Parallel Application on SPECT Data Reconstruction.

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Abstract

The aim of this work is to report the results obtained with a parallel application for the solution of the Single Photon Emission Tomography problem. In particular, we consider the problem of reconstructing several human brain sections from experimental data obtained from a Gamma camera equiped with parallel-hole collimators.

The problem is modeled by a first kind Fredholm integral equation:

$$g(\theta,t) = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} K(x,y,\theta,t) f(x,y) dx dy$$
(1)

where the unknown function f(x, y) represents the photon emission and the kernel $K(x, y, \theta, t)$ models the physical phenomena involved. In our application the kernel takes into account the absorption of primary radiation, the detection of scattered photons and the spatially variable system response as reported in [1] and [2].

It is well known that (1) is an ill-posed problem and the solution of the integral equation in the discrete domain leads to the following linear system:

$$\mathbf{K}\mathbf{f} = \mathbf{g} \tag{2}$$

where the matrix \mathbf{K} is very ill-conditioned. For this reason it is necessary to compute a regularized solution of the least-squares problem:

$$\min \parallel \mathbf{K}\mathbf{f} - \mathbf{g} \parallel_2 \tag{3}$$

Both direct and iterative methods can be utilized, but iterative methods based on the conjugate gradient iterations are more efficient when applied to large size problems [3]. In this work we compute least-squares regularized solutions by means of conjugate gradient iterations coupled with a suitable stopping rule.

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Due to the high storage requirements and computational complexity for the determination of the matrix \mathbf{K} , a parallel application has been studied in order to treat an increasing number of brain sections in a small amount of time.

The rows of the matrix **K** have been distributed among the processors of a 128 nodes Cray T3E and a parallel version of the Conjugate Gradient regularization algorithm has been implemented.

The timing of the reconstruction algorithm can be divided in two parts: the time requied for the generation of the matrix **K** and the time required by the CG iterations. The results obtained with 60 CG iteration in the reconstruction of a 64×64 brain section from 90×64 data projections are reported in the following table.

Table 1: 60 CG iterations reconstruction MSE = 3.6e-1

Nodes	sec. Matrix	sec. CG	total sec.
8	8.5	11.5	19.95
16	4.3	6.4	10.7
32	2.1	4.3	6.4

References

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