IARIA

BIOTECHNO 2024

The Sixteenth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies

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BIOTECHNO 2024 Editors

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BIOTECHNO 2024

Foreword

The Sixteenth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies (BIOTECHNO 2024), held between March 10 – 14, 2024, covered these three main areas: bioinformatics, biomedical technologies, and biocomputing.

Bioinformatics deals with the system-level study of complex interactions in biosystems providing a quantitative systemic approach to understand them and appropriate tool support and concepts to model them. Understanding and modeling biosystems requires simulation of biological behaviors and functions. Bioinformatics itself constitutes a vast area of research and specialization, as many classical domains such as databases, modeling, and regular expressions are used to represent, store, retrieve and process a huge volume of knowledge. There are challenging aspects concerning biocomputation technologies, bioinformatics mechanisms dealing with chemoinformatics, bioimaging, and neuroinformatics.

Biotechnology is defined as the industrial use of living organisms or biological techniques developed through basic research. Bio-oriented technologies became very popular in various research topics and industrial market segments. Current human mechanisms seem to offer significant ways for improving theories, algorithms, technologies, products and systems. The focus is driven by fundamentals in approaching and applying biotechnologies in terms of engineering methods, special electronics, and special materials and systems. Borrowing simplicity and performance from the real life, biodevices cover a large spectrum of areas, from sensors, chips, and biometry to computing. One of the chief domains is represented by the biomedical biotechnologies, from instrumentation to monitoring, from simple sensors to integrated systems, including image processing and visualization systems. As the state-of-the-art in all the domains enumerated in the conference topics evolve with high velocity, new biotechnologes and biosystems become available. Their rapid integration in the real life becomes a challenge.

Brain-computing, biocomputing, and computation biology and microbiology represent advanced methodologies and mechanisms in approaching and understanding the challenging behavior of life mechanisms. Using bio-ontologies, biosemantics and special processing concepts, progress was achieved in dealing with genomics, biopharmaceutical and molecular intelligence, in the biology and microbiology domains. The area brings a rich spectrum of informatics paradigms, such as epidemic models, pattern classification, graph theory, or stochastic models, to support special biocomputing applications in biomedical, genetics, molecular and cellular biology and microbiology. While progress is achieved with a high speed, challenges must be overcome for large-scale bio-subsystems, special genomics cases, bio-nanotechnologies, drugs, or microbial propagation and immunity.

We take here the opportunity to warmly thank all the members of the BIOTECHNO 2024 Technical Program Committee, as well as the numerous reviewers. The creation of such a high quality conference program would not have been possible without their involvement. We also kindly thank all the authors who dedicated much of their time and efforts to contribute to BIOTECHNO 2024.

Also, this event could not have been a reality without the support of many individuals, organizations, and sponsors. We are grateful to the members of the BIOTECHNO 2024 organizing committee for their help in handling the logistics and for their work to make this professional meeting a success.

We hope that BIOTECHNO 2024 was a successful international forum for the exchange of ideas and results between academia and industry and for the promotion of progress in the fields of bioinformatics, biocomputational systems and biotechnologies.

We are convinced that the participants found the event useful and communications very open. We also hope that Athens provided a pleasant environment during the conference and everyone saved some time for exploring this beautiful city

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Table of Contents

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***Abstract*—Nowadays, automatic deep learning-based systems in medical fields play pivotal role in aiding experts with diagnosing diseases through the analysis of medical images and signals. LungQuant, a sophisticated automatic deep learning-based system, specializes in the segmentation of lung structures and lesions. The algorithm comprises two main phases of lung segmentation and lesion segmentation of COVID-19 cases. This study meticulously evaluates the performance of the LungQuant algorithm in its initial phase, leveraging diverse datasets, namely Luna-16 and COVID-19 CT scans. LungQuant demonstrates robust performance in lung segmentation with a Dice Coefficient Similarity (DCS) average of 90% and 88% with Luna-16 and COVID-19 ct datasets, respectively. The study explores various pre-processing techniques, including Anisotropic diffusion and Contrast Limited Adaptive Histogram Equalization (CLAHE), to understand their impact on the algorithm's initial phase. While the outcomes show promising results, future enhancements may include advanced deep networks and further refinement of preprocessing methodologies. The study contributes insights into the practical considerations of noise reduction and edge preservation, underscoring the importance of a stable initial phase in ensuring overall algorithmic efficacy.**

***Index Terms*—LungQuant; Lung Segmentation; COVID-19; Lesion Segmentation**

I. INTRODUCTION

Lung cancer is a serious global health issue affecting both men and women. Computer-Aided Diagnosis (CAD) systems play a crucial role in collaborating with radiologists to detect lung cancer early. This research evaluates LungQuant, an automated system able to automatically segment lung parenchima and lesions in COVID-19 patients [1]. In the realm of lung nodule detection, challenges arise, such as dealing with different intensities and imbalanced target data. Since nodules make up a small part of CT images, advanced deep learning modules are needed for accurate detection. Medical images, with their intricate details, can make neural networks work harder and potentially lead to errors [2]. To make neural networks work efficiently, the initial step involves removing irrelevant parts of the data, focusing on the Region of Interest (ROI). In Lung CT data, segmenting lung parenchyma helps narrow down the search region for nodules. The next phase includes implementing the nodule detection task. This paper introduces and evaluates LungQuant, emphasizing the early stages of the system. It looks into segmenting the ROI from the rest of the image using different datasets and preprocessing methods to show LungQuant's performance in various scenarios. Identifying the ROI is crucial in many deep learning-based methods, with later stages targeting specific abnormalities like nodules or lesions. The rest of this paper is organized as follows. Section II describes the structure of LungQuant. Section III illustrate results and experiments have been applied on LungQuant.

II. HANDS ON LUNGQUANT

To provide a comprehensive understanding, a detailed exploration of LungQuant is imperative. The algorithm is structured into two main phases, with the initial phase focusing on ROI identification, followed by the second phase centered on lung lesion detection. The first phase integrates two distinct deep neural networks: CNN (Convolutional Neural Network) and U-net. The CNN, inspired by Alex-Net, is specifically tailored as the Bounding Box Network (BB-Net). In its original implementation, BB-Net predicts two points in the 3D space of lung CT, forming a cube around the lung. Subsequently, the predicted cube is extracted from the entire CT volume to facilitate the first U-net in accurately segmenting the lung. It's noteworthy that BB-Net was introduced in the second version of the algorithm to enhance the accuracy of the initial phase. The U-net used in this study has undergone slight modifications compared to the original version. It has been fine-tuned using a dataset encompassing both lung CTs with and without COVID-19, aiming to improve the network's robustness and generalization capabilities. In the second phase, another U-net, exclusively fed by the lung portion of CT scans,

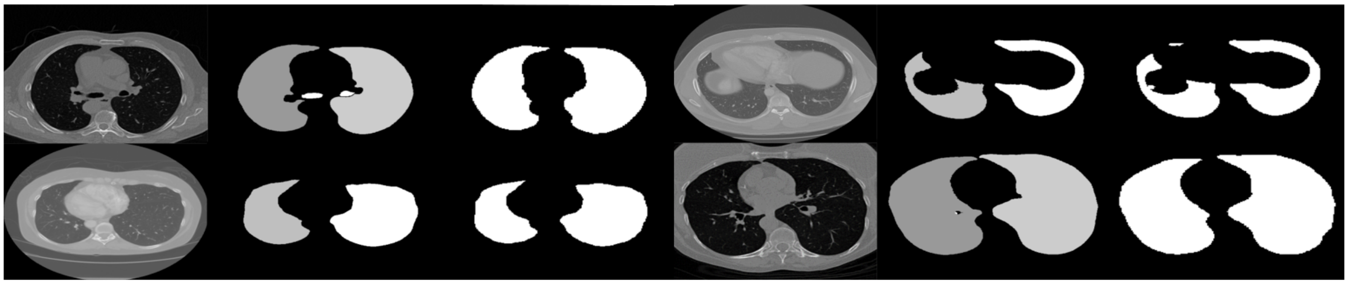

Figure 1. Lung Segmentation samples in columns of Original CT, Mask and Prediction.

is employed to detect lesions [3]. The initial phase begins with pre-processing techniques, standardizing the data range to [0, 1], and adjusting Hounsfield Unit values to [-1000, 1000] within the first U-net. This adjustment enhances lung parenchyma detection, while the Hounsfield Unit is set to [-1000, 300] in the second U-net. Additionally, the input data, characterized by a variable number of slices, is resampled to dimensions of 200 × 150 × 100 for consistency. Following pre-processing, the data is input into BB-net, featuring five Conv 3D layers, three max-pooling layers, and a final layer with six nodes predicting (x, y, z) coordinates for two points, forming a bounding box around the lung. Notably, BB-net is trained with augmented data to accommodate variations in CT configurations across datasets. Furthermore, in the second version of LungQuant, an additional post-processing step has been introduced. This step involves the application of watershed transformation to separate the two lobes of lung parenchyma and eliminate noise from the results.

III. RESULTS

In the original paper, the authors utilized the COVID-19-CT-Seg benchmark dataset and achieved a DCS of 0.96 ± 0.01%. However, in this paper, the evaluation of lung segmentation is extended to two different datasets: Luna-16 and COVID-19 CT scans. The Luna-16 dataset comprises CT scans from 888 patients with masks for lung segmentation. In contrast, the COVID-19 CT scans consist of CT images from 20 patients, including 10 with positive COVID-19 and 10 with negative COVID-19 cases. Luna-16 stands as a benchmark challenge for lung and nodule segmentation, serving as a rigorous evaluation for the lung segmentation performance of LungQuant in its initial phase. LungQuant attained a substantial DCS average of 90% in the lung segmentation task. It is noteworthy, however, that the algorithm yielded slightly lower results in COVID-19 CT scans dataset based on DCS, achieving an average of 88% when compared against the provided ground truth. Figure 1 illustrate performance visually with different type of imaging configuration of lung CTs. This performance metric serves as a testament to the algorithm's efficacy in addressing diverse datasets, underscoring its potential for robust and versatile application within the domain of lung segmentation. Furthermore, this result positions the algorithm as a promising candidate for applications that demand reliability across varied data sources. Nevertheless, in future steps, the utilization of advanced and more complex deep networks holds potential to further enhance the robustness of the results. Additionally, we explore various pre-processing techniques to determine the impact of noise during the implementing of LungQuant's initial phase. Given that the outcomes of the first phase directly feed into the second phase, any errors or deficiencies in the segmentation process can influence the data for subsequent phases. Therefore, the stability and robustness of the first section are pivotal factors in the overall efficacy of the algorithm. firstly, we tested Anisotropic diffusion, which is a type of image filtering technique that is used to remove noise from an image while preserving the edges. It differs from traditional smoothing techniques, such as Gaussian smoothing or mean filtering because it takes into account the orientation of the edges in the image. Results illustrate low efficiency in the result specially with blurring the details nodule detection section can be negatively affected. Furthermore, CLAHE [4] serves as a widely adopted pre-processing technique to address noise and address varying intensity concerns in medical images. It is an image processing technique that enhances contrast by redistributing pixel intensities, maximizing overall brightness, and emphasizing image details.

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