



Artificial Intelligence in Medicine AIME 2015

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Artificial Intelligence in Medicine AIME 2015

This issue of Artificial Intelligence in Medicine includes a selection of papers presented at the Fifteenth Conference on Artificial Intelligence in Medicine (AIME 2015), which was held in Pavia, Italy, from June 17th to 20th, 2015. For its fifteenth edition, AIME was brought back to the city where the first meeting of the European researchers who were applying artificial intelligence (AI) techniques to the medical domain had been organized 30 years earlier. The AIME Society was established just after that first meeting in Pavia, and a cycle of conferences held every two years (the AIME conferences) started in 1987. Since then, these conferences have been an opportunity to witness the most innovative research methodologies and applications building up the state of the art in the field of AI research in biomedicine and health.

The program for AIME 2015 was prepared by the Scientific Chair John H. Holmes (University of Pennsylvania), the Local Organizing Chairs, Riccardo Bellazzi and Lucia Sacchi (University of Pavia), and the AIME 2013 Scientific Program Chair, Niels Peek (University of Manchester). Authors were invited to submit original contributions regarding the development of theory, techniques, and applications of AI in biomedicine and health, including the exploitation of AI approaches to molecular medicine and biomedical informatics and to organisational aspects of healthcare. Besides the traditional tracks for papers, the conference had a specific theme on the challenge of Big Data in biomedical applications.

The conference had two keynote lectures, which dealt with relevant topics in current biomedical informatics research. In his keynote titled “The Physics of the Medical Record”, George Hripcsak (Columbia University) addressed the re-use of data collected in the electronic health record (EHR) for research, focusing on the importance of understanding the temporal dimension in such data. Goran Nenadic (University of Manchester) presented “Contextualization of Biomedical Knowledge through Large-scale Processing of Literature, Clinical Narratives and Social Media”, which focused on mining clinical narratives through natural language processing (NLP). His talk highlighted the value of the information that could be drawn from such source of data, stressing the opportunity of using also novel sources, such as social media for health.

AIME 2015 hosted the fifth edition of the AIME Doctoral Consortium, organized by Niels Peek, where six PhD students had the opportunity to present their work and preliminary results. A scientific panel consisting of experienced researchers provided constructive feedback to the students in an informal atmosphere. In addition, two half-day tutorials took place before, and three workshops took place after, the main programme of the conference.

The main programme received 99 submissions coming from 25 countries, including five from outside Europe. All papers were peer-reviewed by experts from the Program Committee with the support of additional reviewers. At the end of the review process, 19 long papers and 24 short papers were accepted. Each long paper was presented in a 25-minute oral presentation during the conference. Each short paper was presented in a 5-minute presentation and by a poster. The papers were organized according to their topics in the following main themes: Data Mining and Machine Learning; Knowledge Representation and Guidelines; Prediction in Clinical Practice; Process Mining and Phenotyping; Temporal Data Mining; Text Mining; Uncertainty and Bayesian Methods.

Among the accepted full papers, those that scored best during the conference review process were considered suitable for publication in this issue of Artificial Intelligence in Medicine. Authors of these papers were invited to submit a revised and extended version of their contributions, which underwent a review and revision process in addition to that used for the AIME conference. As a result of this process, seven papers were accepted. In the following we present a brief summary of these papers.

The paper by Forestier , *et al.* [1], links two important topics: process modelling and prediction. It focuses on the definition of an automatic methodology to predict the next action a surgeon is going to perform

during surgery. The prediction of the next action is based on a technique involving the alignment of sequences of activities through dynamic time warping, and a strategy to make a prediction only in the case where there is enough confidence to perform it. The evaluation of the methodology on two different datasets shows high prediction accuracies when compared with state of the art approaches. These results are particularly helpful when coupled to the advances in assisted surgery technologies. Their promise is to improve the workflow during surgical procedure, providing useful real-time information to the surgical team (e.g., nurses, anaesthetist, junior surgeon), while allowing the surgeon to focus on more demanding tasks, thus reducing surgical errors and improving efficiency.

Nissim, *et al.* [2], present a study on inter and intra labellers variability for Active Learning (AL), considering experts in the clinical domain. The work is focused on the use of the data collected in EHRs for defining phenotypes, and on predictive models. In analogy to what is reported in Forestier paper, where predictions are performed only when needed, the AL strategies presented in this paper are aimed at requiring experts to label only the situations that are discriminative, to avoid asking the experts to classify too many examples. The authors evaluate one passive and several AL methods, fed by labels provided by seven experts. They analyse the variance of the learning curves of the considered algorithms for all the labellers. Through this analysis, the authors demonstrate that using AL techniques significantly reduces intra-labeller and inter-labeller variance in the performance of the induced models in the training phase.

Tucker, *et al.* [3], deal with the problem of creating longitudinal models of disease progression using large cross-sectional datasets and longitudinal studies. In this context, they investigate the advantages of using a sample of longitudinal data to calibrate the temporal models obtained from cross-sectional studies through the technique of pseudo time-series. Their studies on simulated data and on data collected in a real application on glaucoma progression show that using a relatively small number of time series can dramatically improve the quality of the disease model obtained with pseudo time-series, given that the cross-sectional dataset is large enough. These results have a potential in clinical studies planning, as smaller longitudinal studies, which usually involve higher costs, could be designed while taking advantage from the already available large cross-sectional evaluations.

Pota, *et al.* [4], consider the problem of timely prediction of possible toxicity that might arise during radiotherapy for head-and-neck cancer treatment. They consider parotid shrinkage and xerostomia as symptoms of toxicity. Early detection of these two conditions could result in an adjustment of the treatment schedule to avoid the risk of toxicity and complications. To address the classification problem, the authors extract and integrate features from multiple sources, including clinical, dosimetric, and imaging data. The algorithm selected for classification is an approach based on statistics and fuzzy logic, the likelihood-fuzzy analysis (LFA). This technique allows building simple univariate models, which are then automatically combined to extract a multivariate model including the best features; known risk factors and novel predictors are then extracted by the developed models. Interestingly, the highest levels of accuracy were reached when considering variables coming from all the data sources, and the extraction of accurate predictors from the analysis of CT images is a particularly novel result.

Sadikov, *et al.* [5], designed a decision support system for the long-term monitoring and the management of patients with Parkinson disease. The system is based on machine learning algorithms (logistic regression, Naïve Bayes, Random Forests, and support vector machines), which are used to recognize variations in the spirographic patterns drawn by patients on their smartphones, and consequently detect possible worsening of their condition. The paper addresses the specific problem of differentiating between states of bradykinesia and dyskinesia, and of creating a visual aid to guide neurologists in the interpretation of the algorithms results. The discrimination accuracy of the classifiers was good, reaching AUCs of over 90%, and allowing the identification of the most predictive features to distinguish between the two behaviors. The clinicians who were asked to use the visualization tool judged it useful. Besides the good evaluation results, this system is an interesting example of the importance of telemedicine when used for remote monitoring of chronic diseases. In addition, it highlights the potentials offered by a closer control of patients in delaying

the worsening of the disease thanks to immediate interventions that wouldn't be possible by assessing patients only on periodical encounters.

The paper by Jiang, *et al.* [6], tackles the problem of finding similarities among user profiles derived from online health social websites. Health social websites are modelled as heterogeneous information networks, built by mining the free text extracted from the health forums. Different similarity measures are defined, which rely both on the network structure and on the messages content, to find similar users in such network. This is potentially very useful to help patients finding the support they need from similar subjects, rather than relying on the website search function only. The authors demonstrate that the use of different similarity metrics can help to capture different user behaviours (e.g. active vs inactive users).

The paper by Zamborlini, *et al.* [7], finally, addresses the topic of recommendations interaction in multimorbidity patients followed by guideline-based clinical decision support systems. The problem is addressed by defining a specific model for knowledge formalization, the TMR model, which, if used for recommendation modelling, allows for the automatic calculation of the interaction among the recommendations, independently of the guideline. This can be done thanks to a set of rules for detecting interactions, which are independent both from the specific interactions and the guidelines. The evaluation of the framework is presented on a case study related to the recommendation of exercise therapy for women in the early stages of breast cancer treatment. In the process of prescribing and administering the exercise therapy, the physiotherapist has to take into account the potential side effects of the chemotherapy, possibly adjusting the frequency and intensity level of the activity accordingly. The experts considered that these identified interactions provide correct and relevant alerts to cope with the need for adaptation of exercise therapy.

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