

From Impractical to Practical: Solving an MRI Problem Using Parallelism

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1. INTRODUCTION

Magnetic Resonance Imaging (MRI) is an imaging technique used by radiologists to diagnose disease in the human body. Radiologists are continually looking for ways to extract more information from magnetic resonance images and hence make a better diagnosis. It has been suggested that relaxometry, or the distribution of MRI spin-lattice relaxation rate (R_1) and the spin-spin relaxation rate (R_2), of the tissues may have diagnostic utility. [1] This diagnostic utility is based on R_1 and R_2 being a measure of the mobility of molecules, which is useful as the mobility of molecules in a tissue changes with disease state.

One tool available to determine relaxometry is the implementation of an inverse Laplace transform (ILT) algorithm that is part of CONTIN [2], a general-purpose constrained regularization program for inverting noisy linear algebraic and integral equations. This 6000 line Fortran 77 code developed and maintained by Stephen W. Provencher was last modified in 1982. However, the analysis of a single picture element (pixel) in a series of MRI images using CONTIN may take more than a minute on a sequential machine. Thus, the predicted time for a typical 512x512 pixel series of magnetic resonance images on the same machine is 21 weeks! This is clearly too long for effective use as a diagnostic tool. We hypothesized that if CONTIN could be parallelized, it could become an effective diagnostic tool.

2. MRI AND RELAXOMETRY

The smallest resolvable element in a magnetic resonance image is the volume element or voxel. The magnetic resonance signal from a voxel is represented by the intensity in a pixel. The functional form of the magnetic resonance signal (S) depends on the specific imaging sequence. For the conventional spin-echo imaging sequence, the signal is equal to

$$S = \sum_i \rho_i (1 - e^{-R_{1i}TR}) e^{-R_{2i}TE} \quad (1)$$

where the sum is over all of the different types of tissue (i) in a voxel, TR and TE are instrumental parameters of the imaging sequence, and ρ_i the quantity of each R_1 and R_2 component. R_1 and R_2 are different for healthy tissue and diseased tissue. As a consequence, the MRI signal typically changes when pathology is present. With the number of variables in this equation, it is possible for the signal from pathology to remain the same as healthy tissue, even though the R_1 and R_2 values are different. This could cause missed pathology in some magnetic resonance images.

Relaxometry is the measurement of the R_1 and R_2 values present in an image and the subsequent segmentation of tissues in the image based on this information. Since it is the R_1 and R_2 values that change directly with disease and not pixel intensity, monitoring R_1 and R_2 should be a better way of classifying tissue and

thus diagnosing disease. It is relatively straightforward to process this image data assuming just one average R_1 and R_2 component in a voxel. [2] Here (1) becomes

$$S = \rho (1 - e^{-R_1 TR}) e^{-R_2 TE} . \quad (2)$$

Implementation requires the acquisition of several magnetic resonance images with a fixed TE value and variable TR , and vice versa.

It is difficult to solve (1) simultaneously for a distribution of both R_1 and R_2 values. A more appropriate imaging sequence is the inversion recovery sequence. Here the signal is just a function of R_1 .

$$S = \sum_i \rho_i (1 - 2e^{-R_{1i} TR}) \quad (3)$$

It is this imaging sequence that was used to acquire our data [7] and this functional form that was used to determine ρ_i as a function of R_1 , *i.e.*, $\rho_i(R_1)$. This procedure has not been fully exploited because of the computational power needed to process a complete set of MRI images.

3. PARALLELIZING CONTIN

3.1 What is Parallel Computing?

Parallel computing is the application of multiple processors to the solution of a single task. Traditionally, a parallel computer was one that had multiple processors as part of a single mainframe. Today, software libraries such as Message Passing Interface (MPI) are available that enable programmers to use a cluster of workstations as a parallel computer.

Performance of such computers is measured using metrics such as speedup. Speedup ($S_p(N)$) is defined to be the time to complete the execution of the task using the best algorithm on a single processor, T_1 , divided by the time to execute the same task using a parallel computer using N processors, T_N , *e.g.*,

$$S_p(N) = T_1 / T_N \quad (4)$$

In a perfect world, if N processors were used, the task would be completed N times as fast, *i.e.*, $S_p(N)$ would be N . In reality, however, the cost of communication and coordination amongst processors often undermines the ability to obtain such speedup. Thus, the best performance can be obtained when completing individual subtasks require no information from other subtasks.

3.2 Why Parallelize CONTIN?

There are two main reasons that the MRI relaxometry problem is a good candidate for parallelization. First, as indicated above, the task takes an unacceptably long time to complete. In addition, calculations are done individually on a set of pixels formed by taking a single (the same) pixel from each of a series of images. This means that the calculation of the R_1 and R_2 distribution for a given set of pixels is independent of the calculation for any other set. Thus, the communication and coordination between processors should be minimal and near perfect speedup should be possible.

3.3 The Parallelization Effort

The effort to parallelize CONTIN began as a project in an offering of the Parallel Computing II course in the Computer Science Department at Rochester Institute of Technology. This course had been recently

reorganized to seek out real world problems for students to address using what they had learned in Parallel Computing I. Thus, sponsors are sought, often from outside the department, who have problems suitable for a parallel approach.

The MRI relaxation problem sponsored by Professor Hornak from the Imaging Science Department has been the main programming effort for the past two years. While there was a modicum of success the first year, the project was by no means complete. This was due to several factors:

- The CONTIN program had not yet been used by any of the parties involved.
- The program was written in Fortran 77, a language unfamiliar to most of the students.
- ILT is an unstable technique and proper input data is critical. The MRI data did not fit the input format required by CONTIN. In addition, the program was very sensitive to compiler options. This made testing difficult.
- CONTIN output is strictly numerical with a few printer plots; it was unclear at the start what format the output data needed to be in to be useful, or how much of it there should be.
- In general, the time to accomplish the task was severely underestimated.

The positive results included gaining familiarity with the program, a rewrite of critical subroutines in Fortran 95, which is similar to other programming languages known to the students, generation of fake but useful testing data, and a clearer understanding of the time and information needed to complete the task in a timely fashion.

Between the first and second offerings, Imaging Science students and faculty found a way to scale the MRI data so that it could be used as input to CONTIN. They also used CONTIN to determine the distribution of water R_1 and R_2 values in a set of hydrated synthetic soil samples, [3-6] providing invaluable experience with the program. During this period as well, author Bak, who had been a student in the first offering, began an independent study to complete his team's version of the project. Andrew's work continued in conjunction with the second years offering and was subject to several specification changes. This led him to develop a tool to help with analyzing the output images. Although all programming teams did produce a working parallel version of CONTIN in the second offering, we will focus on Andrew's results here.

4. RESULTS

CONTIN was successfully modified to execute in parallel on a network of workstations using MPI. This approach was chosen as both departments have clusters of workstations and MPI available. Preliminary testing is encouraging. While we have not yet executed the program with a set of 512x512 pixel images, an execution of a real series of 64x64 pixel MRI images that took over 55 hours to execute on a single processor was completed in less than an hour using a 32-node cluster. This represents better than perfect, *i.e.*, super-linear, speedup as is shown in Figure 1. Further testing is required to determine why super-linear speedup was achieved.

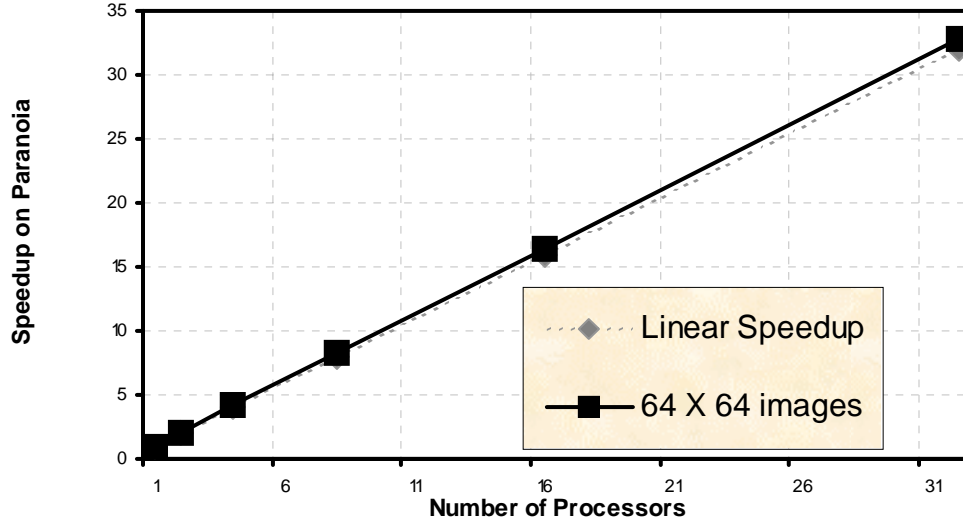


Figure 1. Speedup of determining the ILT on the pixels in a 64x64 pixel MRI data set on 32 node cluster

4.1 The Tool

The output created from the parallel execution of CONTIN is a series of *images* representing the ρ at a given R_1 . Therefore, the pixel intensity equals the spin density ρ at the R_1 represented by the image. Figure 2 shows the interface to the output image analysis tool. Besides displaying the output images scaled in a manner selected by the user, the user may enlarge the image size and has control of its brightness and contrast. In addition, the user may view a plot of a selected pixel's value over the entire series of output images. Histograms of the number of pixels at an R_1 value may also be created to assist in tissue classification by R_1 value. The tool, written in Java, can be easily extended to add other scaling functions.

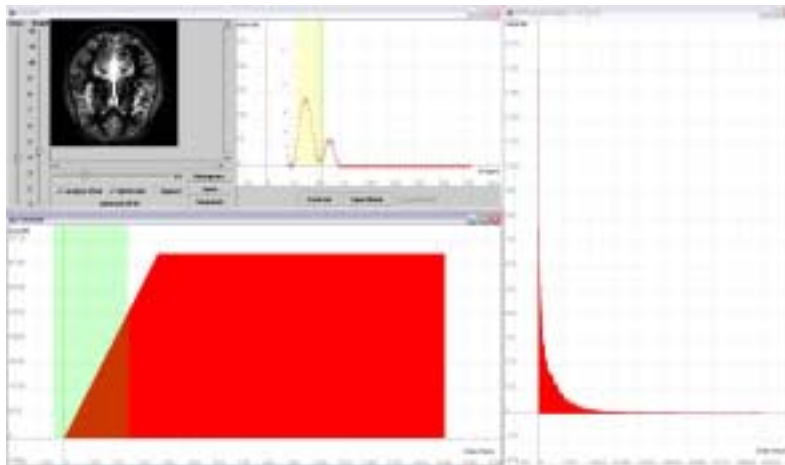


Figure 2. The tool for viewing and analyzing the output from parallel execution of CONTIN.

5. CONCLUSIONS

We are encouraged with the success of the parallelization effort. The implication is that relaxometry may become a more feasible diagnostic tool. However, further extensive testing is required to confirm the super-linear speedup results and to ascertain scalability to larger more realistic 256x256 pixel images.

6. REFERENCES

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