

Recent trends in Medical Image Processing Editorial (Preface) for a special issue of Computer Science Journal of Moldova

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It is said that images bear the greatest density of natural information of all ways of human communication, and biomedical images do not make any exception to this assertion, at least when dealing with morphologic information. The recent rapid advances in medical imaging and automated image analysis will continue and allow us to make significant advances in our understanding of life and disease processes, and our ability to deliver quality healthcare.

Medical imaging and image processing domains mainly manage and process missing, ambiguous, inconsistent, complementary, contradictory, redundant and distorted data, and information has a strong structural character. The processes of human and artificial understanding of any image involve the matching of features extracted from the image with pre-stored models. From the information technology point of view the production of a high-level symbolic model requires the representation of knowledge about the objects to be modeled, their relationships, and how and when to use the information stored within the model.

In general, a distinction is made between (bio)medical imaging and image processing technologies, even if between these fields of knowledge a strong interrelation may be established.

Biomedical imaging concentrates on the capture and display of images for both diagnostic and therapeutic purposes, and modern imaging technology is 100% digital. Snapshots of in vivo physiology and physiological processes can be garnered through advanced sensors and computer technology. Biomedical imaging technologies utilize either x-rays

(CT scans), sound (ultrasound), magnetism (magnetic resonance imaging – MRI), radioactive pharmaceuticals (nuclear medicine: SPECT, PET) or light (endoscopy, OCT) to assess the current condition of an organ or tissue and can monitor a patient over time for diagnostic and treatment evaluation. From the information type point of view, medical imaging can be structural (or morphologic, e.g. CT, MRI, OCT) or functional (PET, SPECT).

Biomedical image processing is similar in concept to biomedical signal processing in multiple dimensions (2D, 3D). It includes the enhancement, analysis and display of images captured via the above mentioned x-ray, ultrasound, MRI, nuclear medicine and optical imaging technologies. Related procedures, like image reconstruction and modeling techniques allow quick processing of 2D signals to create 3D images. Image processing software helps to automatically identify and analyze what might not be apparent to the human eye, even of an expert. Computerized algorithms can provide temporal and spatial analysis to detect patterns and characteristics indicative of tumors and other ailments. Depending on the imaging technique and what diagnosis is being considered, image processing and analysis can be used to determine, for instance, the diameter, volume and vasculature of a tumor or organ, flow parameters of blood or other fluids and microscopic changes that have yet to raise any otherwise discernible flags.

Nowadays some key components of clinical activity are image-guided therapy (IGT) and image-guided surgery (IGS), where localization, targeting, monitoring, and control are main issues. Specifically, in medical imaging and medical image processing we have four key problems: (1) Image Segmentation – dealing with (semi)automated methods that lead to creating patient-specific models of relevant anatomy from images; (2) Image Registration – automated methods that align multiple data sets, eventually coming from different imaging modalities, with each other; (3) Visualization – the technological environment in which image-guided procedures can be displayed; (4) Simulation – software that can be used to rehearse and plan procedures, evaluate access strategies, and simulate planned treatments.

In fact, all traditional and advanced techniques of image processing

and computational vision, analysis and understanding may be used to process medical images, in order to extract useful information for diagnosis and treatment.

A special approach, including that of the editor of this journal issue, directs to the use of Artificial Intelligence (AI), which has proved to yield promising results in medical image processing and analysis. The structural character of information may successfully be approached by using methods of AI such as Knowledge Based Systems, Expert Systems, Decision Support Systems, Neural Networks, Fuzzy Logic and Systems, Neuro-Fuzzy Systems, Evolutionary and Genetic (or bio-inspired) Algorithms, Data Mining, Knowledge Discovery, Semantic Nets, Symbolic Calculus for knowledge representation, etc. The *data fusion* methods successfully solve the aggregation of numerical and linguistic information, and are able to cope with ambiguous, uncertain, conflicting, complementary, imprecise and redundant information, like that occurring in biomedical imaging domain, in order to provide a more accurate and less uncertain interpretation.

One of the main characteristic of the Medical Image Processing domain is its inter- and multidisciplinary nature. In fact, in this field, methodologies of several fundamental and applicative sciences, such as Informatics, Mathematics, Physics, Statistics, Computer science, Medicine, Engineering, Psychology, Artificial Intelligence, (Bio)Mechanics are regularly used. Besides this characteristic, one of the main rationale that promotes the continuous effort being made in this area of human knowledge is the huge number of useful applications in the medical area, some of them being illustrated hereinafter.

This special issue of Computer Science Journal of Moldova contains six invited papers that illustrate new trends and outcomes in medical image processing. It gathers together prominent researches that align to the state-of-the-art of Computational Vision and Medical Image Processing, contributing to the development of both these knowledge areas, and of medical research and clinical activity.

Probably is somehow justified that two of the invited articles deal with retinal images processing. The first one, "Detection of Blood

Vessels in Retinal Fundus Images”, of Oloumi, Dhara, Rangayyan, and Mukhopadhyay approaches automatic detection of blood vessels in retinal fundus images, in order to perform computer-aided diagnosis of some pathologies of the eye such as diabetic retinopathy (DR), retinopathy of prematurity, and maculopathy. The vessels detection techniques include a mix of multiscale and multifeature methods, like multiscale vesselness measures, Gabor filters, line operators, and matched filters. An adaptive threshold selection method is crucial for precise detection of retinal blood vessels. The accuracy of detection is improved by an original postprocessing technique for removal of false-positive pixels around the optic nerve head. The results of detection of blood vessels, evaluated in terms of the area under the receiver operating characteristic curve of up to 0.961, were obtained using the 20 test images of the DRIVE database (which is considered as containing low-resolution retinal images). These results have double meaning: on one hand they outperform other approaches of the chosen topic, and on the other hand they show that a single-scale Gabor filter is capable of detecting blood vessels with accuracy not much different from the best value obtained by means of multifeature and multiscale methods. In this way the authors prove once again the famous Latin saying “non multa, sed multum”.

The second article, “Optic Disc Identification Methods for Retinal Images”, written by Rotaru, Bejinariu, Niță, Luca, and Lazăr, proposes some original methods to identify and model the optic disc in colour retinal images, as well as the blood vessels network, to evaluate different retina diseases such as diabetic macular edema, glaucoma, etc. The paper represents an extension of some early researches of the same authors, in which they heuristically apply certain traditional image processing methods (low-pass filtering, Maximum Difference Method, texture analysis, voting algorithms, morphologic filtering, Otsu binarization) on 40 clinically validated retinal images of high resolution (2592×1728 pixels), 386 images of 720×576 resolution, and more than 100 images from STARE database. The obtained results in terms of accuracy are comparable with the best outcomes in the literature, the proposed techniques are implemented as a Windows application writ-

ten in C++ using Microsoft Visual Studio, and for image manipulation and some processing functions the OpenCV library was used.

The next invited article, “Characterization and Pattern Recognition of Color Images of Dermatological Ulcers: a Pilot Study”, written by L.C. Pereyra, S.M. Pereira, Souza, Frade, Rangayyan, and Azevedo-Marques, approaches content-based image retrieval (CBIR) and computer-aided diagnosis (CAD) applied in dermatological ulcers detection and analysis, which is a very difficult task of color image processing and of tissue composition analysis, respectively. Unsupervised automatic segmentation was performed by using Gaussian mixture modeling, and its performance was assessed by computing the Jacard coefficient between the automatically and manually segmented images. A retrieval engine was implemented using the k -nearest-neighbor method, and classification was made by means of a logistic regression. The performance of CBIR was measured in terms of precision of retrieval, with average values of up to 0.617 obtained with the Chebyshev distance, and the average value of correctly classified instances divided by the total number of instances was 0.738. Results were obtained on a database containing 172 dermatologic images with high geometric and intensity resolution, obtained in a clinical environment and annotated by an expert. Even if the obtained segmentation accuracy is not very high, from clinical and educational utility points of view “objective analysis of color images of skin ulcers using the proposed methods might overcome some of the limitations of visual analysis and lead to the development of improved protocols for the treatment and monitoring of chronic dermatological lesions.”

The last three articles are dedicated to some image processing topics useful in research and clinical practice, but which do not approach image segmentation or classification. They refer to image reconstruction, registration and human genome sequencing, respectively.

“A platform for Image Reconstruction in X-ray Imaging: Medical Applications using CBCT and DTS algorithms”, by Kamarianakis, Buliev, Pallikarakis, presents the architecture of a software platform for the purpose of testing and evaluation of reconstruction algorithms in X-ray imaging. The main elements of the platform are classes, re-

lated together in a logical hierarchy. Real world objects can be defined and implemented as instances of corresponding classes. Different image processing routines (e.g. 3D transformations, loading, saving, filtering of images, etc.) have been incorporated in the software tool as class methods, too. The platform is viewed as a basic tool for future investigations of new reconstruction methods in combination with various scanning configurations. The current tests on Reconstruction Techniques Class Library (RTCL) and the Platform for Image Reconstruction in X-ray Imaging (PIRXI) prove the accuracy and flexibility of this new approach for image reconstruction research and algorithms implementation.

Bejinariu, Costin, Rotaru, Luca, Niță, and Lazăr authored the article “Parallel Processing and Bio-inspired Computing for Biomedical Image Registration”, that deals with image transformations aiming at overlaying one or more image sources to a given model by maximizing a similarity measure. Some bio-inspired metaheuristic optimization algorithms, such as Bacterial Foraging Optimization Algorithm (BFOA), Genetic Algorithms (GAs) and Clonal Selection Algorithm (CSA), are compared in terms of registration accuracy and execution time for area-based and feature-based image registration. Normalized correlation (NCC) and normalized mutual information (NMI) are used as similarity measures. Implementation was made on many images from a publicly available database, mainly using MRI brain images with 256×256 pixels and 8 bits/pixels resolutions, without and with “salt & pepper” noise, respectively. In general, BFOA and GAs yielded comparable results in terms of registration accuracy, GAs performed about three times faster than BFOA, and CSA is too slow for feature-based registration and also with lower registration precision. Even the feature-based image registration performs faster, its use for multimodal images is limited by the procedure’s capability to find common and stable features in the images to be registered.

Last but not least, Voina, Pop, Vaida wrote the article “A New Algorithm for Localized Motif Detection in Long DNA Sequences”, that comes from bioinformatics research domain and approaches human genome sequencing, i.e. the identification of the DNA segments

that have a certain biological significance. The study presents a new algorithm optimized for finding motifs in long DNA sequences and some experiments done to evaluate the performance of the proposed algorithm in comparison with other motifs finding algorithms are described. Some optimizations are introduced, that increase detection accuracy and lower the execution time. Thus, the proposed algorithm proved to have a clear advantage among other similar algorithms due to the detection accuracy of the motifs in long DNA sequences, such as those found in the human genome.

In conclusion we can say that the fundamental, engineering and life sciences are all contributing to a remarkable synergy of efforts to achieve dynamic, quantitative (structural or functional) imaging of the body using minimally invasive, non-invasive or even virtual methods. The structural and functional relationships between the cells, tissues, organs and organ systems of the body are being advanced by molecular imaging, and laboratory imaging techniques. With continuing evolutionary progress in biomedical imaging, visualization and analysis, we can fully expect to benefit from new knowledge about life and disease processes, and from new and efficient methods of diagnosis therapy and prevention.

Iași, 30-th of June, 2014

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Brief biography

Prof. dr. eng. Hariton Costin, B.Sc. in Electronics and Telecommunications, Ph.D. in Applied Informatics, is full professor at the University of Medicine and Pharmacy, Faculty of Medical Bioengineering, Iași, Romania, (www.umfiiasi.ro ; www.bioinginerie.ro). Also, he is senior researcher at the Romanian Academy – Iași Branch, Institute of Computer Science, within the Image Processing and Computer Vision Lab, (http://iit.academiaromana-is.ro/personal/h_costin.html). Here his studies are in image processing and analysis by using Artificial Intelligence methods and data fusion.



Competence areas include: medical electronics and instrumentation, biosignal and image processing and analysis, artificial intelligence (soft-computing, bio-inspired algorithms, expert systems), hybrid systems, HCI (human-computer interfaces), assistive technologies, telemedicine/e-health.

Scientific activity can be resumed by about 145 published papers in peer-reviewed journals and conference proceedings, 9 books, 4 book chapters in foreign publishing houses, 3 patents, 2 national awards.

Research activity: 54 research reports; technical manager (within FP5/INES 2001-32316 project) for a telemedicine application (www.euroines.com; „Medcare” project); responsible for the first Romanian pilot telemedical centre in Iași; director for 9 national funded projects in bioengineering and (biomedical) image processing/analysis. He has served as the program committee member of various international conferences and reviewer for various international journals and conferences. Prof. Costin was invited as postdoc researcher at the University of Science and Technology of Lille (France, 2002, in medical imaging), the University of Applied Sciences Jena (Germany, 2013) and had invited talks at international conferences. Prof. Costin is a member of the I.E.E.E./Engineering in Medicine & Biology Society (EMBS) and of other 5 scientific societies.