

# Special Issue on Novel Applications of Artificial Intelligence in Medicine and Health

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## 1. Introduction

Artificial Intelligence (AI) is one of the big hopes for the future of a positive revolution in the use of medical data to improve clinical routine and personalized medicine. The deep complexity of the learning models allows access to the information not obvious or possible to use by humans, with the opportunity to capture patterns in the clinical data. Those approaches can originate better support systems for clinical decisions and more adequate treatment plans. AI has been used in all areas of the medical field, from cardiovascular disease, immune system disease, cancer detection, or other healthcare application and services. The current special issue was dedicated to innovative solutions of digital technologies that transform healthcare systems for the benefit of patients and their caregivers, clinicians, and the economy as a whole. The papers that compose this special issue cover a part of some interesting developments in healthcare.

## 2. Contributions

Due to the general application of AI, this special issue reflects the broad spectrum with very different works, where AI for healthcare improvement is the common ground between them.

The healthcare systems should be prepared to give assistance during the most extreme conditions, such as emergencies and post-disaster situations; however, these conditions present other kinds of challenges and require specific solutions to deal with them. Drones have been used in several applications and can be efficient to provide essential treatments to patients and victims during those exceptional conditions. The work “*An Efficient Greedy Randomized Heuristic for the Maximum Coverage Facility Location Problem with Drones in Healthcare*” proposed a heuristic named the maximum coverage greedy randomized heuristic (MCGRH) to assign patients to the closest opened facility with the capacity to serve them [1], and achieve high coverage of patients (more than 80% on average) within a very fast processing time (less than 1 s on average). Other possible solutions can be explored based on this problem that can be used for other healthcare applications.

Human immunodeficiency virus (HIV) is still responsible for the death of millions of lives globally. Recently, peptides that have an anti-HIV-1 activity showed promising results in reducing the effects of AIDS. The work “*Rough Set Based Classification and Feature Selection Using Improved Harmony Search for Peptide Analysis and Prediction of Anti-HIV-1 Activities*” proposed a methodology to predict the peptides with an anti-HIV-1 activity using effective feature selection and classification algorithms [2] that achieved a high predictive accuracy of 96% and understanding what essential attributes of an amino acid sequence determine if the treatment is effective against the virus.

Risk stratification is a crucial step in the clinical assessment and the follow-up decision. Oncological patients submitted to radiotherapy and/or chemotherapy have a higher risk



**Citation:** Pereira, T.; Cunha, A.; Oliveira, H. P. Special Issue on Novel Applications of Artificial Intelligence in Medicine and Health. *Appl. Sci.* **2023**, *13*, 881. <https://doi.org/10.3390/app13020881>

Received: 31 December 2022

Accepted: 3 January 2023

Published: 9 January 2023



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of cardiovascular events. Coronary artery calcification (CAC) and muscle mass evaluation have shown diagnostic and prognostic power for cancer patients, and they can be quantitatively evaluated using whole-body positron emission tomography (PET)/computed tomography (CT) which is a standard medical proceeding of patients with malignancy. The work *“Quantification of Coronary Artery Atherosclerotic Burden and Muscle Mass: Exploratory Comparison of Two Freely Available Software Programs”* made an exhaustive and objective comparison of two semiautomatic and free independent software programs that can be applied to the medical image to measure both CAC score and muscle mass [3], and concluded that, for the measurement of the two parameters, both softwares seem to be interchangeable.

Lung cancer is the type of cancer that is still leading the mortality among cancer death, and for this reason, several works are dedicated to this disease, which is clear in this special issue [4,5]. The decision support systems could help clinicians with early detection and better treatment plans. Usually, those systems benefit from the selection of the region of interest, reducing the unuseful information to be processed. The segmentation of the anatomic structures comprises a fundamental step of the preprocessing of medical imaging. This task is difficult due to the variability that can be found in the human body, but also by the heterogeneities induced by the different levels of severity and, sometimes, their co-occurrence. The work *“Lung Segmentation in CT Images: A Residual U-Net Approach on a Cross-Cohort Dataset”* designed on a cross-cohort dataset of CT and uses a combination of two structures, a U-Net and a ResNet34 for lung segmentation [4]. The cross-cohort dataset allows the development of a robust segmentation model even for the most difficult pathological cases. On the other hand, with the development of target therapies, there is a need for a genotype characterization of lung cancer. The work *“Machine Learning and Feature Selection Methods for EGFR Mutation Status Prediction in Lung Cancer”* was dedicated to studying the use of machine learning-based approaches to detect the mutational status of the most relevant oncogene for lung cancer, Epidermal Growth Factor Receptor (EGFR) on the CT images [5]. The analysis was performed using the lungs where the nodules were located based on the relevance of the region for the clinical assessment. The combination of multiple feature selection techniques with several ML methods showed that it can be possible to use imaging information contained in the CT to predict EGFR mutational status of lung cancer.

### 3. Conclusions and Future Needs

This special issue presented works that generated opportunities for a great improvement in the healthcare for oncological patients due to the measurements of cardiovascular risk or the characterization of the genotype of cancer. However, there is still a need for larger datasets to have more confidence in the results and validate the robustness of the solutions created.

The peptide therapeutic field is of great importance for the discovery of new drugs to treat viral infections. ML can help to identify the essential attributes of an amino acid sequence, which is effective against the virus and represents a valuable resource for the development of novel therapies to combat viral infection.

Healthcare systems should be prepared to work and assist patients in emergency situations, and solutions for those occasions must deserve deep attention and resources for strong and confident development.

**Funding:** This work is financed by the ERDF—European Regional Development Fund through the Operational Programme for Competitiveness and Internationalisation—COMPETE 2020 Programme and by National Funds through the Portuguese funding agency, FCT—Foundation for Science and Technology Portugal within project POCI-01-0145-FEDER-030263.

**Acknowledgments:** Thanks to all the authors and peer reviewers for their valuable contributions to this Special Issue ‘Novel Applications of Artificial Intelligence in Medicine and Health’. We would also like to express our gratitude to all the staff and people involved in this Special Issue.

**Conflicts of Interest:** The author declares no conflict of interest.

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