Distributed Medical Image and Volume Registration

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INTRODUCTION

The ability to visualise hidden structures in detail using 3-D volume data has become a valuable resource in medical imaging applications (Maintz & Viergever, 1998). Importantly, the alignment of volumes enables the combination of different structural and functional information for diagnosis and planning purposes (Pluim, Maintz, & Viergever, 2003). Transform optimisation, resampling, and similarity calculation form the basic stages of a registration process (Zitova & Flusser, 2003): During transform optimisation, translation and rotation parameters which geometrically map points in the reference (fixed) image/volume to points in the sensed (moving) image/volume are estimated. Once estimated, pixel/voxel intensities which are mapped into nondiscrete coordinates are interpolated during the resampling stage. After resampling, a metric is used for similarity calculation in which the degree of likeness between corresponding volumes is evaluated (Tait & Schaefer, 2008). Optimisation of the similarity measure is the goal of the registration process and is achieved by seeking the best transform. All possible transform parameters therefore define the search space. Due to the iterative nature of registration algorithms, similarity calculation represents a considerable performance bottleneck which limits the speed of time critical clinical applications.

The use of parallel computing to overcome these time constraints has become an important research area (Nicolescu & Jonker, 2000). Conveniently, many of the similarity calculation strategies employed in medical registration are inherently parallel and therefore well suited to distribution. An important consideration when adopting a parallel processing approach is the architecture of the host system. In a computer constructed of multiple processors with shared-memory, data distribution is not required. These systems are viewed as tightly-coupled architectures. In contrast, a loosely-coupled architecture consists of multiple computers in different locations. Loosely-coupled architectures therefore require data distribution, communication, and accumulation mechanisms. Importantly, the most effective distribution scheme will depend on the architecture of the host system (Seinstra, Koelma, & Geusebroek, 2002). The two contrasting architectures of host systems are illustrated in Figure 1.

BACKGROUND

In the context of parallel processing, registration of medical data has been achieved by Warfield, Jolesz, and Kikinis (1998) who introduced a nonrigid algorithm based on the work-pile paradigm. Their goal was to develop an interpatient registration algorithm which can be applied without operator intervention to a database of several hundred scans. In an initial step, each scan is segmented using a statistical classification method. This preprocessing stage is used to identify different tissue types including skin, white matter, grey matter, and bone structure. Once segmented, a transform which brings these features into alignment is estimated. The system employs a message passing interface and cluster of symmetric multiprocessors to execute parallel similarity calculation operations using multiple threads. Crucially, work is dynamically load balanced. Results published by the group show that successful registration of $256 \times 256 \times 52$ volume brain scans can been achieved in minutes rather than hours.

Christensen (1998) compares two nonthreaded architectures, Multiple Instruction Multiple Data (MIMD) and Single Instruction Multiple Data (SIMD). The work presented raises implementation issues and timing analysis for the registration of $32 \times 32 \times 25$, $64 \times 64 \times 50$ and $128 \times 128 \times 100$ volume datasets. During

Figure 1. Tightly vs. loosely-coupled architectures. Data is either fetched from main memory via a memory bus, or is transferred over a communications network.
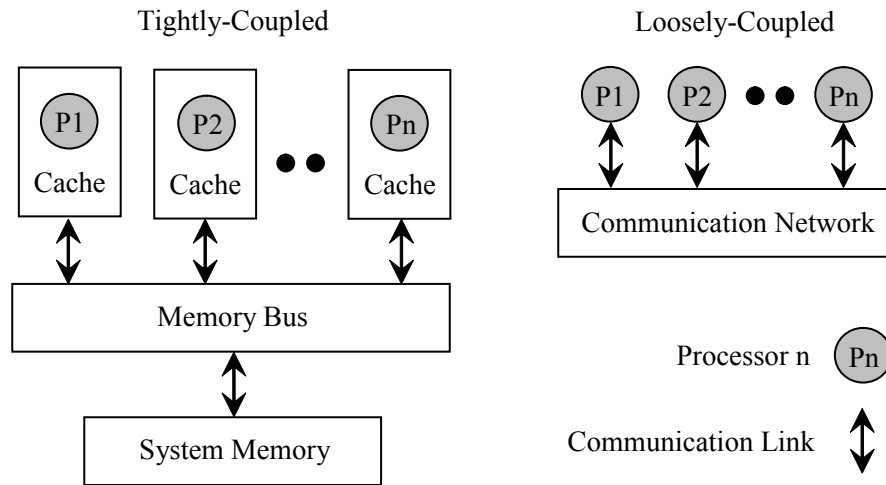
each clock cycle, the SIMD implementation performs calculations in which all processors are performing the same operation. The MIMD implementation, in contrast, breaks an algorithm into independent parts which are solved simultaneously by separate processors. The movement of data in both shared-memory systems is unrestricted and during execution each processor has access to the whole memory. The main performance bottleneck associated with both approaches was reported as scalability of hardware with increasing numbers of processors. Crucially, the MIMD implementation is recorded as being approximately four times faster than its SIMD counterpart. Reduced performance of the SIMD implementation is reportedly caused by overheads during serial portions of the registration algorithm.

More recently, the demands placed on registration algorithms when aligning deformable structures in 3-D space have been discussed. Salomon, Heitz, Perrin, and Armspach (2005) introduce deformable registration of volumes which involves optimisation of several thousand parameters and typically requires several hours processing on a standard workstation. Based on simulation of stochastic differential equations and using simulated annealing, a parallel approach that yields processing times compatible with clinical routines is presented. The approach represents a hierarchical displacement vector field which is estimated by means of an energy function. The energy function is scaled in

relation to the similarly measure and is re-evaluated at the end of each transform parameter optimisation cycle. The algorithm is reportedly suited to massively parallel implementation and has been successfully applied to the registration of $256 \times 256 \times 256$ volumes. Again, the results published demonstrate how alignment can be achieved in minutes rather than hours.

In the next section, a coarse-grained approach to parallelism is described which increases flexibility and allows the issues of fine-grained parallelism to be ignored. Building on a distributed blackboard architecture, the approach adopted supports multiple distributed agents organised in a worker/manager model. Crucially, the basic alignment steps are allocated to individual processors, the most computationally intensive of which are performed concurrently.

SIMILARITY CALCULATION USING A DISTRIBUTED BLACKBOARD ARCHITECTURE

Formally the inputs to a volume-based registration process can be defined as the fixed volume, the moving volume, and the transform used to map voxel coordinates. The goal of the registration process is recovery of a spatial mapping that brings the two volumes into alignment (Yoo, 2004). To achieve this, a metric is employed to generate a measure of similarity based

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