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An island strategy for memetic discrete tomography reconstruction



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ABSTRACT

In this paper we present a parallel island model memetic algorithm for binary discrete tomography reconstruction that uses only four projections without any further a priori information. The underlying combination strategy consists in separated populations of agents that evolve by means of different processes. Agents progress towards a possible solution by using genetic operators, switch and a particular compactness operator. A guided migration scheme is applied to select suitable migrants by considering both their own and their sub-population fitness. That is, from time to time, we allow some individuals to transfer to different subpopulations. The benefits of this paradigm were tested in terms of correctness, robustness and time of the reconstruction by considering publicly available datasets of images. To tackle the so-called stability problem, we considered the case of noisy projections along four directions to simulate an instrumental error. Results show that the proposed method decreases the reconstruction error for all classes of images with respect to a serial implementation recently proposed by the authors, and that such reconstruction error is almost invariant with respect to the number of demes. Moreover, the computation time of the proposed parallel memetic algorithm scales in a quasi-linear manner with respect to the demes number, and is invariant with respect to the used number of migrations.

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1. Introduction

Computerized tomography [21] aims at the three-dimensional recovery of an object from its X-ray projections, by stacking a set of images, called slices. Usually, the gray levels represent different density values within the object and several hundred projections are processed to obtain high resolution slices. During the last decade, it was pointed out that the reconstruction of an object with few density values can be performed by considering a reduced number of projections. *Discrete tomography* [19] deals with geometrical and combinatorial methods to treat discrete structures and its possible applications include medical imaging to detect the presence or the absence of some contrast agent, industrial quality control, internal atomic distribution analysis in crystallography and preliminary investigations to restore works of art.

It is possible to state in polynomial time whether there exists any object compatible with a pair of non-parallel projections, without reconstructing its shape [17,25]. Custom reconstruction algorithms were designed for particular classes of images (e.g. *periodic images* [16], which have repetitions of pixels along some directions, and *hv-convex polyominoes* [7], which are connected sets with 4-connected rows and columns). Besides deterministic methods [3,4,25,27], heuristic [23]

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and evolutionary approaches [5,8,28,13] have also shown their reconstruction ability. Network flows were considered in [3,8,13], too.

Evolutionary algorithms (EAs) and genetic algorithms (GAs) in particular [9] are often considered as global optimization methods to find the optimal solution of a given problem by exploring and stochastically exploiting its solutions space. Since local optima can also be reached (due to the probabilistic nature of these algorithms), the convergence of EAs to a global optimum is guaranteed only in a weak probabilistic sense. Needless to say, EAs are population-based search methods that typically lack space and time efficiency. Nevertheless, they work with independent solutions, which make it feasible to easily distribute the computational load among several processors. Among different kinds of EAs, memetic algorithms [24] (MAs) explore the solutions space by applying co-operative and competitive operators on suitable agents [12]. With respect to EAs, these latter algorithms induce the evolution not only between consecutive generations, but also among the agents within the same generation. This general process can be viewed as a local refinement of a genetic search which further affects the efficiency of the whole evolutionary process.

Parallel evolutionary algorithms (PEAs) are parallel implementations of their corresponding EAs and were introduced not only to avoid their typical slowness, but also to improve the search. In fact, the possibility of using shared memory to improve space efficiency and to use more than one processing unit to evaluate the fitness, does not represent their main feature. Conversely, the most important one is that PEAs can simultaneously span different sub-spaces, thus avoiding traps due to low-quality solutions. In general, a PEA is characterized by a particular parallelization strategy implemented from a serial evolutionary algorithm. The interested reader, can find the main taxonomies of PEAs in [1,10]. Among all possible strategies, the so-called island model requires the division of the population of feasible solutions into a certain number of sub-populations called demes. Demes are generally disjoint, thus each individual competes only with the individuals of the deme to which it belongs. From time to time, some individuals of a deme are migrated. The migration of individuals is ruled by several parameters such as the migration rate, that controls how many individuals migrate, the migration scheme that controls which individuals migrate and a migration interval that determines the frequency of migration. Many studies showed that parallel evolutionary algorithms based on the island model produce good quality solutions even on highly complex problems [1,22].

This paper presents a substantially revised and extended account of research previously reported in [14,11], where we described a memetic tomography reconstructor and its naive island model parallelization, respectively. This latter allowed migration independently of the property of the migrants and their demes. Here, we propose an improved migration strategy that guides decisions about the number and the destinations of the migrants, taking into account the fitness of both the departure and arrival islands. In particular, the adopted strategy imposes the fittest demes to be unwilling to accept immigrants from worse demes. Vice versa, worse demes will try to migrate many individuals towards better demes. In this work, we verify our methodology to reconstruct binary images from four datasets, freely available in the Internet, by considering their noisy projections and without using any a priori information about the objects, but assuming only their compactness. Basic notations are given in Section 2. The proposed parallel memetic algorithm is described in Section 3. Section 4 reports implementation notes and details all experimental results. Future works and possible applications are reported in Section 5.

2. Notations and definitions

Binary images are a convenient representation of the slices which compose three-dimensional objects containing just one density value, and they will be reconstructed by our algorithm. Let us indicate an image I with $n \times m$ pixels by a matrix $A = \{a_{ij}\}$, whose entries are equal to 0 if the corresponding pixels are black (i.e. these points lie on the background) or equal to 1 if they are white (i.e. these points belong to the object). We define the projection line passing through a_{ij} with direction $\mathbf{v} \equiv (r, s)$, where $r, s \in \mathbb{Z}$ and $|r| + |s| \neq 0$, as the subset of A :

$$\ell_{\mathbf{v}}(i, j) = \{a_{i'j'} \in A : i' = i + zs, j' = j - zr \text{ with } z \in \mathbb{Z}\}.$$

Let $t(\mathbf{v})$ be the number of distinct projection lines parallel to \mathbf{v} and $\mathcal{L}_k^{\mathbf{v}}(A)$ be one of these lines that intersect A , with $k = 1, \dots, t(\mathbf{v})$. By denoting with $p_k^{\mathbf{v}}$ the number of 1s on $\mathcal{L}_k^{\mathbf{v}}(A)$ along \mathbf{v} , the projection is:

$$P_{\mathbf{v}} = \left(p_1^{\mathbf{v}}, p_2^{\mathbf{v}}, \dots, p_{t(\mathbf{v})}^{\mathbf{v}} \right) \quad \text{where } p_k^{\mathbf{v}} = \sum_{a_{ij} \in \mathcal{L}_k^{\mathbf{v}}(A)} a_{ij}.$$

It is noteworthy that this definition corresponds to the linear Radon integral transform of A along \mathbf{v} . In order to avoid ambiguities, we will use $P_{\mathbf{v}}(A)$ and $p_k^{\mathbf{v}}(A)$ when more than one matrix is considered. Viceversa, we will adopt the general notation

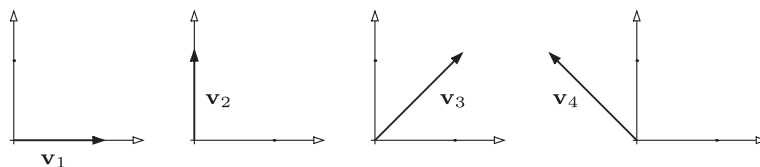


Fig. 1. Directions of the projections used in the proposed parallel memetic algorithm.

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