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Editorial

Special Issue on "Algorithms for Biomedical Image Analysis and Processing"

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Citation: Antonelli, L.; Maddalena, L. Special Issue on "Algorithms for Biomedical Image Analysis and Processing". *Algorithms* **2023**, *16*, 544. https://doi.org/10.3390/a16120544

Received: 6 September 2023
Accepted: 22 November 2023
Published: 28 November 2023

Biomedical imaging is a broad field concerning image capture for diagnostic and therapeutic purposes. Biomedical imaging technologies utilize x-rays (CT scans) [1], magnetism (MRI) [2], sound (ultrasound) [3], radioactive pharmaceuticals (nuclear medicine: SPECT, PET) [4], or light (endoscopy, OCT, light microscopy) [5,6]. Algorithms for processing and analyzing biomedical images are commonly used to visualize anatomical structures or assess the functionality of human organs, point out pathological regions, analyze biological and metabolic processes, set therapy plans, and image-guided surgery [7]. At a different scale, microscopy images are generally produced using light microscopes, which provide structural and temporal information about biological specimens. In the most widely used light microscopy techniques, the light is transmitted from a source on the opposite side of the specimen to the objective lens. On the contrary, fluorescence microscopy uses the reflected light of the specimen [6]. Microscopy imaging requires methods for quantitative, unbiased, and reproducible extraction of meaningful measurements to quantify morphological properties and investigate intra- and inter-cellular dynamics [8]. New technologies have been developed to address this need, such as microscopy-based screening, sequencing, and imaging, with automated analysis (including high-throughput screening and high-content screening) [9], where basic image processing algorithms (e.g., denoising and segmentation) are fundamental tasks.

The large number of applications that rely on biomedical images increases the demand for efficient, accurate, and reliable algorithms for biomedical image processing and analysis, especially with the rising complexity of imaging technologies and the huge amount of images to be processed. This special issue aimed at bringing together both original research articles and topical reviews on the wide area algorithms for biomedical image processing and analysis techniques.

In response to the call for papers, a total of 14 manuscripts were submitted. Out of them, we selected ten submissions to appear in this Special Issue, coming from seven countries in three geographical regions: *America* (Brazil (2), Canada (1)), *Asia* (Indonesia (1), Japan (1)), and *Europe* (Belgium (1), Germany (1), Italy (3)). Two or three experts in the corresponding area have reviewed each submission. The List of Contributions for this Special Issue includes first two reviews and then the other eight published papers in chronological order of publication date, briefly described in the following.

In their review (Contribution 1), Maddalena et al. give an overview of methods, software, data, and metrics for various tasks related to label-free microscopy images, including cell segmentation, event detection and classification, and cell tracking and lineage, providing the reader with a unique source of information, with links for further details.

The review by Conte et al. (Contribution 2) discusses the application of models from polymer physics to understand the machinery underneath the chromosome architecture in the nucleus of the cells. Numerical simulations of the reviewed models are validated against imaging data from multiplexed super-resolution fluorescence in situ hybridization (FISH) imaging for chromatin conformation tracing, which allows unbiased determination of the structural features and their genomic coordinates with high resolution in single cells. This way, they show that this kind of novel data from microscopy can be complemented with quantitative models from physics to understand the mechanisms and function of the genome structure.

Negassi et al. (Contribution 3) afford the problem of automatic data augmentation for semantic image segmentation. They propose an optimal comprehensive method and a sub-optimal one that is computationally less demanding. The performance of these methods is evaluated against four existing annotated datasets for various applications, including crack detection in bridge images, autonomous driving, anomaly detection in cystoscopic medical images, and segmentation of brain electron microscopy images.

In Contribution 4, Rodrigues et al. aim to identify potential brain regions as biomarkers of Autism Spectrum Disorder (ASD) severity. Imaging data come from pre-processing the brain's resting-state functional magnetic resonance imaging (rs-fMRI). Classification of subjects affected by different autism grades is carried out using SVM to select the groups of atlas ROIs (Regions of Interest) that lead to the highest accuracy.

In Contribution 5, Li et al. consider the problem of classifying low and high risk of early prostate cancer. Imaging data consists of DWI and T2 sequences from multi-parametric magnetic resonance imaging (mp-fMRI) aligned and cropped to the prostate region, producing 3D sequences to be fed to a 3D-CNN. The experiments are carried out using various combinations of the input data and different 3D-CNN models and analyse the cancer response maps produced from the last convolution layer of the network.

Contribution 6 by Carvalho et al. affords the problem of classifying healthy and tumor cases in microphotograph images of rats' liver tissue. They consider different texture features and their fusion, combined with three traditional machine learning classifiers.

In Contribution 7, Anam et al. analyze the effect of the iterative application of bilateral filtering to Computed Tomography images. The experiments are carried out on homogeneous phantom images scanned with different tube currents to investigate the impact on noise texture and spatial resolution and on anthropomorphic phantom images of the head to simulate clinical scenarios.

Franchini et al. (Contribution 8) propose an adaptive early stopping technique for optimising the training phase of neural networks for image classification, reducing the required epochs. Numerical experiments are carried out using different CNN models on the standard CIFAR-100 database and two biomedical databases obtained by computed tomography, involving various numbers of classes.

In Contribution 9, Huang et al. present in their work, a derivative-free optimization (DFO) framework that allows direct and model-based search methods in a single algorithm, analyzing their optimal combinations. They propose a smart version of the method that dynamically and adaptively chooses the search strategies. These methods are applied for the design of a solid-tank fan-beam optical CT scanner.

Contribution 10 by Ghafari et al. proposes a clinical validation of recent stent imaging methods. The imaging data consists of coronary angiographies post-processed by two enhanced stent imaging methods, one vendor-specific and the other independent from the angiographic system. The experiments are devoted to comparing the visualization obtained by the two methods in terms of image quality as perceived by expert cardiologists and to quantitatively analyze the stent expansion measurements achieved with the independent method.

As the editors, it is our pleasure to thank the editorial staff of the journal Algorithms for their helpful cooperation during the preparation of the Special Issue and of this volume. We would also like to thank all reviewers for their thorough and timely reports on the reviewed papers and all the authors for submitting many interesting works from a broad spectrum in the field of interest of this volume.

Acknowledgments: This work has been carried out also under the PRIN 2022 project $P2022PMEN2$ and within the activities of the authors as members of the INdAM Research group GNCS and the ICAR-CNR INdAM Research Unit.

Conflicts of Interest: The authors declare no conflict of interest.

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