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P.O. Box 3049, D-6750 Kaiserslautern, West Germany**Abstract**

Complex objects to support non-standard database applications require the use of substantial computing resources because their powerful operations and their related integrity constraints must be performed and maintained in an interactive environment. Since the exploitation of parallelism within such operations seems to be promising, we investigate the principal approaches for processing queries on complex objects (molecules) in parallel. A number of experiments favor methods based on inter-molecule parallelism as well as intra-molecule parallelism. Retrieval of molecules may be supported by multiple storage structures and access paths. Hence, the maintenance of such storage redundancy seems to be another good research area to explore the use of parallelism. Deferred update operations seem to be a bad idea, whereas concurrent update strategies incorporate salient application features. For performance reasons, we have chosen a multiprocessor system sharing an instruction cache and addressable common memory which is used for buffer management, synchronization, and logging/recovery. Activation of concurrent requests is supported by a nested transaction concept which allows a safe and effective execution control within parallel transactions of an operation.

1. Introduction

Non-standard database applications such as 3D-modeling for mechanical parts or VLSI chip design [1] require adequate modeling facilities for their application objects for various reasons. If the data representation is adjusted to the needs of a particular application area, the intended object handling (e.g. composition or decomposition of objects) may be performed in a natural and efficient way, thereby saving a lot of ponderous deviation steps. Existing models supporting such applications embody some degree of object orientation (towards the application objects). The notion of complex objects is used to indicate that such objects have an internal structure (structured components) maintained by the database management system (DBMS) and that access is provided to the object as a whole as well as to its components (structural object orientation). To enhance integrity control and semantic consistency, more object properties beyond the structural relationships have to be specified and preserved by the data model (behavioral object orientation). Such a rich data model supports appropriate forms of data abstraction and encapsulation (e.g. objects) which relieve the application from the burden of maintaining intricate object representations and checking complex integrity constraints.

On the other hand, DBMS requests using such a high-level object-oriented DBMS interface (incorporated by a set of powerful ADTs) suffer from very long execution path lengths since all aspects of complex

object handling have to be performed inside the DBMS. When applying processing concepts known from conventional DBMS, serious performance problems may occur in terms of response time, e.g. in an interactive construction environment. Although an operation is decomposed into a tree of suboperations (Fig. 1b), the classical DBMS processing strategy observes a synchronous activation of each suboperation and its strictly serial execution. Only some conventional systems deviate marginally from this processing strategy by using low-level parallelism for certain house-keeping tasks, e.g. writing modified pages to disk. In general, however, concurrent execution on behalf of a user operation is not achieved [2].

The use of intra-transaction parallelism for higher-level operations was investigated in a number of database machine projects [3]. These approaches focus on the exploitation of parallelism in the framework of the relational model. Complex relational queries are transformed into an operator tree of relational operations in which subtrees are executed concurrently (evaluation of subqueries on different relations) [4]. Other approaches utilize special storage allocation schemes for distributing relations across multiple disks. Parallelism is achieved by evaluating the same subquery on the various partitions of a relation [5, 6].

We are going to investigate possible strategies to exploit parallelism when processing complex objects. In order to be specific, we have to identify our concepts and solutions in the framework of a particular data model and a system design facilitating the use of parallelism. Therefore, we refer to the molecule-atom data model (MAD model [7]) which is implemented by an NDBS kernel system called PRIMA [8]. We use the term NDBS to describe a database management system tailored to the support of non-standard applications.

For this purpose, we introduce the essential concepts of an NDBS architecture and a model of NDBS operations. We focus on the principal ways to process a query on complex objects in parallel. Furthermore, we consider the use of parallelism when redundant storage structures kept for performance reasons have to be maintained. In order to achieve a safe and effective execution control for parallel actions, we tailor the concept of nested transactions to our distributed processing strategies in a series of complex carrying the PRIMA code. Finally, we conclude with a summary of our design proposals.

2. A Model of NDBS Operations

In order to describe our concepts of supporting parallelism in the framework of NDBS processing, we introduce a multi-layered

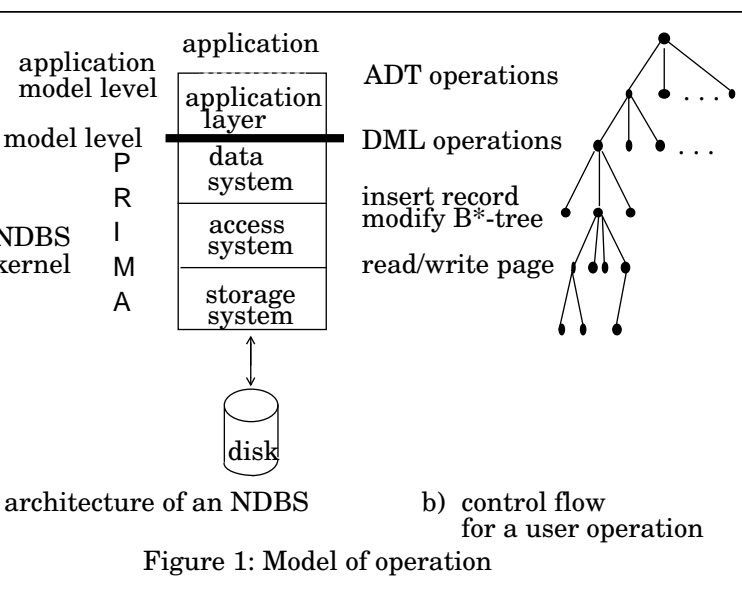
concurrent processing. On the other hand, our architecture shown in Fig. 1a reflects a high degree of data independence attained by explicit interfaces among layers.

The overall architecture consists of a so-called NDBS kernel and a number of different application layers, which map particular applications to the data model interface of the kernel. Our kernel which is considered application-independent is divided into three layers:

The storage system provides a powerful interface between main memory and disk. It maintains a database buffer and enables access to sets of pages organized in segments [8].

The access system manages storage structures for basic objects called atoms and their related access paths. For performance reasons, multiple access paths and redundant storage structures may be defined for atoms.

The data system dynamically builds the objects available at the data model interface. In our case, the kernel interface is characterized by the MAD model and its language called MQL (molecule query language) [7]. Hence, the data system performs composition and decomposition of complex (structured) objects called molecules.



The application layer uses the complex objects and tailors them to more complex objects according to the application model of an application. This mapping is specific for each application (e.g. 3D-CAD, VLSI design, geographic information management). Hence, for each application area a different application layer exists which provides a tailored interface (e.g. in form of a set of ADT operations) for the corresponding application.

The NDBS architecture as exhibited in Fig. 1a lends itself to a workstation-server environment in a smooth and natural way. The application and the corresponding application layer are dedicated to a workstation, whereas the NDBS kernel is assigned either to a server processor or to a server complex consisting of multiple processors. This architectural subdivision is strongly motivated by the properties of the MAD model: Sets of molecules may consist of sets of heterogeneous atoms may be specified as processing units.

So far, we have sketched the static mapping of NDBS objects and operations organized in hierarchical layers. The dynamic processing of user operations may be explained by a tree of operations as illustrated in Fig. 1b. This operation tree reflects

elementary operations: "Each call to a subroutine is an example of a primitive at one level of implementation invoking a set of primitives at a lower level of control [9]".

In conventional DBMS, all operations in such an operation tree are called synchronously and are executed serially (left-most depth first traversal). Given an appropriate run-time environment, operations at a certain level may be called in parallel, i.e. the corresponding subtrees as shown in Fig. 1b are executed (traversed) concurrently. In principle, such a decomposition into parallel execution is conceivable at every level of operation. However, certain prerequisites such as sufficient operation granules are necessary for successful application of concurrency processing a user operation. In this paper, we want to focus on concepts to exploit parallelism within the NDBS kernel, that is, how concurrent and asynchronous actions should be organized on the server complex carrying the NDBS kernel code.

2.1 The Data System Interface

In order to describe the concepts for achieving parallelism in sufficient detail, we have to refine our view of the kernel architecture and the interfaces involved. It is obvious that the data model plays the major role and determines many essential factors which enable reasonable parallelism: sufficiently large data granules, set orientation of request, dynamic construction of objects (result sets), flexible selection of processing sequences,

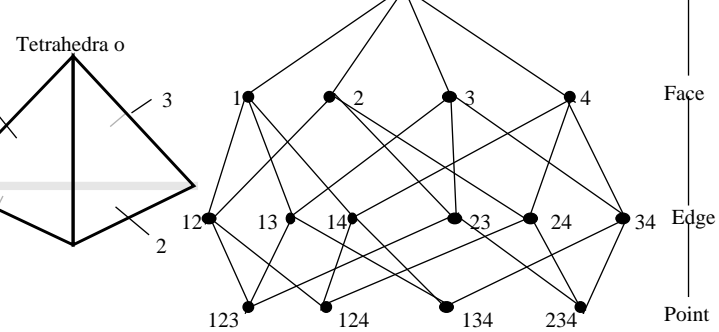
In our system, the data model interface is embodied by the MAD model and its language MQL which is similar to the well-known SQL language. Here, we cannot introduce this model with all its complex details, but only illustrate the most important concepts necessary for our discussion. In the MAD model, atoms are used as a kind of basic element (or building block) in order to represent entities of the real world. In a similar way to tuples in the relational model, they consist of an arbitrary number of attributes. The attributes' data types can, however, be chosen from a rich selection than in the relational model, i.e. apart from conventional types the type concept includes

- the structured types RECORD and ARRAY,
- the repeating group types SET and LIST, both yielding a powerful structuring capability at the attribute level as well as
- the special types IDENTIFIER (serving as surrogates) for identification purposes and REF_TO for the connection of atoms

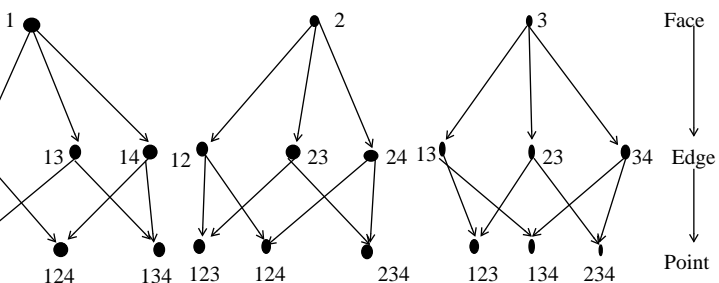
Atoms are grouped to atom types. Relationships between atom types are expressed by so-called links and are defined as link types between atom types. Link types are treated in a symmetric way, i.e. links may be used in either direction in the same manner. Some link types directly map all types of relationships (1:1, 1:n, n:n). The flexibility of the data model is greatly increased by this directed and symmetric mapping. Link types are represented by a pair of REF_TO attributes (reference and "back-reference") one in either involved atom type. For example, a link type may be specified as follows:

- FIDs: SET_OF (REF_TO(Face.EIDs)) in an atom type *Edge*
- EIDs: SET_OF (REF_TO(Edge.FIDs)) in an atom type *Face*.

In the database, all atoms connected by links form mesh-like structures (atom networks) as illustrated in Fig. 2.:



```
SELECT ALL
FROM Face-Edge-Point
WHERE Face.No < 4;
```



```
SELECT ALL
FROM Point - Edge
WHERE Point.No = 134;
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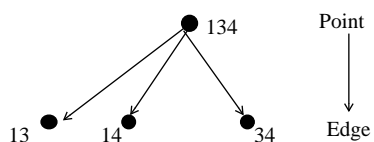


Figure 2: Dynamic construction of molecules from a sample geometric object

Molecules are defined dynamically by using MQL statements and to be derived at run-time. Each molecule belongs to a molecule type (which is specified in the FROM clause). The type description establishes a connected, directed and acyclic type (cycles occur when recursive types are specified), in that a starting point (i.e. root atom type) and all participating atom and edge types (for short "-") are specified. A particular example of a molecule type is Face-Edge-Point. Such a molecule type determines both the molecule structure as well as the molecule set. It groups all molecules with the same structure. At the logical level, the dynamic construction of molecules proceeds in a straight-forward manner using the molecule type description as a template: For each atom belonging to the root atom type all children, grandchildren and so on are connected to the molecule structure, terminating after all leaves of the molecule structure are reached. Connecting children to the molecule structure means forming the hierarchical join which is supported by the link concept. Hence, for each root atom a single molecule is constructed. Figure 2 shows the result of a molecule construction for Face-Edge-Point molecules, where the set of molecules was restricted. Furthermore, it illustrates the most important properties of the interface

MQL request handles a set of molecules.

These molecules as complex objects consist of sets of atoms of different type, i.e., they are embodied by sets of interrelated heterogeneous record structures.

Molecule construction is dynamic and allows symmetric use of the atom networks (e.g. Point-Edge (Fig. 2c)).

allows for direct and navigational retrieval as well as for manipulation of atoms. To satisfy the retrieval requirements of the data system, it supports direct access to a single atom as well as atom-by-atom access to either homogeneous or heterogeneous atom sets.

Manipulation operations (insert, modify, and delete) and direct access operate on single atoms identified by their logical address (or surrogate) which is used to implement the IDENTIFIER attribute as well as the REF_TO attributes. Performing manipulation operations, the access system is responsible for automatic maintenance of the referential integrity defined by the REF_TO attributes. Thus, a manipulation operation on such an attribute requires implicit manipulation operations on other atoms in order to adjust the appropriate back references. These operations however, are triggered by a special consistency manager (section 3.3).

Different kinds of scan operations are introduced as a concept to manage a dynamically defined set of atoms, to hold a current position in such a set, and to successively deliver single atoms. Some scan operations, however, are added in order to optimize retrieval access. Therefore, they may depend on the existence of a certain storage structure (defined by the database administrator).

- The atom-type scan delivers all atoms in a system-defined order, utilizing the basic storage structure which exists for each atom type.
 - The access-path scan provides appropriate means for fast value-dependent access based on different access path structures such as B-trees, grid files, and R-trees.
 - The sort scan processes all atoms following a specified sort criterion also utilizing the basic storage structure of an atom type. However, sorting an entire atom type is expensive and time consuming. Therefore, a sort scan may be supported by an additional storage structure, namely the sort order.
 - The atom-cluster scan speeds up the construction of frequently used molecules by allocating all atoms of a corresponding molecule in physical contiguity using a tailored storage structure, a so-called atom cluster. For example, in Fig. 2 each Face atom and all its associated Edge and Point atoms may be organized to form an atom cluster (Fig. 3). On a logical level, an atom cluster corresponds to a molecule. It is described by a special so-called characteristic atom which consists of references to all atoms belonging to the molecule. This characteristic atom together with all the referenced atoms is mapped onto a single physical record which in turn is stored in a set of pages.
- The underlying concept is to make storage redundancy available outside the access system by offering appropriate retrieval operations (i.e. the choice of several different scans for a particular access decision by the optimizer of the data system), whereas in the case of update operations storage redundancy has to be hidden by the access system. As a consequence, maintaining storage redundancy in an efficient way is a major task of the access system. However, sequential update of all storage structures existing for a corresponding atom results in a lack of efficiency which is not acceptable. Therefore, exploiting parallelism seems to be a natural way to speed up a single manipulation operation.

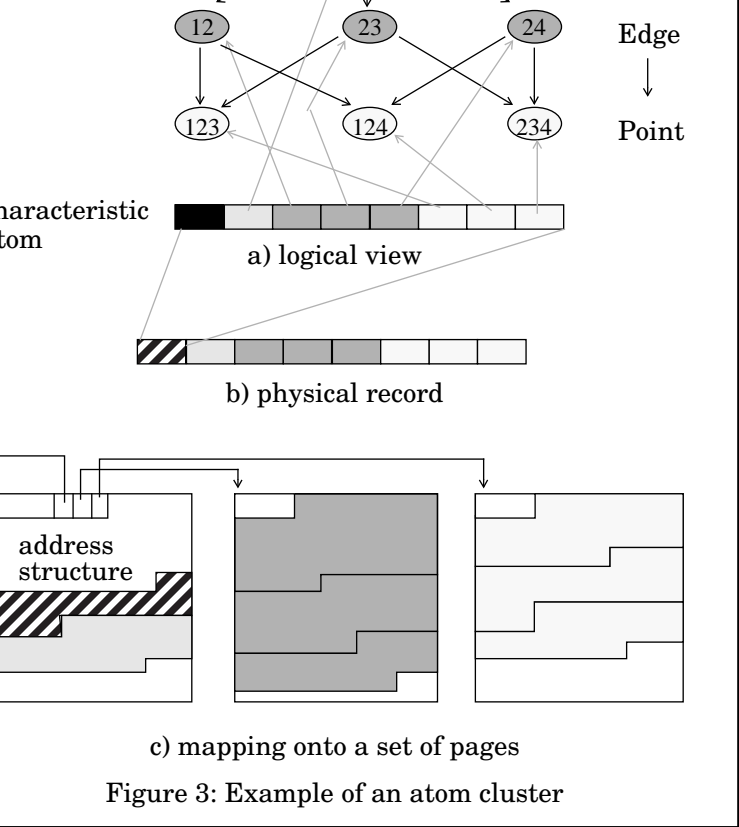


Figure 3: Example of an atom cluster

2.3 Activation of Concurrent Requests

As we start to evaluate our concepts for achieving parallelism in a data system and access system functions, we briefly describe the process (run-time) environment of our DBMS kernel PRIMA. In order to provide suitable computing resources, PRIMA is mapped to a multi-processor system, i.e., the kernel code is

synchronization of concurrent accesses. Due to the frequency of references (issued from concurrent tasks) accessibility of data and synchronization of access must be solved efficiently.

In a so-called DB-distribution architecture [10] every (loosely coupled) processor handles a partition of the database; such static data subdivision and allocation is obviously in conflict with our processing requirements. Therefore, DB-sharing architectures [11] where multiple DBMS share the database at the disk level seem to be much more flexible and appropriate for our purposes. In a loosely coupled system, however, each DBMS has its own system buffer creating the need to cope with fully replicated data; modification of a page in a buffer makes all copies of this page in other buffers obsolete (buffer invalidation problem). Furthermore, the lack of common memory enforces message-based communication for inter-process cooperation (e.g. concurrent control) which seems to be by far too slow for our type of application. As a consequence, use of shared memory for critical functions is mandatory for performance reasons. Hence, we have designed our system to run on a server complex where instruction addressable common memory [12] is available for buffer management, synchronization, and logging/recovery. Such an architecture (sometimes called closely coupled) avoids buffer invalidation (only one buffer) and provides memory-based message exchange as well as instruction-based synchronization primitives. Fig. 4 gives a short illustration of the major architectural issues. Our experimental system for the server complex consists of up to five processors with sufficient private memory, the common memory, an attachment to a file processor, and a high-bandwidth communication system for coupling the server processors with workstations carrying the application layers and corresponding applications..

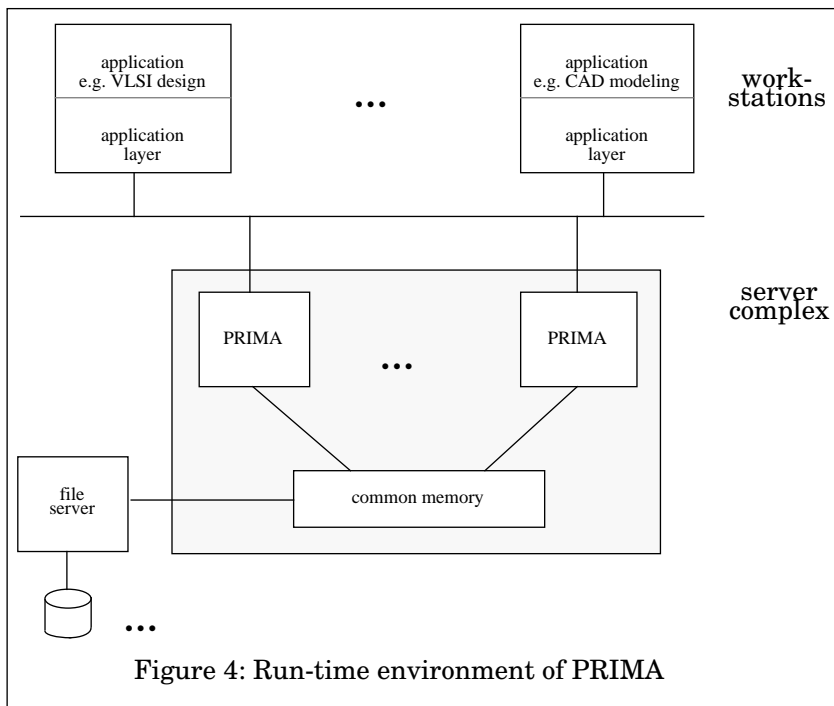


Figure 4: Run-time environment of PRIMA

An instance of PRIMA (running on a particular processor) is divided into a number of processes. Each process may initiate an arbitrary number of tasks which serve as run-units for the execution of single requests. Cooperation among processes is performed by establishing some kind of client-server relationship;

the calling task in the client process issues a request to the server process where a task acts upon the request and returns an answer to the caller. In our model, a client invokes a server asynchronously, i.e. it can proceed after the invocation, and here