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## A note on exact image reconstruction from a limited number of projections

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### Abstract

In a recent paper in this journal by Kesidis and Papamarkos “A new method for the exact reconstruction of any gray-scale image from its projections is proposed.” In this note we point out that this method is a special case of a well-known approach (peeling) and that it can produce exact reconstructions only under assumptions that are not realistic for practical methods of data collection. Further, we point out that some statements made in the paper regarding disadvantages of the algebraic reconstruction techniques (ART) as compared to the method of the paper are false.

### Keywords

Image reconstruction; computerized tomography; peeling; algebraic reconstruction techniques; ART

## 1 Originality and practical applicability of the method of Kesidis and Papamarkos

The method for image reconstruction from projections proposed by Kesidis and Papamarkos [7] is a variant of the well-known technique of “peeling.” The idea is that if we are dealing with an already digitized image (i.e., an image composed of pixels with constant interior gray values), then we can recover this image exactly from integrals taken for a sufficient abundance of rays by sequentially finding pixels for which there exists a ray that only goes through that pixel and pixels for which the gray values have been determined already. If the data consist of integrals that have been calculated by the same model that is assumed for the reconstruction, then the gray values of pixels are determined exactly by such data; see, for example, Theorem 3 and its proof in [4] that was published in 1971. Perfect (mathematical) recovery of a digitized image is possible using this principle from the integrals along a single (but large) set of parallel rays; clearly demonstrating the logical flow in suggesting that something not already digitized is recoverable from data collected for a certain arrangement of rays from the fact that digitized images are recoverable from data for the same arrangement of rays. For a recent paper discussing such issues, see [5]. In order to satisfy the data collection requirements of the peeling method of [7] one needs to collect data for a much larger number of rays than what is common (or even possible) in practice; for example, the authors calculate that in order to reconstruct a

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$64 \times 64$  image (which is several orders of magnitude smaller than what one is likely to come across in an application area; see, e.g., [1]), they need 104 projections with 1197 rays in each. An additional problem with the peeling approach is that it has been demonstrated that it can be highly unstable; even very small inaccuracies in the individual steps might eventually have the accumulative effect of destroying the reliability of the values for pixels recovered late in the process [8]. The paper of Kesidis and Papamarkos [7] discusses some technical matters that will allow efficient implementation of the peeling idea, but the idea itself is not novel and executing it more efficiently will not make it useful in those practical applications where it does not produce efficacious reconstructions using a less computationally efficient version.

## 2 Comparison with ART

The authors of [7] choose to compare their technique with the algebraic reconstruction techniques (ART), but what they say about ART is very incorrect.

1. “The problem is that the image becomes very noisy as the iterations proceed.” This is false for the case considered in the paper. The assumptions there result in an overdetermined consistent system of equations and in such a case ART is known to converge to the (unique) solution; see, for example, Theorem A2 of [6]. This is illustrated in Fig. 1, for a setup that is consistent with what is discussed in [7].
2. “The algebraic methods are computationally intensive and require large amounts of memory.” “The memory required by ART is ...  $M^2$  where  $M$  denotes the total number of image pixels.” These statements are also false. The memory required by ART is in fact  $M$ . This is because ART does its processing ray-by-ray, and for any given line the locations of the pixels intersected by it and lengths of the intersections can be efficiently calculated when they are needed using a digital difference analyzer (DDA) methodology demonstrated in Fig. 2. Thus only the reconstruction needs to be stored and it is updated in-place using the integral associated with the active ray (which is part of the data) and the information provided by the DDA. (For this reason, such approaches have been referred to as “row-action” methods, where the word “row” is used to indicate that only one row of the associated system matrix needs to be considered at any one time, and so the system matrix need not be stored; see [3]). This methodology is not only storage-efficient, but it is quite time-efficient. When applied to data satisfying the restrictive assumptions of [7], the more general-purpose algebraic reconstruction techniques are not as fast as the method of [7], but they are fast enough in real applications to recover in a reasonable time 16,777,216 unknowns from 4,587,520 approximate ray integrals and 884,436 unknowns from 92,160,000 approximate ray integrals; see [1], a paper devoted to reconstruction from electron microscopic projections.

## 3 Summary

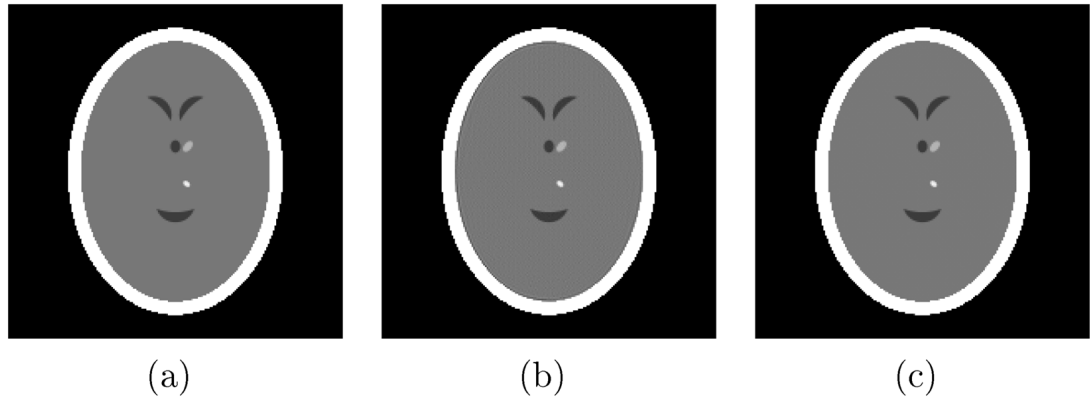
In this note we have discussed the originality and applicability of the method of [7], as well as the comparison made there of that method with ART. In view of relevant material in the previously published literature, the claims made in [7] are questionable.

## Acknowledgments

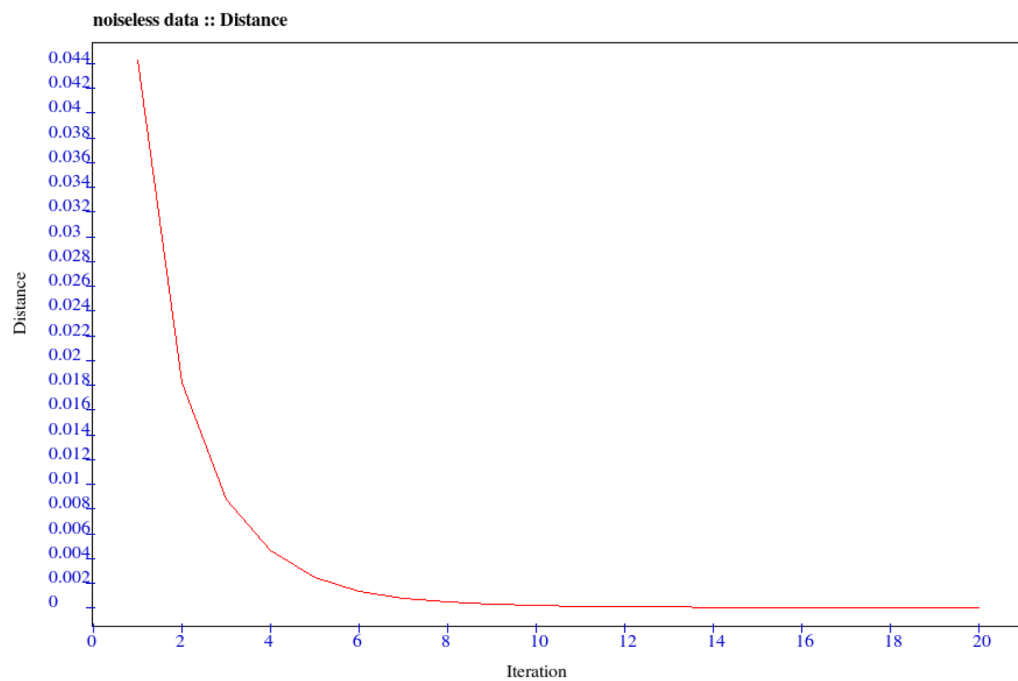
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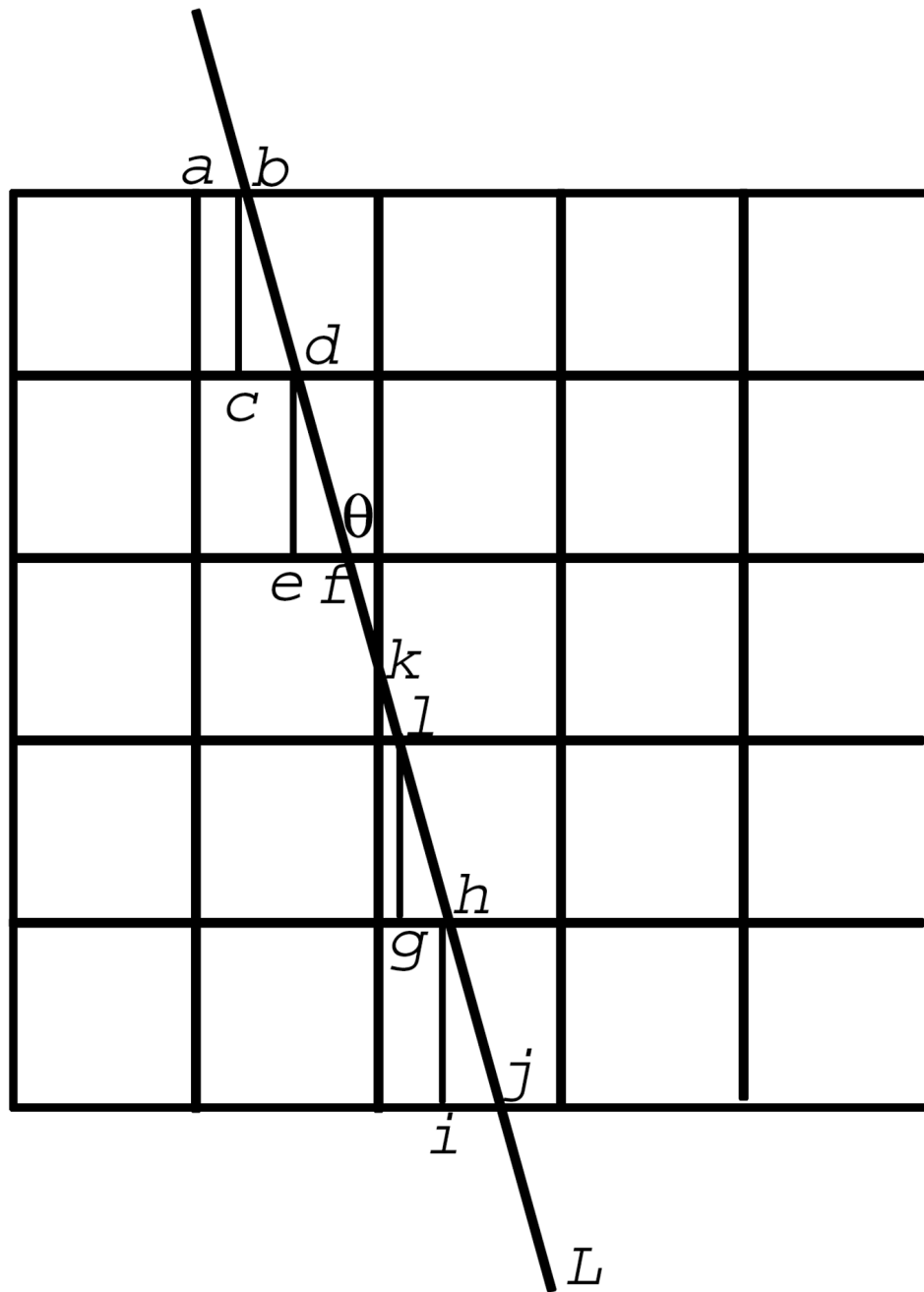
■ ART with relaxation 0.05



(d)

**Figure 1.**

(a) A  $201 \times 201$  digitized head phantom, (b) ART reconstruction from 360 projections with 3,807 rays in each) after four iterations, (c) The same after twenty iterations, (d) Plot of the (normalized) two-norm distance between the phantom and the reconstructions after the first twenty ART iterations. (Phantom, projections, reconstructions and displays produced by the software SNARK05 [2].)



**Figure 2.**

A digital difference analyzer (DDA) for rapidly identifying for any line  $L$  the location of the pixels intersected by it and the lengths of the intersections.