DM algorithms in healthindustry

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Abstract—This survey reviews several approaches of data mining (DM) in healthindustry from many research groups worldwide. The focus is on modern multi-core processors built into today’s commodity computers, which are typically found at universities both as small servers and workstation computers. So they are deliberately not high-performance computers. Modern multi-core processors consist of several (2 to over 100) computer cores, which work independently of each other according to the principle of “multiple instruction multiple data” (MIMD). They have a common main memory (shared memory). Each of these computer cores has several (2-16) arithmetic-logic units, which can simultaneously carry out the same arithmetic operation on several data in a vector-like manner (single instruction multiple data, SIMD). DM algorithms must use both types of parallelism (SIMD and MIMD), with access to the main memory (centralized component) being the main barrier to increased efficiency. This is important for DM in healthindustry applications like ECG, EEG, CT, SPECT, fMRI, DTI, ultrasound, microscopy, dermascopy, etc.

Index Terms—DM, healthindustry.

I. INTRODUCTION
Healthindustry applications like ECG, EEG, CT, SPECT, fMRI, DTI, ultrasound, microscopy, dermascopy, etc. pose high requirements on the runtime performance of data mining (DM). Modern computer hardware supports the development of high-performance applications for data analysis on many different levels. The focus is on modern multi-core processors built into today’s commodity computers, which are typically found at university institutes both as small server and workstation computers. So they are deliberately not high-performance computers. Modern multi-core processors consist of several (2 to over 100) computer cores, which work independently of each other according to the principle of “multiple instruction multiple data” (MIMD). They have a common main memory (shared memory). Each of these computer cores has several (2-16) arithmetic-logic units, which can simultaneously carry out the same arithmetic operation on several data in a vector-like manner (single instruction multiple data, SIMD). DM algorithms must use both types of parallelism (SIMD and MIMD), with access to the main memory (centralized component) being the main barrier to increased efficiency. This is important for DM in healthindustry applications like ECG, EEG, CT, SPECT, fMRI, DTI, ultrasound, microscopy, dermascopy, etc.

The performance shall be further increased compared to the previous approach, e.g. by dynamic load balancing. The usability for various new application algorithms shall be improved, e.g. by developing specialized algorithms to detect data dependencies and to develop convergence criteria for such algorithms. The concept of cache-oblivious loops is to be developed further for better architectures, e.g. GPU or distributed systems (e.g. grid and cloud environments).

II. CACHE-OBlivious LOOPS WITH DYNAMIC LOAD BALANCING
A SIMD and MIMD-based parallelization approach to design loop pairs in such a way that they flexibly support caches of any size divides the total workload of an algorithm by means of so-called space-filling curves into packets that are assigned to the individual cores and make efficient use of the cache memory there. Although the workload can initially be optimally distributed among the computer cores in this way in a very simple manner, it is not yet possible to dynamically rebalance the load if, for example, the cores are subject to an uneven basic load due to external influences. In this work
package, procedures for dynamic load redistribution must be designed in such a way that they do not collide with the overall goal of efficient cache usage.

III. MODELING OF LOOP STRUCTURES

The current approach is limited to traversing two nested loops with fixed loop boundaries in a way that uses caches of any size and also allows MIMD parallelism. A newly developed variant of the Hilbert curve was used for this purpose. In this work package this concept shall be extended to any number of loops and dependencies of the loops among each other shall be modelable. This should make it possible to efficiently process e.g. triangular or band matrices as well as higher order tensors. For the processing of three or more nested loops, the mathematical extensions of the Hilbert curve and other space-filling curves into higher-dimensional spaces basically already exist. However, these methods still have to be extended and adapted in such a way that the calculation can be performed highly efficiently (in constant time per loop pass), which were achieved in the two-dimensional case with the help of different concepts. The extension of these concepts for spaces of arbitrary dimensionality seems to us as a research task demanding but also feasible. For the modelling of dependencies it is possible to define suitable data structures that are oriented towards and support the hierarchical-recursive nature of the space-filling curves.

IV. MODELING OF MONOTONY REQUIREMENTS

This approach, based on a special variant of the Hilbert curve, offers the advantage that in most applications the effect on cache location is strongest compared to comparable space-filling curves. However, some application algorithms require a sequence of loop passes that fulfills certain monotony properties, i.e. certain loop indices are processed before certain other loop indices. The idea is to combine existing space-filling curves such as Hilbert or the Z-order in such a way that even partial monotony requirements can be represented in individual dimensions. In this work package, the concept of cache-oblivious loops will be extended to specify monotonicity properties and automatically apply suitable space-filling curves.

V. GPU AND DISTRIBUTED SYSTEMS

The problem that algorithms work distributed on data in such a way that each processing unit reaches the highest possible access locality does not only arise in multi-core CPU systems, but also in other distributed and parallel architectures. The setting is very similar for graphic processing units (GPU), but the basic problem is similar for distributed systems without shared physical memory (grids, cloud computing). In this work package the extension to such architectures will be investigated. While the basic problem of locality preservation remains the same, in alternative hardware scenarios the considerations about the trade-off between different cost factors of the algorithms, i.e. especially the trade-off between the transmission costs of the data over the network or internal bus connections and the computing time (which also includes the management of space-filling curves and other techniques for locality preservation) can vary in detail.

VI. DERIVATION OF CRITERIA FOR APPLICABILITY

Not all data analysis algorithms are equally suitable for parallelization using cache-oblivious loops, even if they follow the basic pattern of nested loops. Therefore, in this work package a set of criteria is developed to find data dependencies and monotony requirements in the application algorithms manually or (semi-)automatically. In addition, criteria are to be developed to determine when algorithms cannot be transformed equivalently in a provable way, but after a transformation, algorithms result which are also convergent and possibly reach a local optimum deviating from the original algorithm. From a scientific point of view, the latter is even the greater challenge, because automatic techniques for the recognition of data dependencies have already been proposed and are very successfully and widely used in other sub-areas of computer science (e.g. compiler construction). On the other hand, techniques for transformation into merely result-equivalent algorithms are much less known.

VII. TRANSFORMATION OF IMPORTANT APPLICATION ALGORITHMS

Various algorithms are to be transformed exemplarily and to support the development of criteria above in order to be applicable in a SIMD and MIMD parallel architecture with the help of cache-oblivious loops. Very general building blocks such as different matrix decompositions (LU, QR, Jacobi) support dimension transforming or reducing methods such as PCA, Kernel-PCA, ICA or t-SNE, as they are used in the lead application of medical image processing (different modalities of magnetic resonance imaging). In addition, algorithms from network planning techniques for planning in traffic networks or for industrial production planning are also being considered, for example.

VIII. RELATED WORK

There are various approaches for different data types. The data can be of any type, as long as a distance function exists. Fixed-length text data often uses Hamming distance \cite{HOK18} and the similarity between variable length text is often measured using the edit distance \cite{XWL08}. A common measure for set data is the Jaccard distance \cite{DTL18}, \cite{XWL+11}, whereas the similarity of documents is processed with cosine-like similarity measures \cite{AB13}, \cite{SLF17}.

Approximate nearest neighbor search techniques can also be applied to the similarity join problem, however without guarantees on completeness and exactness of the result. There may be false positives as well as false negatives. Recently an approach \cite{YNL+17} to Locality Sensitive Hashing (LSH) is used on a representative point sample, to reduce the number of lookup operations. LSH is of interest in theoretical foundational work, where a recursive and cache-oblivious LSH approach \cite{PPSS17} was proposed. The topic of approximate
solutions for the similarity join is also an emerging field in deep learning [PM13]. There are approximative approaches which target low dimensional cases (spatial joins in 2–3 dimensions [BEF08]) or higher (10–20) dimensional cases [AI06]. Very high-dimensional cases, with dimensions of 128 and above have been targeted with Symbolic Aggregate approXimation (SAX) techniques [MIZ17] to generate approximate candidates. SAX techniques rely on several indirect parameters like PAA size or the iSAX alphabet size.

There are preconstructed indexing techniques, which are based on space-filling curves and applied to the similarity join problem. Specifically, where the data is sorted efficiently with respect to one or more Z-order curves [DS01], [KS00], [LSS08] in order to test the intersection of the hypercubes in the datastructures. Others propose space-filling curves, to reduce the storage cost for the index [CGL+17]. LESS [LSS08] targets GPUs and not multi-core environments. ZC and MSJ [KS00] as well as the SPB-tree index [CGL+17], although simple, require space transformations and preprocessing, which make them hard to parallelize.

EGO family of $\epsilon$-join algorithms. The EGO-join algorithm is the first algorithm in this family introduced by Böhm et al. in [BBKK01]. The Epsilon Grid Order (EGO) was introduced as a strict order (i.e. an order which is irreflexive, asymmetric and transitive). It was shown that all join partners of some point $x$ lie within an $\epsilon$-interval, of the Epsilon Grid Order. Algorithms of the EGO family exploit this knowledge for the join operation. The EGO-join has been re-implemented as a recursive variant with additional heuristics, to quickly decide whether two sequences are non-join-able [KP03]. Further improvements proposed two new members of this family, the EGO* [KP07] algorithm and its extended version called Super-EGO [Kal13] target multi-core environments using a multi-process/multi-thread programming model. Super-EGO proposes a dimensional reordering [Kal13]. In the experiments Super-EGO encounters some difficulties with uniformly distributed data, particularly when the number of data objects exceeds millions of points or the dimensionality is above 32.

If the similarity join runs multiple times on the same instances of the data, one might consider index-based approaches [BK01], [PR09], [CGL+17], such as R-tree [BKS93] or M-tree [CPZ97]. Index-based approaches have the potential to reduce the execution time, since the index stores pre-computed information that significantly reduces query execution time. This pre-computational step could be costly, especially in the case of List of Twin Clusters (LTC) [PR09], where the algorithm needs to build joint or combined indices for every pair of points in the dataset. The D-Index [DGSZ03] and its extensions (i.e. eD-Index [DGZ03] or i-Sim index [PS14]) build a hierarchical structure of index levels, where each level is organized into separable buckets and an exclusion set. The most important drawback of D-Index, eD-Index and i-Sim is that they may require rebuilding the index structure for different $\epsilon$.

Data partitioning across multiple machines is not the main focus of this paper where we assume that the data fits into main memory. The case of relational join algorithms has been studied extensively in the past [SDS99], [WMP13], [FAB+18]. The similarity join has been successfully applied in the distributed environment with different MapReduce variants [LWU16], [MS18], [FAB+18]. Another distributed version is proposed in [ZRDW16]. There, a multi-node solution with load-balancing is used, that does not require re-partitioning on the input data. This variant focuses on minimization of data transfer, network congestion and load-balancing across multiple nodes.

The similarity join has been already implemented for Graphics Processing Units (GPUs). In [BNPZ09] the authors use a directory structure to generate candidate points. On datasets with 8 million points, the proposed GPU algorithm is faster than its CPU variant, when the $\epsilon$-region has at least 1 or 2 average neighbors. LSS [LSS08] is another similarity join variant for the GPU, which is suited for high dimensional data. Unfortunately both [LSS08] and [BNPZ09] are targeted to NVIDIA GPUs and have been optimized for an older version of CUDA.

A. Cache-oblivious Algorithms

Cache-oblivious algorithms [FLPR99] have attracted considerable attention as they are portable to almost all environments and architectures. Algorithms and data structures for basic tasks like sorting, searching, or query processing [HLLY07] or homology search in bioinformatics [FRR14] have been proposed. Two important algorithmic concepts of cache-oblivious algorithms are localized memory access and divide-and-conquer. The Hilbert curve integrates both ideas. The Hilbert curve defines a 1D ordering of the points of an 2-dimensional space such that each point is visited once. Bader et al. proposed to use the Peano curve for matrix multiplication and LU-decomposition [BM06]. [Bad08]. The algorithms process input matrices in a block-wise and recursive fashion where the Peano curve guides the processing order and thus the memory access pattern. In [BPP18], cache-oblivious loops have been applied to K-means clustering and matrix multiplication.

B. Optimized Techniques for Specific Tasks or Hardware

The library BLAS (Basic Linear Algebra Subprograms) [DCH90] provides basic linear algebra operations together with programming interfaces to C and Fortran. BLAS is highly hardware optimized: specific implementations for various infrastructures are available, e.g., ACML for AMD Opteron processors or CUBLAS for NVIDIA GPUs. The Math Kernel Library (MKL) contains highly vectorized math processing routines for Intel processors. These implementations are very hardware-specific and mostly vendor-optimized. Moreover, they are designed to efficiently support specific linear algebra operations. Experiments demonstrate that the cache-oblivious approach reaches a performance better than BLAS on the task of the similarity join for points of dimensions in the range of $\{2, ..., 64\}$. 
IX. APPLICATIONS

These techniques are investigated for DM algorithms in the following applications:

- Electrocardiography (ECG, 1D),
- Electroencephalography (EEG, 1D),
- Computer Tomography (CT, 3D, 4D),
- SPECT (4D),
- Structural Magnetic Resonance Imaging (MRI, 3D),
- Functional Magnetic Resonance Imaging (fMRI, 4D),
- Diffusion Tensor Imaging (DTI, 6D),
- Ultrasound (US, 2D),
- Microscopy, Dermascopy (2D),
- etc.

X. CONCLUSION

This survey reviews several approaches of DM from many research groups world wide. Modern computer hardware supports the development of high-performance applications for data analysis on many different levels. The focus is on modern multi-core processors built into today’s commodity computers, which are typically found at university institutes both as small server and workstation computers. So they are deliberately not high-performance computers. Modern multi-core processors consist of several (2 to over 100) computer cores, which work independently of each other according to the principle of “multiple instruction multiple data” (MIMD). They have a common main memory (shared memory). Each of these computer cores has several (2-16) arithmetic-logic units, which can simultaneously carry out the same arithmetic operation on several data in a vector-like manner (single instruction multiple data, SIMD). DM algorithms must use both types of parallelism (SIMD and MIMD), with access to the main memory (centralized component) being the main barrier to increased efficiency. We investigate these performance issues in the context of health industry applications like ECG, EEG, CT, SPECT, fMRI, DTI, ultrasound, microscopy, dermascopy, etc.

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