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Preface

Special issue: informatics & data-driven medicine-2021

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Abstract: Modern medical diagnosis, treatment, or rehabilitation problems of the patient reach completely different levels due to the rapid development of artificial intelligence tools. Methods of machine learning and optimization based on the intersection of historical data of various volumes provide significant support to physicians in the form of accurate and fast solutions of automated diagnostic systems. It significantly improves the quality of medical services. This special issue deals with the problems of medical diagnosis and prognosis in the case of short datasets. The problem is not new, but existing machine learning methods do not always demonstrate the adequacy of prediction or classification models, especially in the case of limited data to implement the training procedures. That is why the improvement of existing and development of new artificial intelligence tools that will be able to solve it effectively is an urgent task. The special issue contains the latest achievements in medical diagnostics based on the processing of small numerical and image-based datasets. Described methods have a strong theoretical basis, and numerous experimental studies confirm the high efficiency of their application in various applied fields of Medicine.

Keywords: data-driven medicine; small data; machine learning; optimization; predictive modeling; classification; small data approach

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1. Introduction

This special issue covers new science-intensive approaches in Computer Science that solve different tasks in Medicine. The solid theoretical and practical papers have been invited for submission.

Special issue's proposed topics include:

- Big Data and IoT in Medical Applications;
- Small Data Approach in Medicine;
- AI-based data augmentation techniques;
- Ensemble learning for case of Small and Big data processing;
- Surrogating methods for data augmentation;
- Statistical learning in precision medicine;
- Medical and Biomedical Image Processing;
- Deep Learning Models in Healthcare and Biomedicine;
- Machine Learning Approaches for Medicine;
- Bioinformatics for Healthcare Applications;
- Complex Health Monitoring Systems;
- Decision fusion for healthcare applications;
- Semi-supervised learning applied to small data samples;
- Graph signal processing in big data contexts;
- IT-enabled Healthcare Services;
- Analysis and Prediction for Covid'19 Data.

The central part of this special issue was dedicated to the best research presented at the 4th International Conference on Informatics & Data-Driven Medicine (IDDM-2021) [1]. This conference is indexed by Scopus, Web of Science, and dblp databases. In addition, according to the CORE list of conferences 2021, it has ranked C.

We have obtained more than 34 submissions from Ukraine, Poland, China, Brazil, and India scientists and medical experts. After a careful review process, only eight papers were accepted for publication in this special issue.

2. An overview of the published papers

The authors in [2] consider the problem of medical diagnosis based on images in the dermatology domain. They have proposed a solution for solving the image segmentation task for their further identification. This paper improves the vector-difference method for spectral-statistical texture segmentation. It significantly improves the quality of segmented dermatological images in automated medical diagnostic systems. The results of modeling the proposed approach for the segmentation of dermatological images of the psoriatic disease have shown a significant increase in the accuracy of the automated diagnostic system.

In [3], the authors considered the pattern recognition task. The peculiarity of this study is that the authors considered a small set of images. The problem of processing small datasets was solved by modifying the generalized neo-fuzzy system. Experimental studies on the effectiveness of the proposed approach and comparisons with existing methods have shown the high accuracy of its work in a limited amount of data for training.

In [4], it considers a complex problem of medical diagnostics. The authors investigate the difference between diagnosing major depressive disorder and individuals' mental illness. The importance of this problem lies in the timely determination of a person's depressed state due to, for example, the loss of a loved one so as not to inadvertently recognize him as mentally ill. The authors propose an approach based on the combined use of Kohonen maps and guidelines for major depressive disorder diagnosing. Experimental studies have demonstrated the adequacy of the constructed model in terms of the selection of appropriate clusters in the studied cohort.

In [5], the problem of effective processing of short tabular medical datasets was considered. The authors have developed an improved method of data augmentation based on the mega-trend-diffusion technique. Although this method is actively used in many applied tasks, its main problem is the significant deformation of synthetic data in the case of anomalies in the initial training dataset. To avoid this shortcoming, the authors proposed a new distance-based mega-trend-diffusion technique. Experimental modeling on two short sets of medical data in solving both classification and regression tasks showed the developed method's high efficiency compared to the existing.

The authors of [6] also consider the problem of processing short datasets. In this case, the task was to predict severity risk assessment and post-COVID rehabilitation duration for SARS-CoV-2 patients. To solve it, the authors proposed the use of meta-learning techniques. The technological solution is a new three-level stacking ensemble model based on both the principles of meta-learning and the use of associative rules. Experimental modeling of the developed ensemble demonstrated high accuracy of its work in solving the stated task compared to analogs.

It is devoted to studying the relationship between biomarkers for the prognosis of different cancer types in [7]. The authors analyzed the MACC1 expression using the R environment for efficiency in the prediction tasks. A number of known datasets were used to test the proposed approach. Experimental studies have shown the high efficiency of using the proposed method in predicting cancer. In particular, MACC1 can be used to predict the immune response in cancer patients.

It is devoted to the problem of identifying lncRNAs that affect the progression of colorectal cancer in [8]. The importance of solving this problem determines the possibility of effective prediction of the degree of tumor development and, accordingly, selecting an effective strategy for immunotherapy. The authors investigated the existing dataset using the ranking method and comparison of paired gene expression in colorectal cancer. The experiments showed that the studied model could be used to develop an effective immunotherapy strategy to treat the above disease.

In [9], the authors deal with bio-inspired computing tasks. They have improved the mathematical model of the shuffled frog leap algorithm with various modifications. The proposed approach will provide a significantly better result in solving the problem than the primary method. The authors also improved the approach to solve the transmission expansion planning problem based on the results obtained. Experimental modeling on a well-known dataset demonstrated the high efficiency of the developed approach in solving the stated task.

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