algorithm of Guttman and reached a new optimal polynomial algorithm $O(n^d)$, where d is the space dimensionality [49]. In the same paper, the authors give another insertion heuristic, which is called 'sibling-shift'. In particular, the objects of an overflowing node are optimally separated in two sets. Then, one set is stored in the specific node, whereas the other set is inserted in a sibling node that will depict the minimum increase of an objective function (e.g., expected number of disk access). If the latter node can accommodate the specific set, then the algorithm terminates. Otherwise, in a recursive manner the latter node is split. Finally, the process terminates when either a sibling absorbs the insertion or this is not possible, in which case a new node is created to store the pending set. The authors reported that the combined use of the optimal partitioning algorithm and the sibling-shift policy improves the index quality (i.e., node utilization) and the retrieval performance in comparison to the Hilbert R-trees, at the cost of increased

insertion time.

2.1.7 *Branch Grafting.* More recently, in [150] an insertion heuristic is proposed to improve the shape of the R-tree so that the tree achieves a more elegant shape, with a smaller number of nodes and better storage utilization. In particular, when a node overflows, then its father content is checked whether a sibling node with overlapping MBR could accommodate any of the objects of the node in question. This technique is called *branch grafting* and could be considered as an eager method handling overflows locally at a reasonable cost, whereas forced reinsertion could be viewed as a lazy approach with higher costs whenever applied. The comparison regards only various storage utilization parameters and not query processing efficiency.

2.1.8 *Compact R-trees.* Huang et al. proposed 'compact R-trees', a dynamic R-tree version with optimal space overhead [68]. Among the $M+1$ entries of an overflowing node during insertions, a set of M entries is selected to remain in this node, under the constraint that the resulting MBR is the minimum possible. Then, the remaining entry is inserted to a sibling that (i) has available space, and (ii) its MBR is enlarged the minimum possible. Thus, a split takes place only if there is not available space in any sibling. The heuristic is quite simple to implement, it results in storage utilization in the area of 97-99% (as opposed to 70% of the original R-tree) at no extra insertion overhead, whereas the window query performance is similar to that of the original R-tree.

2.1.9 *cR-trees.* Lastly, Brakatsoulas et al. have altered the assumption that an overflowing node has to necessarily be split in exactly two nodes [22]. In particular, they relied on the k-means clustering algorithm and assumed that an overflowing node can be split up to k nodes ($k \geq 2$ being a parameter). Their experimentation showed that the resulting index quality, the retrieval performance and the insertion time are significantly better that those of R-trees (assuming quadratic split) and similar to those of R*-trees.

2.1.10 *Deviating Variations.* Finally, other interesting variants have been proposed, which, however, in some sense deviate drastically from the original idea of R-trees. Among other efforts, we note the following works. The Sphere trees by Oosterom use minimum bounding spheres instead of MBRs [113], whereas the Cell trees by Guenther use minimum bounding polygons designed to accommodate arbitrary shape objects [52]. The Cell tree is a clipping-based structure and, thus, a variant of Cell trees has been proposed to overcome the disadvantages of clipping. The latter variant uses 'oversize shelves', i.e., special nodes attached to internal ones, which contain objects that normally should cause considerable splits [53; 54]. Similarly to Cell trees, Jagadish and Schiwietz proposed independently the structure of Polyhedral trees or P-trees, which use minimum bounding polygons instead of MBRs [70; 148]. The X-tree by Berchtold et al. uses the notion of 'supernodes' (i.e., nodes of greater size) to handle overflows and avoid splits [15]. The S-tree by Aggrawal et al. relaxes the rule that the R-tree is a balanced structure and may have leaves at different tree levels [3]. However, S-trees are static structures in the sense that they demand the data to be known in advance. Another recent effort by

Ang and Tan is the Bitmap R-tree [8], where each node contains bitmap descriptions of the internal and external object regions except the MBRs of the objects. Thus, the extra space demand is paid off by savings in retrieval performance due to better tree pruning. The same trade-off holds for the RS-tree, which is proposed by Park at al. [133] and connects an R*-tree with a signature tree with an one-to-one node correspondence. Agarwal et al. [4] proposed the Box-tree, that is, a bounding-volume hierarchy that uses axis-aligned boxes as bounding volumes. They provide worst-case lower bounds on query complexity, showing that box-trees are close to optimal, and they present algorithms to convert box-trees to R-trees, resulting in R-trees with (almost) optimal query complexity. Lee and Chung [89] developed the DR-tree, which is a main memory structure for multi-dimensional objects. They couple the R*-tree with this structure to improve the spatial query performance. Finally, Bozanis et al. have partitioned the R-tree in a number of smaller R-trees [21], along the lines of the binomial queues that are an efficient variation of heaps.

2.2 Static Versions of R-trees

There are common applications that use static data. For instance, insertions and deletions in census, cartographic and environmental databases are rare or even they are not performed at all. For such applications, special attention should be paid in order to construct an optimal structure with regards to some tree characteristics, such as storage overhead minimization, storage utilization maximization, minimization of overlap or cover between tree nodes, or combinations of the above. Therefore, it is anticipated that query processing performance will be improved. These methods are well known in the literature as 'packing' or 'bulk loading'. Thus, next we examine such methods that require the data to be known in advance.

2.2.1 *The Packed R-tree.* The first packing algorithm was proposed by Roussopoulos and Leifker in 1985, soon after the proposal of the original R-tree [141]. This first effort basically suggests ordering the objects according to some spatial criterion (e.g., according to ascending x-coordinate) and then grouping them in leaf pages. No experimental work is presented to compare the performance of this method to that of the original R-tree. However, based on this simple inspiration a number of other efforts have been proposed later in the literature.

2.2.2 *The Hilbert Packed R-tree.* Kamel and Faloutsos proposed an elaborated method to construct a static R-tree with 100% storage utilization [76]. In particular, among other heuristics they proposed sorting the objects according to the Hilbert value of their centroids and then build the tree in a bottom-up manner. Experiments showed that the latter method achieves significantly better performance than the original R-tree with quadratic split, the R*-tree and the Packed R-tree by Roussopoulos and Leifker in point and window queries. Moreover, Kamel and Faloutsos proposed a formula to estimate the average number of node access, which is independent of the details of the R-tree maintenance algorithms and can be applied to any R-tree variant.

2.2.3 *The STR R-tree.* STR (Sort-Tile-Recursive) is a bulk-loading algorithm for R-trees proposed by Leutenegger et al. in [91]. Let N be a number of rectangles in two-dimensional space. The basic idea of the method is to tile the address space

by using S vertical slices, so that each slice contains enough rectangles to create approximately $\sqrt{N/C}$ nodes, where C is the R-tree node capacity. Initially, the number of leaf nodes is determined, which is $P = \lceil N/C \rceil$. Let $S = \sqrt{P}$. The rectangles are sorted with respect to the x coordinate of the centroids, and S slices are created. Each slice contains $S \cdot C$ rectangles, which are consecutive in the sorted list. In each slice, the objects are sorted by the y coordinate of the centroids and are packed into nodes (placing C objects in a node). The method is applied until all R-tree levels are formulated. The STR method is easily applicable to high dimensionalities. Experimental evaluation performed in [91] has demonstrated that the STR method is generally better than previously proposed bulk-loading methods. However, in some cases the Hilbert packing approach performs marginally better. It has to be noticed that Garcia et al. [50] proposed an R-tree node restructuring algorithm for post-optimizing existing R-trees and improving dynamic insertions, which incurs an optimization cost equal to that of STR. The resulting R-tree outperforms dynamic R-tree versions, like the Hilbert R-tree, with only a small additional cost during insertions. Moreover, an analytical model to predict the number of disk accesses for buffer management is described by Leutenegger and Lopez [90], which evaluates the quality of packing algorithms measured by query performance of the resulting tree.

2.2.4 *Top-Down Greedy Split.* Unlike the aforementioned packing algorithms that build the tree bottom-up, the top-down greedy-split (TGS) method [48] constructs the R-tree in a top-down manner. TGS recursively applies a splitting process that partitions a set of N rectangles into two subsets by applying an orthogonal cut to a selected axis. This process must satisfy the following conditions: 1) the value of an objective function should be minimized, 2) one subset has a cardinality $i \cdot S$ for some i so that the resulting subtrees are packed. The method is recursively applied to both subsets. The objective function has the form $f(r_1, r_2)$, where r_1, r_2 are the MBRs of the two subsets produced. The performance evaluation of the method reported in [48] has demonstrated that the TGS approach is generally better than previously proposed packing algorithms.

2.2.5 *Small-Tree-Large-Tree and GBI.* The previous packing algorithms build an R-tree access method from a set of spatial objects. The small-tree-large-tree method (STLT) [32] performs efficient bulk insertions into an existing R-tree structure. Let R be a set of spatial objects indexed by an already existing R-tree and N a set of new objects that must be inserted. Instead of inserting the objects in the R-tree one-by-one, the STLT method constructs a small R-tree for N and then inserts the small R-tree into the large R-tree. Obviously, the efficiency of the resulting index depends on the data distribution of the small R-tree. If the objects in N cover a large part of the data space, then using the STLT approach will result in increasing overlap in the resulting index. Therefore, the method is best suited for skewed data distributions. STLT is extended in [34], where the Generalized R-tree Bulk-Insertion Strategy (GBI) is proposed. GBI inserts new incoming data sets into active R-trees as follows: it first partitions the data sets into a set of clusters and outliers, then it constructs a small R-tree for each cluster, finding suitable places in the original R-tree to insert the newly created R-trees, and finally it bulk-inserts

the new R-trees and the outliers in the original R-tree.

2.2.6 *Buffer R-tree.* Arge et al. [11] proposed the Buffer R-tree (BR) for performing bulk update and queries. BR is based on the buffer tree lazy buffering technique and exploits the available main memory. Analytical results in [11] show the efficiency of BR, whereas experimental results illustrates its superiority over the the other methods. BR requires smaller execution times to perform bulk updates and produces a better quality index in terms of query performance. Moreover, BR (differently from other methods) allows for simultaneous batch updates and queries.

2.2.7 *R-tree with low stabbing number.* deBerg et al. [40] have proposed an R-tree construction algorithm from a given set of spatial objects (focus is on not very high dimensionality), and they prove that the resulting R-tree has good query complexity for point and range queries with ranges of small width. Their analysis is based on the stabbing number, i.e., the number of rectangles containing a given point. The produced bounds are optimal for certain special cases. Nevertheless, no comparison is performed against other methods.

2.3 Spatiotemporal R-tree Variants

Spatiotemporal access methods (STAMs) provide the necessary tools to query spatiotemporal data. A large number of the proposed methods are based on the well known R-tree structure. In the sequel, we introduce a number of STAMs and query processing techniques related to spatiotemporal applications, such as bitemporal spatial applications, trajectory monitoring, and moving objects. All the presented methods are based on the concept of the R-tree.

2.3.1 *3D R-trees.* The 3D R-tree, proposed in [168], considers time as an extra dimension and represents 2D rectangles with time intervals as three-dimensional boxes. This tree can be the original R-tree [57] or any of its (ephemeral) variants.

The 3D R-tree approach assumes that both ends of the interval $[t_1, t_2)$ of each rectangle are known and fixed. If the end time t_2 is not known, this approach does not work well. For instance, assume that an object extends from some fixed time until the current time, *now* (refer to [35] for a thorough discussion on the notion of *now*). One approach is to represent *now* by a time instance sufficiently far in the future. This leads to excessive boxes and consequent poor performance. Standard spatial access methods (SAMs), such as the R-tree and its variants, are not well suited to handle such 'open' and expanding objects. One special case where this problem can be overcome is when all movements are known a priori. This would cause only 'closed' objects to be entries of the R-tree.

The 3D R-tree was implemented and evaluated analytically and experimentally [168; 171], and it was compared with the alternative solution of maintaining a spatial index (e.g., a 2D R-tree) and a temporal index (e.g., a 1D R-tree or a segment tree). Synthetic (uniform-like) datasets were used, and the retrieval costs for pure temporal (during, before), pure spatial (overlap, above), and spatiotemporal operators (the four combinations) were measured. The results suggest that the unified scheme of a single 3D R-tree is obviously superior when spatiotemporal queries are posed, whereas for mixed workloads, the decision depends on the selectivity of the operators.

2.3.2 *The 2+3 R-tree.* One possible solution to the problem of 'open' geometries is to maintain a pair of two R-trees [108]:

—a 2D R-tree that stores two-dimensional entries that represent current (spatial) information about data, and
—a 3D R-tree that stores three-dimensional entries that represent past (spatiotemporal) information; hence the name 2+3 R-tree.

The 2+3 R-tree approach is a variation of an original idea proposed in [86] in the context of bitemporal databases, and which was later generalized to accommodate more general bitemporal data [19; 18].

As long as the end time t_2 of an object interval is unknown, it is indexed by the (2D) *front* R-tree, keeping the start time t_1 of its position along with its ID. When t_2 becomes known, then:

—the associated entry is migrated from the front R-tree to the (3D) *back* R-tree, and
—a new entry storing the updated current location is inserted into the front R-tree.

Should one know all object movements a priori, the front R-tree would not be used at all, and the 2+3 R-tree reduces to the 3D R-tree presented earlier. It is also important to note that both trees may need to be searched, depending on the time instance related to the posed queries.

2.3.3 *The Historical R-tree.* Historical R-trees (HR-trees, for short) have been proposed in [107], implemented and evaluated in [108] and improved recently in [163]. This STAM is based on the overlapping technique. In the HR-tree, conceptually a new R-tree is created each time an update occurs. Obviously, it is not practical to physically keep an entire R-tree for each update. Because an update is localized, most of the indexed data and thus the index remain unchanged across an update. Consequently, an R-tree and its successor are likely to have many identical nodes. The HR-tree exploits this and represents all R-trees only logically. As such, the HR-tree can be viewed as an acyclic graph, rather than as a collection of independent tree structures.

With the aid of an array pointing to the root of the underlying R-trees, one can easily access the desired R-tree when performing a timeslice query. In fact, once the root node of the desired R-tree for the time instance specified in the query is obtained, the query processing cost is the same as if all R-trees where kept physically.

The concept of overlapping trees is simple to understand and implement. Moreover, when the number of objects that change location in space is relatively small, this approach is space efficient. However, if the number of moving objects from one time instance to another is large, this approach degenerates to independent tree structures, since no common paths are likely to be found.

2.3.4 *The R^{ST}-tree.* The R^{ST}-tree [144] is capable of indexing spatio-bitemporal data with discretely changing spatial extents. In contrast to the indexing structures described previously, the R^{ST}-tree supports data that has two temporal dimensions and two spatial dimensions. The *valid time* of data is the time(s)—past, present, or future—when the data is true in the modeled reality, while the *transaction time*

of data is the time(s) when the data was or is current in the database [71; 158]. Data for which both valid and transaction time is captured is termed *bitemporal*.

2.3.5 *The MV3R-tree.* To overcome the shortcomings of the 3D R-tree and the HR-tree, Tao and Papadias [164] proposed the MV3R-tree, consisting of a multi-version R-tree and small auxiliary 3D R-tree built on the leaves of the former. Through extensive experimentation, the MV3R-tree turned out to be efficient in both timestamp and interval queries with relatively small space requirements.

2.3.6 *The Partially Persistent R-tree.* Kollios et al. in [79] recently proposed the partially-persistent R-tree (PPR-tree), actually a directed acyclic graph of nodes with a number of root nodes, where each root is responsible for recording a subsequent part of the ephemeral R-tree evolution. The disadvantage of both indexing techniques is that space requirements become prohibitive for agile datasets.

2.3.7 *The TB-tree.* The TB-tree (Trajectory Bundle) [136] relaxes a fundamental R-tree property, i.e., keeping neighboring entries together in a node, and strictly preserves trajectories such that a leaf node only contains segments belonging to the same trajectory. This is achieved by giving up on space discrimination. The TB-tree indexes past locations of objects and supports continuous changes.

2.3.8 *The Time-Parameterized R-tree.* The aforementioned access methods focus on providing access paths to present or past values of objects. An access method that is based on the R-tree structure and provides access to present and future values is the Time-Parameterized R-tree [145]. This method is based on the concept of non-static MBRs of leaf and internal nodes. In other words, the MBR of an object or a tree node is a function of time. It is assumed that the velocity vector of each object is known. Based on the last location of the object and its velocity vector, one can determine the current object position in space. One basic characteristic of the TPR-tree structure is that the covering MBRs of the internal nodes are rarely minimum (although they are conservative). In a recent work [138] an efficient variation of the TPR-tree has been proposed that eliminates some basic disadvantages of the structure and shows better performance in query processing.

2.4 R-trees in OLAP, Data Warehouses and Data Mining

R-trees have not been used only for storing and processing spatial or spatiotemporal data. Modifications to the R-tree structure have been also proposed in order to handle queries in OLAP applications, Data Warehouses and Data Mining.

Variations for OLAP and Data Warehouses store summary information in internal nodes, and therefore in many cases it is not necessary to search lower tree levels. Examples of such queries are window aggregate queries, where parts of the dataspace are requested that satisfy certain aggregate constraints. Nodes totally contained by the query window do not have to be accessed. One of the first efforts in this context was the variant of Ra*-tree, which has been proposed for efficient processing of window aggregate queries, where summarized data are stored in internal nodes in addition to the MBR [74]. The same technique has been used in [123] in the case of spatial data warehouses. In [165] the aP-tree has been introduced in order to process aggregate queries on planar point data. Finally, in [124] a combination of aggregate R-trees and B-trees has been proposed for spatiotemporal data

warehouse indexing.

Recently, R-trees have been also used in the context of Data Mining. In particular, Spatial Data Mining systems [58] include methods that gradually refine spatial predicates, based on indexes like the R-tree, to derive spatial patterns, e.g., spatial association rules [80]. Nanopoulos et al. [109], based on the R-tree structure and the closest-pairs query, developed the C^2P algorithm for efficient clustering, whereas [110] proposed a density biased sampling algorithm from R-trees, which performs effective pre-processing to clustering algorithms.

3. QUERY PROCESSING

The processing of spatial queries presents significant requirements, due to the large volumes of spatial data and the complexity of both objects and queries [115] Efficient processing of spatial queries capitalize on the proximity of the objects, achieved by the R-tree, so as to focus the searching on objects that satisfy the queries.

Besides efficiency, one of the main reasons for the popularity of R-tree indexes stems from their versatility, since they can efficiently support many types of spatial operators. The most common types of operators are: a) Topological (e.g., find all objects that overlap or cover a given object), b) Directional (e.g., find all objects that lie north of a given object), c) Distance (e.g., find all objects that lie in less than a given distance from a given object). These operators comprise basic primitives for developing more complex ones in applications that are based on management of spatial data, such as GIS, cartography and many others.

As described, the R-tree abstracts object with complex shapes (polygons, polygons with holes, etc) by using their MBR approximations. To answer queries containing the aforementioned operators, a two-step procedure is followed [24]: (i) Filter step: the collection of all objects whose MBRs satisfy the given query is found, which comprises the *candidate set*. (ii) Refinement step: The actual geometry of each member of the candidate set is examined to eliminate false hits and to find the answer to the query. The two steps are illustrated in Figure 3. In general, the filter step cannot determine the inclusion of an object in the query result. Nevertheless, there are few operators (mostly directional ones) that allow for finding query results from the filter step also. This is shown in Figure 3 by the existence of hits (i.e., answers to the query) in the filter step.

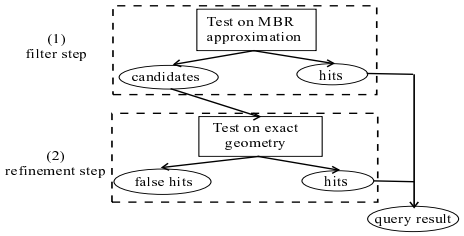


Fig. 3. Two-step query processing procedure.

In the following, we will describe in more detail the query processing techniques that have been developed for each query type. Since the refinement step is orthogonal to the filtering step, the developed techniques have mainly focused on the latter. More details on representations different from the MBR, and their impact on the refinement step can be found in [25].

3.1 Range and Topological Queries

The most common operation with an R-tree index is a range query, that is, the finding of all objects that a query region intersects. In many cases the query region is a rectangle and the query is called window query. The processing of a range/window query is defined in [57]. It commences from the root node of the tree. For each entry whose MBR intersects the query region, the process descends to the corresponding subtree. At the leaf level, for each object bounding rectangle that intersects the query region, the corresponding object is examined (refinement step). Also, it has to be mentioned that point queries (i.e., find all objects that contain a query point) can also be treated as a range query, since the query point can be considered as a degenerated rectangle. In [128] the case of combining the execution of several range queries in order to achieve better overall performance was considered.

The intersection operator, which is examined by the range query, can be considered a special case of a more detailed retrieval of topological relations. Papadias et al. [120] developed a systematic description of the topological information that MBRs convey about the corresponding spatial objects, and proposed an algorithm to minimize the I/O cost of topological queries, that is, queries that involve topological relations. In particular, the intersection test of the range query corresponds to the *disjoint* or *non disjoint* condition between the indexed objects (called primary objects, i.e., those contained in the R-tree) and the query object (called reference object). Although the *disjoint* relation is left unchanged, the *non disjoint* relation is refined further with the following relations: *meet*, *equal*, *overlap*, *contains* and *covers*. Figure 4 depicts all possible relations between two objects.

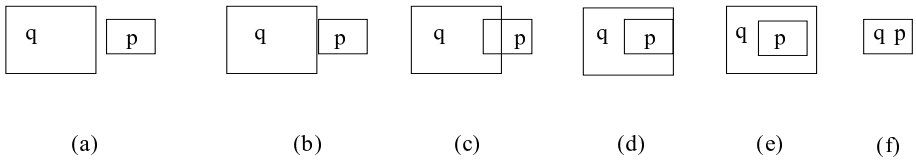


Fig. 4. Topological relations: a) disjoint(q, p), b) meet(q, p), c) overlap(q, p), d) covers(q, p), e) contains(q, p) or inside(p, q), f) equal(q, p).

The topological relation between two MBRs does not necessarily coincide with the topological relations between the two corresponding objects, because MBRs are approximate representations. Therefore, given two objects, the corresponding MBRs satisfy, in general, a number of possible relations [120]. In order to perform a topological query with an R-tree, [120] defines the more general relations that will be used for downwards propagation at the intermediate nodes. For convenience, we denote the aforementioned approach as PTSE (from the names of the authors).

Experimental results in [120] indicate that the topological relations can be divided in three categories, with respect to the incurred I/O cost. The first category contains relation *disjoint*, which requires the larger cost (almost equal to the scanning of the entire R-tree contents), the second contains relations *meet*, *overlap*, *inside* and *covered by*, which require medium cost, and the third the relations *equal*, *cover*, *contains*, which require small cost. Compared to the straightforward case where a range query is first executed and then the topological relations are examined only at the refinement step, the approach of [120] shows an improvement of up to 60%.

3.2 Directional Queries

R-trees have been also used to answer queries involving directional information (left, above, north etc.). Papadias et al. [119] discussed relations between points (e.g. north) and relations between non-point objects approximated by their MBRs (e.g., strong-north, weak-north) and provided a methodology to support these types of queries when objects' MBRs are indexed by an R-tree. The methodology includes two steps:

(1) all node rectangles that could include hits are detected based on a direction relation, possibly different from the target relation,
(2) the candidate hits are accessed based on another direction relation.

As in the case of topological queries, the above procedure that involves MBRs only composes the filter step, while actual hits are detected during the refinement step, which involves the exact geometry of objects. Consider the following example: assume we ask for objects p weak-north of an object q; each object p is approximated by its MBR p' and each rectangle r is defined by its lower-left corner r_l and its upper right corner r_u. The R-tree nodes P that might include hits are those that fulfill the following constraint: P_u north of q'_u and P_l south of q'_u. Respectively, candidate hits p' are those that fulfill the following constraint: p'_u north of q'_u and p'_l north of q'_l and p'_l south of q'_u. Following the same strategy, [119] supported a number of directional queries and showed through experiments their performance.

3.3 Nearest Neighbor Queries

The problem of answering k nearest-neighbor (NN) queries using R-trees has been introduced by Roussopoulos et al. [142]. This approach is based on metrics that measure the optimistic and pessimistic distances between the R-tree contents and the query point[1]. Given a query point P and an object O that is represented by its MBR, [142] describes two metrics. The first is called MINDIST and corresponds to the minimum possible distance of P from O. The second is called MINMAXDIST and corresponds to the minimum of the maximum possible distances from P to a vertex of O's MBR. These two metrics comprise a lower and an upper bound on the actual distance of O from P, respectively. More specifically, MINDIST(P, R) is the distance from P to the closest point on the boundary of R, which does not necessarily have to be a corner point. MINMAXDIST(P, R) is the distance from P to the closest corner of R that is adjacent (i.e., connected with an edge of R) to the

[1]The NN query can be also extended to non-point objects, by providing appropriate distance measures. See [63] for more details.

corner that is farthest from P. Figure 5 illustrates an example of the MINDIST and MINMAXDIST metrics between a two-dimensional query point P and three MBRs (for the rectangle that includes P, MINDIST is equal to 0).

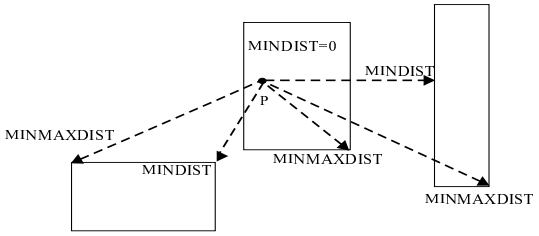


Fig. 5. Example of MINDIST and MINMAXDIST.

In [142], a branch-and-bound R-tree traversal algorithm is presented that uses the aforementioned metrics to order and prune the search tree. The search ordering determines the node visits during the tree traversal. As described in [142], MINDIST produces more optimistic ordering than MINMAXDIST, but there may exist cases of data sets (depending on the sizes and the layouts of MBRs) where the latter produces less costly traversals. For a query point P, the pruning of node visits during the searching is performed according to the following heuristics. The complete algorithm for finding the 1st NN is presented in Figure 6. [2]

(1) An MBR M with MINDIST(P, M) greater than the MINMAXDIST(P, M') of another MBR M', is discarded because it cannot contain the NN. This is used in *downward pruning*.
(2) An actual distance from P to a given object O, which is greater than the MINMAXDIST(P, M) for an MBR M, can be discarded because M contains an object O' that is nearer to P. This is also used in *downward pruning*.
(3) Every MBR M with MINDIST(P, M) greater than the actual distance from P to a given object O is discarded because it cannot enclose an object nearer than O. This is used in *upward pruning*.

Cheung and Fu [33] have observed that a more efficient version of the aforementioned branch-and-bound algorithm can be derived on the basis that pruning with respect to the number of node accesses is considered. It is based on the observation that only the third pruning heuristic is necessary to maintain the same number of pruned nodes. (This observation was independently made also by [63].) However, this pruning heuristic has to be applied in a different position, thus resulting to a modified NN search algorithm, which we denote as MN. For these reasons, the NNSearch procedure of Figure 6 is modified by removing step 12 (which applies the first and second pruning heuristics) and by repositioning of step 3 (third pruning heuristic) before the recursive application of step 15. Thus, the for-loop of steps 13–17 is given in Figure 7.

[2]For finding k-NN ($k > 1$), the previous procedure can be easily modified so as to maintain the current k most closest objects and by pruning with respect to the furthest object each time.

```
Procedure NNSearch(Node, Point, Nearest)
1.  if Node.type == LEAF
2.      for i=1 to Node.count
3.          dist = objectDIST(Point, Node.branch[i].rect)
4.          if dist < Nearest.dist
5.              Nearest.dist = dist
6.              Nearest.rect = Node.branch[i].rect
7.          endif
8.      endfor
9.  else
10.     genBranchList(branchList)
11.     sortBranchList(branchList)
12.     last = pruneBranchList(Node, Point, Nearest, branchList)
13.     for i = 1 to last
14.         newNode = Node.branch[branchList[i]]
15.         NNSearch(newNode, Point, Nearest)
16.         last = pruneBranchList(Node, Point, Nearest, branchList)
17.     endfor
18. endif
19. end
```

Fig. 6. Nearest Neighbor Search Algorithm.

```
13.     for i = 1 to last
14.         Apply Pruning Heuristic 3
15.         newNode = Node.branch[branchList[i]]
16.         NNSearch(newNode, Point, Nearest)
17.     endfor
```

Fig. 7. Modification in the NNSearch.

Finally, it has to be noticed that Belussi et al. [14] have proposed a nearest-neighbor algorithm for the R^+-tree variant. Their method considers information on the reference space to improve the search. The resulting data structure integrates the R^+-tree with a regular grid, indexed by using a hashing technique, combining the advantages of the rectangular space decomposition attained by R^+-trees, with a direct access attained by hashing.

3.4 Incremental Nearest Neighbor Queries

Hjaltason and Samet [63] presented the problem of incremental NN searching with an R-tree. Incremental NN queries find the data objects in their order of distance from the query object (*ranking*). For instance, let a set of cities C and the query: 'find the nearest city to $q \in C$ whose population is larger than 1 million people'. By obtaining the neighbors incrementally, they can be examined against the specified criterion. This operation is defined as *distance browsing* [63]. It has to be noticed that it is different from searching for a prespecified k, because k cannot be known in advance.

The algorithm for incremental NN searching is based on maintaining the set of nodes to be visited in a priority queue (for the case of skewed and high-dimensional data, [63] proposes that the queue should be divided in several tiers, one of which remains in main memory and the others on secondary storage). The entries in the queue are sorted according to the MINDIST metric. It is assumed that the actual objects (e.g., polygons) are stored separately in the data level, as long as each object is completely contained by its corresponding bounding rectangle. Thus, at the leaf-level of the R-tree the object bounding rectangles (i.e., the MBRs of the data objects) can advocate pruning. (In the following, the bounding rectangle of an object O is denoted as $[O]$.) The algorithm is depicted in Figure 8.

```
Procedure IncNNSearch(q)
1.  enqueue(PriorityQueue, root's children)
2.  while PriorityQueue not empty
3.      element ← dequeue(PriorityQueue)
4.      if element is an object O or an object bounding rectangle [O]
5.          if element == [O] and not PriorityQueue empty
              and objectDist(q, O) > First(PriorityQueue).key
6.              enqueue(PriorityQueue, O, objectDist(q, O)
7.          else
8.              Output element  /*or if element is bounding rectangle, the associated object*/
9.          endif
10.     else if element is leaf node
11.         foreach object bounding rectangle [O] in element
12.             enqueue(PriorityQueue, [O], dist(q, [O])
13.         endfor
14.     else  /*non-leaf node*/
15.         foreach entry e in element
16.             enqueue(PriorityQueue, e, dist(q, e)
17.         endfor
18.     endif
19. endwhile
20. end
```

Fig. 8. Optimal Nearest Neighbor Search Algorithm.

For the analysis of the incremental NN searching algorithm, [63] makes the key observation that any algorithm for the R-tree must visit all the nodes that intersect the search region, and notices that the incremental algorithm visits exactly these nodes. Based on the assumption of low dimensionality and uniform data distribution, it is proven in [63] that the expected number of leaf node accesses for k-NN processing is $O(k + \sqrt{k})$.

Evidently, the incremental NN search algorithm can be applied to the problem of finding the k NNs (for a specified k), since it can terminate after having found the first k neighbors. For this case, however, the approach of [63] differs from [142]. The branch-and-bound algorithm of Section 3.3 traverses the index in a depth-first fashion. Once a node is visited, its processing has to be completed even if other (sibling) nodes are more probable to contain the NN object; thus at each step only

local decisions can be made [63]. In contrast, the described algorithm in [63] makes global decisions by using the priority queue to maintain the nodes that are going to be visited, and chooses among the child nodes of all nodes that have been visited, instead of the current one. Thus, it uses a best-first traversal of the tree, and prunes the visiting to nodes according to the third pruning heuristic. This approach has the characteristic of optimality with respect to the number of R-tree node visits, however not to the NN problem itself. (Interestingly enough, [16] have described an analogous k-NN searching algorithm that is based on the approach of [61] (a prior version of [63]), which is called Optimal Nearest Neighbor Search.)

3.4.1 *Comparison of Nearest Neighbor Algorithms.* From the description of all the k-NN algorithms (original branch-and-bound KNN [142], the modified MNN [33], and the incremental INN [63]) it follows that there are three design issues that affect the performance of the NN searching:

(i) the criterion of ordering node visits,
(ii) the manner of ordering node visits (i.e., traversal type), and
(iii) the pruning heuristics.

Table I summarizes the selection made by each algorithm for the above issues, whereas the pruning heuristics are explained in Section 3.3.

	KNN	*MNN*	*INN*
ordering	MINDIST or MINMAXDIST	MINDIST	MINDIST
traversal type	Depth-First	Depth-First	Best-First
pruning heuristics	1,2,3	3	3

Table I. Characterization of NN search algorithms.

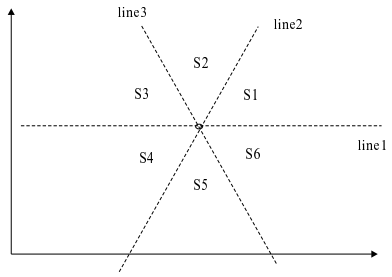
Experimental results in [63] show that INN clearly outperforms KNN. Nevertheless, it has to be noticed that the comparison for high-dimensional data is left as an open issue (where it has to be considered that the size of the priority queue may increase significantly and it has to be stored on disk).

3.5 Reverse and Conditional Nearest Neighbor Queries

3.5.1 *Reverse Nearest Neighbors.* Reverse NN queries find the set of database points that have the query point as the NN. The reverse and the NN problems are asymmetric. If the NN of a query point q is a data point p, then it does not hold in general that q is the NN of p (i.e., q is not necessarily the reverse NN). The aforementioned problem has been introduced in [83], however it was restricted to static data and specialized data structures. Stanoi et al. [159] have developed a reverse NN algorithm for the R-tree, which can handle dynamic data efficiently.

The algorithm of [159] is based on the notion of *space dividing lines*. For the two-dimensional space, each point can be associated with three lines around it. They are denoted as l_1, l_2 and l_3, where l_1 is parallel to the x axis, and the angle between l_1 and l_2, l_2 and l_3, l_3 and l_1 is $2\pi/3$. The left part of Figure 9 illustrates the arrangement of the three space dividing lines, which determine 6 regions (denoted as $S_1, \ldots, S_6$).

According to [159], for a query point q and the corresponding region S_i, either the NN of q in S_i is also the reverse NN, or there does not exist a reverse NN in S_i. Therefore, for each of the S_i regions, the NN of the query point has to be found. This set of points for all regions determine a candidate set that has to be examined so as to identify the reverse NN. Hence, for the two-dimensional space, this limits the choice of RNN(q) to one or two points in each of the six regions [159]. The corresponding algorithm is depicted in the right part of Figure 9. (Note that the computations corresponding to all six regions is done in a single traversal and not separately for each region).




```
Procedure RNNSearch(Point)
1.  RNNResult = ∅
2.  CandidateList = CondNNSearch(q)
3.  EliminateDuplicates(CandidateList)
4.  foreach p ∈CandidateList
5.      NNSearch(p, r)   /*r = NN(p)*/
6.      if objectDist(p, q) ≤ objectDist(p, r)
7.          RNNResult = RNNResult ∪ p
8.      endif
9.  endfor
10. return RRNResult
11. end
```

Fig. 9. Left: Space dividing lines. Right: Reverse Nearest Neighbor Search Algorithm.

3.5.2 *Conditions Determined by Space Dividing Lines.* Given one of the six regions S_i, the conditional NN determines the NN of the query point in S_i. This procedure is based on the observation that the examination of points that belong in MBRs that are out of S_i, can be pruned. However, for an MBR that belongs to S_i, their overlapping is done either fully or partially. This leads to five possible cases for, e.g., the S_2 region:

(1) MBR A: fully contained (all four vertices within S_2).
(2) MBR B: three vertices are in S_2. Thus, there exist some data points in B that are also contained in S_2.
(3) MBR C: two vertices are in S_2. Thus, at least one data point of C is also in S_2 (because an entire edge of C is in S_2 and there exist at least one point on that edge).
(4) MBR D: only one vertex is in S_2. No implication can be done on the existence of points in D that also belong in S_2.
(5) MBR E: no vertices in S_2, but part of E overlaps S_2. No implication can be done on the existence of points in D that also belong in S_2, *nor* on the not existence.

With the consideration of the aforementioned cases, the conditional NN searching traverses the tree and prunes out the sections that cannot lead to an answer either because a) their MBRs do not belong in the examined region, or b) because it can be determined that other points in the region are closer to the query point.

3.5.3 *Generalized Conditional Nearest Neighbor Searching.* The conditional NN searching that is determined by constraints due to space dividing lines is extended by Ferhatosmanoglou et al. [46] to consider more general constraints. They define the constrained NN (CNN) queries as NN queries that are constrained to a specified region (determined by a convex polygon [46]). For instance, let a two-dimensional map, depicted in the left part of Figure 10, which contains several cities that are represented by points. Given the query point q, a CNN query is: find the nearest city to the south of a q.[3] Evidently, in unconditional NN search, the result would be city a. In contrast, the result of the above CNN query is city b. Therefore, CNN queries can combine directional and distance operators. Moreover, CNN queries can involve multiple constraint regions [46].

A straightforward approach for the CNN problem (e.g., to first apply a range query with the specified constrained region and then search for the NNs in the results of the range query, or to use INN [63] for finding nearest points in the order of their distance and testing if they satisfy the given constraint at the same time) may unnecessarily retrieve a large number of points that do not belong in the query region, before finding the desired ones.

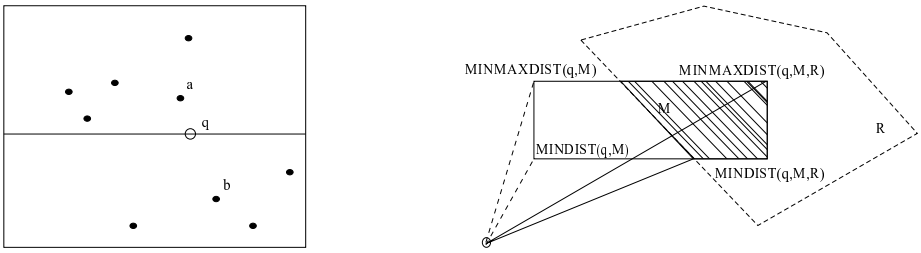


Fig. 10. Left: An example of CNN query. Right: The modified metrics for CNN.

For the above reasons, [46] proposes a new approach that merges the conditions of NN and regional constraints in one phase. It is based on an extension of the work described for the reverse NN, which considers general areas defined by polygons instead of the regions determined by space dividing lines. CNN again considers the five possible cases for the overlap between the query region and an MBR, which were described in Section 3.5.2. The MINDIST and MINMAXDIST metrics, however, are modified in a different way.

Let a query (i.e., constraint) region R, a query point q and an MBR M. Also, let the I_R polygon be the intersection between R and M, i.e., $I_R = R \cap M$ (several well known techniques exist to identify the intersection polygon). Then, having calculated the edges of I_R polygon, [46] defines MINDIST(q, M, R) to be the minimum of all distances from q to these edges. This case is illustrated in the right part of Figure 10, where it has to be noticed that MINDIST(q, M, R) offers a tighter bound compared to MINDIST(q, M). Similarly, MINMAXDIST as defined by [142] does not hold when M is only partially contained in R. Therefore, [46]

[3]Although this constraint does not explicitly determine a convex polygon, as described in [46] the combination of the directional line with the space boundary gives the desired polygon.

defines MINMAXDIST(q, M, R), which is computed only over the edges of M that are completely contained in R (so as to identify the distance that guarantees the inclusion of a point from M in R). This case is illustrated in the right part of Figure 10, where the shaded area represents I_R, the original metrics are depicted with dashed line and the modified ones with solid line.

3.6 Spatial Join Queries

Given two *spatial relations* $A = \{a_1, \ldots, a_n\}$ and $B = \{b_1, \ldots, b_m\}$ (a_i, b_i are spatial objects), the spatial join computes all pairs $(a_i, b_j), a_i \in A, b_j \in B$ that satisfy a spatial predicate, like the topological operators *overlap* (i.e., $a_i \cap b_j \neq \emptyset$) and *coverage* (i.e., a_i covers b_j). For instance, such queries can find all rivers that cross cities. Based on the two-step processing scheme (presented at the beginning of Section 3), the R-tree facilitates the filter step, that is, the determination of all pairs (MBR(a_i), MBR(b_j)) that satisfy the required operator; for instance MBR(a_i) $\cap$ MBR(b_j) $\neq \emptyset$, for the case of overlap. Spatial join queries, differently from selection queries (range and NN) that are single-scan, are characterized as multiple-scan queries, since objects may have to be accessed more than once. Therefore, these types of queries pose increased requirements for efficient query processing. In the following, we examine the case of 2-way join, whereas the multi-way join is examined in the next section.

3.6.1 *Algorithm based on Depth-first Traversal.* Brinkhoff et al. [23] first presented an algorithm for the processing of spatial joins using R-trees. Let R and S be the joined R-trees. The basic form of the algorithm traverses the two R-trees in a depth-first manner, testing each time the entries of two nodes N_R and N_S, one from each tree respectively. Let $E_R \in N_R$ and $E_S \in N_S$. If their MBRs do not intersect, then the further examination of the corresponding subtrees can be avoided. Otherwise, the algorithm proceeds recursively to the entries of the subtrees. This presents a *search pruning* criterion that capitalizes on the clustering properties of the R-tree. The description of the basic form of the algorithm is given in Figure 11.

```
Procedure RJ(N_R, N_S)
1.  foreach E_S ∈ N_S
2.      foreach E_R ∈ N_R with MBR(E_R) ∩ MBR(E_S) ≠ ∅
3.          if N_R is leaf node   /* N_S is also a leaf */
4.              output(E_R, E_S)
5.          else
6.              RJ(E_R.childPtr, E_S.childPtr)
7.          endif
8.          endfor
9.      endfor
10. end
```

Fig. 11. Basic Depth-First Spatial Join Algorithm.

In procedure RJ it is assumed (step 3) that both trees are of equal height. In [23] it is described that when the trees have different heights and the algorithm reaches

a leaf node (whereas the other node is not a leaf), then window queries on the subtrees rooted at the non-leaf node are performed with the MBRs of the entries belonging to the leaf node. Nevertheless, the experimental results in [23] indicate that window queries do not profit very much from the proposed optimizations, that will described in the sequel; thus the performance of the join query may be impacted in this case. Also, to avoid as much as possible the multiple rereading of nodes, an LRU buffer is used.

In the basic form of the algorithm, each node entry is examined against all entries of the other node. For this reason, two optimizations are proposed in [23]:

Restricting the search space: Let two nodes N_R and N_S, and $I = \text{MBR}(N_R) \cap \text{MBR}(N_S)$ the intersection rectangle. This optimization is based on the observation that only the entries $E_R \in N_R$ and $E_S \in N_S$ for which $E_R \cap I \neq \emptyset$ $E_S \cap I \neq \emptyset$ have to be examined, since they are the only that can have a common intersection.

Spatial sorting and plane sweep: Given two nodes N_R and N_S, let R_{seq} and S_{seq} represent the collection of the MBRs of the node entries. R_{seq} and S_{seq} are sorted with respect to the lower-x coordinate values of their entries. The sequences are processed using a plane-sweep algorithm, where the sweep-line is moved each time to the next unmarked rectangle among R_{seq} and S_{seq} with the smaller lower-x value, and the above procedure is repeated, until one of the two sequences has been exhausted. It has to be noted that the sorted node of entries is not maintained in the nodes during insertions/deletions.

The reduction of I/O cost, compared to the basic form of the algorithm, is achieved in [23] with the computation of a read schedule, which controls the way that nodes are fetched from the disk into the buffer. The following local optimization polices are proposed, which are based on spatial locality, and try to maintain in the buffer nodes whose MBRs are close in space:

Local plane-sweep order with pinning: It is based on the plane-sweep sequence, that was described for the tuning of CPU-time. Each time it pins in the buffer MBRs with the maximum number of intersections between it and the MBRs of entries belonging to the other tree that have not been processed. Due to pinning, pages whose MBR frequently intersects other MBRs, are completely processed so as to avoid their rereading.

Local z-order: The intersections between the MBRs of the two nodes is first computed. Then, the MBRs are sorted with respect to a space filling curve, like the Peano curve, opting to bring together MBRs that are closed in space. As in the previous case, the pinning of nodes is applied.

The overall experimental results (those that evaluate all the described optimizations) indicate that the optimized form of the spatial join performs about 5 times faster than the basic one (notice that the basic form is CPU-bounded, whereas the optimized is I/O-bounded).[4]

[4]It has to be noticed that [104] reported an improvement of the join execution time, by applying a grid-based heuristic instead of plane-sweeping. However, no consideration was paid for the case of buffer overflow.

3.6.2 *Algorithm based on Breadth-first Traversal.* Huang et al. [67], differently from the depth-first traversal of [23], propose the synchronous traversal of both R-trees in a breadth-first manner, for the processing of spatial joins. This approach is based on the observation that the method of [23] does not have the ability to achieve a global optimization for the ordering of node visits, because the local optimizations (read-scheduling) performed in [23] do not capture the access pattern of nodes beyond the currently examined nodes. The BFRJ (Breadth-First R-tree Join) algorithm of [67] opts for such global optimizations. The basic form of BFRJ is depicted in Figure 12, where the results, i.e., pairs of intersected entries, at each level l are maintained in the *intermediate join index* (IJI_l) (when the two R-trees do not have the same height, then when reaching the leaf level of one tree, BFRJ will have to proceed by descending the levels of the other tree, until the leaf-level is reached also for this tree).

Procedure BFRJ(R, S)
1. $N_R = \text{root}(R)$, $N_S = \text{root}(S)$
2. $\text{IJI}_0 = \{(E_R, E_S) \mid E_R \in N_R, E_S \in N_S, \text{MBR}(E_R) \cap \text{MBR}(E_S) \neq \emptyset\}$
3. **for** i=1 **to** height$- - 1$
4. **foreach** $(E_R, E_S) \in \text{IJI}_i$
5. $N_R = E_R$.childPtr, $N_S = E_S$.childPtr
6. $\text{IJI}_{i+1} = \text{IJI}_{i+1} \cup \{(E'_R, E'_S) \mid E'_R \in N_R, E'_S \in N_S, \text{MBR}(E_R) \cap \text{MBR}(E_S) \neq \emptyset\}$
7. **endfor**
8. **endfor**
9. output IJI_i /* the IJI of leaf-level */
10. **end**

Fig. 12. Breadth-First R-tree Join Algorithm.

Huang et al. [67] use the CPU-tuning optimizations proposed in [23], but propose three new global optimizations for the tuning of I/O-time, which according to the experimental results in [67] indicate an improvement in terms of disk accesses, compared to the approach of [23]. At level l, the global optimizations of BFRJ are based on IJI_{l-1} to schedule the reading of nodes, and they are described as follows.

IJI Ordering: BFRJ orders the contents of IJI by trying not to spread too widely their multiple appearances. Since each member of IJI corresponds to two MBRs, this form of clustering may have to be performed concurrently for both of them. In [67] several options are considered for the processing, where the most efficient is with respect to the sum of the centers (for each member of IJI, the x coordinates of the centers of the two MBRs are calculated, and their sum is taken).

Memory Management of IJI: If not enough main memory exists, the contents of IJI have to be stored on disk. BFRJ stores the contents only after the corresponding level has been completely written. However, with this option the shuffling of the IJI contents between disk and main memory cannot be avoided.

Buffer management of IJI: The multiple reading of nodes is further minimized by BFRJ by predicting which node will be fetched again in the sequel. Therefore, the buffer can purge nodes that have completed their processing.

For an easy comparison between the two described spatial join algorithms ([23; 67]), Table II summarizes the options followed by each one.

	[23]	[67]
traversal type	depth-first	breadth-first
CPU-time	restrict search space, plane-sweep	restrict search space, plane-sweep
I/O-time	plane-sweep/pinning, z-ordering	IJI ordering, memory and buffer management for IJI

Table II. Characterization of spatial join algorithms.

3.6.3 *Join between an R-tree and a Non-index Data Set.* In the case that an intermediate query result (e.g., of a range query) participates in the join, then an R-tree will not be available for it. A straightforward approach to perform the join in this case is to apply multiple range queries, one for each object in the non-indexed data set, over the R-tree of the other data set. Evidently, this approach is efficient only when the size of the intermediate data set is very small.

An R-tree can be created (e.g., with bulk-loading) for the non-indexed data set in order to apply the already described algorithms for joining two R-trees [134]. This approach, however, may introduce a non-negligible cost, required for the R-tree creation. In order to improve the latter approach, Lo and Ravishankhar [94] propose the use of the existing R-tree as a skeleton to build the *seeded tree* for the non-indexed data set. Also, the *sort-and-match* algorithm [130] sorts the objects of the non-indexed data set (using spatial ordering), creates leaf nodes that can be accommodated in main memory, and examines each of them with leaves of the existing R-tree of the other data set with respect to the join condition. An analogous approach is the Sort/Sweep Algorithm, developed in [56], which is based on plane sweeping. Arge et al. [10] propose the *Priority Queue-Driven Traversal* (PQ) algorithm, which combines the index-based and non-indexed based approaches such that in both forms can be processed using a single algorithm. Mamoulis and Papadias [98] propose the *slot index spatial join* (SISJ), which applies hash-join using the structure of the existing R-tree to determine the extents of the spatial partitions. By additionally considering data that are indexed with quadtrees, [37] proposes an algorithm that joins a quadtree with an R-tree data structure. Moreover, Hoel and Samet [65] present a performance comparison of PMR quadtree join against join for several R-tree-like structures. All the aforementioned methods employ specialized techniques to handle the non-index data set, which do not directly relate to query processing for existing R-trees. The interested reader is directed to the given references.

3.7 Multiway Spatial Join Queries

The spatial join algorithms that were examined in Section 3.6 focus on the case of two R-trees. In GIS applications, large collections of spatial data may have several thematic contents, thus they involve the join between multiple inputs. Multiway spatial joins queries, proposed by Mamoulis and Papadias [100] (an earlier version was presented in [121]), involve an arbitrary number of R-trees. Given n

data sets $D_1, \ldots, D_n$ (each indexed with an R-tree) and a query Q, where Q_{ij} represents the spatial predicate that should hold between D_i and D_j, the multiway join query finds all tuples $\{(r_{1,w}, \ldots, r_{i,x}, \ldots, r_{j,y}, \ldots r_{n,z}) \mid \forall\, i,j : r_{i,x} \in D_i, r_{j,y} \in D_j, r_{i,x}\ Q_{ij}\ r_{j,y}\}$. Therefore, multiway spatial join queries can be considered as a generalization of pairwise spatial join that were presented in Section 3.6. Query Q can be represented by a graph whose nodes correspond to the data sets D_i and edges to join predicates Q_{ij}. In general, the query graph can be a tree (graph without cycles), a graph with cycles or a complete graph (every node connected to each other). For instance, Figure 13 depicts these three different cases of a query graph along with a tuple that satisfies the corresponding predicates (henceforth, based on [100], it is assumed for simplicity that each predicate Q_{ij} corresponds to the spatial operator *overlap*).

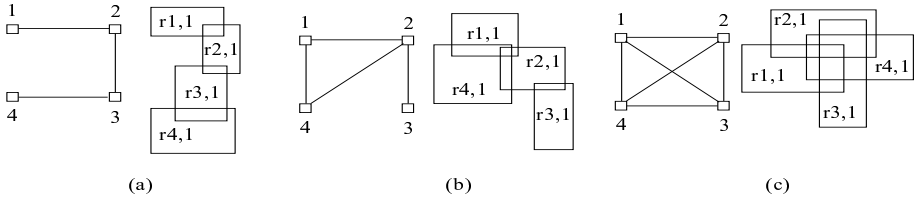


Fig. 13. Examples of multiway queries: a) Acyclic (chain) query. b) Query with cycle. c) Complete graph query.

One method to perform multiway spatial joins is the combination of a sequence of pairwise joins (PJM). The order of pairwise joins is determined by the minimization of expected I/O cost (in terms of page accesses). In this sequence, a pair does not necessarily correspond to a join between two R-trees (i.e., indexed data sets). Therefore, (i) RJ or BFRJ (see Section 3.6) is applied when both inputs are indexed, (ii) Slot Index Spatial Join (SISJ) [98] is applied when only one data set is indexed, and (iii) Hash spatial Join (HJ) [96] when none of the data sets is indexed (i.e., they are intermediate results).

A different approach than PMJ is also described in [100; 121], called Synchronous Traversal (ST). ST starts from the root nodes and synchronously traverses the R-trees. It proceeds only with the combination of nodes that satisfy the query predicates Q_{ij}, until reaching leaf nodes. ST is facilitated by the R-tree structure to decompose the problem into smaller *local* ones at each level. If $f_{\max}$ is the maximum node fanout, then in the worst case each local problem examines $f_{\max}^n$ combinations. The local problem is defined by:

—A set of n variables, $v_1, \ldots, v_n$, each corresponding to an R-tree.
—A domain D_i, for each variable v_i, which consists of the entries $\{E_{i,1}, \ldots E_{i,f_i}\}$ of node N_i in the R_i tree (f_i is the fanout of N_i).
—Each pair of variables (v_i, v_j) is constrained by predicate *overlap*, if Q_{ij} is true.

Based on [100], a binary assignment $\{v_i \leftarrow E_{i,x}, v_j \leftarrow E_{j,y}\}$ is consistent iff (Q_{ij} is true) $\Rightarrow$ ($E_{i,x}$ overlaps $E_{j,y}$). A solution of a local problem is a n-tuple $\tau = (E_{1,w}, \ldots, E_{i,x}, \ldots, E_{j,y}, \ldots, E_{n,z})$ such that $\forall\ i,j\{v_i \leftarrow E_{i,x}, v_j \leftarrow E_{j,y}\}$ is

consistent. The objective of ST is the finding of all assignments of entries to variables so as all predicates are satisfied.

Park et al. [131] made the observation that the optimization techniques of the original 2-way R-tree join algorithm are still required in the case of multiway join, and they proposed the M-way join algorithm. Furthermore, Mamoulis and Papadias [100] propose two optimizations for the ST algorithm, which exploit the spatial structure of the multiway join problem:

Static Variable Ordering (SVO): This heuristic pre-orders the problem variables by placing the most constrained one first. Thus, variables are sorted in decreasing order of their degree. SVO is applied once (before performing ST) and produces a static order that is used in find-combinations and space-restriction procedures.

Plane-Sweep combined with Forward Checking (PSFC): PSFC is an improved implementation of procedure *find-combinations*, which decomposes a local problem into a series of smaller problems, one for each event of the sweep line. With this heuristic, the overhead of searching and backtracking in large domains is avoided.

Experimental results in [100] show that the improvement due to SVO is significant when the few first variables are more constrained, whereas this does not apply for complete query graphs. The combination of SVO-PSFC presents significant reduction in both I/O and CPU cost, compared to the version of ST that does not use these optimizations (PSFC performs better with increasing page size). In general, the savings in CPU cost are considered more significant in [100], since ST is CPU bounded.

Finally, it has to be noticed that [100] proposes the optimization with dynamic programming to derive the query execution plan. Each time, either ST or PJM is selected for the intermediate executions. With this approach, execution plans that are slightly more expensive (12% in the worst case) than the optimal one are selected [100]. Nevertheless, if n (the number of input R-trees) is larger than 10, the cost of the dynamic programming is prohibitive. For this reason, [100] also describes a randomized search algorithm for finding the execution plan of large queries, i.e., for large n.

3.8 Incremental Distance Join and Closest Pair Queries

3.8.1 *Incremental Distance Join.* Given two spatial relations A and B, distance join queries find the subset of the Cartesian product $A \times B$, which satisfies an order that is based on distance. Halation and Samet [62] present an incremental approach for processing distance join and distance semi-join queries (the latter is a variant of the former, and finds for each object in A the nearest object in B). The incremental algorithms for these queries that are described in [62] report the results one-by-one, with respect to the distance ordering. In contrast, the spatial join algorithms, that have been described in Section 3.6, will first have to compute the entire result and then to sort it before starting the output. Evidently, the focus of the incremental algorithm is on starting the output of results as early as possible.

For two R-trees R_1 and R_2, the Incremental Distance Join Algorithm (IDJ) maintains a set P of pairs (each pair has one item from R_1 and R_2 respectively). During the processing of P's entries, each time a pair $p \in P$ is encountered that contains a node item n (i.e., not a data object), it is replaced by all pairs resulting by

substituting n with all its children nodes. The elements of P has to be maintained sorted according to their distance. To achieve this, P is implemented as priority queue. The basic algorithmic form of IDJ is depicted in Figure 14, where the ProcessNode procedure (which is also depicted) uses the same basic loop as the incremental NN algorithm of Section 3.4 (Item_2 corresponds to the query object, for this reason the same notation $[O]$ is used for the object bounding rectangles (OBRs)).

```
Procedure IDJ(R1, R2)
1.  Enqueue(Q, 0, (R1.root, R2.root))
2.  while Q not empty
3.  elem ← Q
4.  if both items of elem are data objects
5.     output elem  /*elem = (O1, O2)*/
6.  else if both items OBRs
7.     D = objectDist(O1, O2)
8.     if Q empty or D ≤ Front(Q).dist
9.        output (O1, O2)
10.    else
11.       Enqueue(Q, D, (O1, O2))
12.    endif
13. else if first item of elem is node
14.    ProcessNode(Q, elem, 1)
15. else
16.    ProcessNode(Q, elem, 2)
17. endif
18. end
```

```
Procedure ProcessNode(Q, elem, order)
    /* elem = (i1, i2) */
1.  if order == 1
2.     Node = i1, Item2 = i1
3.  else
4.     Node = i2, Item2 = i1
5.  endif
6.  if Node is leaf
7.     foreach entry [O] of Node
8.        Enqueue(Q,dist([O],Item2,([O],Item2))
9.     endfor
10. else
11. foreach child c of Node
12.    Enqueue(Q, dist(c, Item2), (c, Item2))
13. endfor
14. endif
15. end
```

Fig. 14. Basic form of Incremental Distance Join Algorithm.

In [62] optimizations are described over the basic form of the algorithm with respect to the tie-braking criteria and the order of processing node items. The evaluation of all described options is given in [62] through experimental results. These results indicate that the best performance is achieved by the combination of the following two optimizations: (i) *Depth-first-like traversal*: Elements containing data objects or object bounding rectangles can be given priority over other elements with the same distance (resolves tie-breaking); also, for elements containing non-leaf items, priority can be given to nodes at smaller level (i.e., deeper in the tree). (ii) *Even*: When a pair (n_1, n_2) with non-leaf nodes is retrieved from the head of the priority queue, the node at a higher level is chosen to be processed, to achieve a more even traversal of the two trees (resolves the order of processing).

During the processing of the distance join, the priority queue may become very large. For the implementation of the priority queue [62] describes an approach that is analogous to the one presented in Section 3.4, which divides the queue in a number of partitions, where one is kept in main memory the others are maintained on disk. Nevertheless, most of the pairs still will have a large distance and they will probably never be retrieved by the queue. In order to limit the number of entries

in the priority queue, [62] proposes the use of restrictions based on a minimum and a maximum specified distance that the query results have to satisfy. If no such constraints on the distance can be posed by the user, [62] sets an upper bound on the number of examined pairs (facilitated by the 'STOP AFTER' clause of SQL, which reports only a specified number K of results). This is done by estimating a lower bound for the distance $D_{\max}$, which can be used to impose the required constraint.

It has to be noticed that recently a k-distance join algorithm has been proposed by Shin et al. [157], which differently from [62], joins the first k pairs with respect to their distance. Their approach is based on a bi-directional expansion of R-tree nodes and on plane-sweeping for pruning distant pairs. Moreover, they develop adaptive, multi-stage algorithms for k-distance join and incremental distance join algorithms. Experimental results illustrate the performance gains due to the adaptive algorithms over previous approaches (including [62]).

3.8.2 *Distance Semi-Join.* As mentioned, the distance semi-join query is a special case of the distance join query, since for each pair (o_1, o_2) in the result, the object o_1 appears only once (i.e., it does not appear in any other pair). In order to achieve this, [62] uses a set S_0 to keep track of all first objects in each pair that is output.

The experimental evaluation in [62] indicates that the *GlobalAll* option presents the best performance. The GlobalAll option operates as follows: for each node and data object in the first R-tree, the smallest $d_{\max}$ distance that has been encountered so far, is maintained. A new pair (i_1, i_2) is enqueued only in the case that its distance is smaller than $d_{\max}$ for i_1. Since this option may require significant memory space, $d_{\max}$ can be maintained for nodes only. Compared to the straightforward approach of applying multiple NN queries (one for each object of the first R-tree), the results of [62] show that the incremental algorithm outperforms the straightforward one by up to 40%.

3.8.3 *Finding Closest Pairs.* As described, the incremental distance join algorithm can be easily modified to produce up to K pairs [62]. In this case, the algorithm finds the K closest pairs between the two data sets, that is, the pairs of objects from the two data sets that have the K smallest distances between them (K=1 yields to the classic closest-pair problem of computational geometry). For instance, given a collection of archaeological sites and holiday resorts, the K closest pair query finds sites that have the K smallest distances to a resort, so as tourists to be accommodated easily.

Corral et al. [38] proposed a different approach, called CP, for closest pair queries than the one of [62]. Two types of algorithms have been investigated in [38], also described briefly in the sequel. (We present the case for K=1, since the extension to $K > 1$ is easy, according to [38]. Also, we assume that the trees have the same height.)

Recursive based on sorting distances. This algorithm, called STD, descends the two R-trees and keeps track of the closest distance T found so far. When two internal nodes are accessed, the MINMAXDIST is calculated for all pairs formed by their contents. T can be updated (a kind of downward pruning) if it is larger than one

of such distances. When reaching the two leaf leaves, the actual object distances are calculated and T is updated.[5]

Non-recursive based on heap Similar to [62], this algorithm, called HEAP, maintains the pairs to be examined within a heap structure, sorted with respect to MINDIST metric. However, differently from [62], HEAP considers only pairs that have MINDIST smaller than T. Moreover, similar to STD, HEAP updates T with respect to the MINMAXDIST metric.

STD is a type of depth-first closest pair algorithm, which considers local optimizations. In contrast, HEAP and the incremental distance join algorithm belong to the type of best-first algorithms, which consider global optimizations. Also, recall that these two different algorithmic types have also been described for NN and join queries. Evidently, closest pair queries combine the characteristics of both these types of queries. Regarding the tie-braking criteria, [38] describes several ones, however the best performance is achieved by resolving ties by giving priority to the pair whose elements have the largest MBR. Also, if different tree heights are addressed with two methods, then [38] proposes the *Fix-at-root* policy, which stops the downwards propagation in the tree with lower level and continues the propagation in the other tree, until a pair of nodes at the same level is found.

The comparison between STD and HEAP, which is experimentally performed in [38], indicates that HEAP outperforms STD for very small buffer sizes and for data sets with large overlapping. For medium and large buffer sizes, STD clearly compares favorably to HEAP. Finally, in [39] the impact of buffering on the performance of CP queries using R-trees was considered for several searching approaches and buffer replacement policies.

3.9 Classification of R-tree Query Processing Algorithms

In this section, we give a summary and a classification of all the described methods. The classification is given in Figure 15 and uses the same notation for the names of the algorithms as the one used throughout the previous sections. The links between the contents of Figure 15 represent the relationships among them.

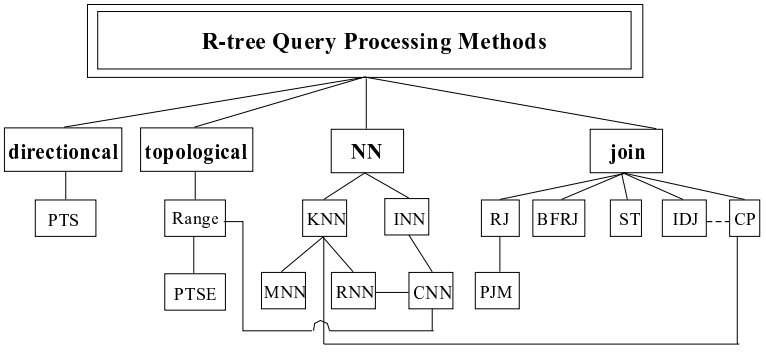


Fig. 15. Classification of the described R-tree based query processing methods.

[5]Note that STD is formed by a number of optimizations, which are presented separately in [38]. Herein we only present STD in its final form because it significantly outperforms the others [38].

Four general types of spatial queries were presented, namely range, topological, NN and join queries. The algorithm for the range query (denoted as Gutt) is the first searching algorithm that was developed for the R-tree. Topological queries (the corresponding algorithm is denoted as PTSE) form a second type of queries, since they generalize the non-disjoint operator used by the range query. NN queries include KNN and its improved version MNN, which address the finding of the k-NN. Moreover, based on KNN, RNN determines the reverse NNs. A different approach is followed by INN, which incrementally finds the NNs in the order of their distance from the query object. By generalizing the constraints of RNN, and based on INN (in order to achieve its 'optimality'), CNN determines the NNs according to a query constraint. Therefore, constrained NN queries is a combination of range and NN queries. Finally, the spatial join query between two R-trees is addressed by RJ (depth-first) and BFRJ (breadth-first). For the multiway join, PJM is based on RJ in order to perform multiple pairwise joins, whereas ST traverses all trees at the same time. IDJ (analogously to INN) focuses on the distance join (i.e., operator *within*) and finds the results incrementally, in the order of the distance between them. Closest pair queries (CP algorithm) find the k closest pairs between two indexed data sets, and can be considered as combination of both NN and join queries. Finally, IDJ can also lead to the finding of closest pairs; for this reason there is a connection between CP and IDJ.

4. QUERY OPTIMIZATION ISSUES

Determining the best execution plan for a spatial query requires tools for measuring (more precisely, estimating) the number of (spatial) data items that are retrieved by a query as well as its cost, in terms of I/O and CPU effort. As in traditional query optimization, such tools include cost-based optimization models, exploiting analytical formulae for selectivity (the hit percentage) and cost of a query, and histogram-based techniques.

In particular for spatial databases supported by R-tree indices, cost-based optimization exploits analytical models and formulae that predict the number of hits among the entries of the R-tree and the cost of a query retrieval, measured in R-tree node accesses (or actual disk accesses, assuming existence of a buffering scheme).

Traditionally, R-tree performance has been evaluated by the ability to answer range queries by accessing the smallest possible number of pages (i.e., nodes) in the disk. Other queries, such as NN [142] and join queries [23] are also of great interest for a spatial query optimizer. Thus, Sections 4.1 and 4.2 survey work on cost models for selection and join queries, respectively, followed by Section 4.3, which presents sampling and histogram-based techniques.

4.1 Cost Models for Selection Queries

Considering that each R-tree node corresponds to a physical page in the disk, the cost estimation of a query (i.e., how many pages are accessed in order to retrieve the result of the query) turns into the problem of estimating the number of nodes visited during R-tree traversal. Apparently, the actual time required (number of disk pages times the time required to read a page resident in disk) could be less than the estimated due to buffering. Therefore, several models have included buffer parameters in their formulae.

4.1.1 *Formulae for Range Queries.* The first attempt to estimate the performance of R-trees for range queries was made by Faloutsos et al. [44]. In that paper, the authors made two fundamental assumptions: (i) uniform distribution of data, and (ii) all the R-tree nodes were supposed to be full of data. For point queries, the cost formula derived expressed the fact that the number of nodes to be visited equals the overlap of parent nodes per level or, in other words, the density of nodes per level summed up for all but the leaf level (the authors did not use the term density in that paper; this was used later in [167] as will be discussed below).

Although the analysis in [44] was restricted by the uniformity assumption and packed trees, it served as a framework for almost all related work that appeared later. Among the proposed formulae, one of the most useful was about the expected height h of an R-tree:

$$h \ = \ log_f \frac{N}{C} \tag{1}$$

where f is the fanout of parent nodes, C is the capacity of leaf nodes, and N is the number of data entries.

Later, Kamel and Faloutsos [76] and Pagel et al. [116] independently extended the analysis in [44] and presented the following formula that gives the average cost C_W of a range query with respect to a query window $q = (q_1, ..., q_d)$, assuming the dataset is indexed by a d-dimensional R-tree and provided that the sides $(s_j, 1, ..., s_j, d)$ of each R-tree node s_j are known (the summation extends over all tree nodes).

$$C_W(R, q) \ = \ \sum_j \left\{ \prod_{i=1}^{d} (s_{j,i} + q_i) \right\} \tag{2}$$

Eq. (2) allows the query optimizer to estimate the cost of a query window (measured in number of node accesses) assumed that the corresponding R-tree has been already built and, hence, the MBR of each node s_j of the R-tree can be measured. This formula, implicitly presents the dependency between the sizes of the R-tree nodes and the query window, on the one hand, and the cost of a range query, on the other hand. Moreover, the influence of the node perimeters is revealed, which helps understanding the R*-tree efficiency as, it was the first method among the R-tree variants to take into account the node perimeter during its construction phase (see Section 2.1 for relevant discussion and [166] for a performance-wise comparison of the most popular members of the R-tree family until that time).

Extending the work performed in [116], Pagel et al. in [117] proposed an optimal algorithm that established a lower bound result for the performance of packed R-trees. It was also shown through experimental results that the best known static and dynamic R-tree variants, the packed R-tree by Kamel and Faloutsos [76] and the R*-tree [12], respectively, performed about 10%-20% worse than the lower bound. [117] defined the problem of measuring the performance of SAMs like R-trees, as follows: For a bucket set B and a query model QM, let Prob(q meets B_i) be the probability that performing query q forces an access of bucket B_i. Then the expected number of bucket accesses needed to evaluate query q is called the performance measure

PM for QM and is given by:

$$PM(QM, B) = \sum_{i=1}^{m} \text{Prob}(q \text{ meets } B_i) \quad (3)$$

[117] also formalized the so called Bucket Set Problem (BSP): Given a set of geometric objects, a bucket capacity $C_b \geq 2$, and a query model QM, determine the bucket set B_{opt} for which the performance measure PM is minimal. They also distinguished two cases, the simple case (called, SBSP) where C_b=2, and the universal case (called, UBSP) where $C_b \geq 3$, and proved that SBSP can be solved in polynomial time, while UBSP is NP-hard. Practically, this means that in R-trees etc. (where $C_b = M >> 2$), it is not possible to find and integrate an optimal construction algorithm.

The impact of the three parameters that are involved in Eq. (2), namely the area sum of rectangles, the perimeter sum, and the number of rectangles, was further studied in [118], where formulae for various kinds of range queries, such as intersection, containment and enclosure queries of various shapes (points, lines, circles, windows, etc.), were derived. One of the main conclusions of that paper was that window queries can be considered as representative for range queries in general.

However, Eq. (2) could not predict the cost of a range query just by taking into consideration the dataset properties only since R-tree properties were involved (namely, the R-tree node extents s_j). Faloutsos and Kamel [45] and Theodoridis and Sellis [167] extended this formula towards this goal. [45] used a property of the dataset, called fractal dimension. The fractal dimension fd of a dataset (consisting of points) can be mathematically computed and constitutes a simple way to describe non-uniform datasets, using just a single number. According to the model proposed in [45], the estimation of the number of disk accesses at level 1 (i.e., leaf level), denoted by $C_W(R^1, q)$, is given by:

$$C_W(R^1, q) = \frac{N}{f} \cdot \prod_{i=1}^{d} (s_{1,i} + q_i) \quad (4)$$

where $s_{1,i} = (f/N)^{1/fd}$, $\forall i = 1, ..., d$ and f is the average fanout of the R-tree nodes.

In [45], the Hausdorff fractal dimension (D_0) was used to estimate the cost of a range query. In [13], another fractal dimension, the correlation one (D_2), was used to make selectivity estimation. In both cases, the accuracy of the estimations was very good, a fact that illustrated how surprisingly often real (point) datasets behave like fractals. [45; 13] were also the first attempts to support analytically non-uniform distributions of data (with uniform distribution being a special case: $fd = d$) superseding [44] analysis that assumed uniformity. However the models proposed are applicable to point datasets only.

In a different line, [167] used another property of the dataset, called density surface. The density D of a set of N (hyper-)rectangles with average extent $s = (s_1, ..., s_d)$ is the average number of rectangles that contain a given point in d-dimensional space. Equivalently, D can be expressed as the ratio of the global data area over the work space area. If we consider a unit workspace $[0, 1)^d$ then the

density $D(N, s)$ is given by the following formula:

$$D(N,s) \;=\; \sum_{N} \prod_{i=1}^{d} s_i = N \cdot \prod_{i=1}^{d} s_i \tag{5}$$

Using the framework proposed in [116] and based on the investigations that: (i) the expected number of node accesses $C_W(R, q)$ for a query window q is equal to the expected number of intersected nodes at each level, (ii) the average number of intersected nodes is equal to the density D of the node rectangles inflated by q_i at each direction, (iii) the average number of nodes N_j at level j is $N_j = N/f$, where N is the cardinality of the dataset and f is the fanout, and (iv) an expression of the density D_j of node rectangles at each level j can be expressed as a function of the density of the dataset, [167] proposed the following formula:

$$C_W(R,q) \;=\; \sum_{j=1}^{1+log_f \frac{N}{f}} \left\{ \frac{N}{f^j} \cdot \prod_{i=1}^{d} \left((D_j \cdot \frac{f^j}{N})^{1/d} + q_i \right) \right\} \tag{6}$$

To reach this formula, the authors assumed 'square' node rectangles and argued that this is a reasonable simplification and a nice property for an efficient R-tree (the same was also argued in [76]). They also assumed uniform distribution of data as well as of node rectangles. Under these assumptions, the above formula estimates the number of node accesses by only using the dataset properties N and D, the typical R-tree parameter f and the extents of query window q.

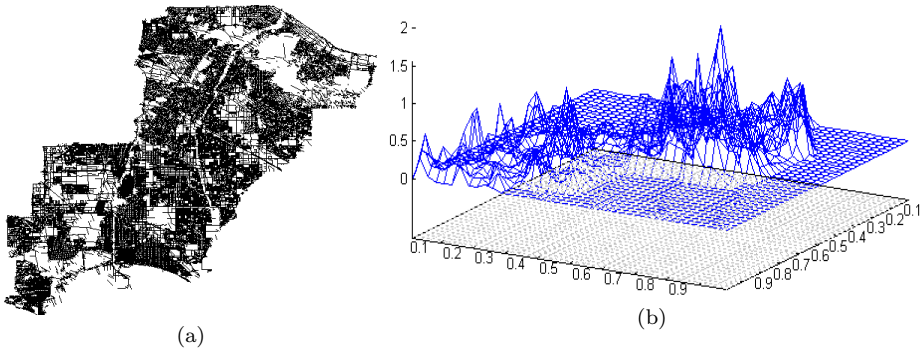
[167] also provided a formula for the selectivity S of a range query specified by a query window q, i.e., the ratio of the expected number of hits in the dataset over the total number N of entries. Since, S is equal to the ratio of the number of intersected rectangles among the N rectangles of the input dataset over N, the formula proposed for the selectivity is the following:

$$S \;=\; \prod_{i=1}^{d} \left((\frac{D}{N})^{1/d} + q_i \right) \tag{7}$$

However, Eqs. (6) and (7) assumed uniformity of data (in particular, in order to express the density of parent nodes at a level j+1 as a function of the density of child nodes at level j). This assumption is restrictive as already discussed, and, to overcome it, the authors proposed the evolution of density from a single number D to a varying parameter (graphically, a surface in two-dimensional space) showing deviations, if projected in different points of the work space, with respect to the average value D. For example, in Figure 16, a real dataset is illustrated together with its density surface, which is actually a two-dimensional histogram.

Using the introduced density surface, [167] showed that non-uniform distributions of data could be supported as well, after the following modifications were made in Eqs. 5 and 6: (i) the average density D_0 of the dataset is replaced by the actual density D'_0 of the dataset within the area of the query window q. (ii) the cardinality N of the dataset is replaced by a transformation of it, called N', computed as follows: $N' = \frac{D'_0}{D_0} \cdot N$

It was also noted that in order for the above formulae to be usable for point datasets also, the average density of a dataset is considered to be always $D_0 > 0$,



(a) (b)

Fig. 16. (a) A real dataset (LB county TIGER dataset), (b) Its density surface.

even for point datasets, since zero density corresponds to zero-populated work area. A comparison of the analytical estimates with experimental results using R*-trees on synthetic and real datasets showed that the estimates were accurate enough, with the relative error being below 10% (20%) for C_W on uniform (non-uniform) data and below 5% (10%, respectively) for S.

A similar idea was proposed by Jin et al. [72], where a density file was proposed to be maintained in addition to the R-tree. In particular, the density file proposed in [72] is an auxiliary data structure that contains the number of points (assuming a point dataset) falling within a specific Hilbert range. In case of rectangular data items, a cumulative density scheme was proposed, gridding spatial extents and keeping four values for each Hilbert cell about the number of rectangles whose lower-left / lower-right / upper-left / upper-right corner lies in the cell. Based on this density file, models for estimating the selectivity as well as the cost of a range query were proposed with their accuracy shown to be high (usually less than 5% errors for uniform to skewed datasets using the packed R-tree [76] as a case-study).

More recently, in [139] the authors studied the distribution of the MBRs of R-tree nodes and observed that it follows the distribution of the underlying data set. Therefore, accurate estimations of the number of accessed nodes for range queries can be obtained, by taking into consideration the MBR distribution.

All the above models can provide cost estimations measured in number of R-tree nodes accessed, which is an upper bound for the number of actual disk accesses. The latter can be significantly lower than the former with the existence of a buffering scheme, which is always the case in real life systems. The effect of the buffering on the R-tree performance for selection queries was studied in [92].

In particular, Leutenegger and Lopez [92] modified Eq. (2), originally proposed in [76; 116], by introducing the buffer size following the LRU replacement policy. The authors also discussed the appropriate number of R-tree levels to be pinned, and argued that pinning may mostly benefit point queries and, but only under special conditions. For example, for point queries, it was argued that pinning R-tree levels is advantageous, but only when the total number of nodes pinned is within a factor of two of the buffer size, while for range queries the benefit is even more modest. Practically, if the buffer is shared among many applications, [92] suggested that

pinning R-trees should be done only when the rest applications do not need the full buffer size.

4.1.2 *Formulae for NN Queries.* Exploiting the branch-and-bound algorithm for NN query processing proposed in [142], Papadopoulos and Manolopoulos [126] derived lower and upper bounds for its performance (number of disk accesses to R-tree leaf pages). In particular, they first proved two propositions for the expected number of R-tree leaf pages accessed in order to find the NN of a point P: the minimum (maximum) number of leaf pages touched is the number of leaf pages intersected by a circle C_1 (C_2) with center P and radius d_{nn} (d_m), where d_{nn} is the actual distance between P and its NN (not known in advance) and d_m is the MINMAXDIST between P and the first touched leaf page. (cf. subsection 3.2 for a definition and discussion on MINMAXDIST metric) Then, extending Eq. (4) proposed in [45] for range queries on uniform datasets, [126] came up with the following pair of formulae for lower and upper bounds:

$$C_{NN}(R,P)_{lower} = \frac{N-1}{f} \cdot (s + 2 \cdot d_{nn})^{D_2} \quad (8)$$

$$C_{NN}(R,P)^{upper} = \frac{N-1}{f} \cdot (s + 2 \cdot d_m)^{D_2} \quad (9)$$

The experimental results presented in that work showed that the actual cost is well bounded by the two proposed bounds and, in general, the measured cost is closer to the lower than to the upper bound.

The above analysis was restricted to estimating the cost for the first NN and its extension to support k-NN queries is not straightforward at all. Recently, Bohm [20] and Tao et al. [162] tackled the problem of estimating the average d_k distance between P and its k-th NN. The model proposed in [20] involves integrals in the computation of d_k, which can be solved only numerically, thus making it not easily applicable for query optimization purposes. On the other hand, [162] proposed the following closed formula:

$$d_k = \frac{2}{C_V} \cdot \left\{ 1 - \sqrt{1 - (k/N)^{1/d}} \right\} \quad (10)$$

where $C_V = \frac{\sqrt{\pi}}{\Gamma(d/2+1)^{1/d}}$ and $\Gamma(x+1) = x \cdot \Gamma(x)$, $\Gamma(1)=1$, $\Gamma(1/2)=\pi^{1/2}$. A side effect of the above analysis is also the estimation of the smallest value for k for which sequential scan would surpass R-tree based search, as a side effect of the curse of dimensionality. According to the authors' experiments, the threshold value decreases dramatically with the dimensionality, a conclusion consistent with the related work of [173].

4.2 Cost Models for Join Queries

Spatial join requires high processing cost due to the high complexity and large volume of spatial data. Therefore, the accurate estimation of the selectivity and cost of spatial join queries has a great influence on the query optimizer. Unlike range queries, the number of input datasets in join queries is variable, thus we distinguish between models proposed for pair-wise joins and those proposed for multi-way joins.

4.2.1 *Formulae for Pair-wise Joins.* The first work on predicting the selectivity of join queries was by Aref and Samet [9]. In that paper, the authors proposed analytical formulae for the number of hits, based on uniformity assumption and the R-tree analysis provided in [76]. The motivating idea was the consideration of a join query as a set of selection queries (with the first R-tree playing the role of the target index and the second R-tree assumed to be the source of query windows). Demonstrated experimental results showed the accuracy of the proposed selectivity estimation formula.

Also assuming uniform distribution of data, Huang et al. [66] proposed a cost model for R-tree-based spatial joins distinguishing two cases: either lack or existence of a buffering mechanism. Two corresponding formulae were proposed, one estimating cost assuming no buffering and one estimating actual cost taking into account the probability of a page not to be (re-)visited due to buffering mechanism:

$$C_{SJ}(R_1, R_2) \;=\; 2 \cdot \sum_{l=1}^{h-1} \sum_{i=1}^{N_1^l} \sum_{j=1}^{N_2^l} \prod_{k=1}^{d} (s_{R_1,k} + s_{R_2,k}) \tag{11}$$

and

$$C_{SJ}(R_1, R_2)^{actual} \;=\; n + m + (C_{SJ}(R_1, R_2) - n - m) \cdot \text{Prob}(x \geq b) \tag{12}$$

The triple sum in Eq. (11) denotes the pairs of considered node MBRs, one for each tree, for all levels. Thus, to find the cost this number is counted twice (once for each tree). Also, in Eq. (12), the first two terms (n+m) represent the total number of first accesses for all tree pages traversed during join (every node will be traversed at least once), while the term $C_{SJ}(R_1, R_2)$–n–m represents the expected number of non-first accesses with the probability of one such access causing a page fault being $Prob(x \geq b)$. The accuracy of the two formulae was also demonstrated after a comparison with experimental results for varying buffer size (with the relative error being around 10%-20%).

Theodoridis et al. [169; 170] also considered the depth-first approach for a join query between two R-trees R_1 and R_2 as a series of query windows, where e.g., the node rectangles of R_1 at a level l could play the role of query windows on a 'dataset' consisting of the node rectangles of R_2 at a corresponding level. Under this consideration, Eq. (6), proposed in [167] for range queries, was modified to calculate the cost of a join query. In particular, the cost for each R-tree at level l is the sum of costs of $N_{R_2,l}$+1 different window queries on R_1:

$$C_W(R_1^l, R_2^l) \;=\; C_W(R_2^l, R_1^l) \;=\; N_{R_2,l+1} \cdot N_{R_1,l+1} \cdot (|s_{R_1,l+1}| + |s_{R_2,l+1}|)^d \tag{13}$$

for $0 \leq l \leq h-2$.

Hence, for R-trees with equal height h, the total cost of a spatial join between R_1 and R_2 is the sum of node accesses at each level:

$$\begin{aligned} C_{SJ}(R_1, R_2) \;&=\; \sum_{l=0}^{h-2} \left\{ C_W(R_1^l, R_2^l) + C_W(R_2^l, R_1^l) \right\} \\ &=\; 2 \cdot \sum_{l=1}^{h-1} \left\{ N_{R_2,l} \cdot N_{R_1,l} \cdot (|s_{R_1,l}| + |s_{R_2,l}|)^d \right\} \end{aligned} \tag{14}$$

Evidently, the cost shown in Eq. (14) is an upper bound where no buffer is considered and every node access in R_i corresponds to a node access in R_j. [170] provided a detailed description of cost formulae for R_j, including the case of R-trees with different heights. As in [167], all the involved parameters were expressed as functions of dataset properties, namely cardinality N and density D. Experimental results suggested that the above cost model is accurate for uniform data (where the density remains almost invariant through the workspace), and reasonably good for non-uniform data distributions, where the density surface is used (similar results were shown in [97]).

4.2.2 *Formulae for Multi-way Joins.* As already discussed in Section 3.6, multi-way spatial join queries between n R-trees $R_1, ..., R_n$, can be represented by a graph Q, where Q_{ij} denotes the join condition between R_i and R_j. Papadias et al. [121; 122] provided formulae for the selectivity (i.e., the number of solutions among all possible n-tuples in the cartesian product) and the cost (in terms of node accesses) of some special cases of multi-way queries. In particular, taking into consideration the general idea that the total number of solutions is given by the following formula:

$$\#\text{solutions} \;=\; \#(\text{all possible n}-\text{tuples}) \cdot \text{Prob}(\text{a n}-\text{tuple constitutes a solution}) \tag{15}$$

and the fact that the pairwise probabilities are independent in case of acyclic graphs, the selectivity of an acyclic join graph is:

$$\text{Prob}(\text{a n}-\text{tuple is a solution}) \;=\; \prod_{\forall i,j:Q(i,j)=TRUE} \left(|s_{R_i}| + |s_{R_j}|\right)^d \tag{16}$$

and the total number of solutions at tree level l is:

$$\#\text{solutions}(Q,l) \;=\; \prod_{i=1}^{n} N_{R_i,l} \cdot \prod_{\forall i,j:Q(i,j)=TRUE} \left(|s_{R_i,l}| + |s_{R_j,l}|\right)^d \tag{17}$$

However, in case of cycles, the assignments are not independent anymore and Eq. (16) does not accurately estimate the probability that a random tuple constitutes a solution. For the special case of cliques only, [122] provided a formula for selectivity, based on the fact that if a set of rectangles mutually overlap then they must share a common area (the proof is extensive and can be found in [122]):

$$\#\text{solutions}(Q,l) \;=\; \prod_{i=1}^{n} N_{R_i,l} \cdot \left(\sum_{i=1}^{n} \prod_{j=1, j\neq i}^{n} |s_{R_j,l}| \right)^d \tag{18}$$

In order to provide cost formulae for multi-way joins, [122] decomposed the query graph Q into a set of legal subgraphs $Q_{x,y}$ (legal, means connected graph), which could be processed e.g., by applying Synchronous Traversal (cf. ST algorithm in Figure 14). Since, according to ST algorithm, the x roots of R-trees must be accessed in order to find root level solutions and, in turn, each solution will lead to x accesses at the next (lower) level, in its generalization at level l, there will be $x \cdot \#solutions(Qx, y, l+1)$ node accesses and the total cost for processing $Q_{x,y}$

using ST would be:

$$C_{mSJ}(R_1, R_2, ..., R_n, Q_{x,y}) \;=\; x + \sum_{l=0}^{h-2} x \cdot \#\text{solutions}(Q_{x,y}, l+1) \qquad (19)$$

Again, this formula is useful for query optimization purposes only when an accurate estimation of the number of solution is possible, i.e., in the cases of acyclic graphs and cliques only. Experimental results on those types of query graphs and uniform distributions of data demonstrated the accuracy of Eqs. (16-19), with the relative error being below 10% on the average and below 25% on the worst case. The extension of the cost models to support arbitrary query graphs and non-uniform data distribution was left as an open issue.

Extending [121], Park and Chung [132] analyzed the time and temporary space complexity of the formulae for tree and clique multi-way joins and showed that the complexity for the former type is much more than that for the latter type.

In a different line, Mamoulis and Papadias [99] addressed the problem of complex query processing, in which a n-way join follows n independent selection queries on the original (R-tree indexed) spatial datasets (see an example illustration in Figure 17, for n=2). Assuming that the original datasets share a common workspace, the authors anticipated that the spatial selections would affect not only the number of objects that would participate in the succeeding join, but also their spatial distribution, adding a dependency overhead. Two selectivity formulae, one for acyclic and one for clique joins, were proposed. The experimental results provided in [99] showed that the formulae were accurate enough, especially for pair-wise joins (the relative error was 8% for n=2, while it was raised up to 38% for n=4). Although the above analysis assumed uniformity, the model was also extended to work for arbitrary data distributions, taking into account the density surface concept [167; 169]. However, in that case the accuracy of the estimation was lowered.

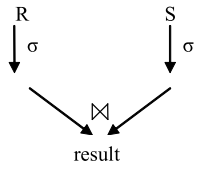


Fig. 17. A complex query execution plan.

4.3 Sampling and Histogram-based Techniques

Recalling the query optimization problem illustrated in Figure 4.2, selectivity estimation could be based on samples of the two (or n, in general) spatial datasets involved. An et al. [6] proposed the following three-step methodology: (i) pick samples from input datasets, either exploiting their R-tree indices or not; (ii) construct an R-tree for each of the samples; (iii) perform an R-tree join on the constructed R-trees. This was evaluated in comparison with the alternative of joining one sample with the entire other dataset. The conclusions drawn from the experimentation were clearly in favor of the proposed methodology.

Recently, a significant research effort has also focused on selectivity estimation based on histograms. In particular, [6] and [161] introduced novel types of histograms for estimating the selectivity of spatial selections and spatial joins, respectively, while [1] addressed the issue of accuracy in estimations of related work due to the ignorance of the cost of the refinement step and proposed new types of histograms that capture the complexity, size and location of the spatial objects. We do not provide further details about these works because they are not directly related to R-tree-based query optimization. The interested reader can find more in the cited papers.

5. IMPLEMENTATION ISSUES

The implementation of an access method in a commercial DBMS or a research prototype raises many issues that must be considered in order to provide an effective and efficient access to the underlying data. An access method is useless, unless it can be efficiently implemented in real-life data intensive applications. Making the access method part of a larger (usually multi-user) system is not an easy task. The access method must be adjusted to the underlying system architecture and therefore issues like concurrency control and parallelism must be handled carefully. In this section we discuss implementation issues regarding the R-tree access method. More specifically we investigate the following issues:

—the adjustment of the R-tree to parallel architectures
—the management of concurrent accesses
—R-tree implementations in research prototypes and commercial systems

5.1 Parallel Systems

One of the primary goals in database research is the investigation of innovative techniques in order to provide more efficient query processing. This goal becomes much more important considering that modern applications are more resource demanding, and are usually based on multi-user systems. A database research direction that has been widely accepted by developers is the exploitation of multiple resources (processors and disks) towards more efficient processing.

The design of algorithms for parallel database machines is not an easy task. Although in some cases the parallel version of a serial algorithm is straightforward, one must look carefully at three fundamental performance measures:

—*speed-up*: shows the capability of the algorithm when the number of processors is increased and the input size is constant. The perfect speed-up is the linear speed-up, meaning that if T seconds are required to perform the operation with one processor, then $T/2$ seconds are required to perform the same operation using two processors.
—*size-up*: shows the behavior of the algorithm when the input size is increased and the number of processors remains constant.
—*scale-up*: shows the performance of the algorithm when both the input size and the number of processors are increased.

There are three basic parallel architectures that have been used in research and development fields [41]:

—*shared everything*: all processors share the same resources (memory and disks) and the communication among processors is performed by means of the global memory.
—*shared disk*: all processors share the disks but each one has its own memory.
—*shared nothing*: the processors use different disks and different memory units and the communication among processors is performed using message passing mechanisms.

In addition to the above basic parallel architectures, several hybrid schemes have been proposed, in order to combine the advantages and avoid the disadvantages of each one. For example, the *shared virtual memory* [156; 26] scheme combines the shared nothing and the shared memory scheme in order to provide a global address space.

Parallelism can also be categorized in:

—*CPU parallelism*, where a task is partitioned to several processors for execution
—*I/O parallelism*, where the data are partitioned to several secondary storage units (disks or CD-ROMs) in order to achieve better I/O performance.

5.1.1 *Multi-disk Systems.* Using more than one disk devices leads to increased system throughput, since the workload is balanced among the participating disks and many operations can be processed in parallel. RAID systems have been introduced in [135] as an inexpensive solution to the I/O bottleneck. Using more than one disk devices, leads to increased system throughput, since the workload is balanced among the participating disks and many operations can be processed in parallel [29; 30].

Given a disk array, one faces the problem of partitioning the data and the associated access information, in order to take advantage of the I/O parallelism. The way data is partitioned reflects the performance of read/write operations. The declustering problem attracted many researchers and a lot of work has been performed towards taking advantage of the I/O parallelism, to support data intensive applications. Techniques for B^+-tree declustering have been reported in [151]. In [175] the authors study effective declustering schemes for the grid file structure. The challenge is to decluster an R-tree structure among the available disks, in order to:

—distribute the workload during query processing as evenly as possible among the disks, and
—activate as few disks as possible

There are several alternative designs that could be followed in order to take advantage of the multiple disk architecture. These alternatives have been studied in [75].

5.1.1.1 *Independent R-trees.* The data are partitioned among the available disks, and an R-tree is build for each disk. The performance depends on how the data distribution is performed:

—*Data Distribution.* The data objects are assigned to different disks in a round robin manner, or by using a hash function. This method guarantees that each disk will host approximately the same number of objects. However, even for small queries, all disks are likely to be activated in order to answer the query.

—*Space Distribution.* The space is divided to d partitions, where d is the number of available disks. The drawback of this approach is that due to the non-uniformity of real-life datasets, some disks may host more number of objects than the others, and therefore may become a bottleneck. Moreover, for large queries (large query regions) this method fails to balance the load equally among all the disks.

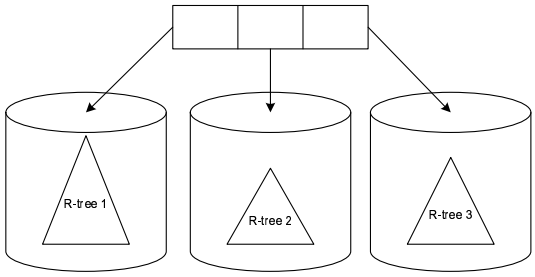


Fig. 18. Independent R-trees.

5.1.1.2 *R-tree with Super-Nodes.* This alternative uses only one R-tree. The exploitation of the multiple disks is obtained by expanding each tree node. More specifically, the logical tree node size becomes d times larger, and therefore each node is partitioned to all d disks (disk stripping). Although the load is equally balanced during query processing, all disks are activated in each query. This happens because since there is no total order of the rectangles (MBRs) that are hosted in a tree node, each node must be reconstructed by accessing all the disks (each node is partitioned among all disks).

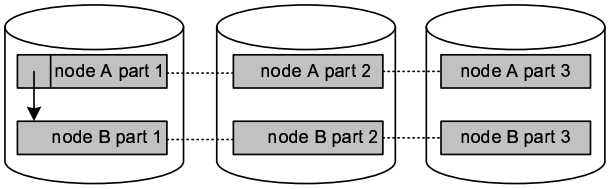


Fig. 19. R-tree with super-nodes.

5.1.1.3 *Multiplexed (MX) R-trees.* This alternative uses a single R-tree, having its nodes distributed among the disks. The main difference with an ordinary R-tree is that inter-disk pointers are used in order to formulate the tree structure. Each node pointer is a pair of the form $< diskID, pageID >$, where $diskID$ is the disk identifier that contains the page $pageID$. An example of an MX R-tree with 10 nodes distributed in 3 disks is given in Figure 20. It is assumed that the R-tree root is maintained in memory.

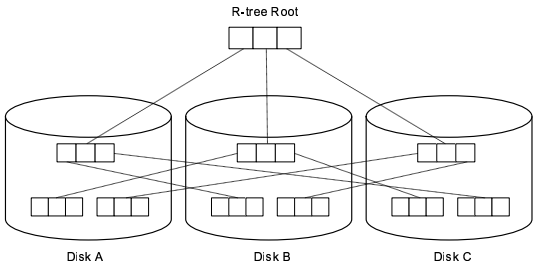


Fig. 20. MX R-tree example.

The main issue that must be explained is the node-to-disk assignment policy. The insertion of new objects will cause some nodes to split. The problem is to which disk the newly created node N_n will be assigned, whereas the target is to minimize the query response time. In order to obtain the best result, we could examine all nodes that lie in the same tree level. However, this operation is very costly because it results in many I/O operations. Instead, only the sibling nodes are examined, i.e., the nodes that have the same parent with N_n. Moreover, it is not necessary to fetch the sibling nodes, since the information that we require (MBRs) resides in the parent node (which has been fetched already in memory in order to insert the new object). There are several criteria that could be used in order to perform the placement of the new node N_n:

—*data balance*: In the best case, all disks must host the same number of tree nodes. If a disk contains more nodes than the others, it may become a bottleneck during query processing.
—*area balance*: The area that each disk covers plays a very important role when we answer range queries. A disk that covers a large area, will be accessed with higher probability than the others, and therefore it may become a bottleneck.
—*proximity*: If two nodes are near in space, the probability that they will be accessed together is high. Therefore, proximal nodes should be stored to different disks in order to maximize parallelism.

Although it is very difficult to satisfy all criteria simultaneously, some heuristics have been proposed in order to attack the problem:

—*round-robin*: The new node is assigned to a disk using the round-robin algorithm.
—*minimum area*: This heuristic assigned the new node to the disk that covers the smallest area.
—*minimum intersection*: This heuristic assigned the new node to a disk in order to minimize the overlap between the new node and the nodes that are already stored in this disk.
—*proximity index*: This heuristic is based on the proximity measure, which compares two rectangles and calculates the probability that they will be accessed together by the same query. Therefore, rectangles (which correspond to tree nodes) with high proximity must be stored in different disks.

Several experimental results have been reported in [75]. The main conclusion is that the MXR-tree with the proximity index method for node-to-disk assignment outper-

forms the other methods for range query processing. The performance evaluation has been conducted by using uniformly distributed spatial objects and uniformly distributed range queries. The proposed method manages to activate few disks for small range queries, and activate all disks for large queries, achieving good load balancing, and therefore can be used as an efficient method for parallelizing the R-tree structure. It would be interesting to investigate the performance of the method for non-uniform distributions.

5.1.1.4 *Parallel Query Processing.* The parallel version of the R-tree answers the same type of queries as the original R-tree structure much more efficiently. Although [75] focuses on range queries, parallel algorithms exist for other types of queries. In [129] parallel algorithms for NN queries on a multi-disk system have been studied. Three possible similarity search techniques are presented and studied in detail: Branch-and-Bound (BBSS), Full-parallel (FPSS) and Candidate Reduction (CRSS). Moreover, an optimal approach (WOPTSS) is defined, which assumes that the distance D_k from the query point to the k-th NN is known in advance, and therefore only the relevant nodes are inspected. Unfortunately, this algorithm is hypothetical, since the distance D_k is generally not known. However, useful lower bounds are derived by studying the behavior of the optimal method. All methods are studied under extensive experimentation through simulation. Among the studied algorithms, the proposed one (CRSS), which is based on a careful inspection of the R*-tree nodes, and leads to an effective candidate reduction, shows the best performance. However, the performance difference between CRSS and WOPTSS suggests that further research is required in order to approach the lower bound as much as possible.

5.1.2 *Multi-processor Systems.* The exploitation of multi-processor systems for spatial query processing has been used in order to achieve better performance of spatial data intensive applications. The ability to execute several operations in parallel may have a dramatic impact on the efficiency of the database system. While in multi-disk systems the main target is to achieve I/O parallelism, in multi-processor systems I/O and processing parallelism may be achieved (each processor may control one or many disks).

Although the use of parallelism seems extremely attractive towards query performance efficiency, several factors must be taken into consideration in order to provide a viable solution. Parallel query execution plans must be constructed in order to exploit the multiple processors. Therefore, careful decomposition of the query must be performed to achieve good load-balancing among the processors. Otherwise a processor to whom the largest task has been assigned will become a bottleneck. Moreover, if the processors communicate by means of a local area network (LAN) communication costs for interprocessor data exchange must be taken into account. These costs must also be included during query optimization and query cost estimation. Although the proposed techniques are applied in the case where processors communicate by means of a local area network (loosely coupled architecture), they can be applied as well in the case where processors are hosted in the same computer (tightly coupled architecture). In the latter case communication costs are reduced significantly.

5.1.2.1 *Independent R-trees.* Some of the methods used for multi-disk R-tree declustering can be used in the multi-processor case. For example, the spatial data could be partitioned allowing each processor to manipulate its own local R-tree structure (independent R-trees). If such a scheme is used, the following disadvantages are observed:

—If the majority of the queries refer to a subset of the data that most of them are hosted to a single processor, this processor may become a bottleneck, and therefore parallelism is not being exploited to a sufficient degree.
—In the case where the spatial data are partitioned with respect to a partitioning scheme based on a non-spatial attribute, all processors must be activated to answer a single query, even if a processor contains irrelevant data with respect to the query's spatial attributes.

5.1.2.2 *Leaf-Based Declustering.* In [85] a parallel version of the R-tree has been proposed in order to exploit parallelism in a multi-computer system, such as a network of workstations. The system architecture is composed of a master processor (primary site) and a number of slave processors (secondary sites). All sites communicate via an ethernet network. The allocation of pages to sites is carefully performed, in order to achieve efficiency in range query processing. The leaves and the corresponding data objects are stored in the secondary sites, whereas the upper tree levels are maintained in the primary site. More specifically, the leaf-level stored at the master contains entries of the form (MBR, serverID, pageID). Since the upper tree levels occupy relatively little space, they can be maintained in the main memory of the primary processor.

Given that the dataset is known in advance, Koudas et. al. suggest sorting the data with respect to the Hilbert value of the object's MBR centroid. Then, the leaf tree level is formed, and the assignment of leaves to sites is performed in a round-robin manner. This method guarantees that leaves that contain objects close in the address space will be assigned to different sites (processors), thus increasing the parallelization during range query processing. In Figure 21 we present a way to decluster an R-tree in four processors, one primary and three secondary. For simplicity it is assumed that each processor controls only one disk.

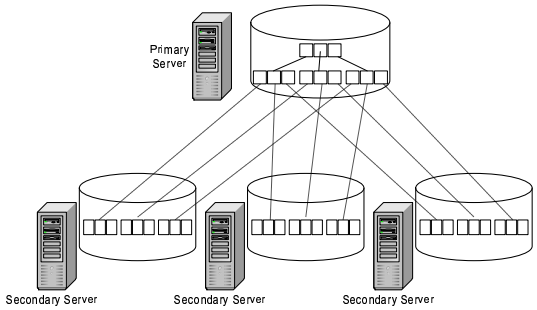


Fig. 21. Declustering an R-tree over three sites.

The parallel version of the R-tree described above can be implemented easily in

a multi-computer system (e.g., network of workstations). The main drawback of this approach is that the processor, which contains the upper levels of the R-tree, may become a bottleneck during intensive demands.

5.1.2.3 *GPR-tree.* The GPR-tree proposed in [174] utilizes a global index structure shared by a number of processors in a multi-computer system. Each processor maintains in memory a fraction of the GPR-tree, having its nodes partitioned into two groups: 1) local, when the corresponding page resides in the local disk, and 2) remote, when the corresponding page is managed by another processor.

5.1.2.4 *Master-Client R-trees.* This technique has been proposed in [149] and as in the leaf-based declustering approach uses a master-slave architecture. The master holds the upper levels of the R-tree. Unlike the previous approach, the leaf-level of the master contains entries of the form (MBR, serverID). Each client maintains its own local R-tree that is used to index the portion of the data that has been assigned to it. A potential problem with this method is that the master may become a hot-spot.

5.1.2.5 *Upgraded Parallel R-trees.* In [87] an upgraded parallel R-tree structure has been proposed. A partition function is used to partition the area into several sub-areas. The partition function is determined according to the distribution of the underlying data. Each sub-area is indexed by an R-tree structure. The whole structure is composed of: 1) a number of sub-trees, 2) data partitioning functions, 3) primary mapping category, and 4) secondary mapping category. Each item in primary mapping category is of the form (processorID, number of objects). Each item in secondary mapping category is of the form (subtree pointer, number of objects). In order to reduce communication costs, each processor hosts the complete structure, although only a fraction of the database is stored locally. In [87] experimental results are offered demonstrating the performance of the method. However, a comparison with previous approaches in not provided.

5.1.2.6 *Parallel Query Processing.* Several methods have been proposed towards parallel query processing using R-trees. In [64] a performance evaluation has been performed by comparing the parallel equivalents of R-trees and PMR quadtrees in a shared memory architecture. Experimental results have been reported for range query and spatial join queries.

Brinkhoff et al. in [26] study efficient parallel algorithms for parallel spatial join processing using R-trees. In their work the *shared virtual memory* architecture has been used (a special implementation of shared-nothing with a global address space, [156]) to implement the access methods and the proposed algorithms.

Parallel range query processing using R-trees with leaf-based declustering has been studied in [85]. The authors also provide cost estimates, taking into consideration the communication costs incurred due to message passing among processors.

Parallel NN query processing techniques are provided in [125; 127], which are based on the multi-computer architecture of [85] described previously. The main motivation is that although the branch-and-bound NN algorithm proposed in [142] can be directly applied in a parallel R-trees structure, intraquery parallelism is not being exploited due to the serial nature of the algorithm. Several parallel algorithms

have been proposed, implemented and evaluated using synthetic and real-life spatial datasets.

In [5] the authors discuss R-tree implementation issues in a multi-computer architecture. The performance of parallel R-trees has been evaluated using insertions, range queries with large query window, and range queries with small query window. Uniform and non-uniform datasets have been used for the performance evaluation. Two metrics have been used: query response time and system throughput when multiple queries are executed concurrently. It has been shown that parallel implementation of R-trees on a cluster of workstations comprising of eight Sun Ultra-Sparc processors give significant improvement in response time and throughput.

Parallel range query processing in distributed shared virtual memory architecture has been reported in [172]. A range query is decomposed to a number of subqueries, and each subquery is assigned to a processor. Two phases are identified: (i) in the *workload phase*, a number of internal tree nodes are determined, (ii) in the *search phase* the corresponding subqueries are executed in parallel. Performance results based on query response time and speed-up are provided.

A very important issue in parallel and distributed query processing is the migration of data from one disk to another or from one server to another, according to the access patterns used to access the data. In [93] the authors study migration issues for R-trees.

5.2 Concurrency Control

The management of concurrent operations in access methods is considered very important because it is strongly related to the system performance, the data consistency and the data integrity. When index updates interfere with access operations, a synchronization mechanism must exist in order to guarantee that the result of each operation is correct. Moreover, this synchronization must be efficient, preventing exclusive index locking for long time periods. In [143] two main categories for scheduling operations have been identified:

—top-down approaches, where an update operation locks its scope to prevent other updates. Read operations might not be allowed in the scope of an update operation until the latter commits or they may be allowed during the search phase or the restructuring phase of the update.
—bottom-up approaches, where an update operation behaves like a read operation on the way to the leaf-level of the index, and then moves up the tree, locking only a few nodes simultaneously and making the necessary changes.

Since the B-tree is implemented in many commercial systems, concurrency control issues in B-trees have been extensively studied [73; 106; 143; 155]. As concurrent operations can improve the efficiency of B-trees, similarly they can also improve R-tree efficiency. However, due to the different nature of the tree structure, the B-tree can not be applied directly. Moreover, although some straightforward modifications could be applied, the results are not efficient enough.

5.2.1 *R-link.* Ng and Kameda in [111] discuss methods for concurrency control in spatial access methods, and particularly in R-trees. The first method that we discuss is similar to the B-link method for the case of B-trees. The R-link method

have been proposed by Ng and Kameda in [112] and almost simultaneously by Kronacker and Banks in [81] as a solution for the concurrency control problem in R-tree based access methods. The R-link is an R-tree variant, where each tree node contains a number of pointers, one for each child node, and an additional link pointer used for concurrency control. All nodes that reside at a specific level of the tree are linked together. The main purpose of the link pointers is to be able to decompose operations into smaller atomic actions.

In the following study two types of locks are used. An R-lock is used for shared reading, and an X-lock is used as an exclusive lock. As in the case of B-link, when a search takes place, a concurrent insertion or delete might split or merge a node respectively. As a result, link pointers should be followed to check for cases where the split has not yet been propagated to the parent node.

Search operations start at the root and descent the tree using R-locks. Upon visiting a tree node an R-lock is applied to the node. The R-lock is released when the child nodes that must be visited have been determined. The problem is that some insertions may not have been committed, which means that some split nodes may not have been recorded in their parent nodes but have only been recorded as link pointers to their siblings. Therefore, we have to examine all nodes emanating from horizontal pointers. If the MBRs of these nodes overlap with the query region, we check if their parent node is valid. If it is valid, the corresponding search path would be examined from the parent node according to the R-tree search algorithm. Otherwise, we include in the search path the subtree emanating from the corresponding split node, since it contains relevant data that their existence have not yet been recorder in the parent node.

Insertion operations start at the root and descent the tree until the appropriate leaf node is detected. If the leaf can not hold more entries, a split operation is performed. Changes must be propagated upwards. Only MBRs that need enlargement are going to change. In order to avoid conflicts with other operations, the MBR enlargement is deferred. During tree descent the expanded MBR is stored in a list of pending updates. This list is used in the second phase, where MBR enlargement takes place. Subsequent operations must examine this list. During the first phase of descending the tree, the corresponding MBRs are enlarged and parent nodes are updated with the new split nodes that only existed as linked nodes until now.

In the case of deletions, during tree descent multiple paths are examines, and in every node we execute the pending updates that have been registered by previously executed insertions, deletions or splits. If a node becomes empty, it is marked as *deleted* and it is not yet removed because other operations may be using it. A garbage collection algorithm is executed periodically in order to delete all marked nodes. If a node underflows, it is appended to a list, and when the size of the list reaches a threshold a condense algorithm is executed.

A slightly different approach has been followed in [81], where a more sophisticated technique is used in order to provide ordering of sibling nodes. Logical sequence numbers (LSN) are assigned to the nodes. These numbers are similar to timestamps since they monotonically increase over time. The LSN numbers are used during search and insert operations in order to make correct decisions about tree traversal. During tree descent no lock-coupling is needed, and therefore only one

node is locked at any given time. The comparison of the method with lock-coupling concurrency control mechanisms in R-trees has shown that R-link trees maintain high throughput and low response times as the load increases.

5.2.2 *Top-down Approaches.* Although B-link is widely recognized as a structure of theoretical and practical importance, this is not the case for R-link. Commercial systems are using the classical R-tree [57] structure or the R*-tree [12]. In [31] concurrency control techniques have been proposed, by using different methods than the R-link structure. Three types of locks are used, R-locks, W-locks and X-locks. Lock-coupling and breadth-first search are used to locate the set of objects that satisfy the query. A node that is examined remains locked until the search operation commits.

A search operation starts at the root, and descends the tree by inserting each visited node into a queue. An element of the queue is extracted and examined in order to determine which of it's children's MBR overlap with the query region. If the examined node is not a leaf the children that are relevant to the query region are R-locked and inserted into the queue left-to-right.On the other hand, if the examined node is a leaf the corresponding children are data objects and must be examined further (refinement step) to check if they satisfy the query. The search operations terminated when the queue is empty. Since all nodes in the queue are R-locked, update operations can not be applied to these nodes.

Insertions are performed in two phases. During the first phase, lock coupling is used to the path from the root to the corresponding leaf node that will host the new object. At each node the appropriate path is selected and followed. The MBRs of the nodes are adjusted properly. In the second phase the new object is placed into the corresponding leaf node. If the leaf node is full, a split operation must be applied. To avoid interference of other update operations, the leaf and its parent are W-locked before the execution of the split. The same is applied to other ascendants if they are full. Therefore, all full nodes from the leaf to the root are W-locked. The set of these nodes is the scope of the current operation. During reconstruction of the tree the W-lock of a node must be converted to an X-lock before modification. After the split operations, the MBRs of the parent nodes are adjusted accordingly to cover the MBRs of their children.

Deletions are applied in a similar manner and are also characterized by two phases. During the first phase an appropriate leaf is found and the corresponding path from the root to the leaf is W-locked. We note that several paths may qualify, since many MBRs may totally cover the deleted object. In order to guarantee that the deleted object will not be missed, all paths must be examined in a breadth-first search manner. In the second phase the corresponding object is deleted. Appropriate actions must take place in order to deal with node underutilization. Changes are propagated upwards and the appropriate MBRs are adjusted accordingly. In general, there are three techniques that can be used in underutilized nodes:

(1) *reinsertion*, where objects in the underutilized node are reinserted in the tree,
(2) *merge-at-half*, where the node is merged, and
(3) *free-at-empty*, where the node is deleted when it is completely empty.

The proposed algorithm used the last technique since it is the most efficient one

according to [73]. A study of granular locking in R-trees can be found in [28].

5.3 Research Prototypes and Commercial Systems

By studying the literature in SAMs it is evident that the R-tree structure and its variants attracted a lot of attention. The simplicity of the structure and its ability to handle spatial objects efficiently are two very tempting reasons in order to incorporate the structure in research prototypes and commercial database systems. It is well known that it is not sufficient to support spatial objects in a database system. Efficient methods to access these data are of great importance taking into consideration the requirements of modern demanding applications [154].

There are several implementations of the R-tree access method and its variants that are offered by researchers all over the world. Most of these implementations have been performed in order to conduct experiments and performance comparisons with other structures, to investigate the performance of a proposed algorithm, or to provide modifications and enhancements to the structure in order to improve its efficiency. However, these implementations have been performed for research purposes and therefore issues like concurrency control, recovery, buffering issues and other implementation details have generally been neglected. Moreover, the majority of these implementations are stand-alone, meaning that they only serve the needs of the experimental evaluation rather than being an integral part of a platform. In the sequel we briefly describe efforts for R-tree implementations in research prototypes and commercial database systems.

5.3.1 *BASIS.* The BASIS prototype system (Benchmarking Approach for Spatial Index Structures) has been proposed in [55] in order to provide a platform for experimental evaluation of access methods and query processing algorithms. An outline of the architecture is depicted in Fig. 22. The platform has been implemented in C++ and runs on top of UNIX or Windows. The platform is organized in three modules:

—the *storage manager*: Provides I/Os and caching services,
—the *SAM toolkit*: It is a set of commonly used SAMs and defines some design patterns, which support an easy development of new structures, and
—the *query processor*: It is a library of algorithms whose design follows the general framework of the iterator model [51].

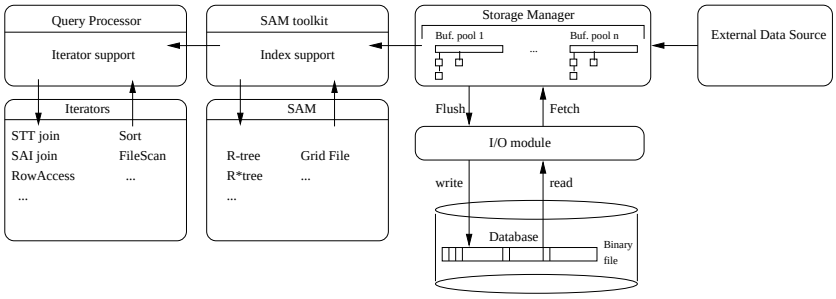


Fig. 22. The BASIS architecture.

The storage manager is essentially in charge of managing a database. A database is a set of binary files that store either datasets (i.e., sequential collection of records) or SAMs. A SAM or index refers to records in an indexed data file through record identifiers.

The buffer manager handles one or several buffer pools. A data file or index (SAM) is assigned to one buffer pool, but a buffer pool can handle several indices. This allows much flexibility, when assigning memory to the different parts of a query execution plan. The buffer pool is a constant-size cache with LRU or FIFO replacement policy (LRU by default). Pages can be pinned in memory. A pinned page is never flushed until it is unpinned.

There are two main types of files that are handled by the storage manager:

(1) *data files* are sequential collections of formatted pages storing *records* of a same type. Records in a data file can either be accessed sequentially, or by their address.
(2) *SAMs* are structured collections of index entries. An index entry is a built-in record type with two attributes: the key and a record address. The key is the geometric key, usually the MBR. The currently implemented SAMs are a grid file, an R-tree, an R*-tree and several R-tree variants based on bulk-loading techniques.

The BASIS architecture allows an easy customization and extension. Depending on the query processing experiment, each level is easily extendible: the designer may add a new SAM, add a new spatial operator or algorithm at the query processor level, or decide to implement her own query processing module on top of the buffer management (I/O) module, which implements adequate functionality. As an example, a performance evaluation of spatial join processing algorithms implemented in BASIS has been reported in [130]. Generally, the BASIS prototype system can be used for experimental evaluation of SAMs and spatial query processing algorithms, by allowing the designer to create various query execution plans according to the needs of the experimentation. Moreover, the platform offers a fair comparison among the competing methods since the same storage and buffer management policies are used. Some issues, however, have not been taken into consideration, like concurrency control and recovery.

5.3.2 *Generalized Search Trees (GiST).* Extensibility of data types and queries are very important in order to allow database systems to support new non-traditional applications. GiST (Generalized Search Trees) is an index structure, which supports an extensible set of data types and queries. GiST is a balanced tree (all leaf nodes are at the same tree level) that provides template algorithms for searching and modifying the tree structure [60; 82]. In leaf nodes pairs of $(key, recordID)$ are stored, whereas in internal nodes the GiST stores $(predicate, treePTR)$ pairs. GiST supports the standard search, insert and delete operations. However, in order for these operations to work properly, external functions must be provided. Therefore, the combination of the generic functionality of GiST and the functionality provided by the designer results in a fully functional access method.

An overview of the GiST architecture is presented in Figure 23. External functions are called by the GiST core in order to provide the required functionality.

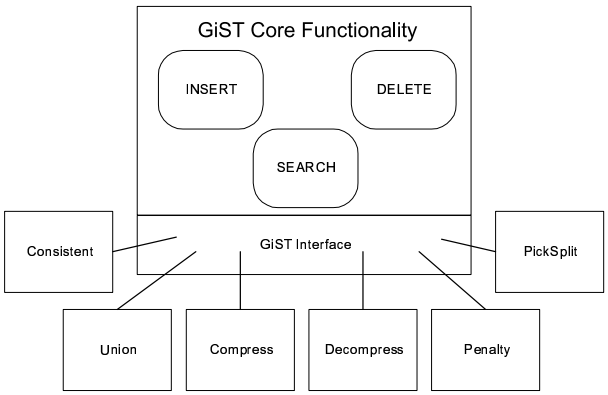


Fig. 23. Overview of GiST architecture.

These external functions, which comprise the GiST interface, are briefly described below [60]:

—*Consistent*(E, q): Given an entry $E = (p, ptr)$ and a query predicate q, the function returns true if and only if the p matches q.
—*Union*$(\mathcal{P})$: Given a set $\mathcal{P}$ of entries $(p_1, ptr_1), ..., (p_n, ptr_n)$ the function returns the union of $p_1, ..., p_n$.
—*Compress*(E): Given an entry $E = (p, ptr)$, the function returns the entry $E' = (p', ptr)$, where p' is a compressed representation of p.
—*Decompress*(E): Returns a decompressed representation of E.
—*Penalty*(E_1, E_2): Given two entries $E_1 = (p_1, ptr_1)$ and $E_2 = (p_2, ptr_2)$ returns a domain-specific penalty for inserting E_2 in the subtree rooted at E_1. This function is used for insertion and splitting purposes, where criteria for selecting a subtree and splitting a node must be specified.
—*PickSplit*$(\mathcal{P})$: Given a set $\mathcal{P}$ of $N+1$ entries, the function divides $\mathcal{P}$ into two subsets $\mathcal{P}_1$ and $\mathcal{P}_2$. The function is used for splitting purposes, where criteria for node splitting must be defined.

By providing implementations for the above functions, all R-tree variants can be supported by GiST, except the R^+-tree. This is due to the fact that the R^+-tree performs object splitting allowing pieces of an object to be stored in several leaf nodes. This functionality is not supported by GiST, which assumes that the tree is a hierarchical partitioning of the data. In [60] support for B^+-trees, R-trees, and RD-trees [59] is provided, and several performance and implementation issues are discussed.

5.3.3 *The SHORE Project.* SHORE integrates concepts and services from file systems and object-oriented databases. The main objective of the SHORE project [27] is to provide a persistent object system to serve the needs of modern demanding applications such as CAD systems, persistent programming languages, geographic information systems (GIS), satellite data repositories and multimedia applications. SHORE extends the EXODUS storage manager providing more features and support for typed objects and multiple programming languages. The

SHORE architecture is based on the following layers:

—*SHORE Storage Manager (SSM)*: It is a persistent object storage engine that supports creation of persistent files of records. The storage manager offers concurrency control and recovery, supporting two-phase locking and write-ahead logging.
—*SHORE Value-Added Server (SVAS)*: It is based on the functionality of SSM in order to provide support for types objects, a UNIX-like naming, access control mechanisms and client-server capabilities.
—*SHORE Data Language (SDL)*: It is based on ODMG ODL and supports object-oriented data types independently of the programming language used.

Paradise [42] is a parallel geographic information system, based on SHORE, with many capabilities in handling large geographic datasets. Paradise applies object-oriented and parallel database features to provide efficiency in storing and querying large amounts of spatial data. The Paradise server is implemented as a SHORE value-added server on top of SHORE storage manager. Paradise adds extra functionality to the basic SHORE server: catalog manager, extend manager, tuple manager, query optimizer and query execution engine, support for spatial abstract data types (points, polylines, polygons and raster). Efficient access of the stored spatial objects is enhanced by the use of R*-trees. The R*-tree has been implemented in the SHORE storage manager relatively easily, since a lot of B^+-tree code (already supported by SHORE) was reused. In addition, Paradise supports bulk-loaded R-trees. The packing algorithm used in Paradise is similar to the packing algorithm used in [76], which is based on the Hilbert curve.

5.3.4 *R-trees in Commercial Database Systems.* The support of complex data types (non alphanumeric) and access methods is a key issue in modern database industry, since it allows the DBMS to extend its functionality beyond pure relational data handling. A simple approach for complex data handling is to use BLOBs (binary large objects) to store the complex data. The limitation of this approach is that the DBMS is not aware of what is stored in the BLOB, and therefore the management of the BLOB contents must be performed by the user application. The operations and algorithms to manipulate the contents of the BLOB are not available to the query processor. Another approach is to allow the DBMS to provide the needed functionality for complex data types (e.g., polygons, line segments) and access methods. These data types are supported by the DBMS just like the ordinary alphanumeric data types. The problem is that it is not possible for each DBMS vendor to implement all the data types and access methods that any application demands (or will require in the future). A more revolutionary approach is to allow the user to define additional data types and access methods for data handling according to application needs (extendible DBMS). In the sequel we briefly describe efforts from database vendors for spatial query processing using R-trees:

—*PostgreSQL*: PostgreSQL provides support for B-trees, R-trees, GiST and Hashing. Therefore, a user can rely on the provided R-tree implementation, or can implement other R-tree variants using the GiST approach. The R-tree supported is based on the original proposal by Guttman and it is based on the quadratic split policy. To create an R-tree index using SQL, one should issue the command:

CREATE INDEX *myindex* ON *mytable* USING RTREE (*mycolumn*). Details regarding PostgreSQL features can be found in [137].

—*Mapinfo SpatialWare*: SpatialWare extends an Informix, Microsoft SQL Server, IBM DB2 or Oracle database to handle spatial data such as points, lines and polygons. It extends database capabilities avoiding a middleware architecture. All functionality is contained directly into the DBMS environment. SpatialWare is implemented in the following ways: 1) in Informix as a datablade, 2) in SQL Server using the Extended Stored Procedure mechanism, 3) in IBM DB2 as an extender, and 4) in Oracle as Spatial Server. SpatialWare provides R-tree support for spatial data indexing purposes [102; 105].

—*Oracle Locator and Oracle Spatial*: Oracle Locator, which is a feature of Oracle Intermedia, provides support for location-based queries in Oracle 9i DBMS. Geographic and location data are integrated in the Oracle 9i server, just like ordinary data types like CHAR and INTEGER. Oracle Spatial provides location-based facilities allowing the extension of Oracle-based applications. It provides data manipulation tools for accessing location information such as road networks, wireless service boundaries, and geocoded customer addresses. Both Oracle Locator and Oracle Spatial provide support for linear quadtrees and R-trees for spatial data indexing purposes [84; 114].

—*IBM Informix and DB2* In Informix, the R-tree is built-in to the database kernel and works directly with the extended spatial data types. The Informix R-tree implementation supports full transaction management, concurrency control, recovery and parallelism. A detailed description of the Informix R-tree implementation can be found in [69]. A description of spatial data handling in a DB2 database can be found in [2].

—*Other Vendors* Apart from large database vendors, the R-tree has been adopted by other application vendors as well. Examples include the EzGIS and EzCAD applications that exploit the R-tree to index spatial objects [43].

6. EPILOG

Although 'trees have grown everywhere' because of their simplicity and their satisfactory average performance, only a small subset of them have been successfully used by researchers and developers in prototype and commercial database systems. The R-tree is the most influential SAM and has been adopted as the index of choice in many research works regarding spatial and multidimensional query processing. Taking into consideration the work performed so far, we can state that the R-tree is for the spatial databases, what the B-tree is for alphanumeric data types. In fact, a serious reason for its acceptance is exactly the resemblance to the B-tree.

Considering the work performed on R-trees we realize that contains almost all aspects concerning a database system: query processing, query optimization, cost models, parallelism, concurrency control, recovery. This is the main reason why gradually database vendors adopted the R-tree and implemented it in their products for spatial data management purposes.

In this survey paper we presented research performed during the last 18 years, after Guttman had presented the R-tree access method in 1984 [57]. We described several modifications to the original structure that improve its query processing

performance, ranging from structural modifications to algorithmic enhancements. Also, query processing algorithms were described in detail, that enable the structure to answer range, NN, spatial joins and other query types. Several cost models estimating the output size and the number of node accesses were presented, according to the query type used. These cost estimates are invaluable for query optimizers. Finally, implementation issues were covered, regarding concurrency control, recovery and parallel processing, along with a presentation of R-tree implementations by several database vendors.

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