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Strategies for Tomography

Preface

Image reconstruction from collected data is an inverse problem that frequently appears in several applications. It is encountered in various research areas, such as biomedical imaging, reconstruction algorithms, image processing, stereology, and mathematical morphology. It turns out that the same methodologies and strategies can be frequently adapted to different frames and disciplines. One of the main tools is the Radon Transform, and its inversion formula which is used, in particular, in many problems of tomographic research where the information is usually acquired by means of data obtained from X-rays projections.

Since the 1990s specialistic meetings have been organized devoted to both theoretical advances and practical applications of Tomography. Among them, the Meeting on Tomography and Applications, now in its 6th edition, succeeds in attracting some of the main researchers involved in the various aspects of Tomography. The presentations consists of technical contributions as well as talks outlining the state-of-the-arts and proposing future research directions.

The main purpose of this edition of the meeting was to focus on connections and overlaps among Discrete Tomography, Geometric Tomography, and Computerized Tomography, with a special focus on applications.

This special issue consists of invited papers. Some of them have been presented at the 6th Meeting on Tomography and Applications held at Politecnico di Milano on April 26-27, 2012, but in order to provide a better perspective on current research also additional papers were invited. The papers went through a thorough refereeing process and the accepted papers are presented in this issue.

The reminder of this preface consists of two parts. In the first part we provide brief overviews for each of the papers from this issue. In the second part we provide summaries for talks presented at the 6th Meeting on Tomography and Applications. In this way the reader can get a better insight into the nature of the meeting and hence also into the current research in the area covered by this special issue.

1. Overview of the papers from this issue

• H. Segers, W. Jan Palenstijn, K.J. Batenburg, and J. Sijbers, *Discrete tomography in MRI: a simulation study*.

This paper exploits the possibilities of using the Discrete Algebraic Reconstruction Technique (DART) that performs extremely well for the discrete tomography reconstruction problem, with the data obtained from the Magnetic Resonance imaging (MRI). The MRI is a well-known technique that uses a magnetic field to produce images of various structures like organs, soft tissues, bone, or biological samples. The actual MRI reconstruction methods either use fast inversion Fourier transform techniques from a huge number of measurements, or apply compressed sensing methods that use few measurements, but must be used under some a priori assumptions.

In this paper a new type of a prior knowledge about the homogeneity of the unknown structure (that reflects the poorness of grey levels in the MRI image) is exploited. The authors adapt the DART technique to this scenario, they carry on experiments on MRI data obtaining extremely accurate reconstructions, and they prove that DART outperforms a commonly used reconstruction method.

• K.J. Batenburg, W. Fortes, and R. Tijdeman, Approximate discrete reconstruction algorithm.

The paper presents an approximate algorithm to reconstruct images with a small number of grey levels from projections, i.e., quantitative data on the number of pixels, weighted with respect to their grey level, along a finite set of directions. This problem is one of the most studied in the field of Discrete Tomography, and a range of reconstruction algorithms have been proposed in the literature with most of them assuming the presence of only two grey levels. However, since the general problem is not polynomially solvable, all these algorithms do not guarantee the exact reconstruction of the image, and moreover the error, i.e., the misclassified pixels, depends on the particular problem instance and so it cannot be bounded sharply.

The authors approach the reconstruction problem by means of a mixed technique that relies both on algebraic methods for the solution of linear equation systems and on combinatorics. The algorithm they define requires that the grey levels of the image belong to a fixed set of real values. The reconstructed solution is really close to the unknown starting image, and the difference between the given projections and the projections of this reconstructed image is bounded. A remarkable fact is that this bound is explicitly computable, and moreover it is independent of the image size and scales linearly with the number of projection angles.

• R.A. Fiorini, and G. Laguteta, *Discrete Tomography Data Footprint Reduction by Information Conservation*.

The authors deal with the problem concerning the storage of a huge amount of collected data. One of the aims of Discrete Tomography is the reconstruction of nanocrystals at atomic resolution. This is carried out through suitable algorithms which allow a fast and accurate reconstruction from a limited number of projection images. These algorithms produce a large amount of available data, and one of the underlying problems is their storage in a smaller space. The usually employed processes to achieve this are known as Data Footprint Reduction (DFR), including, for instance, deduplication and lossless compression. However, they fail to match high end data imaging application requirements, so that no contemporary lossless compression/decompression algorithm is completely satisfactory. In this paper a proposal is presented for an original and convenient algorithm for numeric images that offers both Arbitrary Bit Depth (ABD) resolution and Dynamic Upscale Regeneration (DUR), with full information conservation, at no extra computational cost. An original application example is presented and critically discussed.

• A. Condorelli, R.A. Fiorini, and G. Laguteta, *Discrete Tomography Data Footprint Reduction via Natural Compression*.

The paper continues the discussion carried out in the previous contribution, starting from the remark that the usual probabilistic models employed in modern lossless compressors are unable to match high end application requirements with full information conservation. In particular, it would be desirable to manage suitably, and at the same time, an *Arbitrary Bit Depth* (ABD) resolution and a *Dynamic Upscale Regeneration* (DUR). In order to achieve information compression and regeneration at digit level with arbitrary precision, arithmetic and exponential numeric reversible closure of the field \mathbb{Q} of rational numbers are presented and explored. Illustrative examples are provided which point out strong connections with modular group theory and combinatorial optimization. It turns out that traditional \mathbb{Q} Arithmetic can be interpreted as a formal numeric language of languages, with self-defining consistent numeric words and rules. This new approach seems to be very promising for the development of more convenient algorithms and applications.

• S. Petra, C. Schnörr, and A. Schröder, *Critical Parameter Values and Reconstruction Properties of Discrete Tonography: Application to Experimental Fluid Dynamics.*

The paper analyzes the possibility of a unique reconstruction of a 3D image from projections matrices obtained using the technique Particle Image Velocimetry (PIV). The target unique solution is a highly sparse volume function that represents the time-varying motion of a series of particles inside a fluid, while the projections are 2D images taken simultaneously by few cameras from different view angles.

In general, if the reconstruction problem is considered from an algebraic point of view as a system of linear equations, it immediately reveals its high indeterminateness. Here, the authors use most recent results in the field of compressed sensing to investigate the conditions on the sparsity of the particles inside the fluid in order to force the system to have a unique nonnegative solution. They show that if the measurements satisfy certain properties, then nonnegative sparse matrices can be reconstructed exactly from a surprisingly small number of samples. Furthermore, it has been proved that there exist thresholds on sparsity below which a unique solution is guaranteed, while for sparsities above the thresholds the uniqueness is lost with high probability. Such a threshold depends on the numbers of the measurements used for the reconstruction.

Finally, the authors show that similar thresholds can be obtained even from different geometries of the environments, i.e., varying the dimension of the 2D images, the number of projections and projecting directions.

• E. Barcucci, and S. Brocchi, Solving multicolor discrete tomography problems by using prior knowledge.

The authors study the reconstruction problem from the horizontal and vertical projections for several classes of discrete sets that are both connected and convex, say convex polyominoes, and that include colored elements. Both of these properties, singularly, have been extensively studied in the field of discrete tomography due to their connections with practical applications. On the other hand, multicolored sets are used to model the situation where several types of different atoms exist inside an unknown object. Since the reconstruction problem of c-colored objects from two projections has been proved to be NP-complete for c > 1, heuristic algorithms or procedures that handle subclasses of the problem have been proposed. This paper considers multicolored discrete sets with both of these properties: the cells of the set can assume more than one color, and the union of the colored cells is a convex polyomino. A simple reconstruction algorithm is given for two colored sets where the polyomino has an unique solution. Then the authors consider the case of the reconstruction of two nested convex polyominoes of different colors, and they are able to furnish a polynomial reconstruction algorithm by using previous algorithmic results for the same class of polyominoes. They also extend this procedure to nested 8-connected colored sets. Finally, they define some sufficient conditions for a generic multicolored convex polyomino to be uniquely determined by its horizontal and vertical projections.

• S. Bilotta, S. Rinaldi, and S. Socci, On polygons drawn from a permutation.

This paper considers binary matrices, where the elements 1 are connected, and column convex. An interesting subclass of these objects have a close relationship with the permutation diagrams, namely the class of column-convex permutominoes, and they can be defined by a pair of permutations (π_1, π_2) . In recent literature, they have been considered first from a combinatorial point of view, and then they have been applied to some problems which fit in the field of discrete and computational geometry, including the random generation of grid n-ogons with the aim of providing a quadratic-time algorithm for the random generation of orthogonal polygons with a fixed number of vertices, the Minimum Vertex Guard problem (a special case of the popular Art Gallery Problem) for the class of grid n-ogons, and also in theoretical studies of xyz-graphs, that can be thought as a generalization of permutominoes to 3-dimensions. Using a geometric construction, the authors prove that for every permutation π there is at least one column-convex permutomino P such that $\pi_1(P) = \pi$ or $\pi_2(P) = \pi$. Then, they prove that for any given permutation π , it is possible to define a set of logical implications $\mathcal{F}(\pi)$ about the points of π , and that there exists a column-convex permutomino P such that $\pi_1(P) = \pi$ if and only if $\mathcal{F}(\pi)$ is satisfiable. This property can be then used to give a characterization of the set of column-convex permutominoes P such that $\pi_1(P) = \pi$.

• N. Hantos, and P. Balazs, *The Reconstruction of Polyominoes from Horizontal and Vertical Projections and Morphological Skeleton is NP-complete.*

This paper is concerned with one of the main problems in Binary Tomography, i.e., a possibility of reconstructing a binary image from a small number of projections, in polynomial time.

Usually, a small number of available projections does not allow a faithful reconstruction of an unknown binary image, since in general the class of the solutions is really huge and its elements can be extremely different. In the case of only two projections, various researchers use additional information about the unknown image in order to reduce the number of possible solutions, but, in same cases, this leads to dramatically lowering the reconstruction performances till reaching the NP-hardness. Recently, the authors began to study the reconstruction from an additional shape descriptor, the so called morphological skeleton.

In this paper, they provide an NP-completeness proof of the reconstruction problem from two projections of a binary 4-connected images when the morphological skeleton is given. This result

is achieved by means of a remarkable reduction that involves the classical NP-complete problem Three Partition. This result gives rise to a series of interesting open questions concerning the true potential of the morphological skeleton knowledge in the reconstruction process.

• R. Fedele, A. Ciani, L. Galantucci, M. Bettuzzi, and L. Andena, A regularized, pyramidal multigrid approach to global 3D-Volume Digital Image Correlation based on X-ray micro-tomography.

The authors present a robust strategy for 3D-Volume Digital Image Correlation (DIC).

The bulk deformation of a sample, opaque to natural light, can be estimated through 3D-Volume DIC algorithms on the basis of truly three-dimensional tomographic images at different loading steps, achieved by synchrotron radiation or advanced X-ray laboratory sources. X-ray tomography has experienced a significant growth, due, on one side, to the availability of high resolution and ultra-fast X-ray scan systems, and, on the other side, to highly optimized algorithms and multi-core computing platforms. High-accuracy, full-field measurements collected during mechanical tests are able to greatly enrich experimental information.

In particular, formulation of DIC based on a Galerkin, finite element discretisation of the displacement field, offers a unified framework for material parameter identification procedures, consistent with mechanical modeling. However, being the above inverse problem ill-posed, unstable response may occur in the estimation of displacement fields. This leads to spurious oscillations which corrupt the deformation scenario and make it hardly legible. To partially overcome such problems, multi-resolution approaches have been proposed in the recent literature on digital image processing. An important conceptual meaning of these strategies is their similarity with the multi-scale nature of human vision, which can focus both on details and on the global scenario, passing rapidly and iteratively from one scale to another.

The 3D-Volume DIC implementation proposed in this paper allows accurate kinematic measurements within a loaded sample on the basis of three-dimensional digital images reconstructed by means of X-ray computed microtomography. A non destructive methodology i.e. a 3D-Volume Digital Image Correlation procedure based on a Galerkin, finite element approach, is presented. The noveltie of our method is the employment of a full multi-grid approach.

It aims to furnish a good compromise between conflicting requirements of computational efficiency and architectural simplicity of the strategy.

2. Outline of the talks presented in the Meeting on Tomography and Applications, 2012

Optical Tomography of biological organisms *Andrea Bassi, Politecnico di Milano*

The talk by Andrea Bassi discussed image reconstruction by means of Optical Projection Tomography. Optical Projection Tomography [1] is a three dimensional imaging technique, which is particularly suitable to study millimeter sized biological samples and organisms. Similarly to x-ray computed tomography, OPT is based on the acquisition of a sequence of optical transmission (or fluorescence) images of the sample at several orientations. The acquired images, or projections, are combined to reconstruct

the 3-D volume of the sample, typically using a back-projection algorithm. The principles of OPT were described, showing various examples of ex-vivo and in-vivo imaging. The protocol for ex-vivo imaging of fixed biological samples, which includes chemical clearing in an index matching solution, were presented. Then a protocol for in-vivo imaging of various biological organisms (such as zebrafish) was given. Results obtained with absorption and fluorescence OPT were shown and then a new contrast mechanism in OPT, given by the movement of cells present in bloodstream, was described, showing that the circulatory system of a living biological organism such as zebrafish can be visualized in 3D, in vivo, without the need of any labeling [2]. Nevertheless, in vivo OPT is usually limited by tissue light scattering, especially when zebrafish at the juvenile and adult stage are under study. To reduce this problem, a technique called Time-Gated Optical Projection Tomography (TGOPT) [3] was presented. This technique is able to reconstruct adult zebrafish internal structures without staining or chemical clearing procedures. The use of a time gating mechanism, based on non-linear optical upconversion of an infrared ultrashort laser pulse, allows the rejection of multiply scattered photons and the exclusive detection of ballistic ones within a 100 fs temporal gate. This results in a strong increase of contrast and resolution with respect to conventional OPT. Artifacts in the reconstructed images are reduced as well. Results showing that TGOPT is well suited for imaging the skeletal system and nervous structures of adult zebrafish, were presented.

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Optimized limited angle tomography Alberto Borghese, Università di Milano

The talk of Alberto Borghese is based on a joint work with Iuri Frosio (both authors are members of the Applied Intelligence Systems Laboratory, Department of Computer Science, University of Milano), where innovative algorithms have been developed for managing truncation and band artifacts.

Computerized tomography (CT) is nowadays widely used for imaging the patients body in many clinical fields. However, the cost of the machinery and the high dose delivered to the patient is not justified for many applications. Accordingly to the ALARA (As Low As Reasonably Achievable) principle, much effort has been done to develop techniques and machines aimed at reconstructing the local anatomical districts of interest, reducing the potential damage that can be produced inside the irradiated volume. Such limited volume reconstruction is often associated to limited angle acquisition and therefore it rises several problems unique to the tomographic process. In particular, band and truncation artifacts arise, that may significantly degrade the quality of the reconstructed volume: correction algorithms are required to get satisfactory results.

A close analysis of the results, shows that band artifacts are generated by SART during the iterative reconstruction process as the projection cone associated to each projection only partially crosses the volume. As a consequence, a discontinuity is generated at the margins of the projection cone, because the voxels inside the cone are updated whereas the external ones are not. To avoid the introduction of the band artifacts, a local equalization strategy inspired by Zhang et al., 2009 has been adopted. In particular, after each volume update trough and for each slice of the volume, the margins of the projection cone are detected and the difference of the absorption coefficients across the border is computed. This difference is locally averaged along the border to identify the average difference in the volume generated by any new projection. Such difference is then used to smoothly increase or decrease the absorption coefficients along each voxels line in the direction mostly perpendicular to the border.

The modified algebraic tomography has been applied to the dental field to obtain 3D images that are clinically valid for implantology and prosthesis. Final implementation has been realized in CUDA parallel architecture. CUDA extends the C language and it furnishes a set of functions that permits the usage of the GPU as a parallel multiprocessor, and it is therefore particularly suitable to image processing, and tomography in particular. A CUDA architecture consists of many computational cores (on the GPU) executing the same code (CUDA kernels) on different data (SIMD = Single Instruction Multiple Data architecture). Each thread (and the corresponding core) has its own (limited) register and memory. Shared memory and global memory are also present (higher latency). To maximize the efficiency, parallelization should follow some principles: Avoid CPU / GPU data transfer; Data alignment for optimal access; Optimize the resource usage for each kernel (e.g.number of registers).

The research group of Alberto Borghese has implemented the algorithm on a set of 11 projections (1536 x 562 pixels), acquired from -30° to $+30^{\circ}$ equally spaced. A volume of 50mm x 40mm x 105mm has been reconstructed with anisotropic voxels of 1mm x 0.15mm x 0.15mm for a dimension of 50 x 267 x 700 voxels. A total of five iterations on the full images data-set has shown to be sufficient. The order of the images was randomly extracted and the overall computational time was of 60s on a CPU (Intel Centrino Duo @ 3.06GHz, RAM 4M) that dropped to less than 6 seconds when a GPU was fully used. In particular a Quadro FX 770M GPU board has been employed, with 512MByte on-board memory (2008). Three main kernels were identified: CUDA Kernel 1: forward projection and error computing 1 Thread per ray tracing (per pixel). CUDA Kernel 2: back projection 1 Thread per voxel. CUDA Kernel 3: band artifact correction 1 Thread per band.

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Bounded sets in Discrete Tomography: Non-Uniqueness vs Uniqueness Sara Brunetti, Università di Siena

Problems of Discrete Tomography concern the recovery of lattice sets from their X-rays in a prescribed set S of lattice directions. The uniqueness problem consists in deciding whether there exists just one lattice set having the given X-rays. Uniqueness in the reconstruction ensures that the computed set of points is the original one.

These problems have been widely studied in the literature for both their theoretical relevance, and the main role they play in some important related problems (see [4, 5] for an overview). For the two directions case Ryser and Wang have found necessary and sufficient conditions; in the case of more than two directions, the uniqueness problem is NP-complete.

In her talk, Sara Brunetti considered a finite grid $\mathcal{A} = \{(i, j) \in \mathbb{Z}^2 : 0 \le i < m, 0 \le j < n\}$ and defined as *bounded sets* each subset of points contained in A. The problem, she focused on, can be posed as follows: determine any set S of lattice directions for which every bounded set in \mathcal{A} is unique. To avoid trivial cases the notion of "valid" set of directions was introduced by Hajdu and Tijdman in [2] in order to exclude those sets whose sum of the elements overcomes the dimensions of \mathcal{A} . Sara Brunetti discussed uniqueness issues, and extended some results of [3] by showing that, for any fixed $\mathcal{A} \subset \mathbb{Z}^2$ of size $m \times n$, families of suitable sets of four directions can be selected such that any two subsets of \mathcal{A} can be distinguished by means of their X-rays in these directions. These have been determined in cooperation with P. Dulio and C. Peri.

She proposed an algebraic approach to deal with the uniqueness issues, and she gave a characterization of the sets S, consisting of four lattice directions, which provide uniqueness in A. A crucial notion to investigate uniqueness is that of *bad configuration*, since any lattice set is unique if and only if it has no bad configuration. Moreover any lattice set is additive if and only if it has no *weakly bad configuration*. Additive sets are also unique, and this fact furnishes conditions, involving the set of directions and the dimensions m and n of the grid, which forbid a weakly bad configuration to be transformed into a bad configuration inside the given grid, so that possible non-additive bounded sets are unique.

Relying on these notions, L.Hajdu and R.Tijdman gave an algebraic condition that a function $g : \mathcal{A} \to \mathbb{Z}$ has to satisfy in order to have zero line sums along the lines taken in a set of directions S ([2, Lemma 3.1]). Geometrically, such a function corresponds to a weakly bad configuration if |g| > 1, or to a bad configuration if |g| = 1 (in the Euclidean norm). In order to get uniqueness g cannot be the difference of two characteristic functions.

Finally, she defined some conditions that characterize a set S of four directions in order to uniquely determine the bounded sets of \mathcal{A} [1]. In contrast with the general case, this result permits to efficiently solve some related problems asking to find one of the two parameters given the other one in order to get uniqueness.

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Project CINEMAT based on X-ray micro-tomography: from digital images to material properties. Some preliminary results *Roberto Fedele, Politecnico di Milano*

In his communication Roberto Fedele outlined some preliminary results, both experimental and numerical, achieved during the first year of the multidisciplinary Project CINEMAT. Such a project, including in a tight and coordinated collaboration researchers belonging to different disciplines, has been funded in 2010 by Politecnico di Milano, in the framework of 5 per mille Call for Young Researchers. The aim of this research is to develop a novel experimental-numerical methodology, suitable to estimate material parameters on the basis of full-field kinematic measurements throughout a loaded specimen. The proposed methodology combines synergistically: (i) a sequence of 3D digital images provided at different instants by high-resolution X-ray micro-tomography, (improved with advanced technological solutions) and interfaced with an ad-hoc loading device (see e.g. [1]); (ii) mathematical models describing the material behavior at different scales; (iii) inverse analysis in a sequence, namely volume Digital Image Correlation (DIC) for the estimation of kinematic fields inside the bulk material (i.e. displacements and strains, see e.g. [3]), and model calibration/validation through stochastic parameter identification techniques [2].

For the material samples and constructs selected as a reference for their impact in the scientific community and the wide social concern, the proposed methodology is expected to provide not only qualitative but truly quantitative high-quality information on the heterogeneous structure, allowing one to reconstruct the local strain states and use them as a basis for the subsequent mathematical modeling and relevant calibration/validation stages. Roberto Fedele also pointed out a few preliminary results to be discussed. These concern (i) development and validation of micro-loading devices, to be interfaced with the tomograph; (ii) tomos of a biodegradable scaffold, to replace injured cartilaginous tissues (see [4]), and polymeric foam samples under loading; (iii) development of a Digital Image Correlation code.

Special attention has been devoted to no-contact Digital Image Correlation (2D DIC) procedures, which have been widely applied to monitor a variety of experimental tests at different observation scales, both in the laboratory and in situ. In the proposed algorithm an image pyramid is generated recursively by averaging non-overlapping 2×2 domains, in such a way that images progressively smoother and smaller are located at higher levels; at each pyramid level, a unique grid is considered, including finite elements with the same number of pixels; several computational cycles differently shaped are performed along the pyramid, where suitably transfer operators are defined (prolongation and restriction); to compare a pair of image at each scale, the conventional, least-square matching function for DIC is enriched by a Tychonoff regularization term weighted by a penalty factor tuned by the user, preserving the solution against unstable response; inexact convergence is considered at each grid (and scale), and satisfactory results can be achieved even by one Newton iteration per scale, with a drastic decrease of the computing effort. Results are presented concerning a laboratory X-ray micro-tomography experiment on a polymer sample under loading.

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Discrete Tomography Natural Lossless Compression Rodolfo Fiorini, Politecnico di Milano

The lecture by Rodolfo Fiorini dealt with image compression. For a deeper treatment of this topic, and its connection with Discrete Tomography, as well as for a comprehensive list of references, we address the reader to the papers of R. Fiorini which appear in this issue. Here we just give a sketch of his lecture.

The first impact of nanoscale technology has been to generate new challenges associated with the problems of formation, acquisition, compression, transmission, and analysis of humongous quantity of data. Data Footprint Reduction (DFR) is the process of employing one or more techniques to store a given set of data in less storage space. One of the most popular ones is data lossless compression. The very best modern lossless compressors use classical probabilistic models, but are unable to match high end application requirements, such as Arbitrary Bit Depth (ABD) resolution and full information conservation. In particular, contemporary lossless image compression algorithms are affected by three main weaknesses:

- (1) image type compression effectiveness and efficiency dependence;
- (2) image size compression/decompression speed and space limitations;
- (3) no true lossless compression achieved: a few pixels may vary by com/decom processing.

The focus has been devoted to the third point, which is especially inadequate for discrete tomography applications where high data reliability is required. A natural modular arithmetic approach to achieve true lossless com/decom and to overcome those constraints has been presented. Also, test image results to well-known techniques comparison have been discussed.

Starting from basic properties and relationships of the set \mathbb{Q} of rational numbers, one can achieve full numeric algorithmic information conservation first, and then take advantage of that knowledge to show strong connections with modular group theory and combinatorial optimization. Traditional rational number system can be even regarded as a highly sophisticated open logic, powerful and flexible LTR and RTL formal language, with self-defining consistent words and rules, starting from elementary generators and relations. This new awareness can guide the development of successful new convenient algorithm and application. A real first algorithmic example is presented (NC, Natural Compression algorithm), benchmarked to standard lossless JPEG2000 implementation and discussed. Its raw overall lossless compression performance compares quite well to the standard one, and moreover it offers true ABD and achieving full information conservation and regeneration, with no hidden extra burden.

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How to decompose a binary matrix into hv-convex polyominoes Andrea Frosini, Università di Firenze

In his contribution Andrea Frosini presented original results obtained in cooperation with C. Picouleau, concerning the problem of the minimum decomposition of a planar shape, regarded as a binary matrix, into convex parts. This problem finds its practical applications in the Intensity Modulated Radiation Therapy (IMRT). For cancer treatment IMRT consists in delivering a radiation dose to destroy the tumor while maintaining the functionality of organs surrounding it. The collimator is the medical machine that delivers the radiation dose (dose matrix). Technically, the collimator cannot deliver all shapes of matrices. The shape decomposition problem consists in decomposing the dose matrix into a set of deliverable shape matrices. Baatar et al. [1] show that the problem of deciding whether a binary matrix A can be decomposed into at most K horizontally convex (briefly h-convex) matrices is \mathcal{NP} -complete in the strong sense even in the case where A has one single row.

Jarray et al. [2] consider the problem of deciding whether it is possible to decompose a binary matrix into a (small) fixed number of binary matrices fulfilling some specific requirements as it is usual in the field of the theoretical discrete tomography. They show that the decomposition into three horizontally and vertically convex, abbreviated hv-convex, matrices is \mathcal{NP} -complete in the strong sense whereas the decomposition into two of them is polynomial even in the case where each of the two matrices is connected, i.e. it is a polynomia. Note that this last requirement is of great importance for the applications in IMRT.

Andrea Frosini briefly sketched the idea that lie behind the \mathcal{NP} -completeness proof in [2], and then presented an algorithm to decompose a binary matrix A into three hv-convex polyominoes X, Y, and Z that performs the task in polynomial time with respect to the dimension of the input binary matrix, if possible, otherwise gives failure.

This algorithm relies on a theoretical result that characterizes the hv-convex polyominoes by means of the presence of a monotone path that runs from any two of its elements, where monotone path is defined as a path internal to the polyomino and that uses at most two of the four north, south, east and west types of steps.

After preprocessing A in order to detect trivial cases, the algorithm starts the detection of the borders of X, Y, or Z using two different procedures:

geometrical detection: the connectedness and the convexity constraints imposed on X, Y, and Z allow to immediately assign to each of them some elements of A;

2-face permutation detection: it can be proved that if the decomposition problem on A has a solution, then its non convex parts can be arranged so as to form a 2-face permutation matrix (for definitions see [3]). Thus this part of the algorithm proceeds in detecting these square permutations and assigns their elements to the borders of X, Y, or Z.

In the final step, the algorithm joins by means of monotone paths the elements of the border already assigned to the same polyomino, and the detection of X, Y, and Z is fully performed.

Finally, Andrea Frosini proposed some open problems related to the decomposition of a binary matrix, and discussed a series of hints about the possible generalizations of the algorithm.

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Reconstruction of convex bodies from X-rays: Old and new, including an application to nanowire reconstruction

Richard Gardner, Western Washington University

In Geometric Tomography the usual density functions of Computerized Tomography are replaced by geometric sets (equivalently, density functions taking only 0 or 1 as values), and one of the main goals is to find conditions which guarantee uniqueness of reconstruction within a given geometric class. Data are usually collected by means of (continuous) X-rays, namely line integrals along lines parallel to given directions (parallel X-rays), or issuing from a finite source point (point X-rays). These are routinely called *projections* in Computerized Tomography, but, in a mathematical contest, where projection means shadow, the term X-ray is more appropriate.

During the AMS Symposium of Pure Mathematics in 1963, P. C. Hammer proposed the following X-ray problems.

Suppose there is a convex hole in an otherwise homogeneous solid and that X-ray pictures taken are so sharp that the "darkness" at each point determines the length of a chord along an X-ray line. (No diffusion, please.) How many pictures must be taken to permit exact reconstruction of the body if: a. The X-rays issue from a finite point source?

b. The X-rays are assumed parallel?

In his lecture, Richard Gardner considered part (b), i.e., the case of parallel X-rays. From earlier theoretical work [1], [2], based among other things on geometrical properties of affinely regular polygons, it is known that there are certain sets of four directions in the plane, for example those specified by the four vectors (0, 1), (1, 0), (2, 1), and (-1, 2), such that the exact X-rays of a planar convex body in these directions determine it uniquely among all planar convex bodies. This, of course, is a very different situation from the one usually encountered in computer tomography, in which there is a complete

lack of uniqueness in general; there, reconstructions are by necessity approximate, the accuracy of the approximation depending on the number of X-rays taken.

The lecture also addressed an implementation and application of an algorithm [3] developed together with Markus Kiderlen for reconstructing planar convex bodies from a finite set of X-rays. The algorithm takes k values of each X-ray in such a set of four directions and returns a convex polygon which converges to the convex body as k tends to infinity, even when the measurements are affected by Gaussian noise of fixed variance. In practice the implementation uses simulated annealing to avoid local minima, and pre-processing of noisy measurements with a smoothing procedure.

Three possible applications having physical relevance were pointed out:

1. The reconstruction of structural maps of polycrystalline materials from data collected using a new 3D X-ray diffraction method (3DXRD), due to Henning Poulsen, that presently employs highly penetrating (and so highly destructive) X-rays from a synchrotron.

2. The reconstruction of platinum catalyst nanoparticles from data obtained by the High-Angle Annular Dark-Field electron tomography (HAADF), a new tomography method that forms images with a scanning transmission electron microscope.

3. The application to nanowire reconstruction [4] mentioned in the title of the lecture. In this case, the algorithm has been employed. Pictures were shown comparing the reconstruction of a nanowire by means of this and other algorithms.

At the end of the lecture, some related open theoretical problems were mentioned.

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Elementary Algorithms in Multi-Resolution Geometric Tomography with Area Model *Yan Gérard, Université d'Auvergne*

Geometric Tomography [1] deals with the reconstruction of an unknown compact shape S from projections in some directions. Several models of projections can be considered. The most classical one is the length ray model. It provides the sum of the length of the segments of the intersection between the beam and S. We choose however to consider a different model called the area model. The projection is the area of the intersection of the shape S and the strip between the consecutive parallel lines.

The area model seams suitable for applications because captors of cameras have a non-null width. They register signals coming from strips and not necessarily from lines.

In his talk, Yan Gérard presented some experiments in the framework of geometric tomography with the area model without assuming any prior knowledge on the solution. After showing how to express this problem by linear constraints on real variables and how to solve it by linear programming, he focused on other algorithms.

First he considered a greedy approach, starting from a decomposition of the domain in cells (it could be pixels or quads of different sizes in a multiresolution framework). The principle of the algorithm is to work with a current shape S described by its list of cells. The shape will grow during the process by adding at each step a new cell according to a local criterion of error: for each cell which is not in S, it is computed its contribution to the errors on the projections, and the maximal one is chosen. If it is positive, then the cell is added to S and the error table updated, otherwise, it stops.

Yan Gérard showed tests on several error criteria on the cells, and proposed as the best option to weight the error between the area of the intersection of S and a strip by the area of the cell with the strip. This algorithm is used as routine for the next one that relies on a multiresolution greedy approach.

In previous approach, the cell structure is given as input and does not change during the process. One can however think that close to the boundaries of the shape, it could be useful to work with smaller cells than in the middle of white or black regions. Then the idea is the following:

Initialization - take an initial cell decomposition of the domain.

Loop - perform greedy algorithm and refine the cell structure close to the boundaries.

This approach provides a sequence of shapes with an increasing level of details without increasing too much the time of computation.

Yan Gérard also presented a final simulated annealing algorithm [3]: here the state is made of a cell decomposition of the domain and a shape S given by a list of cells. At each step, the local state of a cell can change with a certain probability that depends on several criteria (temperature, error contribution, neighborhood). Three kinds of transitions are possible: cells can split, merge or just change their colors. In order to control the number of cells, a minimal area is defined under which no split is authorized. The method seems promising because it is easy to introduce many significative criteria which are difficult to optimize with global algorithms, as for instance a control of the topology of the shape.

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Bounds for the differences between discrete tomography solutions *Lajos Hajdu, University of Debrecen,*

The notion of projection of a discrete object, regarded as a finite set of points in the integer lattice, along a (discrete) direction (a, b) is commonly defined as the vector whose entries are the number of points that lie on each line of the form ay = bx + t, and intersecting the set. The research field of Discrete Tomography concerns the retrieval of geometrical information about an unknown discrete objects from its projections along a finite set of directions. Obviously, the final aim is a faithful reconstruction of the object itself, but, in general, this is prevented from the existence of different objects that are compatible with the same projections, i.e., objects that contain subsets of positions, say switching components,

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where the elements can be moved without changing the projections. So, a crucial step is the estimation of the maximal distance between these solutions, and their stability.

Lajos Hajdu, starting from the basic notions of Discrete Tomography, presented a series of results that are both already known and original, using a purely algebraic setting, and real valued density functions. The original results have been obtained in cooperation with K. J. Batenburg, B. E. van Dalen, W. Fortes, and R. Tijdeman.

In formulating the main problems of the field, he introduced the interesting notion of valid set of directions for a discrete set, i.e., a set of directions S whose sum does not overcame the bounding rectangle, say A, of the set itself.

The definition of a valid set S for A is strictly related to the existence of different sets of points having the same projections along the directions of S, as shown in [5]. Under this assumption, Lajos Hajdu defined the real function f_0 as the shortest real solution (w.r.t. the Euclidean norm) of the reconstruction problem, and he showed that f_0 can be expressed as a rational linear combination of the line sums [1]. In the case of the row and column sums only, this linear combination greatly simplifies, and each value of f_0 can be easily expressed in terms of the entries of the two vectors [4].

The function f_0 shows interesting properties, and it can be used to determine bounds concerning the differences between the solutions of a discrete tomography problem, i.e., between binary matrices having the same line sums along lines in finitely many given directions. This result follows from the fact that all the binary solutions are situated on a hypersphere, with center f_0 [4]. It is therefore crucial to estimate the radius of the hypersphere to approach the problem of their stability.

So, he presented various bounds between any two binary solutions. In the case where only row and column sums are considered, van Dalen [3] derived upper bounds for the number of places where two binary solutions may differ. Lajos Hajdu also presented an algorithm to make these bounds rather sharp in concrete cases, and also showed the results of some practical experiments obtained in [1] and [2].

Then, he proposed extensions of some of the mentioned results to various other cases: to the continuous case; to the case where the entries of the unknown matrix are integers; and to the case where the fundamental domain is not a matrix, but a torus. Finally, he outlined a method to estimate the maximal distance between two binary solutions, and he deduced an upper bound for the distance from any given real solution to the nearest integer solution.

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Innovative methods to seismic tomography and examples of their applications *Tatyana Smaglichenko, Russian Academy of Sciences*

The contribution by Tatyana Smaglichenko focused on seismic tomography, which aims at determining the interior Earth structure by using information about seismic waves registered by seismometers.

Under suitable assumptions one can solve the problem in the ray approximation, and consider propagation of seismic wave along the ray connecting the source point with the receiver on surface. The Earth medium can be divided in blocks, or cells, and then according to this discretization [1], one can speak about transmission tomography and solve the system of linear equations. To invert the system the following three techniques are mainly employed:

- (1) LSQR algorithm or Lanczos method [4];
- (2) Consecutive Subtraction of Selected Anomalies method (CSSA) [6];
- (3) the differentiated approach or the Modification of Gauss Elimination (MGE) [8].

All the methods belong to the group of projection techniques i.e., they are mainly working with columns of the initial matrix. This makes seismic tomography different from the medical X-ray tomography, where iterative techniques (such as ART, or SART) are employed. In seismic tomography columns correspond to blocks of seismic medium, which could be some rocks. Geological information represents visible observation data to seismic tomography, and it can be incorporated in the inversion process. In contrast, seismic rays are unreliable assistants because levels of their noise can be unpredictable high.

Different Inversion techniques have different ability in reconstructing different structures (tests). In 1993 Leveque et al. published a research where resolution parameters are recommended, instead of the so-called *checker-board resolution test*, to check reliability of solution. A reason is that LSQR retrieves the *checker-board* model, which is a small-size structure, but, at the same time, it fails in reconstructing large-size structures. In 2003 T. Smaglichenko introduced the CSSA scheme that corresponds to relaxation technique of the method of steepest descent. Being an alternative to the standard method, CSSA easily reconstructs a single large anomaly surrounded by uniform homogeneous zone, i.e., simple case of large-size structure. However, it was pointed out that both methods could not reconstruct a single large high anomaly surrounded by uniform low zone, i.e., complex large-size structures. Recently, T. Smaglichenko developed the MGE technique, due application of which allow the reconstruction of this model.

In general a combination of the three techniques can be employed. Technologies have been recently developed and tested by using models of different structures (small-size and large-size), and possible applications can be outlined based on the study of seismic active area in Japan and in Iceland.

In August 1996 a relatively large earthquake (Magnitude 5.9) occurred in north-east Japan in Onikobe district, on the boundary of Miyagi, Iwate and Akita prefectures. The main shock was followed by numerous aftershocks, which were distributed inside prefectures and formed Onikobe aftershock area. This area is located in few tens kilometer from the wide aftershock zone that followed tsunami in 2011. In order to investigate the Onikobe area the structure has been studied using two data sets before and after the main shock of 1996. The first data were shallow and intermediate-depth earthquakes selected for the period 1989-1996 [5] and the second one were shallow earthquakes that occurred in 1996 [6]. CSSA has been applied twice. In the case of the first data set the horizontal size of block was 23x25 km, while, in the second case, the size was 4x4 km. Both results show that hypocenter of the Onikobe earthquake is located exactly on the edge of low velocity zone that is surrounded by weak high velocity anomaly. Note

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that, before application to real observations, CSSA twice successfully passed the checking by using *the checkerboard resolution test* for both data sets. Thus, one can assume that the produced images are close to reality.

A similar conclusion has been reached in studying the Tjornes Fracture Zone (TFZ), that is located at the north-east of Iceland. In collaboration with colleagues from Mainz University (Germany), T. Smaglichenko investigated seismicity from 1986 to 1989, mainly along Grimsey Lineament. In 2000-2003 they inverted data by applying CSSA, but the resolution of revealed images was insufficient, due to noise in observations. It can be explained by non-uniform distribution of earthquakes in sea, and location of stations at coast [7]. In 2008 they repeated the inversion by employing the MGE approach, which is stable under errors in data. This most accurate result pointed out that hypocenters are close to the boundary of low and high velocity anomalies or inside strong low zone.

In order to increase details of an image one should normally select the small size of blocks. However, if LSQR is employed, then an estimation of a very large resolution matrix must be considered. Experience of many researchers shows that computer programs are often stumbled working with such matrix. MDE has been developed to overcome this inconvenience. Initial matrix is subdivided into many cells and few sub-systems must be solved applying different schemes, which can include standard method too. Due to this approach the accurate image of Nagano fault area (Central Japan) was constructed using data of aftershocks that were collected during 1995-1998 years after the 1984 Nagano-Seibu earthquake (Magnitude 6.8). By using small enough block size (1.0 x 0.19 x 0.3 km) the visualization of the fault plane projection has been obtained, based on velocity images. Extremely low velocities can determine the fault location in space. This result encourages in probing the hydrocarbon model. Simple geological knowledge tells that dipping thin reservoir model is similar to the fault projection model. The construction of accurate velocity images in areas of mining could facilitate both finding hydrocarbons and taking care of the Earth. The experience of seismic tomography indicates that the passive seismic exploration seems to be a modern perspective direction for human scientific activity [2].

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