Spatial Join Techniques

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A variety of techniques for performing a spatial join are reviewed. Instead of just summarizing the literature and presenting each technique in its entirety, distinct components of the different techniques are described and each technique is decomposed into an overall framework for performing a spatial join. A typical spatial join technique consists of the following components: partitioning the data, performing internal memory spatial joins on subsets of the data, and checking if the full polygons intersect. Each technique is decomposed into these components and each component is addressed in a separate section so as to compare and contrast the similar aspects of each technique. The goal of this survey is to describe algorithms within each component in detail, comparing and contrasting competing methods, thereby enabling further analysis and experimentation with each component and allowing for the best algorithms for a particular situation to be built piecemeal, or, even better, enabling an optimizer to choose which algorithms to use.

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General Terms: Algorithms,Design

Additional Key Words and Phrases: external memory algorithms, plane-sweep, spatial join

1. INTRODUCTION

This article presents an in-depth survey and analysis of spatial joins. A large body of diverse literature exists on the topic of spatial joins. The goal of this article is not only to survey the literature on spatial joins, but also to extract algorithms and techniques from the literature and to present a coherent description of the state of the art in the design of spatial join algorithms. Frequently, an article presents a complete framework for performing a spatial join. Instead of summarizing each complete framework individually, we decompose them into components in two ways. First, if several methods are similar, then a common algorithm is extracted from the frameworks to show specifically how each framework differs from the others.

Table I. Components of spatial join algorithms.

Internal Memory Methods	A.3 Nested Loop Join [Mishra and Eich 1992] A.3 Index Nested-Loop Join [Elmasri and Navathe 2000] 3.1 Plane Sweep [Arge et al. 1998; Preparata and Shamos 1985] 3.2 Z-Order [Aref and Samet 1994b; Orenstein 1986]
Section 4.1 External Memory Methods (Both Datasets Indexed)	4.1.1 Hierarchical Traversal [Brinkhoff et al. 1993; Günther 1993; Huang et al. 1997b; Kim et al. 1995] 4.1.2 Non-Hierarchical Methods [Harada et al. 1990; Kitsuregawa et al. 1989] 4.1.3 Multi-Dimensional Point Methods [Song et al. 1999]
Section 4.2 External Memory Methods (One Dataset Not Indexed)	4.2.1 Construct a Second Index [Lo and Ravishankar 1994] 4.2.2 The Index as Partitioned Data [van den Bercken et al. 1999; Mamoulis and Papadias 2003] 4.2.3 The Index as Sorted Data [Arge et al. 2000; Gurret and Rigaux 2000]
Appendix 4.3 External Memory Methods (Neither Dataset Indexed)	B.1 External Plane Sweep [Jacox and Samet 2003] 4.3.1 Generic Partitioning Algorithm B.2 Grid Partitioning [Patel and DeWitt 1996; Zhou et al. 1997] B.3 Strip Partitioning [Arge et al. 1998] B.4 Size Partitioning [Koudas and Sevcik 1997; Arge et al. 1998] B.5 Data Partitioning [Lo and Ravishankar 1995; 1996]
Appendix D Refinement	D.1 Ordering Candidate Pairs [Abel et al. 1999] D.2 Polygon Intersection Test [Preparata and Shamos 1985; Brinkhoff et al. 1994] D.3 Alternate Intersection Test [Brinkhoff et al. 1994]

Table II. Spatial join issues.

Fundamentals and Concepts	Section 2 Spatial Join Basics Appendix A.1 Minimum Bounding Rectangles Appendix A.2 Linear Orderings
Processing Issues	4.1.4 Joining Data Nodes
Partitioning Issues	4.3.2 Determining the Number of Partitions 4.3.3 Repartitioning 4.3.4 Avoiding Duplicate Results
Section 6 Selectivity Estimation	Uniform Dataset Estimates [Aref and Samet 1994a] Non-Uniform Dataset Estimates [Belussi and Faloutsos 1995; Das et al. 2004; Faloutsos et al. 2000; Mamoulis and Papadias 2001b]
Appendix C Alternate Filtering Techniques	C.1 False Hit Filtering [Brinkhoff et al. 1993; Koudas and Sevcik 1997; Veenhof et al. 1995; Zimbrao and de Souza 1998] C.2 True Hit Filtering [Brinkhoff and Kriegel 1994a] C.3 Non-Blocking Filtering [Luo et al. 2002]

For instance, there exist several methods for performing a spatial join on R-trees [Guttman 1984], each using a hierarchical traversal method. From these different algorithms, we create a generic hierarchical traversal algorithm and show how each method slightly varies the generic algorithm (see Section 4.1.1). Thus, each method is presented in a simpler manner that allows it to be more thoroughly compared and contrasted with similar algorithms. By doing so, the strengths and weaknesses of each competing algorithm become more apparent. The various components are tabulated in Table I along with the sections in which they are discussed. The second approach to decomposing the various methods is to extract common issues from

Table III. Specialized spatial joins.

Section 5.1 Multiway Spatial Joins	5.1.1 Multiway Indexed Nested Loop [Mamoullis and Papadias 1998; Mamoulis and Papadias 2001a; Papadias et al. 1998] 5.1.2 Multiway Hierarchical Traversal [Mamoullis and Papadias 1998; Mamoulis and Papadias 2001a; Papadias et al. 1998]
Section 5.2 Parallel Spatial Joins	Parallel Hierarchical Traversal [Brinkhoff et al. 1996] Parallel Grid Partitioning Methods [Luo et al. 2002; Patel and DeWitt 2000; Zhou et al. 1997] Hypercube Spatial Joins [Hoel and Samet 1994]
Section 5.3 Distributed Spatial Joins	Distributed Filter and Refine [Abel et al. 1995; Mamoulis et al. 2003]

each and address these issues in separate sections. For example, many of the spatial join methods for handling unindexed data must deal with the issue of removing duplicate results from the different stages of spatial join processing. Rather than separately show how each framework handles duplicate results, different techniques for handling duplicate results are described in a separate section (Section 4.3.4). The sections dealing with issues that arise in algorithms are tabulated in Table II. Furthermore, spatial joins for specialized environments are discussed in separate sections, as tabulated in Table III.

The rest of the paper is organized as follows. Section 2 defines the spatial join operation and discusses design parameters that influence the performance of a spatial join. Typically, a spatial join is performed in two stages: the *filter* stage in which complicated polygonal objects are approximated by rectangles and the *refinement* stage which removes any results produced during the filtering stage that do not satisfy the join condition [Orenstein 1989b]. Section 3 describes internal memory filtering techniques, while Section 4 describes external memory filtering techniques. Section 5 explains how spatial joins are handled in specialized situations, such as in parallel architectures, while Section 6 discusses selectivity estimation. Concluding remarks are drawn in Section 7. In addition, Appendix A describes the following two concepts that are important to many spatial join algorithms: the *minimum bounding rectangle* (also known as a *minimum bounding box*) and *linear orderings*. Appendix B provides details of the methods that do not rely on the input datasets being indexed. The remaining appendices elaborate further on the filter and refine stages. In particular, Appendix C presents extended or alternate filtering techniques, while Appendix D discusses the refinement phase.

2. SPATIAL JOIN BASICS

Given two datasets of multi-dimensional objects in Euclidean space, a spatial join finds all pairs of objects satisfying a given relation between the objects that involves the values of their spatial components, such as intersection. For example, a spatial join answers such queries as *find all of the rural areas that are below sea level*, given an elevation map and a land use map [Veenhof et al. 1995]. To illustrate the concept further, a simplified version of a spatial join is as follows: given two sets of rectangles, R and S, find all of the pairs of intersecting rectangles between the two sets, that is, for each rectangle r in dataset R, find each intersecting rectangle, s, from dataset S, as illustrated in Figure 1. The general spatial join problem, also

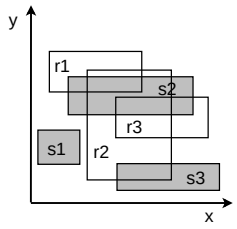


Fig. 1. A spatial join to find the intersecting objects of datasets R, consisting of objects $r1$, $r2$, and $r3$, and S, consisting of objects $s1$, $s2$, and $s3$, will report the intersection of objects $r1/s2$, $r2/s2$, $r2/s3$ and $r3/s2$.

known as a *spatial overlay join*, extends the simplified version in several ways:

(1) The datasets can be objects other than rectangles such as points, segments, or polygons [1].
(2) The datasets might have more than two dimensions [2].
(3) The relationship between pairs of objects can be any relation between the objects that involves the values of the spatial components, such as intersection, nearness, enclosure, or a directional relation (for example, find all pairs of objects such that r is northwest of s [Zhu et al. 2001]).
(4) There might be more than two datasets in the relation (a *multiway spatial join*) or only one dataset (a *self spatial join*).

The problem of spatial join has been the subject of much attention in fields other than spatial databases. In particular, its solutions make use of the same principles as interference detection in robotics applications (for example, [Gottschalk et al. 1996]), game programming (for example, [Ulrich 2000]), and design rule checking in VLSI applications (for example, [Rosenberg 1985]). These topics are beyond the scope of this review, but for more details, the interested reader should consult texts such as [Samet 2006].

Spatial joins are distinguished from a standard relational join [Mishra and Eich 1992] in that the join condition involves the multi-dimensional spatial attribute of the joined relation. This property prevents the use of the more sophisticated relational join algorithms. For instance, because the data objects are multi-dimensional, there is no ordering of the data that preserves proximity. Relational join techniques that rely on sorting the data, such as the sort-merge join [Mishra and Eich 1992], work because neighboring objects (those with the next higher and lower value) are adjacent to each other in the ordering. However, in more than one dimension, the data can not be sorted so that this property holds for all directions and dimensions. For example, in two dimensions, the left and right neighbors can be adjacent to an

[1] An extensive amount of research has also examined the related operation, the segment join [Balaban 1995; Brinkmann and Hinrichs 1998; Chazelle and Edelsbrunner 1992; Mairson and Stolfi 1988; van Oosterom 1994], and the more general overlay operation which also addresses the effects of the result of the spatial join on the way in which the combined attributes of the join are handled [van Roessel 1987; 1991; 1994].
[2] A one dimensional version of the spatial join would be an interval join [Enderle et al. 2004].

object in an ordering, but then the top and bottom neighbors will need to go elsewhere in the order (see Appendix A.2 for a further discussion of multi-dimensional orderings).

Other relational join techniques are also inapplicable because the data objects might have extent. For example, equijoin techniques [Mishra and Eich 1992] (for example, hash joins), will not work with spatial data because they rely on grouping objects with the same value, which is not possible when the objects have extent. This is the same reason that equijoin techniques will not work with intervals (extent in one dimension) or inequalities. As an example, for a one-dimensional hash join on datasets R and S, a group of objects from R is mapped to the same bucket, G, if their keys, key, are mapped by the hash function $f(key)$ to the same value. An object g in bucket G can only be paired with an object from S whose key is also mapped to the same value ($f(key)$) by the same hash function. This property does not hold for objects with extent, such as a rectangle, because the objects can overlap each other and a disjoint grouping might not exist. In fact, an object from dataset R could potentially intersect every object from dataset S. Because of these two factors (that is, failure to satisfy proximity preservation and extent) relational join algorithms cannot be used directly to perform a spatial join.

The computational geometry approach to solving the simplified spatial join (a two-set rectangle intersection) is to use a plane-sweep technique [Preparata and Shamos 1985] (see Section 3.1). In order to use the plane-sweep method for a general spatial join, two problems must be overcome: the objects are not necessarily rectangles and there might not be sufficient internal memory for the plane-sweep algorithm. Furthermore, calculating whether two complex objects satisfy the join condition, such as intersection, can be an expensive operation, and performing as few of these operations as possible improves overall performance. To overcome these problems, a spatial join is typically performed using a two stage filter-and-refine approach [Orenstein 1989b].

In the filter-and-refine approach, the spatial join is first solved using approximations of the objects in the filtering stage and any incorrect results due to the approximations are removed in the refinement stage using the full objects [3]. In the filtering stage, objects are typically approximated using *minimum bounding rectangles* (see Appendix A.1), hereafter referred to as MBRs, which require less storage space than the full object, resulting in faster processing and less expensive I/O operations [4]. For example, GIS objects might be polygons, each consisting of thousands, or even millions, of points. Reading these objects in and out of memory could easily be the dominant cost of performing a spatial join, depending upon the available amount of internal memory and the ratio of I/O to CPU performance, whereas a filter-and-refine approach alleviates this problem. Furthermore, a spatial join on rectangles presents a more tractable problem. For smaller datasets, the filtering stage of the spatial join can be solved using internal memory techniques, which are described in Section 3. For larger datasets, external (secondary) memory

[3] While the filter and refine stages can be considered two phases of one technique, Park et al. [1999] propose separating the filter and refinement steps for query optimization so that each stage can be combined with non-spatial queries.

[4] Other approximations also can be used (see Appendix C).

techniques are required for the filtering stage, which are described in Section 4.

The output of the filtering stage is a list of all pairs of objects whose approximations satisfy the join condition, which is referred to as the *candidate set*, and is typically represented by pairs of object ids. The candidate set includes all of the desired pairs, those whose full objects satisfy the join condition, but also includes pairs whose approximations satisfy the join condition, but whose full objects do not. The extra pairs appear because of the inaccuracy of the object approximations (see Appendix A.1). The purpose of the refinement stage is to remove the undesired pairs using the full objects, producing the final list of object pairs that satisfy the given join condition. Refinement techniques are described in Appendix D.

As mentioned above, the dominant cost of a spatial join with very large objects can be the I/O cost of reading the large objects, depending upon the amount of internal memory and the ratio of I/O to CPU performance. Early filtering techniques were dominated by I/O costs [Brinkhoff et al. 1993]. Later techniques have improved I/O performance so that it is no longer an axiom that I/O costs dominate the CPU costs [Patel and DeWitt 1996]. Even though filtering reduces the I/O costs, reading large objects can still be the major cost of the refinement stage, which is generally more expensive than the filtering stage [Patel and DeWitt 1996]. Furthermore, while the performance improvement from using a filter-and-refine approach might be obvious for very large objects, it remains an open question as to whether it is the best approach for smaller, simpler objects. As an example of an alternative approach, Zhu et al. [2000a; 2000b] have proposed methods for extending the plane-sweep algorithm (Section 3.1) to trapezoids and recti-linear polygons, thereby avoiding the need for the filter-and-refine approach for objects having such shapes.

Throughout the review of the spatial join techniques, we do not discuss experimental results. Most of the methods described in this survey were shown to outperform some other method. Unfortunately, we found it difficult to compare methods using only the literature since the techniques are compared with one or no other technique, and the implementations of the techniques can vary dramatically, which has a large impact on the experimental results. Furthermore, the variety of computer hardware, software and networks used make it difficult to compare results between methods. For these reasons, we do not discuss most experimental results.

Also, to simplify the discussion of the techniques, it is assumed that the data is two dimensional and that we are interested in determining pairs of intersecting objects. Both of these assumptions are common in the literature. The two-dimensional assumption is made because the applications of these techniques to higher dimensional data has not been extensively addressed in the literature and many of the techniques presented might not work or might not perform well in higher dimensions. The intersection assumption is made only to simplify the discussion. We believe that this assumption does not effect the generality of the algorithms. For example, a nearness relation can easily be calculated by extending the size of the MBRs so that nearness is calculated by an intersection test [Koudas and Sevcik 1998]. However, for some predicates, such as a directional predicate, the algorithms need to be modified appropriately. For instance Zhu et al. [2001] use a modified plane-sweep algorithm (see Section 3.1) to search for all objects in the desired di-

rection for a directional predicate. When appropriate, a generic join condition is used, rather than intersection.

Furthermore, although many spatial join techniques depend on spatial indices, the discussion of spatial indices is left to other work [Gaede and Günther 1998; Samet 1990]. Knowledge of these structures can be crucial to a deeper understanding of many of the techniques for processing spatial data. Where appropriate, these index structures are described, but in general, the algorithms are presented in such a way that little or no knowledge of the underlying spatial indices is required.

Many factors contribute to the performance of a spatial join and influence the design of algorithms. The foremost factor, of course, is the processor speed and I/O performance, and in particular, the ratio of these two factors. Early spatial joins algorithms were constrained by I/O, which dominated CPU time, and the focus of improvements was on minimizing the amount of data that needed to be read from and written to external memory. As spatial join algorithms improved, experiments showed that CPU time accounted for an equal share of performance and that the algorithms were no longer I/O dominated [Brinkhoff et al. 1993]. In addition, ever increasing amounts of internal memory allow larger portions of the data to reside in memory, which also improves the performance of the spatial join. Today, algorithms need to account for both CPU performance and I/O performance. These two factors can be balanced somewhat by tuning page sizes and buffer sizes (the amount of internal memory available to the algorithm), two factors which also play an important role in performance. However, as processor, I/O speeds, and internal memory sizes continue to improve, algorithms need to account for these factors and thus tuning will always be necessary for the best performance.

The characteristics of the datasets and whether the datasets are indexed are also major influences on performance. The dataset sizes obviously effect overall performance, but a more important issue is whether the dataset fits into the available internal memory. If the entire dataset does fit in internal memory, then the spatial join can be done entirely in memory (Section 3) [5], which can be significantly faster than using external memory methods (Section 4). One of the most confounding factors for spatial join design is the distribution of data. Algorithms for uniformly distributed datasets are easy to develop, but the development of algorithms for handling skewed datasets is significantly more complicated. A poorly designed algorithm can thrash with skewed datasets by repeatedly reading the same data in and out of external memory, which severely degrades performance. These factors are mitigated if the data is indexed appropriately. If a dataset is indexed, then in general, algorithms that use the index will be faster than those that do not. Section 4 classifies spatial join algorithms by whether they assume that both datasets are indexed (Section 4.1), only one dataset is indexed (Section 4.2), or neither of the datasets are indexed (Section 4.3).

How the data is stored is another factor that contributes to the design of spatial joins. Vectors (a list of vertices) are commonly used to store polygons, but raster approaches are also used [Orenstein 1986]. The choice of storage method for the

[5] If the plane-sweep technique is used (Section 3.1), then the dataset can be processed in internal memory even if its total size exceeds the size of the internal memory provided that the data is already sorted and that the active set fits into internal memory.

full object mostly effects the complexity of the object intersection test during the refinement stage, since an approximation of the full object is used during the filtering stage. This article only discusses refinement techniques for the more common vector representation. During the filtering stage, an object is represented by an approximation and an object id or a pointer is used to access the full object. An MBR is generally chosen as the approximation, but other approximations can also be used (see Appendix C).

The environment in which the algorithm is executed also plays a role in the design of spatial join algorithms. In a demand-driven pipelined system [Graefe 1993], which is typical for a DBMS, each stage of the spatial join algorithm needs to output results continuously in order for the pipeline to run efficiently. In this case, each stage is said to be *non-blocking* because the next stage does not need to wait for results. Unfortunately, filtering methods that sort or partition the data are blocking, although there is a method to produce some results earlier (see Appendix C.3). Also, specialized algorithms can be used to improve the performance of multiway spatial joins, and modified algorithms are required to perform spatial joins that run in parallel environments and distributed environments (see Section 5).

3. THE FILTERING STAGE – INTERNAL MEMORY

During the filtering stage, a spatial join is performed on approximations of the objects. This section describes techniques for performing a spatial join without using external memory, that is, no data is written to external memory (only read once if necessary). In particular, we note that if there is insufficient internal memory to process a spatial join entirely in memory, then external memory must be used to store all or portions of the datasets during processing (see Section 4). Even so, at some point, most external memory spatial join algorithms reduce the size of the problem and process subsets of the data using internal memory techniques.

Two simple methods are not addressed here, but in Appendix A.3, which first describes the brute force nested-loop join, and the related index nested-loop join, which is presented as an internal memory method even though it can be used as an external memory algorithm if the indices are stored in external memory. Two more sophisticated approaches are described here: the plane-sweep algorithm, rooted in computational geometry, in Section 3.1, and a variant of the plane-sweep that uses a linear ordering of the data, in Section 3.2.

3.1 Plane Sweep

A two-dimensional plane-sweep [Preparata and Shamos 1985] of a set of axis-aligned rectangles finds all of the rectangles that intersect. The algorithm has two passes. The first pass sorts the rectangles in ascending order on the basis of their left sides (i.e., x coordinate values) and forms a list. The second pass sweeps a vertical scan line through the sorted list from left to right, halting at each one of these points, say p. At any instant, all rectangles that intersect the scan line are considered *active* and are the only ones whose intersection needs to be checked with the rectangle associated with p. This means that each time the sweep line halts, a rectangle becomes active, causing it to be inserted into the set of active rectangles, and any rectangles entirely to the left of the scan line are removed from the set of

```
1  procedure PLANE_SWEEP(setA, setB)
2  begin
3    listA←SORT_BY_LEFT_SIDE(setA);
4    listB←SORT_BY_LEFT_SIDE(setB);
5    sweepStructureA←CREATE_SWEEP_STRUCTURE();
6    sweepStructureB←CREATE_SWEEP_STRUCTURE();
7    while NOT listA.END() OR NOT listB.END() do
8      /* get leftmost rectangle from the two lists */
9      if listA.FIRST() < listB.FIRST() then
10       sweepStructureA.INSERT(listA.FIRST());
11       sweepStructureB.REMOVE_INACTIVE(listA.FIRST());
12       sweepStructureB.SEARCH(listA.FIRST());
13       listA.NEXT();
14     else
15       sweepStructureB.INSERT(listB.FIRST());
16       sweepStructureA.REMOVE_INACTIVE(listB.FIRST());
17       sweepStructureA.SEARCH(listB.FIRST());
18       listB.NEXT();
19     endif;
20   enddo;
21 end;
```

Fig. 2. A two set plane-sweep algorithm to find the intersections between two sets of rectangles.

active rectangles [6]. Thus, the key to the algorithm is its ability to keep track of the active rectangles (actually, just their vertical sides), as well as performing the actual intersection test.

To keep track of the active rectangles, the plane-sweep algorithm uses a structure (referred to as a *sweep structure* or `sweepStructure` in Figure 2) that supports three operations needed to track the active rectangles. The first, `INSERT`, inserts a rectangle by adding it to the active set. The second, referred to as `REMOVE_INACTIVE`, removes from the active set all rectangles that do not overlap a given rectangle (or line). These rectangles become inactive when the sweep line halts. The third operation, `SEARCH`, searches for all active rectangles that intersect a given rectangle and outputs them. Examples of structures that support these operations are discussed later in this section.

The classical rectangle intersection problem, given a set of rectangles, S, determines the pairs of intersecting rectangles in S. A spatial join, given two sets of rectangles, A and B, determines all pairs of intersecting rectangles in A and B — that is, for each rectangle r in A, find all of the rectangles in B intersected by r. To apply the plane-sweep algorithm, a sweep structure is needed for both A and B. Rectangles from A are inserted into A's sweep structure and rectangles from B are inserted into B's sweep structure. Also, a rectangle r from A will perform a search on B's sweep structure, thereby finding all the intersections with the rectangles in B, and vice versa. Such an algorithm in given in Figure 2.

The data structure used to implement the sweep structures in Figure 2 can have a significant impact on performance, as Arge et al. [1998] show in their performance

[6] A variant of the plane-sweep algorithm also stops at the right sides of each rectangle, which also must be included in the original sorted list, and removes that rectangle from the active set.

studies. The choice of a simple list structure or a block list structure (multiple objects in each list entry) [Arge et al. 1998] is appropriate for smaller datasets, where the overhead of more sophisticated structures is not needed [Dittrich and Seeger 2000]. For larger datasets or highly skewed datasets, more sophisticated structures are appropriate. Some examples of data structures that will work as sweep structures are:

(1) A simple linked list [Cormen et al. 1990].
(2) Interval tries [Knuth 1973], as used by Dittrich and Seeger [2000].
(3) A dynamic segment tree [Cormen et al. 1990].
(4) An interval tree [Edelsbrunner 1983] with a skip list [Pugh 1990], as described by Hanson [1991] and used by Arge et al. [1998].
(5) A dynamic priority search tree [McCreight 1985].

Except for the linked list implementation, the search operation on the sweep structure is $O(log(n))$, where n is the size of the combined datasets $(n_a + n_b)$, giving a running time for the plane-sweep algorithm of $O(n \cdot log(n))$, which includes the initial sort of the data.

Arge et al. [1998] modify the plane-sweep algorithm slightly to dramatically increase the size of datasets that can be processed without resorting to external memory. The traditional version of the plane-sweep algorithm assumes that all of the data is in internal memory. If the data is in external memory, then the entire dataset is first read into internal memory before performing the plane sweep. Arge et al. [1998], revisiting work by Güting and Schilling [1987], observed that only the data in the sweep structures needs to be kept in internal memory. If the data is in external memory and sorted, then each object can be read one at time from external memory, inserted into the sweep structure, and then purged from internal memory when it is deleted from the sweep structure. In this way, only the data intersecting the sweep line needs to be kept in internal memory, reducing the internal memory requirements of the algorithm and increasing the size of datasets that can be processed without resorting to more sophisticated spatial join techniques. A rough calculation estimates that a typical dataset will have $O(\sqrt{n})$ objects intersecting the sweep line [Ottmann and Wood 1986], meaning that datasets of size $O(m^2)$, can be processed, where m is the number of objects that can fit in internal memory. The plane-sweep technique can also be extended to process datasets of any size by using external memory (see Appendix B.1).

3.2 Z-Order Methods

The plane-sweep method described in Section 3.1 only uses input sorted in one dimension, but can be adapted to use more than one dimension using a more general linear ordering that sorts the points using multiple dimensions (see Appendix A.2). Thus, instead of a sweep line, a point or grid cell is swept over the data space, creating an *active border* [Aref and Samet 1994b; Dillencourt and Samet 1996]. Since fewer objects will intersect a point than will intersect a line, the sweep structure will be kept smaller, decreasing search times and the amount of internal memory needed. However, since the enclosing cells used for a linear ordering are bigger than MBRs, the number of objects in the sweep structure will increase, thereby

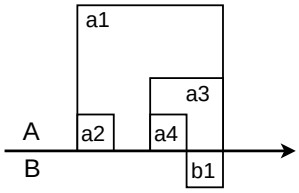


Fig. 3. Objects are shown from dataset A and dataset B in the order in which they appear in the Z-order, where large objects are encountered first (that is, in the following order: $a1$, $a2$, $a3$, $a4$, $b1$). Since the stack for the B dataset will be empty until $b1$ is inserted, $a2$ and $a4$ do not need to be inserted into A's stack. In other words, when $b1$ is inserted into B's stack, $a1$ and $a3$ are the only elements in A's stack, and $a2$ and $a4$ will never be in A's stack when an element of B is in B's stack. Therefore, $a2$ and $a4$ do not need to be inserted into A's stack.

offsetting some of the benefit. Orenstein [1986] first used a variation of the Z-order method in his work on spatial joins. This section shows how to adapt the plane-sweep method to use a Z-order (a Peano-Hilbert order would work as well) and relates the algorithm to Orenstein's work.

The Z-order algorithm is nearly identical to the plane-sweep algorithm, shown in Figure 2, and this section only describes the two minor modifications needed for the Z-order algorithm, rather than presenting the entire algorithm. First, the objects from both datasets are assigned to Z-order grid cells (see Appendix A.2). Next, the objects are sorted in Z-order rather than one-dimensionally. The remainder of the Z-order algorithm, which consists of creating the sweep structures and the `while` loop, is identical to the plane-sweep algorithm, shown in Figure 2. In this case, the active set, instead of being the objects that intersect the sweep line, are the enclosing cells of the objects that intersect the current Z-order grid cell. Since a sufficiently fine grid cell will intersect fewer objects, the active set will be smaller and the sweep structure can be simpler, such as a linked list [Cormen et al. 1990]. Also, the sweep structure can be modified to take advantage of the regular decomposition of the Z-order cells. All of the objects in the active set (sweep structure), which are the enclosing Z-order grid cells, will have either a containment relation to each other or be identical. In early work on spatial joins, Orenstein [1988] used a stack which he called a *nest* to implement the sweep structure. Because the input is sorted in Z-order, large objects can be inserted into the sweep structure before the smaller objects that are enclosed by the object. These small objects will be removed before their enclosing objects are removed. This LIFO property makes a stack the natural choice for the sweep structure. The `INSERT` and `REMOVE_INACTIVE` methods will be simple because they either push elements on to the stack or pop elements from the stack, respectively. The `SEARCH` method is also simple since all objects in the stack will intersect the input object. If the enclosing cells intersect, the MBRs can also be checked for intersection to further filter false hits from the candidate set, assuming the MBRs are available.

Aref and Samet [1994c] further improved the use of the sweep structure by avoiding some insertions, using a technique similar to a zig-zag join [Garcia-Molina et al. 2000]. They point out that if one stack is empty, for example, `sweepStructureB`, then it might not be necessary to insert elements into the other stack, `sweep-`

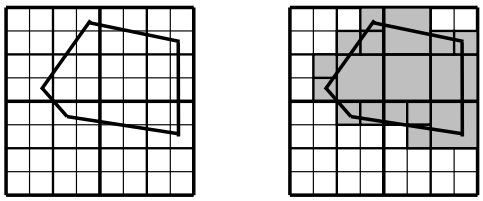


Fig. 4. An object can be decomposed into multiple cells.

`StructureA`. The objects to skip can be determined by examining the next object to be inserted into the empty stack. For example, in Figure 3, if dataset A contains the objects $a1$, $a2$, $a3$ and $a4$, then objects $a2$ and $a4$ will not intersect any objects in dataset B, which contains only $b1$. The objects $a2$ and $a4$ do not need to be inserted into A's stack. If one stack, `sweepStructureB`, is empty, then the algorithm can look ahead to the next element, say $bTop$, that will be inserted into the empty stack, and avoid inserting any elements into the other stack, `sweepStructureA`, that do not intersect $bTop$. In Figure 3, `sweepStructureB` will be empty until $b1$ is encountered, which becomes $bTop$. Therefore, $a2$ and $a4$ do not need to be inserted into the stack for dataset A, `sweepStructureA`. In a further extension, Aref and Samet [1996] modify the Z-order sweep to report larger pairs first, at each stopping point (iteration of the `while` loop), by reporting from the bottom of the stack up, rather than from the top. Thus, the output is already in Z-order, which can be useful for performing a cascaded join.

One drawback of the Z-order sweep method is that the stacks can be filled with objects that have large enclosing cells, even when the objects are small. For instance, any object that overlaps the center point of the space will be contained in the highest level enclosing cell, which encloses the entire space. Such an object will be one of the first objects to enter a stack and will remain in the stack until the algorithm is through processing. This increased stack size will impair performance. To alleviate this problem, Orenstein [1989a] suggested decomposing objects into multiple cells, as shown in Figure 4. This decomposition not only reduces the size of the stack, but creates a more accurate approximation of the object, which reduces the number of false hits. However, these benefits are offset by the increased number of objects introduced by the redundancy and the need to remove duplicate results (see Appendix A.1). Even so, Orenstein [1989a] found that performance rapidly improves with a modest amount of decomposition. In a further study, Gaede [1995] developed a formula for determining the optimal amount of redundancy.

4. THE FILTERING STAGE – EXTERNAL MEMORY

The internal memory techniques mentioned in Section 3 require sufficient levels of internal memory in order to operate efficiently. For instance, to perform the nested-loop join (Appendix A.3), both datasets need to be in internal memory in order to avoid repeatedly reading the same objects in and out of external memory. To efficiently process datasets of any size, an algorithm must use external memory to store subsets of the data (or references to the data) during processing or the

data must be indexed. This section describes filtering methods that use external memory to efficiently process datasets of any size.

If the data is already indexed, then it is generally advantageous to use the index for the filtering stage of a spatial join. Section 4.1 describes techniques for filtering when both datasets are indexed. Even if there is sufficient internal memory to use the internal memory techniques from Section 3, if both datasets are indexed, then it can be faster to use the two-index filtering techniques [7]. Section 4.2 addresses the case where only one of the datasets is indexed. Of course, the unindexed dataset can be indexed and the two-index techniques from Section 4.1 can be used. Another approach, if only one dataset is indexed, is to consider the index as a source of sorted or partitioned data and use the techniques for performing a spatial join when neither dataset is indexed, which are addressed separately, in Section 4.3. If neither dataset is indexed, then it might not be efficient to build indices in order to do a spatial join, especially if the indices will not be used again and immediately discarded, as is the case if the spatial join is an intermediate step in solving a complex query.

Even though the internal memory techniques in Section 3 cannot be used directly, at some point during processing, two subsets of the data that do fit in internal memory are joined. These subsets can be two pages from indices, as in Section 4.1.1, or subsets created by partitioning the data, as in Section 4.3. In these cases, when the internal memory techniques from Section 3 become applicable, the reader is referred to that section, rather than elaborating on the in-memory join aspects of the particular algorithm.

4.1 Both Datasets Indexed

If both datasets are indexed, but with incompatible types of indices, such as an R-tree [Guttman 1984] and a point quadtree [Finkel and Bentley 1974], Corral et al. [1999] suggest ignoring one index and performing an index-nested loop join, as described in Appendix A.3. If both datasets are indexed using the same type of index, then the technique for performing the filtering stage of the spatial join depends on the structure of the index. Since many spatial indices are hierarchical, a spatial join algorithm for these indices also has a hierarchical nature. These methods are described in Section 4.1.1. Early work on spatial joins used a more general non-hierarchical approach, which are described in Section 4.1.2. Section 4.1.3 discusses a method that works with indices that transform objects into points in higher-dimensional space. Since most methods in this section join data pages or index nodes, this issue is discussed separately, in Section 4.1.4.

4.1.1 *Hierarchical Traversal.* A common type of spatial index is one that can be described as a *hierarchical containment index* or a *generalization tree* [Günther 1993; Hellerstein et al. 1995], such as an R-tree [Guttman 1984] or a multi-level grid file [Whang 1991]. This type of index is a tree structure in which every node of the tree corresponds to a region of the data space. An internal node's region covers the regions of its sub-nodes and each node might or might not overlap other

[7] When an external memory filtering technique should be used instead of an internal memory algorithm is an open question.

```
1  procedure INDEX_TRAVERSAL_SPATIAL_JOIN(rootA, rootB)
2  begin
3    priorityQueue←CREATE_PRIORITY_QUEUE();
4    priorityQueue.ADD_PAIR(rootA, rootB);
5    while NOT priorityQueue.EMPTY() do
6      nodePair←priorityQueue.POP();
7      rectanglePairs←FIND_INTERSECTING_PAIRS(nodePair);
8      foreach p ∈ rectanglePairs do
9        if p is a pair of leaves then
10          REPORT_INTERSECTIONS(p);
11       else
12          priorityQueue.ADD_PAIR(p);
13       endif;
14     enddo;
15   enddo;
16 end;
```

Fig. 5. A generic hierarchical traversal spatial join algorithm for data indexed by hierarchical indices.

nodes, depending on the index type. Each node is typically stored on one page of external memory, which is determined by the underlying DBMS and typically has a size ranging between 1KB and 8KB. This section assumes that the data objects are only stored in the leaves of the tree, though the techniques can be adapted to handle data in the internal nodes. If both datasets are indexed using generalization trees, then a spatial join can be performed efficiently with a *synchronized traversal* of the indices. This section describes a generic synchronized traversal algorithm, and then presents variations that differ in how the indices are traversed, attributable to Günther [1993], Brinkhoff et al. [1993], Kim et al. [1995], and Huang et al. [1997b] [8].

The generic synchronized traversal algorithm is shown in Figure 5. To simplify the explanation, both indices are required to have the same height. For indices of different heights, the join of a leaf of one index with a sub-tree of the other can be accomplished using a window query [Brinkhoff et al. 1993], or handling leaf-to-node comparison as special cases [Kim et al. 1995]. Starting with the two root nodes of the indices, `rootA` and `rootB`, the algorithm finds intersections between the sub nodes of `rootA` and `rootB` using the `FIND_INTERSECTING_PAIRS` function. The intersecting sub-node pairs are added to the priority queue [Cormen et al. 1990], `priorityQueue`, and these pairs are checked for intersecting sub-nodes in later iterations. If the two nodes are leaves, then the `REPORT_INTERSECTIONS` function is used to compare the leaves and report any intersecting objects. Section 4.1.4 discusses the methods used to find object or sub-node intersections within two nodes, as used by the `FIND_INTERSECTING_PAIRS` and `REPORT_INTERSECTIONS` functions.

The three variations of the synchronized traversal algorithm differ in the implementation of the `ADD_PAIR` function, or, in other words, the priority (i.e., the sort order) that is used by the priority queue. Each variation attempts to minimize disk accesses. However, the algorithms must use heuristic methods, as a similar disk scheduling problem for relational joins has been shown to be NP-hard [Fotouhi and Pramanik 1989; Merrett et al. 1981]. Günther [1993] and Huang et al. [1997b] both

[8] See Huang et al. [1997a] and Theodoridis et al. [1998] for cost models for these approaches.

perform a breadth-first traversal, where priority is given to higher-level node pairs. In this way, all of the nodes at one level of the indices are examined before any nodes in the next level. Since all of the intersecting node pairs for a given level are known before any pair is processed, Huang et al. [1997b] further sort the pairs for a level, that is, the pairs in the priority queue, to reduce the number of page faults and buffer misses. In this approach, priority is still given to higher level nodes, but a secondary sort is used within each level. They investigated using the following heuristics as a secondary sort:

(1) A secondary sort on one dataset's nodes, say A, to achieve clustering for that dataset. For example, for each element of A, say a, all node pairs containing a will be adjacent in the order.
(2) A secondary sort on the sum of the centers of the pair in one dimension. In effect, objects pairs whose centers are closer in the x-dimension are given priority.
(3) A secondary sort on the center of the MBR enclosing the pair, in one dimension.
(4) A secondary sort on the center of the MBR enclosing the pair using a Peano-Hilbert order.

In their experiments, Huang et al. [1997b] found that ordering by the sum of the centers of the pair in one direction outperformed the other orders in terms of I/O for realistic buffers sizes. One of the drawbacks of the breadth-first approach is that, as the algorithm progresses, the priority queue can grow extremely large and portions of it might need to be kept in external memory.

Brinkhoff et al. [1993] and Kim et al. [1995] use a depth-first approach in which all of the sub-node pairs for a given node pair, p, are processed before proceeding to the next node pair at the same level. In this case, priority is given to lower-level node pairs. As with the breadth-first approach, heuristics can be used to reduce I/O by secondarily ordering $p's$ intersecting sub-node pairs. Brinkhoff et al. experimented with several ordering heuristics that secondarily sort the intersecting region of the node pairs [9]:

(1) In one-dimension.
(2) By frequency (maximal degree), determining which node, say a, is contained in the most node-pairs, and processing a's node pairs first.
(3) In Z-order.

Brinkhoff et al. found that the Z-order approach worked best for smaller buffer sizes and that the frequency method worked best for larger buffer sizes. To improve performance, Brinkhoff et al. [1993] use two *path buffers*, which keep in memory all of the ancestor nodes of the current node pair. They also advocate the use of an LRU buffer to improve performance. Additionally, Brinkhoff and Kriegel [1994b] suggest that the performance of the spatial join could be improved by organizing

[9] A sorted list of intersecting regions of node pairs can easily be determined by using a plane-sweep technique (see Section 3.1), which outputs the interesting regions of the node pairs in sorted order. Brinkhoff et al. [1993] use a variation of the algorithm described in Section 3.1 that does not require a sweep structure, but instead searches the sorted lists of rectangles for intersections.

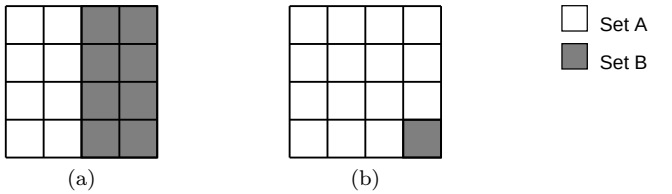


Fig. 6. When joining datasets A and B, internal memory, represented as data pages in the grid, can be (a) half filled by each of datasets A and B or (b) filled almost entirely with dataset A, leaving only one data page for dataset B.

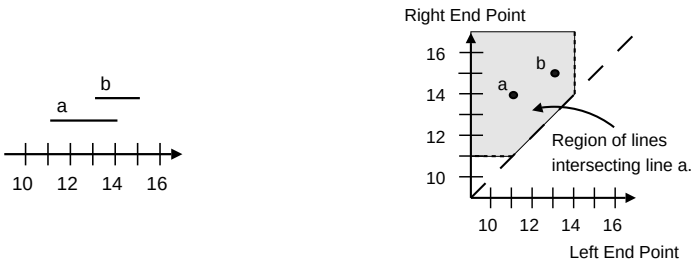
the nodes of the index into clusters which are physically close on disk. During join processing, a cluster would be read into memory as a whole.

4.1.2 *Non-Hierarchical Methods.* A more general approach to performing a spatial join on indexed data is to treat the indices as simply a partitioned dataset, where the data pages of the indices are the partitions. In this approach, the data pages are read in an order that is meant to minimize I/O, which is a generalization of the I/O minimization heuristic orders described in Section 4.1.1. Each pair of intersecting data pages is then read into memory and joined (see Section 4.1.4 for a discussion of joining data pages). This method is applicable to any index type with data pages. Kitsuregawa et al. [1989] applied it with k-d trees [Bentley 1975], while Harada et al. [1990] applied it with grid files [Nievergelt et al. 1984].

In this technique [Harada et al. 1990; Kitsuregawa et al. 1989], the overlapping partitions (data pages) need to be determined first, which is just a spatial join on the areas covered by the data pages, and internal memory techniques (Section 3) can be used to find the overlapping partitions [10]. Once the overlapping partition pairs are determined, partitions are read from one dataset, A, in sorted order [11]. Either enough data pages from dataset A are read to fill half of the available internal memory or enough are read to fill all but one data page of internal memory, as shown in Figure 6. Then, the intersecting data pages from the other dataset, B, are read into the remaining internal memory and joined. Since all of the intersecting data pages from dataset B might not fit in memory, the data pages from dataset B are purged from memory once they are joined and more pages from dataset B are read into memory, until all of the intersecting data pages from dataset B have been read. To enhance performance, Lu et al. [1995] propose precomputing overlapping index nodes if the index will receive few updates, much like a spatial join index [Rotem 1991].

Corral et al. [1999] apply a similar strategy for performing a spatial join between an R-tree [Guttman 1984] (hierarchical and non-disjoint) and a quadtree [Finkel and Bentley 1974] (hierarchical and disjoint) index. They propose filling internal memory efficiently by reading data pages in groups as shown in Figure 6. Additionally, they propose ordering the first dataset of data pages using a linear ordering

[10] This approach assumes that the boundary information for the partitions (i.e. the extent of the data pages) is in internal memory.
[11] Note that any linear ordering would suffice (see Appendix A.2).



(a) (b)

Fig. 7. As an example of the transformation to multi-dimensional points in a higher-dimensional space, (a) two one-dimensional intervals, a and b, that overlap (b) will be near each other when mapped to two-dimensional points. Any interval that overlaps interval a will be contained within the dotted lines when represented as a point. Furthermore, since the left end point of the interval is represented by the x-axis, all points will be above the dashed, diagonal line since the left end point is always less than or equal to the right end point.

(see Appendix A.2). Even though the two indices are of different types, the method works because the data pages of the indices are treated as partitions.

The methods described in this section use heuristics to determine the order of reading partitions. In a relevant analysis, Neyer and Widmayer [1997] showed that determining the optimal read schedule to minimize the number of disk reads is *NP-hard* if no restrictions are placed on the partitions. However, if the partitions do not share boundaries (that is, they do not have any sides in common), they show that the problem is easy to solve. If G is a graph where the vertices represent the MBRs of the index nodes and an edge is placed between all of the intersecting nodes between the two datasets, then the optimal read schedule is the Hamiltonian path through G, which can be found using an algorithm by Chiba and Nishizeki [1989].

4.1.3 *Transform to Multi-Dimensional Points.* Unlike points, rectangles have extent, which complicates spatial join algorithms. For instance, since an object will not fit neatly into a partition, either the object must be replicated into multiple partitions or the partitions must overlap, as in an R-tree [Guttman 1984]. Transformation methods avoid this problem by transforming objects into multi-dimensional points in a higher dimensional space, such as used by the grid file index [Nievergelt et al. 1984]. For example, a two-dimensional rectangle can be transformed into a point in four-dimensional space by using the coordinate values of the center point, half of the width, and half of the height as the four values representing the rectangle. Alternatively, the rectangle can be transformed using the coordinate values of the opposing corner points of the rectangle as the four values, which is a technique known as the *corner transformation*.

Song et al. [1999] propose a spatial join for data that is indexed using the corner transformation method. The indices create a partitioning of the multi-dimensional points, and the method for joining the partitions is similar to the non-hierarchical spatial join methods (Section 4.1.2), which order the processing of overlapping partition pairs between the two datasets. However, in the transformed space, the search space substantially increases. For instance, when joining two indexed datasets, R

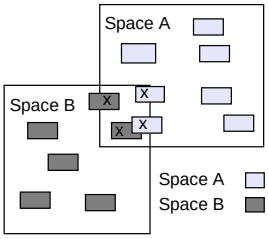


Fig. 8. When joining two data pages, only the objects within the intersecting region of the pages (marked with an x) need to be considered.

and S, a region (data page) containing points from a dataset R needs to be compared against a larger region containing points from dataset S. To see why this is so, consider the one-dimensional intervals, a and b, shown in Figure 7a. In two-dimensional space, any interval that overlaps a, such as b, will be contained within the region shown in Figure 7b, lying between the dashed and dotted lines. Note that all data points in transformed space are above the diagonal since the terminating point of the interval is always greater than the starting point. Similarly, for two-dimensional objects, such as a rectangle r (for example, the MBR of an index node), all rectangles overlapping r will occupy a space in four dimensions similar to the region shown in Figure 7b (see Song et al. [1999] for the exact calculation of this region in four dimensions). Once the overlapping partition pairs have been determined, the methods in Section 4.1.2 can be used to order the reading of the data pages from memory.

4.1.4 *Node to Node Comparison.* When joining two regions A and B, which could represent two index nodes, two data pages, or two partitions, if both regions cover the same space and fit in internal memory, then every object in region A needs to be joined with every other object in region B. This, of course, is an internal memory spatial join and an appropriate internal memory technique from Section 3 should be used. For smaller page sizes, a nested-loop join (Appendix A.3) might be best because of the low overhead. For larger page sizes, the plane-sweep method (Section 3.1), as suggested by Brinkhoff et al. [1993], or a Z-order sweep (Section 3.2) would be more appropriate.

If the regions do not cover the same space, as is likely when joining index nodes, then the search space can be reduced [Brinkhoff et al. 1993]. Only objects within the intersecting region of the two nodes need to be compared, as shown in Figure 8. For example, if the plane sweep method is used to join the nodes, then only these objects will be processed by the plane sweep.

4.2 One Dataset Not Indexed

If only one dataset is indexed, then the spatial join can be performed using an index nested loop join (Appendix A.3), which uses the index to do window queries. For example, given two datasets to be joined, A and B, if dataset A is indexed with an R-tree, then for every element b in B, a window query is performed on the R-tree index of A using each b, which finds all of the objects in A that intersect

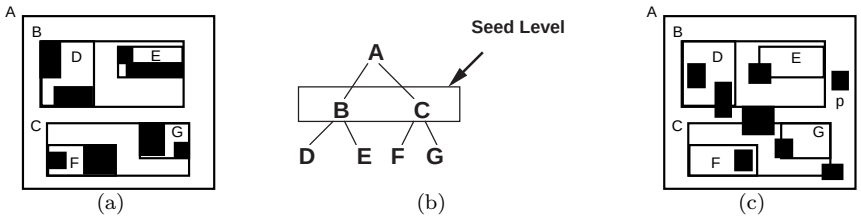


Fig. 9. (a) The data (dark rectangles) and regions (lettered squares) covered by the nodes of an R-tree. (b) As shown in a hierarchical representation of the index node structure, the second level of the R-tree is used as a seed level. (c) Since object p, from the second, unindexed dataset, does not overlap any seed level region (regions B and C), p can be discarded.

b. Another approach is to construct an index on the unindexed data and then use the spatial join techniques for when both datasets are indexed, which are described in Section 4.1. In support of this approach, techniques for efficiently constructing the second index are surveyed in Section 4.2.1. Still another approach is to take advantage of the structure of the indexed data, without using the index directly, as described in Section 4.2.2, which reviews techniques that partition the leaves of the index, and Section 4.2.3, which reviews methods that adapt the plane-sweep algorithm (Section 3.1) to use the index as a source of sorted data.

4.2.1 *Constructing A Second Index.* If only one dataset is indexed, then the other dataset can be indexed efficiently using bulk-loading techniques [Hjaltason and Samet 1999; van den Bercken et al. 1997], which exist for many types of indices, and then the techniques described in Section 4.1 can be used to perform the spatial join. This approach is especially useful when the index will be saved and used later. Conversely, if the index is not going to be reused, then Lo and Ravishankar [1994] suggest building a special purpose index that improves the performance of the spatial join. However, the index might not be reusable because some of the data will be excluded from the specially built index. This constructed index, which is an R-tree [Guttman 1984], is built so that it mirrors the structure of the existing index, thereby minimizing node overlap between the two indices and reducing the number of node-to-node comparisons, which speeds the spatial join.

Lo and Ravishankar [1994] call their constructed index a *seeded tree* since it is built using the upper levels of the existing index to seed the construction of the second index. An upper level of the existing index, termed a *seed level*, is used to partition the second dataset. For efficiency, the level should be chosen such that each node is assigned a write buffer. The number of write buffers is limited by the amount of internal memory, which, therefore, determines the lowest level of the index that can be used. Lo and Ravishankar discuss techniques for choosing a level in [Lo and Ravishankar 1995]. In a slightly different approach, Mamoulis and Papadias [1999] point out that trying to create too many partitions will cause buffer thrashing and propose a bottom-up approach instead (see Section 4.2.3). One level of the existing index forms a collection of non-disjoint regions that do not necessarily cover the data space. This is illustrated in Figure 9a and b by regions B and C. Each region's centroid, for example, the center points of the MBRs of the data pages, serves as the basis for partitioning the second dataset. Initially,

each partition of the new index has no area. As objects from the unindexed dataset are inserted into a selected partition, the partition is enlarged to enclose all of its objects. Lo and Ravishankar experimented with different techniques for choosing the partition in which to insert objects for the unindexed dataset. The technique that performed the best in their experiments is to insert an object into the partition with the nearest centroid. Another technique, which performed slightly worse, is to insert the object into the partition whose size is enlarged the least.

Once the data is partitioned, each partition is transformed into an R-tree using bulk-loading techniques [van den Bercken et al. 1997]. The resulting forest of R-trees is attached to the upper seed levels, which are duplicated from the original index, and the new seed levels are adjusted to cover the newly created forest of R-trees, resulting in a regular R-tree. Once this is done, the techniques given in Section 4.1.1 can be used to perform the spatial join. Since the trees are similar, performance improves because the number of overlapping nodes is reduced. To improve performance even further, Papadopoulos et al. [1999] note that during construction of the R-tree, the leaves of the R-tree (or partitions in general) do not need to be written to external memory to form the full external memory index if the R-tree is not going to be reused. Instead, the leaves or partitions can be joined to the other dataset immediately and then thrown out, saving I/O cost and speeding the spatial join.

Lo and Ravishankar [1994] also propose extensions to filter the second dataset, reducing the size of the second dataset and, thus, further speeding the join. Given two datasets A and B, where A is indexed and B is not, they note that any object in B, say b, that does not intersect with the regions covered by the upper level nodes of the existing index on dataset A, could not intersect any object in A. Therefore, b does not need to be inserted into the constructed index for dataset B. This makes the join faster, but renders the second index unusable for processing other operations in the future since it does not contain the entire dataset. For example, if the constructed R-tree is not going to be reused, then objects from the second dataset that do not intersect the regions covered by the seed levels do not need to be inserted into the partitions because they will not intersect any object in the indexed dataset, as shown in Figure 9c for object p.

4.2.2 *An Index as Partitioned Data.* Even if just one dataset is indexed, the best approach to performing a spatial join might not be to construct a second index, but rather to use the synchronized traversal methods from Section 4.1.1. In this case, the pre-existing index can be viewed as a partition of the dataset and methods similar to the non-hierarchical methods (Section 4.1.2) can be used to perform the spatial join. To create partitions from an index, the data pages are grouped to form the partitions. The data pages can be grouped either in a top-down manner for hierarchical indices by using sub-trees as the partitions [van den Bercken et al. 1999] or in a bottom-up fashion by grouping data pages, which can be used for any index type [Mamoulis and Papadias 2003].

In a top-down method to partitioning, proposed by van den Bercken et al. [1999], the unindexed dataset is partitioned based on one of the levels of the existing hierarchical index, for example, the sub-nodes of the root of the indexed dataset, which is similar to the seeded tree technique in Section 4.2.1 and shown in Figure 9b.

Fig. 10. (a) A set of index data pages (b) are grouped to form slots, shown by thick-lined rectangles.

The partition boundaries are the MBRs of the internal index nodes for the chosen level, for example, regions B and C in Figure 9. The unindexed data is partitioned based on these regions, placing each object into each partition that it overlaps, which replicates the data, requiring that duplicate removal techniques be used on the result pairs (see Section 4.3.4).

Once the partitioning is done, each partition is joined with the objects in the sub-tree of the corresponding index node using any appropriate internal memory method (Section 3). If the data pages and partitions for a sub-node do not fit in memory, then the method can be recursively applied by descending to the next level of the index. This approach works best if the depth of the tree is small or, conversely, if the index has a large fan out. For this reason, van den Bercken et al. [1999] propose this approach as a technique for joining two unindexed datasets, in which case an index is created with the largest possible fan out on one dataset before the method is applied.

In a bottom-up approach to partitioning the data pages, Mamoulis and Papadias [1999; 2003] propose a technique that creates a target number of partitions, which they call *slots*, by grouping the data pages of the existing index, as shown in Figure 10. The unindexed dataset is partitioned based on the slots. To create the slots, the amount of data in each slot is first determined, which is roughly half of the available internal memory. The data pages of the existing index are grouped by traversing them in a linear order (Appendix A.2) and adding them to a slot until the slot's capacity is reached. Then, the next slot is filled and so forth. The region covered by the data pages in the slot form a partition for the unindexed data. As with the top-down approach, once the unindexed dataset is partitioned, a group of data pages from the original index (a slot) and its corresponding partition of the unindexed dataset are read into memory and joined. Due to skew, however, a slot and its partition might not fit in internal memory. In this case, the partitioning method is applied recursively until each slot and its partition fit in memory.

4.2.3 *An Index as Sorted Data.* An index can also be viewed as a sorted dataset, since extracting the data from an index in sorted order is inexpensive using an in-order traversal of the index. In this case, the plane-sweep method (Section 3.1) can used to perform the spatial join. Generally, the plane-sweep method is performed after sorting both datasets. Since extracting data from an index in sorted order (sorted in one-dimension) is fast in this situation, the plane-sweep technique is less expensive than sorting both datasets since only one dataset needs to be sorted [Arge et al. 2000].

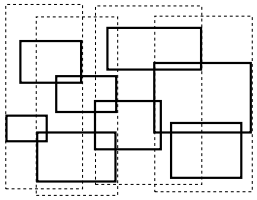


Fig. 11. The leaves of an R-tree are grouped into strips, which can flushed to external memory if internal memory overflows. Here, four strips (dashed lines) are formed, each containing two objects.

Another approach, one that modifies the plane-sweep method, proposed by Gurret and Rigaux [2000], is to read the data pages from an index (they use an R-tree) in a one-dimensional sorted order and insert entire data pages into the sweep structure. In this case, one sweep structure will contain objects, as is normal, while the other sweep structure will contain data pages. This technique only requires a modification of the plane-sweep `SEARCH` routine (see Figure 2) to search for intersections between an object and a data page. Since the `REMOVE_INACTIVE` and `INSERT` routines work with MBRs and the enclosing rectangle of a data page is an MBR, these two methods do not need to be modified. Additionally, the initial sort step of the plane-sweep algorithm needs to extract the data pages of the index as well as to sort the unindexed dataset.

If memory overflows (that is, the active set is too large to fit in internal memory), then Gurret and Rigaux [2000] propose using a method in which some of the data pages of the index are removed (or *flushed*) from the sweep structure and written to disk for later processing. To do this, before the plane-sweep phase of the algorithm starts, each data page is assigned to a strip, as shown in Figure 11. The strips are created using a method that is similar to forming slots in Section 4.2.2, except that a one-dimensional sort is used. Only entire strips of data pages are flushed at a time. After a strip is flushed, the plane-sweep algorithm continues. Any rectangle from the unindexed dataset that overlaps the flushed strip is also written to external memory. After the plane-sweep algorithm finishes, it is run again on the flushed data pages and the rectangles written to external memory, starting from the point where the flush occurred. If a plane sweep on the flushed data also overflows memory, then the flushed data can be partitioned further into strips and the entire algorithm applied recursively.

4.3 Neither Dataset Indexed

The inputs to a spatial join operation are usually assumed to be indexed. However, the situation is often different when the input to the spatial join are themselves the result of a spatial join. In particular, there is no requirement that the output of a spatial join be indexed (but see Hoel and Samet [1995], which evaluates different spatial indices by taking into account the time necessary to construct an index for the result of a spatial join). If neither dataset is indexed, then an index can be built on one or both datasets, and then the techniques from Sections 4.1 and 4.2, respectively, can be used. If the index is to be saved and reused, this can make

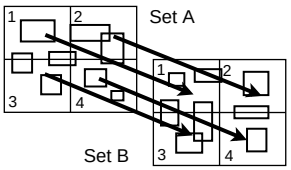


Fig. 12. If both datasets, A and B, are partitioned using the same grid, then each grid cell is joined with exactly one other, corresponding cell.

sense. If not, then other techniques that do not necessarily create an index might be faster [12]. These techniques are useful when an index would not be used later, such as for a one-time operation on the data, where the extra cost of building the index would be more expensive. For example, in a complex query, intermediate results can be processed faster with these techniques. The key to most of these techniques lies in partitioning the datasets so that the partitions are small enough to fit in internal memory. In other words, a divide-and-conquer approach is used to decompose the datasets into manageable pieces.

Once the data is partitioned, each pair of overlapping partitions, one from each dataset, is read into internal memory and internal memory techniques are used (see Section 3). This assumes that the partition pairs fit into internal memory. If they do not, then they can be repartitioned until the pairs fit (see Section 4.3.3).

As a foundation for describing the partitioning methods in this section, Section 4.3.1 describes a generic algorithm for performing a spatial join using a partitioning technique. The algorithm also serves to introduce several common issues associated with the partitioning approach: determining the number of partitions is discussed in Section 4.3.2, repartitioning, if any of the partition pairs do not fit in internal memory, is discussed in Section 4.3.3, and handling duplicate results is discussed in Section 4.3.4.

Details of specific methods are found in Appendix B. Appendix B.1 discusses an extension to the plane-sweep algorithm (Section 3.1) that can process datasets of any size by using external memory. The distinction between the sort-and-sweep method and the partitioning method is analogous to the distinction between sort-merge joins and hash-based joins. Next more sophisticated partitioning algorithms from the literature are described, grouped by how they partition the data: using grids in Appendix B.2, using strips in Appendix B.3, by size in Appendix B.4, and clustering in Appendix B.5.

4.3.1 *Basic Partitioning Algorithm.* This section uses a simplified algorithm to illustrate a spatial join technique based on partitioning. While the algorithm has limited practical applications, it is used as the basis for describing more sophisticated algorithms and to discuss the common issues associated with partitioning techniques. The basic concept is to define a grid and use it to partition the data from each dataset, datasets A and B, into external memory. Each data object is placed into each grid cell (partition) that it overlaps. Once the data is partitioned,

[12]Some techniques for unindexed data create a usable index as a byproduct of the spatial join, for example, the filter tree [Koudas and Sevcik 1997].

```
1  procedure GRID_JOIN(setA, setB)
2  begin
3    /* determine the number of partitions */
4    m←AVAILABLE_INTERNAL_MEMORY;
5    mbrSize←BYTES_TO_STORE_MBR;
6    minNumberOfPartitions←(SIZE(setA)+SIZE(setB))*mbrSize/m;
7    partitionList←DETERMINE_PARTITIONS(minNumberOfPartitions,
8                                       AREA_OF_DATA_SPACE);
9    /* partition data to external memory */
10   partitionPointersA←PARTITION_DATA(partitionList, setA);
11   partitionPointersB←PARTITION_DATA(partitionList, setB);
12   /* join partitions */
13   foreach partition ∈ partitionList do
14     partitionA←READ_PARTITION(partitionPointersA, partition);
15     partitionB←READ_PARTITION(partitionPointersB, partition);
16     PLANE_SWEEP(partitionA, partitionB);
17   enddo;
18 end;
```

Fig. 13. A simple partitioning technique for performing a spatial join on unindexed data.

the partitions for each grid cell of dataset A are joined with the corresponding partition of dataset B using one of the internal memory methods from Section 3. For example, in Figure 12, both datasets A and B are partitioned using the same grid, and then, each corresponding cell is joined with the other. Grid cell 1 from dataset A, for instance, is joined with cell 1 from dataset B, and so forth.

In the algorithm, shown in Figure 13, the first step is to determine how many partitions are needed. The goal is to create partitions that are small enough, when paired with a corresponding partition, to fit in internal memory. To do this, the algorithm first calculates the minimum number of partitions needed, `minNumberOfPartitions`, as the total storage costs of the objects in both datasets divided by the available internal memory. The algorithm uses the `DETERMINE_PARTITIONS` function to create the smallest grid that has at least `minNumberOfPartitions`. However, the calculation of `minNumberOfPartitions` is inaccurate for two reasons. First, if a dataset is skewed, then some grid cells might contain more objects than can fit in internal memory. The more sophisticated techniques described later in this section correspond to different ways of dealing with skewed data. The simplified algorithm assumes that the data is uniform. Second, since a data object is placed into each cell it overlaps, the number of data objects will increase since the object is replicated into each cell. To address this issue, the calculation of the minimum number of partitions can be adjusted using methods described in Section 4.3.2. Alternatively, the algorithm can continue and when a partition pair to be joined is encountered that is too large for internal memory, then one or both of the partitions can be repartitioned, creating smaller partitions that can be processed. Section 4.3.3 addresses repartitioning. Note that since objects are replicated into multiple cells for both datasets, duplicate results will arise. Section 4.3.4 addresses the issue of removing duplicates from the result dataset.

Once the partitions are created, the algorithm scans the datasets, placing each object into each partition that it overlaps using the `PARTITION_DATA` function, which writes the objects to external memory. In the final step of the algorithm, each

partition pair is read into internal memory using the `READ_PARTITION` function and joined using the plane-sweep technique from Section 3.1 (note that any internal memory spatial join would be appropriate), which will report all of the intersecting pairs between the partitions.

4.3.2 *Determining the number of partitions.* Many partitioning techniques must first determine a target number of partitions. The goal is to create pairs of partition to be joined that will fit in memory. However, because of data skew, no simple partitioning scheme can guarantee that all of the partition pairs will fit in memory. Therefore, a heuristic calculation must be used. This calculation is constrained by the following factors:

(1) The amount of internal memory, which determines the number of objects that can be joined at a time using internal memory techniques.
(2) The replication rate, which is the actual number of objects inserted into the partitions, which includes duplicates.
(3) The amount of internal memory also limits the number of write buffers that can be used to partition the data to external memory.

Within these constraints, different techniques either try to maximize or minimize the number of partitions. A minimum number of partitions might be calculated in order to reduce replication, which reduces the number of pairs that need to be joined. A maximum number of partitions minimizes the chances of a costly repartitioning.

The simplest calculation, ignoring data skew and replication, derives the target number of partitions by dividing the total storage costs of the objects by the available internal memory. The total storage costs of the objects is the number of objects multiplied by the size of an object in bytes, referred to as $objectSize$. In an implementation, $objectSize$ might be the sum of the size of a rectangle (MBR) in bytes and the size of an object pointer or object key. To account for replication, a scale factor, r, can be added to the calculation. The replication rate depends on the dataset and the partitioning scheme. In one set of experiments [Patel and DeWitt 1996], the replication rate was found to be 3-10%. Incorporating the replication scale factor, r, the calculation for the minimum number of initial partitions is:

$$\frac{r \cdot (|setA| + |setB|) \cdot objectSize}{m}, \tag{1}$$

where m is the available internal memory. However, this equation does not take into account data skew and is only an estimate. In the worst case, with severely skewed data, most of the data could be in one partition. In this case, repartitioning is required (see Section 4.3.3).

Equation 1 applies to internal memory methods that require all of the data to be read into internal memory before processing begins. Arge et al. [1998] showed that the plane-sweep method can process more data than can fit into internal memory, see Section 3.1. However, the exact amount of data that can be processed is dependent on the dataset, specifically the *maximum density* of the dataset [Faloutsos and Kamel 1994; Jacox and Samet 2003; Theodoridis et al. 1998], which is just the maximum number of objects in the active set. However, this value is difficult to calculate for a given dataset.

The maximum number of partitions is limited by internal memory in that internal memory limits the number of external memory write buffers. Typically, for better performance, when writing to external memory, a page of internal memory is filled before it is flushed to external memory. This places a hard limit on the maximum number of partitions.

The principal motivation for getting the number of partitions right is to avoid repartitioning (see Section 4.3.3). However, the more partitions there are, the greater the replication. Some evidence suggests that this replication does not have a significant impact on the total processing time [Zhou et al. 1997]. In this case, creating the maximum number of partitions might optimize performance. Conversely, internal memory algorithms might perform better with smaller partitions, thereby improving overall performance. From the literature, it is unclear what the best choice is for the number of partitions and thus, we leave this choice as an open question.

4.3.3 *Repartitioning.* The goal of partitioning is to create partitions that are small enough to be processed by internal memory techniques (Section 3). However, the initial partitioning phase (Section 4.3.2) might create partitions that are too large because of data replication or skewed data. If this occurs, then the partition pairs that are too large can be further sub-divided using the original partitioning scheme, creating a finer grid. If this repartitioning fails, then the process can be repeated recursively until all of the partition pairs can be processed by internal memory methods.

Repartitioning can occur immediately after the initial partitioning, or it might be necessary to do it later, after some partition pairs have been joined because it might not be known if a repartitioning will be necessary. With the basic internal memory techniques, such as the nested-loop join (Section 3), the size of the datasets that can be processed is known, in which case, any over-full partition pairs can be repartitioned immediately, before joining any of the partitions. However, with other internal memory techniques, such as the plane-sweep extension [Arge et al. 1998], it might not be known whether or not a partition pair is small enough. In this case, repartitioning is done only when an internal memory technique fails because its sweep structure has grown too large for the available internal memory. Any result pairs generated for the current partition pair need to be discarded since the results will be regenerated after repartitioning.

If a partition pair to be joined, say A and B, is too large for the available internal memory, Dittrich and Seeger [2000] propose repartitioning only one of the datasets, say A, first, and then joining each sub-partition with B. If this fails to create small enough partitions, then the other dataset, B can be repartitioned. This process can also occur recursively until small enough partitions are achieved.

4.3.4 *Avoiding Duplicate Results.* If partitioning the data results in object replication, then duplicate results will be reported. For instance, if a pair of overlapping objects is split by a partition boundary, then the intersecting pair will be reported when each partition is processed, as shown in Figure 14a. Some experiments have shown that replication does not add considerably to processing [Zhou et al. 1997], though other experiments have shown the opposite [Luo et al. 2002]. In either case,

(a) (b)

Fig. 14. (a) An intersection between objects a and b is reported from both partitions into which they are inserted, creating a duplicate result. (b) The reference point method for online duplicate avoidance only reports an intersecting pair if a point in the intersecting region, x, is within the current partition. The point must be chosen consistently, such as always the lower left corner.

duplicate results need to be removed from the candidate set to avoid extra processing during the refinement stage (Appendix D). The duplicates can be removed with an extra step between the filtering stage and the refinement stage or combined with refinement. With some algorithms, duplicate results can be detected during filtering and removed online.

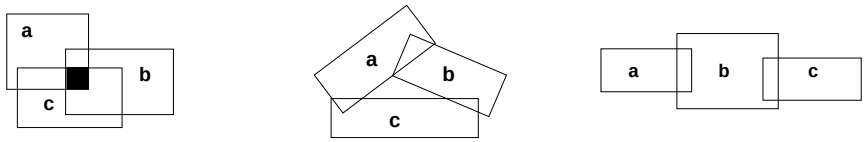
One way to remove duplicate results from the candidate set after the filtering stage is to sort the candidate set and then scan the sorted list, removing duplicates. Some refinement techniques sort the candidate set first, and thus, this duplicate removal technique can be used without a loss of performance (see Appendix D). However, to sort the candidate set, the entire candidate set must be produced first. In most database systems, that is, demand-driven pipelined systems [Graefe 1993], results need to be produced continuously. In this case, *online duplicate removal* techniques, which remove duplicates as they appear in the filtering stage, are preferred.

To implement online duplicate removal, the internal memory spatial join techniques (Section 3) can be modified with a simple test which is applied when the rectangles are checked for intersection. The technique, termed the *reference point method* [Aref and Samet 1994b; Dittrich and Seeger 2000; Seeger 1991], calculates a point within the intersecting region of the two objects. The pair is reported only if this point is within the current partition. The test point can lie anywhere within the intersecting region of the two objects, such as the centroid of the region or a corner point, but must be chosen consistently [13]. For instance, as shown in Figure 14b, reference point x is the lower left corner point of the intersecting region of the two rectangles. Since point x only lies within the B partition, the intersecting rectangles will only be reported when the B partition is processed, but not when the A partition is processed, even though the A partition also includes the rectangle pair.

5. SPECIALIZED SPATIAL JOINS

A basic spatial join is executed between two sets of objects on the same machine with a single processor. Modifications of the spatial join can be made to improve performance when more than two sets of objects are joined in a *multiway* join, as described in Section 5.1. Also, the spatial join requires special considerations

[13] To use the reference point method, the approximations of the objects cannot be clipped, that is, the full MBR must be stored and not just the portion of the object within a partition (most partitioning methods don't use clipping).



(a) (b) (c)

Fig. 15. Three objects with (a) mutual intersection, (b) pair-wise intersection, (c) two of the objects not intersecting.

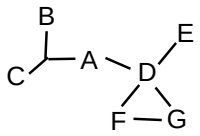


Fig. 16. A graph representing the relations between datasets in a complex query between multiple datasets. Each edge is a join condition between the objects, which might be more than a binary relation, such as the ternary relation joining A, B, and C.

when it is performed using a parallel architecture, described in Section 5.2, or on distributed computers, described in Section 5.3.

5.1 Multiway Joins

A complex query could contain multiple spatial joins. As an example, consider the query – *find all regions between 500 meters and 700 meters above sea level that receive 10 to 15 centimeters of rainfall and are in a forested area*. This query requires a spatial join to find the intersecting regions of rainfall and elevation and also the intersection with land type (forest). This query can be answered by performing a spatial join between any two of the datasets and joining the results with the third dataset. The intermediate results are the intersecting regions of the result candidate set, which is then joined with the third dataset. In the example, rainfall and elevation can be joined, creating a new dataset that represents regions with 10 to 15 centimeters of rainfall and which are between 500 and 700 meters above sea level. This intermediate dataset is then joined with the land type data to create the final result.

The previous example illustrates a query with mutual intersection between the datasets. A spatial query might not require that the datasets mutually intersect. For example, the query – *find all roads that cross a river and a railroad track* – does not require that the river and the railroad track in a result triplet intersect. In Figure 15a, the three objects have a mutually intersecting region, but in Figure 15b, each object pair-wise intersects. Furthermore, it is not necessarily the case that a relationship exists between all of the datasets in the query. For instance, as shown in Figure 15c, the query could only require that objects from dataset B intersect an object from both A and C, but no restriction is placed on intersections between A and C, such as with the road, river, and railroad example. In general, a multiway spatial query can be represented by a graph, as shown in Figure 16, in which n-

```
1  procedure MULTI_INDEX_NLJ(joinCondition, setA, setB, setC)
2  begin
3    spatialIndexB←CREATE_SPATIAL_INDEX(setB);
4    spatialIndexC←CREATE_SPATIAL_INDEX(setC);
5    foreach a ∈ setA do
6      tempSetB = spatialIndexB.SEARCH(a);
7      foreach b ∈ tempSetB do
8        tempSetC = spatialIndexC.SEARCH(b);
9        foreach c ∈ tempSetC do
10         if SATISFIED(a, b, c, joinCondition) then
11           REPORT(a, b, c);
12         endif;
13       enddo;
14     enddo;
15   enddo;
16 end;
```

Fig. 17. A multiway index nested loop join that finds objects from three datasets that satisfy any type of multiway intersection (see Figure 15).

ary relations are used to represent mutually intersecting regions. For instance, in Figure 16, objects from A, B, and C are required to mutually intersect, as in Figure 15a, as opposed to objects D, F, and G, which are only required to pair-wise intersect, as in Figure 15b.

As mentioned, a multiway spatial join can be solved by joining two datasets at a time and creating intermediate datasets. Furthermore, traditional database optimization approaches [Graefe 1993] that order the pair-wise joins to efficiently solve the query can be used [Mamoulis and Papadias 1999]. To do this, selectivity estimates (Section 6) are required in order to efficiently determine which pair of datasets to process first, typically processing the pair that produces the smallest intermediate result set first. Moreover, query optimizers also need selectivity information in order to efficiently perform queries that involve a mix of spatial and aspatial data.

To be more efficient, several techniques have been proposed for extending the filtering algorithms (Sections 3 and 4) to process multiple datasets at once. For example, the nested-loop join (Appendix A.3) can be extended to process three datasets simultaneously by nesting another loop and using a join condition that takes three arguments, which tests for a three-way intersection. Section 5.1.1 describes a similar extension to the index nested-loop join (Appendix A.3), which serves as a basis for describing a more sophisticated technique that is derived from *constraint satisfaction problem* (CSP) techniques [Kumar 1992]. Next, Section 5.1.2 describes extending the synchronized traversal spatial join (Section 4.1.1) to perform a multiway spatial join.

5.1.1 *Multiway Indexed Nested-Loop Spatial Joins.* A multiway version of the index nested loop algorithm (Appendix A.3) can be created by nesting each additional dataset. This algorithm, shown in Figure 17, is a simplification of algorithms by Mamoulis and Papadias [1998] and Papadias et al. [1998], and only joins three datasets. More datasets could be joined with further nesting, but the temporary candidate sets can grow significantly larger with more datasets. A generic join

condition, termed `joinCondition`, that specifies the desired relation between the datasets, is used since a relation other than intersection might be required. However, each dataset is assumed to be involved in some form of an intersection relation with another dataset. Otherwise, the multiway spatial join might not be appropriate.

The first step in the algorithm, shown in Figure 17, indexes `setB` and `setC`. Then, for each element of `setA`, a window query is performed on the index of `setB` using the `SEARCH` method. This assumes that the relation specifies that `setA` and `setB` intersect. Each of the search results from `setB` is used to perform a window query on `setC`, which produces another intermediate result set. Note that not all elements of `setC` need to intersect elements of `setA` as intersection is not a transitive relation (for example, objects a and c in Figure 15c do not intersect each other, even though they both intersect object b). Finally, each result from `setC`, along with the current value for `setA` and `setB` are checked to ensure that they satisfy the given relation using the `SATISFIED` function, and if so, the values are reported. The `SATISFIED` function ensures that the specified join condition is met. For example, if mutual intersection is required, as in Figure 15a, then the intersections of the type shown in Figures 15b and c will not be reported. Note that the algorithm explicitly instantiates the temporary result sets, for example, `tempSetB`. This is done in order to give the reader an idea of the internal memory requirements of the algorithm. A database iterator could be used instead, thereby letting the database engine optimize storage and retrieval of the temporary result set.

To enhance the performance of the algorithm, if the query seeks mutually intersecting rectangles, each search can use the intersections of the current values of the previous datasets to further improve performance. For instance, when the index on `setC` is searched, the intersection of `a` and `b` would be the search window, rather than just `b`. Papadias et al. [1998] refer to this approach as a *window reduction*. In a hybrid approach, Papadias et al. [1998] propose performing a normal spatial join on two of the datasets first, which should be faster than a nested-loop join, and then using window reduction for the remaining values.

To enhance the performance of the algorithm further, each temporary result set could be checked against all previous relations to further prune the result set. For example, the algorithm only considers the relations between `setA`/`setB` and `setB`/`setC`. A relation could exist between `setA` and `setC`, as in Figure 15a. If more datasets were being joined with further nesting, then reducing the size of `tempSetC` would be advantageous. In this case, after the temporary result set for `setC` is generated (`tempSetC`), it could be checked against the current value from `setA`, `a`, to further reduce the size of `tempSetC`.

The previous enhancement can be carried even further by having each current set immediately prune each following dataset. For instance, in the algorithm in Figure 17, each value from `setA` could be used to produce temporary sets for every other dataset, `setB` and `setC`, before scanning any other dataset. Papadias et al. [1998] and Mamoulis and Papadias [1998; 2001a] use this approach to solve the multiway spatial join, which is a constraint satisfaction problem (CSP) technique [Kumar 1992] called *multi-level forward checking*. In the CSP approach, temporary

```
1  procedure MULTI_INDEX_CSP(joinCondition, setA, setB, setC)
2  begin
3    tempSetA←∅
4    tempSetB←∅
5    foreach a ∈ setA do
6      foreach b ∈ setB do
7       if SATISFIED(a, b, joinCondtion) then
8          tempSetB←tempSetB ∪ b
9       endif;
10     enddo;
11     if relation between setA and setC then
12        foreach c ∈ setC do
13         if SATISFIED(a, c, joinCondtion) then
14            tempSetC←tempSetC ∪ c
15            endif;
16        enddo;
17     else
18        tempSetC = setC;
19     endif;
20     /* inner loop */
21     foreach b ∈ tempSetB do
22        foreach c ∈ tempSetC do
23           if SATISFIED(a, b, c, joinCondtion) then
24              REPORT(a, b, c);
25           endif;
26        enddo;
27     enddo;
28   enddo;
29 end;
```

Fig. 18. A multiway index nested loop join that finds objects from three datasets that satisfy any type of multiway intersection using constraint satisfaction problem (CSP) techniques to prune temporary datasets.

result sets are generated as soon as possible. In this algorithm, shown in Figure 18, if a relation exists between `setA` and `setC`, then a temporary result set, `tempSetC`, is generated in the outer loop using the current value from `setA`. If a relation exists between each dataset, then all temporary results are generated in the outer loop with each object from `setA`. These sets are pruned as each object is instantiated for each dataset in the nested loops. As a further possible enhancement, another CSP technique is to dynamically vary the order in which the datasets are processed, choosing the one with the smallest temporary result set first.

5.1.2 *Multiway Hierarchical Traversal.* Papadias et al. [1998] and Mamoulis and Papadias [1998; 2001a] extend the hierarchical traversal method (Section 4.1.1) to do a multiway spatial join. This technique applies if each dataset is indexed using a hierarchical index, such as an R-tree [Guttman 1984]. For two datasets, the original method compares overlapping nodes of the two indices. If the nodes are leaves, the intersecting objects within the node are reported, else the intersecting child node pairs are placed on a priority queue to be processed later. To do a multiway join, the queue is modified to hold multiple nodes, one from each dataset, instead of pairs. To start, the root nodes of the indices are checked and combinations of

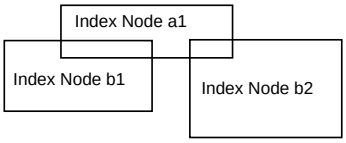


Fig. 19. Objects in multiple partitions might be read from memory multiple times.

the root node's children that satisfy the join condition are placed on the queue. Next, the first set of nodes on the queue is checked and combinations of children are put on the queue. This process repeats until the queue is empty. Papadias et al. [1998] and Mamoulis and Papadias [1998] suggest using multi-level forward checking (Section 5.1.1) to check the nodes, but any appropriate multiway version of an internal memory spatial join could be used. For instance, Park et al. [1999] propose using a pair-wise plane-sweep method for comparing multiple nodes at once, that is, a plane-sweep method is used on the first two datasets and the results are joined with the third dataset with the plane-sweep method, and so forth. As an alternate hybrid approach, Papadias et al. [1999] propose using the hierarchical traversal approach to instantiate the first few variables, then finishing with window reduction (Section 5.1.1) to instantiate the remaining variables.

5.2 Parallel

In a parallel architecture, work is distributed amongst several processors. For a spatial join, the work can be distributed in both the filtering and refinement stages, and also for partitioning unindexed data. For the filtering stage, parallel techniques that extend the synchronized hierarchical traversal approach (Section 4.1.1) have been used for indexed data [Brinkhoff et al. 1996], and techniques that extend the grid partitioning methods (Appendix B.2) have been used for unindexed data [Luo et al. 2002; Patel and DeWitt 2000; Zhou et al. 1997]. These techniques assume a shared nothing architecture (each processor has it's own memory), although some algorithms have extensions that use shared memory architectures to improve performance [Brinkhoff et al. 1996; Zhou et al. 1997]. Most of these methods have shown a near linear speed increase with more processors. However, the key to achieving linear speed increases during filtering depends on load balancing. An algorithm that uses a specialized hypercube architecture to join two indexed datasets is also discussed [Hoel and Samet 1994].

Brinkhoff et al. [1996] investigated extending the synchronized hierarchical traversal approach (Section 4.1.1) to parallel architectures by assigning sub-trees of the index to each processor. In the simplest approach to distributing the work amongst n processors, a single processor first performs a hierarchical traversal, one level at a time, until the number of node pairs on the priority queue exceeds n. At that time, the node pairs are distributed to the processors, which perform a sequential spatial join. However, as shown in Figure 19, one processor might be assigned nodes $a1$ and $b1$ and another processor the node pair $a1$ and $b2$. In this case, node $a1$ will be read from memory twice. To overcome this inefficiency, Brinkhoff et al. propose using global buffers (in a shared memory architecture) so that one processor can access a node that another processor has read into internal memory. However, this

approach does incur extra communication costs to synchronize usage of the buffers. Additionally, the workloads might not be balanced since the processing time for each sub-tree could be different. Rather than assigning all of the node pairs from the queue at once, Brinkhoff et al. suggest assigning only one node pair at a time to each processor. Once a processor finishes with one node pair, another is requested while the queue is not empty. When the queue is empty, they further suggest that one processor can share the work of another processor by taking node pairs from another processor's local queue, i.e., sub-trees of the original sub-trees.

For unindexed data, Zhou et al. [1997] adapt the variation of the grid partitioning method (Appendix B.2) that physically creates the grid cells. In their approach, the random data is evenly divided amongst the n processors, which then partition the data using the same tiling scheme. Then, with the sizes of the grid cells known, a single processor determines the merging of grid cells into n partitions using a Z-order merge, creating, on average, an even load distribution amongst the processors. Next, each processor is assigned a partition and the data is redistributed appropriately. Finally, each processor filters the data using a sequential spatial join filtering technique. Both Patel and Dewitt [2000] and Luo et al. [2002] investigated a similar approach. Rather than physically tiling the data, though, they both use the virtual tiling method (Appendix B.2), relying on a good hash function to distribute the data evenly.

For parallel refinement, each processor could refine the candidate pairs it produces. However, Zhou et al. [1997] point out that it is difficult without much selectivity information to balance the number of candidates produced by each processor during the filtering stage. If the candidate pairs are redistributed, then the workload for refinement can be close to optimal since the number of vertices in each polygon are good estimates of performance. Like sequential refinement, performance can be improved by ordering the candidate set to minimize the number of times each full object is read. Zhou et al. argue that an efficient approach is to use one processor to sort the candidates into a linear order, and then assign the candidates to each processor in a round-robin fashion. Each processor will be processing candidate pairs that are near each other (exhibiting locality), increasing the likelihood that an object only needs to be read into internal memory once (assuming a shared memory architecture), rather than continually reading some of the same objects throughout refinement. Zhou et al. took the approach of assigning full objects to processors, which are responsible for reading the object into memory and distributing the object to other processors. They found that the redistribution costs are negligible.

Hoel and Samet [1994] describe parallel algorithms for PMR bucket quadtrees [Nelson and Samet 1987] and R-trees [Guttman 1984] using a specialized hypercube architecture. The algorithms require that the data fit in memory, but result in extremely fast algorithms. In their quadtree approach, regions of one of the quadtrees are associated with half of the nodes (processors), termed the *source nodes*, and corresponding regions of the other quadtree are associated with the other nodes, termed the *target nodes*. Each quadtree is assumed to cover the same area, and thus, because of the regular decomposition, there is a one-to-one correspondence between source nodes and target nodes. The source nodes send their objects to

the target nodes, which check for intersections. Hoel and Samet also describe a similar algorithm for R-trees in which the index nodes of the R-tree are associated with the processor nodes. However, because of the irregular decomposition, each source node will be associated with multiple target nodes, dramatically increasing the communication costs and slowing the join.

5.3 Distributed

In a distributed spatial join, the datasets reside at different locations. Abel et al. [1995] show how to combine the semi-join [Mishra and Eich 1992] concept for distributed join processing and the filter-and-refine approach for spatial join processing. Given two sets of objects, R and S, that are at different locations (physically distributed), they send the MBRs of dataset R to the S location and filter the objects there. Then, they send the full objects from S that are in the candidate set to R's location to perform the refinement step. Tan et al. [2000] point out that unlike a relational semi-join [Ozsu and Valduriez 1999], where the transmission cost is dominant, the processing cost can be just as large of a factor for spatial joins.

Mamoulis et al. [2003] explore the distributed spatial join problem in which the data resides on different servers between which there is no communication and the servers will not perform a spatial join. This would be the case if the servers are commercially owned and contain proprietary data. Additionally, it is assumed that the servers will not provide statistics on the data. In this case, the spatial join must be performed at a third, possibly small, site, such as a mobile device. They point out that any processing at the data server sites is relatively inexpensive compared to a mobile device. Therefore, as much work as possible should be done on the data servers, such as running queries to build useful statistics on the data. To do the spatial join, they propose a grid-based partitioning spatial join (Appendix B.2) and use the detailed statistics to determine the best grid such that data fits within the available internal memory. The statistics are also used to identify empty regions in a dataset for which no spatial join needs to be performed, thus saving valuable transmission costs.

6. SELECTIVITY ESTIMATION

Techniques for estimating the selectivity of a spatial join are important as an aid for analyzing spatial join algorithms, for use in query optimizers, and as a data mining tool. Günther et al. [1998] have shown that along with the size of the dataset, selectivity is crucial in determining the performance of an algorithm. Query optimizers assist a database engine in determining the order of operations in a complex query. Also, selectivity estimates could play a roll in determining which spatial join algorithm to use. For instance, a very dense dataset in which nearly every pair is reported, could be computed faster using the simple nested loop join (Appendix A.3), rather than a more complex algorithm with a large overhead. For data mining applications, selectivity estimates can give approximate answers to queries, which can be used to rule out hypotheses [Belussi and Faloutsos 1995].

For uniform datasets in two dimensions, a rudimentary estimate of the selectivity for the filtering stage of a spatial join can be derived from the probability that two average sized rectangles overlap [Aref and Samet 1994a]. Given that both datasets are enclosed in a universe of finite area, which is represented as $TotalArea$, the

probability that two rectangles with widths w_a and w_b and heights h_a and h_b intersect is:

$$\frac{(w_a + w_b) \cdot (h_a + h_b)}{TotalArea} = \frac{area_a + area_b + (w_a \cdot h_b) + (w_b \cdot h_a)}{TotalArea}, \quad (2)$$

where $area_a$ and $area_b$ are the areas of two rectangles [14]. To derive a selectivity estimate for a spatial join between two uniform datasets, the average sizes of the rectangles in the two datasets A and B are substituted into Equation 2. In this case, the selectivity is approximately:

$$\frac{\overline{area_A} + \overline{area_b} + (\overline{w_A} \cdot \overline{h_B}) + (\overline{w_B} \cdot \overline{h_A})}{TotalArea}. \quad (3)$$

However, the situation is more complicated for non-uniform datasets. Mamoulis and Papadias [2001b], An et al. [2001], and Belussi et al. [2004] propose using a two-dimensional histogram on each dataset, which can be a grid with occupancy counts. Within each grid cell, the selectivity estimate for uniform datasets, Equation 3, can be applied. The results for each cell are then combined to get an overall estimate of selectivity. The finer the histogram, the more accurate the results will be. An et al. also studied sampling techniques and proposed a novel technique for estimating intersections within a grid cell by counting the number of sides and corners of rectangles within each grid cell.

Das et al. [2004] present a method that provides a selectivity estimate of a spatial join for skewed datasets. The method requires one scan of the dataset, and has a provable, adjustable error bound. Each object in the dataset is represented by a fixed set of objects from a *dyadic* cover, with a total size $O(\log(n))$, where n is the size of the dataset. As each object, r, is encountered, summary statistics for each dyadic object composing r are updated. By combining these statistics in a manner that does not count particular intersections more than once, the method estimates the selectivity of the spatial join.

In another approach, working with point datasets, Belussi and Faloutsos [1995] expressed the selectivity of a self-spatial join in terms of a fractal dimension. Since the data is points, the spatial join finds all pairs of points within a distance ϵ, which is expressed as $\overline{nb}(\epsilon)$, and is analogous to the average number of intersecting pairs, that is, the selectivity of the spatial join [15]. The average number of nearby, or *neighboring*, points captures information about the distribution of the data. If the data is clustered, then the average number of neighbors increases. The problem, then, is to find a good estimate of the number of neighbors. To do so, Belussi and Faloutsos use the fractal *correlation dimension* D_2, which is a characteristic of the dataset, and calculate the average number of neighbors as:

$$\overline{nb}(\epsilon) = (n - 1) \cdot (2 \cdot \epsilon)^{D_2}, \quad (4)$$

where n is the number of points. Using this equation, the selectivity of a self-spatial

[14] Equation 2 assumes that the space wraps around and does not account for the need for rectangles to be within the boundaries of the space. However, the difference is negligible if the rectangle is a small fraction of the space. Also, a minus one value is also dropped from the sums, for simplicity.
[15] Though, $\overline{nb}(\epsilon)$ as defined by Belussi and Faloutsos [1995] is the number of points within a circle, here, their generalization to other shapes is used. In this case, a rectangle.

join is estimated as $(2 \cdot \epsilon)^{D_2}$. The correlation dimension, D_2, can be calculated in $O(n \cdot \log(n))$ time [Belussi and Faloutsos 1995] or even in constant time according to Faloutsos et al. [2000], who describe algorithms for efficiently calculating the correlation dimension for a given dataset and show the effectiveness of the calculation for predicting the selectivity of a self-spatial join [16].

7. CONCLUDING REMARKS

We have provided an in-depth survey and analysis of the various techniques used to perform a spatial join using a filter-and-refine approach in which complex objects are approximated, typically by a minimum bounding rectangle. The approximations are joined, producing a candidate set which is refined to produce the final results using the full objects. We examined various techniques for performing a spatial join using the available internal memory, using either nested loop joins, indexed nested loop joins, or variants of the plane-sweep technique. If there is insufficient internal memory, then external memory can be used to process larger datasets. We examined cases where the data is indexed or not indexed. If the datasets are indexed, then overlapping data pages can be read in a predetermined order or the two indices can be traversed synchronously if the indices are hierarchical. Pairs of overlapping data pages are joined using internal memory techniques. Alternatively, if the data is not indexed, then the data can be partitioned using a variety of techniques, and then overlapping partition pairs can be joined using internal memory techniques. We also examined the techniques and issues involved with refining the candidate set produced during the filtering stage. Finally, we looked at spatial joins in a variety of situations: multiway spatial joins, parallel spatial joins, and distributed spatial joins.

Of course, there are many other variations of spatial joins and techniques which space limitations have prevented us from elaborating upon. We now briefly mention a few of them. There has been some interest recently in improving performance of spatial joins through the use of specialized hardware such as graphics processing units (GPUs). Such an approach has been proposed by Sun et al. [2003] who suggest assigning a different color to each dataset and then letting the graphics hardware render the datasets for the screen. In this case, the frame buffer can be searched for regions containing a combination of the colors, which indicates intersecting objects. From an analytical standpoint, the algorithm will be worse because of the scan of the frame buffer, but the overall performance will be improved due to the advanced hardware. However, the drawback of this approach is that the graphics hardware typically only works on convex polygons and only a limited resolution can be achieved, thereby leading to false hits that still need to be refined. In addition, Sun et al. propose using a similar approach to determine whether two polygons intersect. In this case, the edges of one polygon are assigned one color while the other polygon's edges are colored differently.

When the dataset is not updated often and speed is critical, Günther [1993] suggest the use of a spatial join index [Rotem 1991]. In this case, all of the intersecting objects are determined in advance and the resulting pairs of ids are stored in an

[16] Faloutsos et al. [2000] use the formula $K \cdot r^{\mathcal{P}}$ for selectivity, instead of Equation 3, where r replaces $2 \cdot \epsilon$ and $\mathcal{P}$ replaces D_2, and they also use the multiplier K.

index. A spatial join algorithm must be used, though, to create the original set of results pairs.

Zhu et al. [2005] address the issue that at times we are not interested in all of the intersecting pairs. In particular, given two spatial data sets A and B, they are interested in obtaining the k objects from A or B that intersect the highest number of objects from the other set, termed a *top-k spatial join*. They achieve this by making use of the synchronized traversal methods from Section 4.1.1.

Finally, we point out that Papadias and Arkoumanis [2002] take a different approach to the issue of not reporting all of the intersecting pairs. They are motivated by the desire to perform a multiway spatial join in a given amount of time due to the prohibitive expense, timewise, of performing the full multiway spatial join. Their approach searches for approximate solutions, which are defined as solutions that may violate some constraints. For instance, for a 3-way intersection, a solution with only two of the required intersections would be an approximate answer. The method they use is a combination of search heuristics, randomized algorithms, and R-tree spatial indexes [Guttman 1984]. In essence, a candidate pair is guessed and then improved upon using a search through the R-trees. This operation is repeated until time runs out.

At this point, we mention that our main goal in this survey was to provide a guide as to what techniques work best in particular situations. However, we were not able to conclusively determine which techniques are superior for each scenario as we observed that the experiments comparing techniques were inconclusive and could easily be skewed by the choice of experimental data or details of implementation. Nevertheless, we feel that this survey illuminates some of these issues and hope that it motivates further analyses and experimentation.

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Spatial Join Techniques

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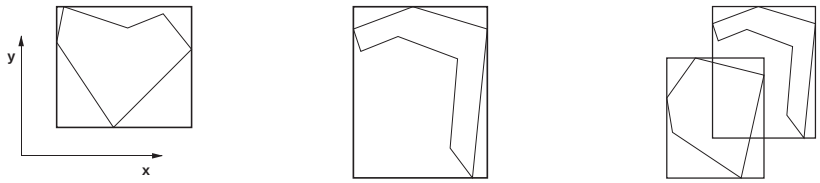
A. SPATIAL JOIN CONCEPTS

Appendices A.1 and A.2 review MBRs and linear orderings, respectively, which are concepts that are fundamental to many spatial join techniques. Also, Appendix A.3 describes a simple method for performing an in-memory spatial join, the nested-loop join.

A.1 Minimum Bounding Rectangles and Approximations

For the filtering stage, most algorithms use a minimum bounding rectangle (MBR) to approximate the full object, though other approximations might be used instead or as a secondary filter (Appendix C). An MBR of an object is the smallest enclosing rectangle whose sides are parallel to the axes of the space (axis-aligned), as shown in Figure 20a. MBRs are preferred over the full object because they require less memory and intersections between MBRs are easier to calculate. Objects, especially in GIS applications, can be very large, requiring many points or lines to represent a polygon, and for large datasets, which are also typical in GIS applications, reading thousands, millions, or more of these objects from external memory and performing intersection tests on them can be extremely expensive in terms of I/O performance. Instead, if MBRs are used in the filtering stage, the MBRs can be read from external memory faster than the full object and the intersection tests can be performed faster. Unfortunately, using MBRs, or any approximation, will produce some wrong answers. As shown in Figure 20b, an object might only occupy a fraction of its MBR, leaving a portion of *dead space*. Two MBRs might intersect, but the objects they represent might not intersect, as shown in Figure 20c. This result is referred to as a *false hit*, whereas the result is termed a *true hit* if the MBRs intersect and the objects they represent also intersect.



(a) (b) (c)

Fig. 20. (a) A minimum bounding rectangle (MBR) is the smallest rectangle that fully encloses an object and whose sides are parallel to the axes. (b) The area of an MBR might be significantly larger than the area of the enclosed object. The extra area is referred to as *dead space*. (c) Two MBRs might intersect even though the objects that they enclose do not intersect.

(a) (b)

Fig. 21. (a) In order to reduce dead space, an object can be approximated by two disjoint rectangles. (b) However, both rectangles might intersect a second object, thereby producing duplicate results.

Before performing a spatial join, the MBRs for the full objects must be calculated. If the data is indexed using a spatial indexing method [Gaede and Günther 1998; Samet 1990], then typically the MBRs exist already. If they do not, then a scan of the full dataset is required to create the MBRs. Forming the MBR of an object simply involves checking each corner point of the object, which is an $O(n)$ operation for a polygonal object with n vertices.

Use of the filter and refine approach for spatial joins was first introduced by Orenstein [1989b]. Orenstein was concerned that a poor approximation would degrade performance [Orenstein 1989a] and experimented with using a set of disjoint rectangles to approximate each object. For example, to use this representation, the object in Figure 20b is decomposed into the two MBRs shown in Figure 21a, improving the approximation by reducing the dead space, but also increasing the size of the dataset. While this approach improves the accuracy of the filter stage, it also creates the need for an extra step after the filtering stage to remove duplicates from the candidate set. As shown in Figure 21, both pieces of the decomposed object in Figure 21a might intersect the same object, as shown in Figure 21b. Both of these intersections create a candidate pair. The duplicate results generally need to be removed for most applications and this typically should be done before the more costly refinement stage in order to avoid extra processing (see Section 4.3.4 for a discussion of duplicate removal techniques).

Nevertheless, most algorithms use one MBR, rather than approximating an object by a set of rectangles, and rely on the refinement stage to efficiently remove false hits. However, many algorithms intentionally duplicate objects. For instance, if

(a) (b)

Fig. 22. (a) A linear order, where object a's neighbors, b and c are nearby. (b) A linear order in which one of object a's neighbors, c, is nearby, but the other neighbor, b, is not.

(a) (b)

Fig. 23. (a) Z-Order (Peano order) and (b) Peano-Hilbert order.

an algorithm creates a disjoint partition of the objects in a divide-and-conquer approach, as is done with a grid partitioning approach (see Appendix B.2), then each object will appear in each partition it overlaps. Similarly, some spatial indices that can be used to perform a spatial join use disjoint nodes and the objects again are copied into each node they overlap (for example, the R^+-tree [Sellis et al. 1987]). In both cases, duplicate removal (or avoidance) techniques are required (see Section 4.3.4).

A.2 Linear Orderings

A linear order [Jagadish 1990a; Samet 1990] creates a total order on multi-dimensional objects. In other words, a linear order is a traversal of all of the objects, as shown in Figure 22. Linear orderings play an important role in many spatial join techniques, in a similar way that sorted orders (a one-dimensional linear ordering) play an important role in creating efficient algorithms for relational joins (for example, the sort-merge join [Mishra and Eich 1992]). The benefit of a sorted order in one dimension is that neighboring objects (close in value) are next to each other in the sorted order, leading to algorithms such as the sort-merge join [Mishra and Eich 1992]. In more than one dimension, no natural linear order exists and spatially neighboring objects will not necessarily be close in the linear order. For example, in Figure 22a, neighboring objects a and b are next to each other in the order indicated by the arrows, but in Figure 22b, they are widely separated. Nevertheless, because linear orders keep some of the neighboring objects near each other in the order, they can be useful in spatial join techniques.

Linear orders that keep neighboring objects closer in the order, on average, such as the Z-order or the Peano-Hilbert order, tend to be more useful for spatial join algorithms. The Z-order (also known as a Peano or Morton order), shown in Figure 23a, and the Peano-Hilbert order, shown in Figure 23b, traverse the grid in a

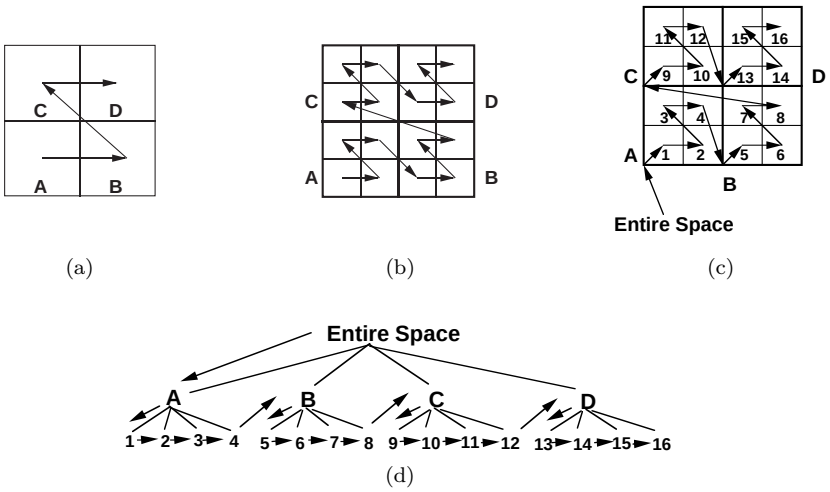


Fig. 24. (a) A four cell grid traversed in a Z-order. (b) A sixteen cell grid traversed in a Z-order. (c) A sixteen cell grid traversal that includes enclosing blocks (lettered blocks). (d) A sixteen cell grid traversal as a tree traversal.

pattern that helps to preserve locality. They are also known as space-filling curves (see [Samet 2006] for other such curves). Both of these linear orders first order objects in a block before moving to the next block. For example, the Z-order is a traversal through a regular grid using a 'Z' pattern, as shown in Figure 24a. If there are more than four cells in the grid, then each top-level block is fully traversed before moving to the next block. In Figure 24b, block A from Figure 24a is traversed in a 'Z' pattern before moving to block B. This pattern is repeated at finer levels, where a block at any level is fully traversed before moving to the next block. In this way, a linear order is imposed on the cells. The Peano-Hilbert order is similar, as shown in Figure 23b, though each block is traversed in a rotation that might be clockwise or counter-clockwise, avoiding the large jumps between the constituent grid cells of a Z-order.

Additionally, an order might visit both the grid cells and the enclosing blocks, for instance, ordering both the blocks in Figure 24a and the constituent grid cells in Figure 24b. To accomplish this order, one convention is to visit enclosing regions (the blocks in Figure 24a) before visiting smaller regions (the cells in Figure 24b), as shown in Figure 24c, which also includes the top level cell (the enclosing space) in the ordering. In essence, this a hierarchical traversal of the nodes, as shown in Figure 24d, which is a preorder tree traversal.

To traverse points in a linear order, the grid cells can be made small enough such that each point is in its own grid cell. To traverse objects in a linear order, either a point in the objects, such as the centroid, is used to represent each object or the objects are assigned to the smallest enclosing block or grid cell, which is similar to creating an MBR for the object, but with more dead space, as shown in Figure 25a. Note that an object, no matter how small, that intersects the center point will always be in the top level cell (root space), as shown in Figure 25b. Some algorithms can take advantage of the regular structure of the enclosing cells, but

(a) (b)

Fig. 25. (a) In a linear ordering, objects can be assigned to the smallest enclosing block or grid cell. Object r is assigned to the root space since it is not within any block. Object s is assigned to the lower right block, B, and object t is assigned to cell 14. (b) An object overlapping the center point, no matter how small, will be assigned to the top level, which is the entire space.

```
1  procedure NESTED_LOOP_JOIN(setA, setB, joinCondition)
2  begin
3    foreach a ∈ setA do
4      foreach b ∈ SetB do
5        if SATISFIED(a, b, joinCondition) then
6           REPORT(a, b);
7        endif;
8      enddo;
9    enddo;
10 end;
```

Fig. 26. The basic nested loop join with running time $O(n_a \cdot n_b)$, for datasets of size n_a and n_b, using an arbitrary join condition (`joinCondition`).

```
1  procedure INDEX_NESTED_LOOP_JOIN(setA, setB)
2  begin
3    spatialIndex←CREATE_SPATIAL_INDEX(setA);
4    foreach a ∈ setA do
5      spatialIndex.INSERT(a)
6    enddo;
7    foreach b ∈ setB do
8      searchResults←spatialIndex.SEARCH(b)
9      REPORT(searchResults)
10   enddo;
11 end;
```

Fig. 27. An index nested-loop join improves the performance of the spatial join to $O((n_a + n_b) \cdot log(n_a) + f)$, assuming search times of the index are $O(log(n_a) + f)$, where f is the number of results found, n_a is the size of the indexed dataset, and n_b is the size of the unindexed dataset.

at the price of more false hits due to the increased dead space (see Section 3.2 and Appendix B.4).

A.3 Nested Loop Joins

The most basic spatial join method is the nested-loop join, which compares every object in one dataset to every object in the other dataset [Mishra and Eich 1992]. The algorithm, shown in Figure 26, takes every possible pair of objects and passes it to the `SATISFY` function to check if the pair of objects meets the given join condition,

termed `joinCondition` in the algorithm. If a pair satisfies the join condition, then it is reported using the `REPORT` function. Given two datasets, A and B, with n_a and n_b objects in each, respectively, the nested-loop join takes $O(n_a \cdot n_b)$ time. Despite this larger cost, the nested-loop join can be useful when there are too few objects to justify the overhead of more complex methods. Note that this algorithm works with any object type and with any arbitrary join condition.

A variant of the nested-loop join algorithm, called the index nested-loop join [Elmasri and Navathe 2000], improves performance for larger datasets by first creating a spatial index on one dataset, say A. In this algorithm, given in Figure 27, the spatial index is first created and every element of dataset A is inserted into the index using the `INSERT` function. Next, the other dataset, say B, is scanned, and each element is used to search the index on dataset A for intersections. The index is searched using the `SEARCH` function, which in this context becomes a *window query* [Gaede and Günther 1998] on the index, where the window is the object from dataset B. Generally, the search window is a rectangle, which limits the types of join conditions to intersection tests or related relations that can be solved with a window query, such as proximity. Typically, for each object in dataset B, the time to search the index is, on average, $O(log(n_a) + f)$, where n_a is the size of dataset A and f is the number of intersections found. For example, the search and insert time, on average, for an R-tree [Guttman 1984] is $O(log(n_a) + f)$. In theory, an object could intersect every object in the index, creating an $O(n)$ search time. In practice though, the number of intersections is small and the running time of the entire algorithm is $O((n_a + n_b) \cdot log(n_a) + f)$, which includes the time to construct the index, which is typically $O(n_a \cdot log(n_a))$. Since all of dataset A is inserted first, more efficient static indices and bulk-loading techniques [Arge et al. 1999; Hjaltason and Samet 1999; Kamel and Faloutsos 1993; van den Bercken et al. 1997] can be used to improve the construction time and the performance of the index.

The index nested-loop algorithm can be executed entirely in memory, using in memory indices, and is useful as a component in other spatial join algorithms (see Section 4). The algorithm can also be used as a stand alone external memory spatial join algorithm by using external memory indices, which allows the algorithm to process larger datasets. For instance, Becker et al. [1993] used grid files [Nievergelt et al. 1984] as the index and Henrich and Möller [1995] used an LSD tree [Henrich et al. 1989] as the index. However, more sophisticated methods exist for using an external spatial index to perform a spatial join (see Section 4).

B. NEITHER DATASET INDEXED TECHNIQUES

This Appendix provides more details of specific methods for performing a spatial join on unindexed data that were mentioned in Section 4.3. Appendix B.1 discusses an extension to the plane-sweep algorithm (Section 3.1) that can process datasets of any size by using external memory. Next more sophisticated partitioning algorithms from the literature are described, grouped by how they partition the data: using grids in Appendix B.2, using strips in Appendix B.3, by size in Appendix B.4, and clustering in Appendix B.5.

```
1  procedure EXTERNAL_PLANE_SWEEP(setA, setB)
2  begin
3    mergedSet←SET_MERGE(setA, setB);
4    sortedSet←SORT_BY_LEFT_SIDE(mergedSet);
5    insertList←sortedSet;
6    sweepStructureA←CREATE_SWEEP_STRUCTURE();
7    sweepStructureB←CREATE_SWEEP_STRUCTURE();
8    while insertList ≠ ∅ do
9      sweepStructureA.INITIALIZE();
10     sweepStructureB.INITIALIZE();
11     doOverFile←new File();
12     foreach r in sortedSet do
13       if r ∈ setA then
14          sweepStructureB.REMOVE_INACTIVE(r);
15          sweepStructureB.SEARCH(r);
16          if r = insertList.FIRST() then
17            insertList.POP();
18            errorStatus←sweepStructureA.INSERT(r);
19            if errorStatus = InsufficientMemoryError then
20               doOverFile.WRITE(r);
21            endif;
22          endif;
23       else
24         sweepStructureA.REMOVE_INACTIVE(r);
25         sweepStructureA.SEARCH(r);
26         if r = insertList.FIRST() then
27            insertList.POP();
28            errorStatus←sweepStructureB.INSERT(r);
29            if errorStatus = InsufficientMemoryError then
30               doOverFile.WRITE(r);
31            endif;
32          endif;
33       endif;
34     enddo;
35     insertList←doOverFile.READ_ENTIRE_FILE();
36   enddo;
37 end;
```

Fig. 28. An external memory version of the plane-sweep algorithm with the ability to process datasets of any size.

B.1 External Plane Sweep

Jacox and Samet [2003] extended the modified plane-sweep algorithm of Arge et al. [1998] (see Section 3.1) to process datasets of any size by using external memory. The algorithm, shown in Figure 28, adds an outer loop to the plane-sweep algorithm that keeps track of which objects have been inserted into the sweep structure. Initially, all objects are included in the list of objects to insert, which are stored in the `insertList` variable. In the first pass of the outer loop, the plane-sweep runs normally. If there is sufficient internal memory, the external plane-sweep performs exactly as the internal version (see Figure 2), and the outer loop does not need to be run again. However, if internal memory is full, then the current object is not inserted into the sweep structure, but marked as not having been added to the sweep structure. In this case, a reference to the object is saved to a file (or some other

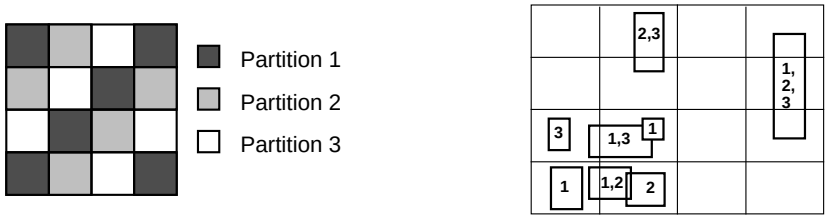


Fig. 29. (a) Noncontiguous grid cells are grouped to form three partitions. (b) Forming partitions from noncontiguous grid cells helps to prevent data skew problems by creating partitions of equal size. Even though the data is clustered in the lower left corner, the partitioning scheme results in each partition containing either four or five objects. Each object is labeled with the partitions in which it will be placed.

external memory storage), called `doOverFile`. When a pass of the plane-sweep finishes, this list of objects in `doOverFile` serves as the list of objects to insert into the sweep structure in the next pass of the outer loop, which just performs the same plane-sweep again, but doesn't insert the objects that were inserted on the first pass. The plane-sweep algorithm is run repeatedly until all objects have been inserted into the sweep structure. Note that on every pass, every object is used to search the sweep structure, thereby not missing any intersecting pairs. Also note that the algorithm merges the two datasets into one dataset at the beginning of the algorithm with the `SET_MERGE` function so that the algorithm only needs to manage one `doOverFile` instead of two.

B.2 Partitioning Using Grids

No technique uses a simple grid as did the generic algorithm in Figure 13, since it is only useful for uniform distributions. However, Patel and Dewitt [1996] use a uniform grid as a starting point. First, the data space is divided into a uniform grid, where the number of grid cells, which they call *tiles*, is greater (typically much greater) than the number of desired partitions. The grid cells are then grouped into partitions using a mapping function in such a way as to minimize skew by, hopefully, creating partitions that contain a similar numbers of objects. For example, in Figure 29a, the grid cells are grouped to form three partitions. Even if the data is skewed, each partition will cover part of the dataset, as shown in Figure 29d. Note that the data is not physically partitioned into the grid cells, but only into the final partitions. In other words, grid cells are assigned to partitions first, and then the data is partitioned.

Patel and Dewitt [1996] do not proscribe a particular mapping, but only suggest using some form of a hashing function to assign the cells to partitions. The hash function should be chosen to distribute the data evenly amongst the partitions and is dependent on the dataset. As an example, Patel and Dewitt use a round-robin order, that scans the grid in row-major order and alternates assigning the cells among the partitions, as is shown in Figure 29a. In the figure, because the grid cells are not contiguous, the partitions have a larger total perimeter, leading to increased data replication since a larger perimeter provides more opportunities for an object

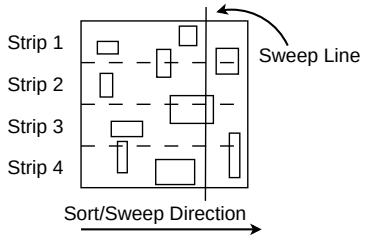


Fig. 30. In strip partitioning, the data is partitioned into strips and sorted parallel to the strip to take advantage of the plane-sweep modification described in Section 3.1. In this example, the sweep is repeated four times, once for each strip. The actual height of the sweep line is the height of the strip.

to intersect the perimeter. Using more initial grid cells increases the uniformity of the distribution because areas of skewed, dense data are distributed amongst several partitions, but using more grid cells also increases the replication of objects across partitions. Experiments [Patel and DeWitt 1996] showed that increasing the number of grid cells can create near uniform distributions from skewed datasets, but the replication rate can also increase rapidly. In their experiments, Patel and Dewitt [1996] found that Tiger data [U.S. Bureau of the Census 1992] had a replication rate of about 2.5% with 100 grid cells per partition while Sequoia data [Stonebraker et al. 1993] had a replication rate of 10%.

Zhou et al. [1997] use a variation of this technique in which the data is physically partitioned into the grid cells, first. Since the grid cell sizes are known, the partitions can be formed by grouping contiguous cells until a desired partition size, as determined using methods from Section 4.3.2, is reached. This approach reduces the amount of replication because the partition boundary is smaller. The cells can be grouped using any linear order, such as a Z-order (Appendix A.2). If any grid cells remain after the maximum number of partitions have been formed, then they can be assigned to the partitions with the least objects.

B.3 Partitioning With Strips

Arge et al. [1998] partition the data into strips so that they can take advantage of their modification to the plane-sweep algorithm (Section 3.1). They show a lower bound for their method of $O(n \log_m(n)+t)$ I/O transfers, which is optimal, where n is the number of objects in both sets divided by the block size, B (that is, $n = N/B$, where N is the total number of objects in the datasets), m is the amount of internal memory divided by block size, and t is the number of result pairs divided by block size. For the plane-sweep method, after the data is sorted, it is partitioned into strips that are parallel to the sort direction, as shown in Figure 30 [17]. With the modified plane-sweep method, the amount of data that can be processed with a given amount of internal memory is limited by the maximum size of the active set. When the data is partitioned into strips, the maximum size of the active set is the maximum number of objects that intersect the sweep line, which is a function of

[17] Güting and Schilling [1987] also used a form of strip partitioning to solve the rectangle intersection problem using external memory.

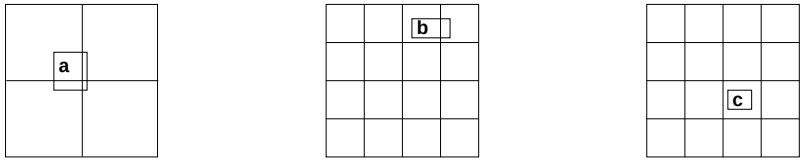


Fig. 31. To partition by size, objects are associated with the level where they first intersect a grid. (a) Object a is associated with the root space, the highest level, since it intersects the first (coarsest) grid level with four grid cells. (b) Object b is associated with the next level since it intersects the next finer grid level with sixteen cells. (c) Object c is associated with an even lower level.

the height of the strip. By appropriately limiting the height of the strip, which can be a difficult calculation (see Section 4.3.2), the width of the strip can be of any length, even infinite, in theory. Also, because strips are used, fewer partitions are needed than in the grid method of Appendix B.2. Thus, if the grid method needs k partitions to process the data without repartitioning, then the strip method can process the same data with only $\sqrt{k}$ partitions. For instance, if the grid method creates a regular grid with sixteen cells, then the strip method can process the same data with four strips. In other words, the strip method would just ignore the vertical lines of the grid method. Additionally, since fewer partitions are used, less data is replicated.

B.4 Partitioning By Size

Koudas and Sevcik [1997] roughly partition the data by size, using a series of finer and finer grids, as shown in Figure 31. Each successive grid is derived by subdividing each cell into four equal sized cells. To partition the data, each object is placed into the partition associated with the finest grid in which the object does not intersect the grid lines [18]. For example, as shown in Figure 31a, object a crosses the coarsest partitioning, and therefore, goes into the first partition. The next partition is similarly composed of objects that do not fit in the first partition and which cross partition boundaries for sixteen equal sized partitions, as shown Figure 31b. Each lower level partition, such as the one containing object c in Figure 31c, is similarly formed. In essence, each partition is a filter and objects fall through to the lowest level partition where a partition boundary is crossed.

The algorithm for joining two datasets partitioned by size is shown in Figure 32. It is a variant of the Z-order method described in Section 3.2. The main difference is that the data is partitioned into multiple levels using the `DETERMINE_LEVEL` function and several sweep structures are used for each dataset, one for each level. Note that the data need not be physically partitioned into the levels, but only partitioned into

[18] In addition to using this structure for the spatial join, Koudas and Sevcik [1997] build an index from the level partitions by saving them to data pages and adding an access structure to the data pages. They call the index a *filter tree*, which in essence is an MX-CIF quadtree [Kedem 1981] where an object is associated with its maximum enclosing quadtree block. Arge et al. [1998] use a concept similar to the filter tree in conjunction with the strip partitioning method (Appendix B.3) to avoid inserting large objects into the partitions, improving the performance of the join on each partition and limiting the amount of replication.

```
1  procedure PARTITION_BY_SIZE(setA, setB)
2  begin
3    /* determine number of levels */
4    minSize←FIND_SMALLEST_OBJECT(setA, setB);
5    levels←CEILING(log4(TotalArea/minSize));
6    listA←SORT_IN_Z-ORDER(setA);
7    listB←SORT_IN_Z-ORDER(setB);
8    sweepStructuresA[]←CREATE_SWEEP_STRUCTURES(levels);
9    sweepStructuresB[]←CREATE_SWEEP_STRUCTURES(levels);
10   while NOT listA.END() OR NOT listB.END() do
11     /* get next rectangle from the two lists */
12     if listA.FIRST() < listB.FIRST() then
13       object←listA.POP();
14       level←DETERMINE_LEVEL(object)
15       sweepStructuresA[level].INSERT(object);
16       for( i=level; i<=0; i-- )  do
17          sweepStructuresB[i].REMOVE_INACTIVE(object);
18          sweepStructuresB[i].SEARCH(object);
19       enddo;
20       listA.NEXT();
21     else
22       object←listB.POP()
23       level←DETERMINE_LEVEL(object)
24       sweepStructuresB[level].INSERT(object);
25       for( i=level; i<=0; i-- ) do
26          sweepStructuresA[i].REMOVE_INACTIVE(object);
27          sweepStructuresA[i].SEARCH(object);
28       enddo;
29       listB.NEXT();
30     endif;
31   enddo;
32 end;
```

Fig. 32. A modified Z-order algorithm that partitions the data by size.

distinct sweep structures, which is a modification suggested by Dittrich and Seeger [2000]. The first step in the algorithm is to determine how many levels are needed, which is done with a simple calculation. The smallest grid cells should be about the same size as the smallest object, which is found using the `FIND_SMALLEST_OBJECT` function. The number of levels then is roughly the base four logarithm of the total number of grid cells at the finest level, which is estimated as the enclosing area of the data space, `TotalArea`, divided by the size of the smallest object, `minSize`. The algorithm then proceeds nearly identically to the Z-order method from Section 3.2, accounting for multiple sweep structures. Each object is read (in Z-order) and inserted into its dataset's sweep structure for its level using the `INSERT` function. Next, after the inactive objects are removed using the `REMOVE_INACTIVE` function, the sweep structures for the other dataset are searched for intersections using the `SEARCH` function. Only sweep structures at the same level or shallower (coarser) need to be searched since the Z-order can ensure that larger objects will be seen first. For instance, the two root space sweep structures will be searched after every insertion of the opposing data set.

The finest level partition needed depends on the size of the smallest objects.

The algorithm in Figure 32 assumes that all of the coarser levels contain objects, but this might not be the case. The algorithm can be modified to ignore empty levels. Note that because the objects are partitioned by size, they are not replicated between partitions. Also, there is no way to repartition the data. Since the sizes of partitions are determined by grid divisions and not by the number of objects in each partition, there could be too many objects in a particular partition and the sweep structures could overflow the available internal memory. However, in their experiments, Koudas and Sevcik [1997] found that sweep structures, which they implemented as stacks, tend to contain few objects, and internal memory is unlikely to overflow.

Small objects might be in level partitions meant for larger objects if they cross partition boundaries for that level, as was shown in Figure 25b in Appendix A.2. This hinders performance. Dittrich and Seeger [2000] suggest replicating small objects to allow them to be placed into more appropriate partitions. If an object is smaller than the grid cells of the boundary that it overlaps, then the object is divided using the boundary. Each divided piece is then used to find a finer level partition in which to insert the full object. For example, the object in Figure 25b would be divided into four pieces and inserted into the four middle partitions. Duplicate removal methods will then be needed (see Section 4.3.4).

B.5 Data-Centric Partitioning

Lo and Ravishankar [1995; 1996] cluster the data into partitions. One of the datasets, say dataset A, is first sampled and a nearest-center heuristic is used to identify clusters of the sampled objects. The centroids of the clusters form the basis of the partitions. Initially, each partition is just the identified point, with no area. As objects from dataset A are inserted into the partitions, the partition boundaries are expanded to enclose the inserted objects. Thus, a partition boundary is the enclosing MBR of the objects in the partition. Data is inserted into the partitions using a choice of heuristics, such as inserting into the partition whose size grows the least by area or into the partition whose centroid is closest. Note that this process results in non-disjoint partitions. Once dataset A is inserted into the partition, the resulting partition boundaries are used to partition the second dataset, say B. Objects from dataset B are inserted into each partition that they overlap. Each partition for dataset A then needs to be joined with only one partition from dataset B using any appropriate internal memory method (Section 3). Duplicate results do not occur since each object from dataset A is only in one partition. One benefit of building non-disjoint partitions is that the partitions might not cover the entire data space. If this is the case with dataset A, then objects from dataset B that do not overlap any partition can be discarded since they could not be joined with any object in dataset A.

C. FILTERING EXTENSIONS

This section discusses approximations other than MBRs that can be used for filtering, and a method for making the filtering phase non-blocking. Appendix C.1 surveys techniques for producing better candidate sets with fewer false hits by using better approximations. Appendix C.2 discusses tests and approximations that can be used to identify true hits, that is, pairs of objects that definitely intersect. These

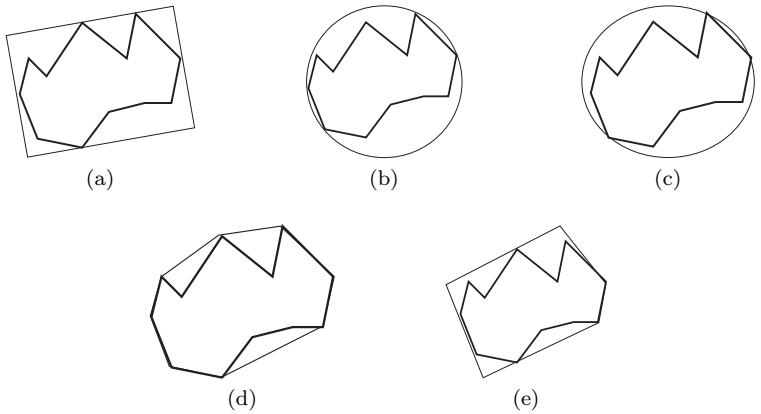


Fig. 33. Alternate approximations to MBRs include: (a) the rotated minimum bounding rectangle, (b) the minimum bounding circle, (c) the minimum bounding ellipse, (d) the convex hull, and (e) the minimum bounding n-corner polygon (for example, 5-corner).

pairs can be immediately reported and then removed from the candidate set, meaning that they are not passed to the more expensive refinement stage. Appendix C.3 describes a technique for making the filtering phase non-blocking.

C.1 False Hit Filtering

The MBR is not the only approximation that can be used during the filtering stage. Other approximations can be used if the filtering method is adapted to use the alternate approximation. Additionally, other approximations can be used as a secondary filter after the initial filtering stage to prune some false hits from the candidate set. To do this, the candidate set is scanned and an intersection test is performed on each pair of objects using a different approximation than was used to do the initial filtering. This second approximation should be stored since calculating the approximation on the fly requires the full object to be read into memory.

Brinkhoff et al. [1993] investigated false hit filtering methods that use approximations other than the MBR, which are shown in Figure 33. The approximations are:

(1) The rotated minimum bounding rectangle.
(2) The minimum bounding circle.
(3) The minimum bounding ellipse.
(4) The convex hull.
(5) The minimum bounding n-corner polygon (for example, 5-corner).

They found that using a better approximation generally reduces the number of false hits. The convex hull and 5-corner approximation performed especially well. However, the higher storage costs, the increased complexity of calculating the approximation, and the increased complexity of the intersection test can mitigate the

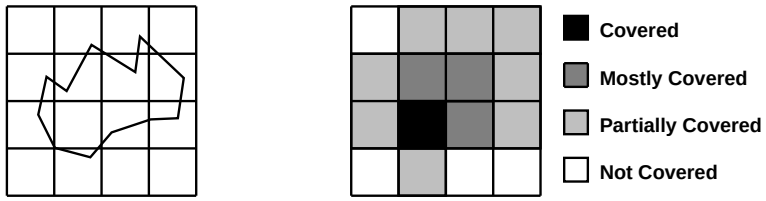


Fig. 34. An object (a) is approximated using a four color scheme (b) by imposing a grid over the object and coloring the cells depending on whether they are covered, mostly covered, partially covered, or not covered.

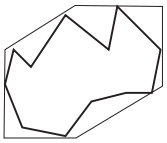


Fig. 35. An MBR approximation can be improved by adding two more sides, parallel to each other.

benefit. Even so, Brinkhoff and Kriegel [1994a] found that additional filtering with these approximations can improve total performance significantly.

Zimbrao and de Souza [1998] propose using a 4-color raster approximation for secondary filtering. As shown in Figure 34, a grid is imposed over each object and grid cells are colored depending on whether they are covered, mostly covered, partially covered, or not covered. To check for intersections, the two raster approximations of the objects are compared, taking into account the different offsets and scales of the grids. The number of grid cells can be adjusted to obtain more accurate results for filtering, but at the expense of higher storage costs.

Veenhoff et al. [1995] propose an approximation that is constructed by rotating two parallel lines around the object [19]. In other words, two more sides, parallel to each other, are added by chopping two corners of the MBR, as shown in Figure 35, creating a better approximation than the MBR, but still relatively inexpensive to calculate, (i.e., $O(n)$). The tighter approximation reduces the number of false hits.

A number of techniques have been proposed in the spatial indexing, robotics, and computer graphics literature for improving the quality of the approximation yielded by the MBR whose sides are parallel to the axes. For example, an index termed an *oriented bounding box tree* (OBBTree) (for example, [Gottschalk et al. 1996; Reddy and Rubin 1978]) uses a rotated minimum bounding box; a P-tree [Jagadish 1990b] uses an n-corner polygon; a k-DOP data structure [Klosowski et al. 1998], where the number k of possible orientations of the approximation is bounded; and a general spatial filtering mechanism [Brodsky et al. 1995], which attempts to find the optimal orientations, uses a minimum bounding polybox. The most general

[19] This approximation is also used by Duncan et al. [2001] in the BAR tree index.

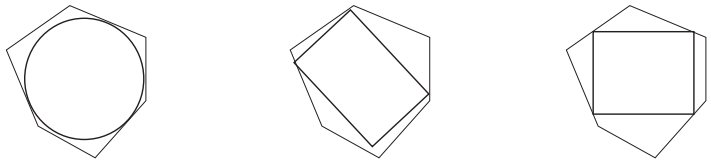


Fig. 36. An object approximated by: (a) a maximum enclosed circle, (b) a maximum enclosed rectangle, and (c) a maximum enclosed axis-aligned rectangle.

solution is the convex hull, which is often approximated by a minimum bounding polygon of a fixed number of sides having either an arbitrary orientation (for example, the minimum bounding n-corner [Dori and Ben-Bassat 1983; Schiwietz and Kriegel 1993]) or a fixed orientation, usually parallel to the coordinate axes (for example, [Esperança and Samet 1997]). The minimum bounding box may also be replaced by a circle, sphere (for example, the sphere tree [Hubbard 1996; Omohundro 1989; van Oosterom and Claassen 1990; White and Jain 1996]), ellipse, or intersection of the minimum bounding box with the minimum bounding sphere (for example, the SR-tree [Katayama and Satoh 1997]). In more than two-dimensions, Kriegel et al. [2004] present approximations for high-resolution three-dimensional objects.

In addition to alternate approximations, Koudas and Sevcik [1997] propose an additional filtering mechanism that might be useful for sparser datasets. They propose building a bitmap for one of the datasets, say A, where each bit represents a cell in a fine grid over the data space. If any object from dataset A intersects a grid cell, then the bit is turned on for that cell. Then, as objects from the second data are processed, each object is checked against the bit map. If the object does not intersect a cell with the bit turned on, then the object can be discarded.

C.2 True Hit Filtering

The traditional filtering phase identifies a candidate set, which is a super set of intersecting objects that also includes pairs of objects that do not intersect, but whose approximations intersect. In true hit filtering, additional approximations are used to find object pairs that definitely intersect, termed *true hits*, and thus can be reported immediately or later combined with the results of the refinement stage. While reducing the size of the candidate set is beneficial, Brinkhoff and Kriegel [1994a] point out that multiple filters might not combine well, that is, adding more than one filter might not significantly improve performance.

To identify true hits, Brinkhoff and Kriegel [1994a] propose using what they call a *progressive approximation*, where the approximation is entirely enclosed by the full object. In contrast to enclosing approximations, such as the MBR, the progressive approximation does not include extra dead space, but rather excludes portions of the full object. If the progressive approximations of two objects intersect, then the full objects must intersect. Brinkhoff and Kriegel [1994a] investigated three different progressive approximations, shown in Figure 36:

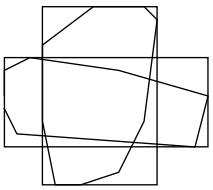


Fig. 37. If the MBRs of two objects cross, then the two objects must intersect.

(1) A maximum enclosed circle.
(2) A maximum enclosed rectangle.
(3) A maximum enclosed axis-aligned rectangle.

These approximations were shown to be effective at identifying true hits, but they are more expensive to calculate than MBRs and require extra storage space.

Brinkhoff and Kriegel [1994a] also describe a *cross test* that looks for enclosing approximations, such as MBRs, that cross, as shown in Figure 37 [20]. For example, assuming the objects are contiguous, if the MBRs of two objects *c*ross, then the objects must intersect. This is because the objects must also cross at some point and thereby intersect. This is most clearly seen by trying to imagine a counter example where the MBRs cross, as in Figure 37, without the objects intersecting. In their experiments, Brinkhoff and Kriegel found that very few intersecting MBRs will cross. However, they argue that since the cross test is so simple, it is worth applying, even if it identifies only a few true hits.

C.3 Non-Blocking Filtering

During the filtering phase, any algorithm will block while building an index, sorting the data, or partitioning the data. No output will be produced while this occurs, which delays overall processing in a pipelined system [Graefe 1993]. This section first describes a variant of the index nested-loop join (Appendix A.3) which is non-blocking and then presents a method to make any filtering technique non-blocking.

The indexed nested-loop join in Appendix A.3 blocks while it is building an index, that is, it doesn't produce any result pairs, which can slow processing in pipelined systems [Graefe 1993]. To overcome this limitation, Luo et al. [2002] use a non-blocking variation of the index nested-loop join so that some results are returned immediately. In the algorithm, shown in Figure 38, each dataset is indexed using a dynamic index, such as an R-tree [Guttman 1984]. A dynamic index must be used, which can be less efficient than static indices, but static indices block while being built. The input to the algorithm is the combined datasets. If the datasets are separate, as shown in previous algorithms, then either one data element or blocks of elements should be read from each dataset, alternating between the two datasets. Otherwise, no results will be reported until items from the second dataset are encountered. As each element is encountered, it is inserted into the index

[20] The cross test is similar to the intersection test of Ballard [1981] and Peucker [1976].

```
1  procedure NON-BLOCKING_NESTED_LOOP_JOIN(combinedDataSets)
2  begin
3    spatialIndexA←INTIALIZE_DYNAMIC_SPATIAL_INDEX();
4    spatialIndexB←INTIALIZE_DYNAMIC_SPATIAL_INDEX();
5    foreach dataElement ∈ combinedDataSets do
6      if dataElement ∈ setA then
7         spatialIndexA.INSERT(dataElement)
8         intersections←spatialIndexB.SEARCH(dataElement)
9      else
10        spatialIndexB.INSERT(dataElement)
11        intersections←spatialIndexA.SEARCH(dataElement)
12     endif;
13     REPORT(intersections)
14   enddo;
15 end;
```

Fig. 38. A non-blocking index nested loop join allows results to be reported immediately and continuously.

belonging to it's own dataset and the other index is searched for intersections. In this way, results can appear after only a few objects have been seen, though at the expense of building a second index.

A similar technique can be used to make any filtering technique non-blocking. Luo et al. [2002] propose a simple extension, that is conceptually similar to a pipelining hash join [Wilschut and Apers 1991], and is applicable to most filtering methods. They propose devoting a portion of internal memory to maintaining an in-memory R-tree (or any other spatial index) for each dataset, say datasets A and B, and then using the non-blocking nested loop join as a front-end to the filtering method. Only a subset of datasets A and B is inserted into the R-trees, which is processed like the non-blocking nested loop join shown in Figure 38. Once the R-trees are full, that is, the allotted internal memory is used up, the remaining data is processed using a more efficient external memory method (Section 4). However, the R-trees are still searched using the remaining objects in order to find all of the intersections with the objects in the indices. Once all of the data has been encountered, the objects in the indices can be discarded since all intersections with them have been reported, thereby freeing more internal memory for use by the external memory method used for the remaining objects.

D. THE REFINEMENT STAGE

The filtering stage (Section 4) produces a set of candidate object pairs that are typically represented as pairs of object ids. The candidate set contains pairs whose approximations intersect, but do not necessarily intersect themselves. The refinement stage checks the full objects to remove any of these false hits from the candidate set. Unless all of the full objects in the candidate set can fit into internal memory, the key to the refinement stage is ordering the reading of the full objects to minimize I/O. This issue is discussed in Appendix D.1. Since objects are often polygons, Appendix D.2 describes a common algorithm for checking if a pair of polygonal objects intersect. This test can be performed faster if the polygons are indexed using a spatial access method [Gaede and Günther 1998; Samet 1990],

which is discussed in Appendix D.3.

The candidate set might contain duplicate results, which should be removed first to avoid any extra intersection tests on the full objects. If online techniques for duplicate removal are used (Section 4.3.4), then the candidate set will not contain any duplicate results. However, some methods cannot use the online techniques and will introduce duplicates into the candidate set. A straight-forward approach to duplicate removal is to sort the id pair list, then scan the list and remove the duplicates. This extra step might not impact performance because it can be combined with techniques for efficiently reading the full objects from external memory in order to do the full object intersection tests, as discussed in Appendix D.1.

D.1 Ordering Pairs

Before performing an intersection test on a pair of objects, each object must be read into memory. Since the full objects might be large, it is unlikely that every object in the candidate set will fit into internal memory. In the best case, each object will be read once, and in the worst case, both objects will need to be read for each candidate pair. The pairs can be processed in the order in which the filtering stage produces them, which is necessary in a pipelined system [Graefe 1993]. Otherwise, if the extra cost of sorting is acceptable, then the candidate pairs can be sorted by ids or by the MBRs using a one-dimensional sort or a linear order (see Appendix A.2). Sorting improves performance and avoids the worst case of reading two objects for each candidate pair by minimizing the number of repeated reads of an object.

When the candidate pairs are not sorted, Abel et al. [1999] showed that the filtering method used impacts the performance of the refinement stage. In their experiments, they showed that the output of Z-order methods (see, for example, Appendix A.1 and Appendix B.4) were processed faster in the refinement stage than the output of the hierarchical traversal methods (Section 4.1.1). To explain this phenomenon, they suggest that the Z-order methods produce candidates that have more locality, making it more likely that the candidate pairs for an object are near each other in the output order, and thus, the object is more likely to remain in internal memory until it is needed again.

Alternatively, sorting the candidate pairs can reduce the number of times an object is read into memory, although the cost of sorting the pairs might offset some of the performance benefit. The pairs can be sorted using objects from only one dataset or a combination of both objects, using, for example, the centroid of the two objects or the MBR enclosing the two objects. Also, different amounts of internal memory can be devoted to each dataset, which is similar to the techniques used to read partitions in a non-hierarchical spatial join (Section 4.1.2). In one approach, the candidate pairs can be sorted for one dataset, say R. The objects in dataset R will be read into memory only once, while the objects from the other dataset, say S, will be read a multiple number of times. The objects from dataset S might be read as often as once for each candidate set pair, which is still better than the worst case of reading two objects into memory for each candidate pair. In another approach, Patel and Dewitt [1996] modify this process slightly by reading as much of the sorted dataset R into memory as possible, leaving room for one object from the dataset S. Then, the objects from dataset S are read one at a time, testing for intersections with each object with which it is paired in the candidate set that

```
1 function EDGE_INTERSECTION_TEST(edgesA, edgesB, MBRoverlap): boolean
2 begin
3   allEdges←edgesA ∪ edgesB;
4   allEdgesInRegion←EDGES_IN_REGION(allEdges, MBRoverlap);
5   allEndPoints←DOUBLE_EDGES(allEdgesInRegion);
6   edgeList=SORT_BY_END_POINT(allEndPoints);
7   activeEdges←CREATE_SWEEP_STRUCTURE();
8   while edgeList ≠ ∅ do
9     edge←edgeList.POP();
10    edgeAbove←activeEdges.EDGE_ABOVE(edge);
11    edgeBelow←activeEdges.EDGE_BELOW(edge);
12    if edge is the beginning of the edge then
13      activeEdges.INSERT(edge);
14      if INTERSECT(edge, edgeAbove) OR INTERSECT(edge, edgeBelow) then
15        return true;
16      endif;
17    else
18      if INTERSECT(edgeAbove, edgeBelow) then
19        return true;
20      endif;
21      activeEdges.REMOVE(edge);
22    endif;
23  enddo;
24  return false;  /* No intersection detected. */
25 end;
```

Fig. 39. A plane-sweep algorithm for detecting the intersection of simple polygons whose MBRs intersect.

is present within the portion of dataset R that is in memory. While objects from dataset R are still read one at a time, objects from dataset S will likely be read less often, since on each read, they can be compared to a multiple number of objects from R.

In a more sophisticated approach for polygonal datasets, Xiao et al. [1998] propose clustering the candidate pairs using matrix calculations. In their approach, they pose the read scheduling as an optimization problem that minimizes the number of fetches, weighted by object size. In the matrix, rows represent one dataset and columns represent the other dataset. The matrix values are the sums of the number of vertices in two intersecting polygons or zero for non-candidate pairs. This approach, unlike other methods, takes into account object sizes. Matrix calculations, termed the *Bond Energy Algorithm*, are used to cluster objects into datasets that fit in memory, where an object might be in multiple clusters. This algorithm runs in $O(n^3)$ time, where n is the number of objects.

D.2 Polygon Intersection Test

If the objects are polygons, a common approach to test if the objects intersect is a plane-sweep technique [Preparata and Shamos 1985], which is conceptually similar to the plane-sweep technique described in Section 3.1. The algorithm, shown in Figure 39, determines if two polygons have any intersecting edges. As with the plane-sweep technique in Section 3.1, this algorithm works by sweeping an axis-aligned line across the plane. The end points of the edges from both polygons

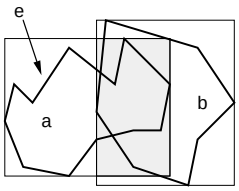


Fig. 40. Only the edges contained within the intersecting region of the MBRs could intersect each other. Edge e of object a, which is outside of the intersecting region, could not possibly intersect object b.

are the stopping points of the sweep line and the edges intersecting the sweep line form the active set. If the polygons do not have intersecting edges, one polygon could be contained within the other and a separate test for containment needs to be performed, which is described later.

The typical plane-sweep polygon intersection algorithm has been modified to improve its performance for the refinement stage using a technique of Brinkhoff et al. [1994]. Since only edges within the intersecting region of the MBRs of the two polygons could possibly intersect, only those edges are used in the plane-sweep method. Any other edges are removed from consideration using the `EDGES_IN_REGION` function in the algorithm. For example, in Figure 40, edge e of polygon a is not contained in the intersecting region of the MBRs and could not possibly intersect polygon b.

The algorithm has also been simplified by assuming that the polygons are simple, that is, they do not intersect themselves. In the algorithm, as soon as an intersecting edge is found, the algorithm can report that the polygons intersect without checking if the intersecting edges belong to the same polygon because the polygons are simple [21].

The first step of the algorithm in Figure 39 combines the edges from both polygons into one dataset and removes any edges that do not overlap the intersecting region of the MBRs, `MBRoverlap`, using the `EDGES_IN_REGION` function. Next, the `DOUBLE_EDGES` function creates two entries for each edge, one for each end point, which are the stopping points of the sweep line. Then, the end points are sorted in one dimension using the `SORT_BY_END_POINT` function. As with the plane-sweep algorithm in Section 3.1, a sweep structure is needed to store the edges that intersect the sweep line. In this case, the sweep structure, referred to as `activeEdges`, must perform two additional operations, `EDGE_ABOVE` and `EDGE_BELOW`, which identify edges that intersect the sweep line just above the given edge or just below, respectively. After initializing the `activeEdges` structure with the `CREATE_SWEEP_STRUCTURE` function, the list of edges is scanned. When an edge is first encountered, it is inserted into the `activeEdges` structure, using the `INSERT` function. When the end of an edge is encountered, it is removed from the `activeEdges` structure

[21] Becker et al. [1999] review and propose algorithms for non-simple polygons and efficient algorithms for finding all of the intersecting edges.

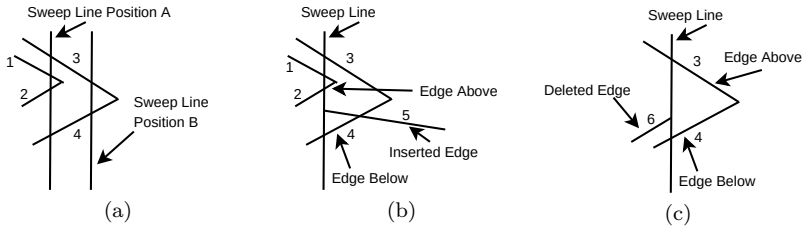


Fig. 41. (a) Two intersecting edges will intersect the sweep line at adjacent points as the sweep line approaches their intersect point. (b) When an edge is inserted, it could intersect the edge just above it or below it. (c) When an edge is deleted, the edges adjacent to it might intersect.

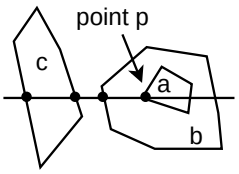


Fig. 42. Object a will be reported as contained within object b since the horizontal line through a point, p, in a intersects object b once to the left of point p. Object a will not be reported as contained within object c since it intersects the horizontal line twice to the left of point p.

using the `REMOVE` function.

In the algorithm, an edge intersection test is performed when an edge is inserted or removed from the sweep structure. As the sweep line moves, the relative positions of the intersection points of the sweep line with the edges change. For example, as shown in Figure 41a, the edges intersect the sweep line at position A, in the order 3, 1, 2, and 4, from top to bottom. At position B, the sweep line does not intersect edges 1 or 2 and edge 3 has moved down the sweep line while edge 4 has moved up. The edges continuously change their intersection point with the sweep line as the sweep progresses, but the relative order of the edges only change when an edge is inserted or removed (or when two edges intersect). Furthermore, only the two edges adjacent to the inserted or removed edge will move in the relative order. For instance, when edge 5 is inserted in Figure 41b, only edges 2 and 4 have changed order and are no longer adjacent. Therefore, when an edge is inserted, an intersection test is performed with it and the edge above and the edge below using the `EDGE_ABOVE` and `EDGE_BELOW` functions, respectively, to find the edges to be tested. Similarly, when an edge is deleted, only the relative order of the edges above and below it are effected. For instance, when edge 6 is deleted in Figure 41c, edges 3 and 4 become adjacent. Therefore, when an edge is deleted, an intersection test is performed between the edge that was above it and the edge that was below it, using the `EDGE_ABOVE` and `EDGE_BELOW` functions, respectively.

Because the polygons are assumed to be simple, if any edges intersect, then the polygons must intersect and true is returned. Otherwise, the sweep completes

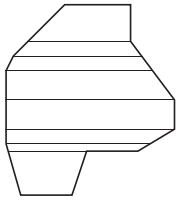


Fig. 43. A polygon can be approximated by trapezoids, which can be used to perform a faster polygon intersection test.

without finding any intersections and false is returned [22]. Since a polygon could be contained within the other, a containment test is necessary if false is returned to confirm that the polygons do not overlap. A containment test [Preparata and Shamos 1985], which typically has an $O(n)$ running time, needs to be run twice to conclude that neither object is contained within the other. One such algorithm, briefly described here, takes a point from one polygon, say a, and the edges from the other, say b, and checks if the point is contained within the polygon. If so, then a must be contained within b. Any point on or in polygon a will suffice. Using a horizontal line through the point from polygon a, the algorithm counts the number of edges of b that intersect the horizontal line to the left of the given point. As shown in Figure 42, the point is contained within the polygon only if the horizontal line intersects the edges an odd number of times to the left of the point. The algorithm concludes by returning true if an odd number of intersections to the left of the point were detected and false otherwise. Care must be taken in counting intersections with horizontal edges, which can be counted as either no intersection or as two intersections. Care must also be taken with intersections involving the end points of edges, which can be counted as half of an intersection. For more details on this issue, see the discussion of the point-in-polygon test in any computer graphics book, such as [Foley and van Dam 1982].

D.3 An Alternate Intersection Test

To improve the speed of the polygon intersection test, at the expense of higher storage costs, a spatial access method can be used to store each full polygon [Gaede and Günther 1998; Samet 1990]. When the polygons are represented by a containment hierarchy (for example, an R^+-tree [Sellis et al. 1987] or a region quadtree [Klinger 1971]), a synchronized traversal similar to that described in Section 4.1.1 can be used to check for intersections between the full polygons. For example, Brinkhoff et al. [1994] propose that each full polygon be decomposed into trapezoids, as shown in Figure 43, and storing the pieces in an R^*-tree like structure called a TR^*-tree. The entire TR^*-tree for each polygon is stored with the polygon. When two polygons are checked for intersection, both TR^*-trees are read into memory and then

[22] In the full polygon intersection test, where all of the intersecting edges need to be found or the polygons are not simple, intersections with adjacent edges also need to be checked when an intersection point occurs since the two edges switch positions in the list, creating new adjacencies for the edges. The algorithm shown in Figure 39 just reports success as soon as any intersection is found since the polygons are simple and will not self-intersect.

a synchronized traversal is performed to check for intersections. This process can be further improved by using heuristics that detect intersections between partial polygons [Badawy and Aref 1999; Huang et al. 1997].