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Predictive Intelligence in Medicine


Third International Workshop, PRIME 2020
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Proceedings

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Preface

It would constitute a stunning progress in medicine if, in a few years, we contribute to engineering a predictive intelligence, able to predict missing clinical data with high precision. Given the outburst of big and complex medical data with multiple modalities (e.g., structural magnetic resonance imaging (MRI) and resting function MRI (rsfMRI)) and multiple acquisition timepoints (e.g., longitudinal data), more intelligent predictive models are needed to improve diagnosis of a wide spectrum of diseases and disorders while leveraging minimal medical data. Basically, the predictive intelligence in medicine (PRIME) workshop primarily aims to diagnose in the earliest stage using minimal clinically non-invasive data. For instance, PRIME would constitute a breakthrough in early neurological disorder diagnosis as it would allow accurate early diagnosis using multimodal MRI data (e.g., diffusion and functional MRIs) and follow-up observations all predicted from only T1-weighted MRI acquired at baseline time point.

Existing computer-aided diagnosis methods can be divided into two main categories: (1) analytical methods and (2) predictive methods. While analytical methods aim to efficiently analyze, represent, and interpret data (static or longitudinal), predictive methods leverage the data currently available to predict observations at later time points (i.e., forecasting the future) or predicting observations at earlier time points (i.e., predicting the past for missing data completion). For instance, a method which only focuses on classifying patients with mild cognitive impairment (MCI) and patients with Alzheimer's disease (AD) is an analytical method, while a method which predicts if a subject diagnosed with MCI will remain stable or convert to AD over time is a predictive method. Similar examples can be established for various neurodegenerative or neuropsychiatric disorders, degenerative arthritis, or in cancer studies, in which the disease/disorder develops over time.

Following the success of the first two editions of PRIME MICCAI in 2018 and 2019, the third edition of PRIME 2020 aims to drive the field of 'high-precision predictive medicine,' where late medical observations are predicted with high precision, while providing explanation via machine and deep learning and statistically, mathematically, or physically-based models of healthy, disordered development and aging. Despite the terrific progress that analytical methods have made in the last 20 years in medical image segmentation, registration, or other related applications, and efficient predictive intelligent models and methods are somewhat lagging behind. As such predictive intelligence develops and improves – and this is likely to do so exponentially in the coming years – it will have far-reaching consequences for the development of new treatment procedures and novel technologies. These predictive models will begin to shed light on one of the most complex healthcare and medical challenges we have ever encountered, and, in doing so, change our basic understanding of who we are.

What are the key challenges we aim to address?

The main aim of PRIME MICCAI is to propel the advent of predictive models in a broad sense, with application to medical data. The workshop accepted 8 to 12-page papers describing new cutting-edge predictive models and methods that solve challenging problems in the medical field. We envision that the PRIME workshop will become a nest for high-precision predictive medicine, one that is set to transform multiple fields of healthcare technologies in unprecedented ways. Topics of interests for the workshop included, but were not limited to, predictive methods dedicated to the following topics:

- Modeling and predicting disease development or evolution from a limited number of observations
- Computer-aided prognostic methods (e.g., for brain diseases, prostate cancer, cervical cancer, dementia, acute disease, neurodevelopmental disorders)
- Forecasting disease or cancer progression over time
- Predicting low-dimensional data (e.g., behavioral scores, clinical outcome, age, gender)
- Predicting the evolution or development of high-dimensional data (e.g., shapes, graphs, images, patches, abstract features, learned features)
- Predicting high-resolution data from low-resolution data
- Prediction methods using 2D, 2D+t, 3D, 3D+t, ND, and ND+t data
- Predicting data of one image modality from a different modality (e.g., data synthesis)
- Predicting lesion evolution
- Predicting missing data (e.g., data imputation or data completion problems)
- Predicting clinical outcome from medical data (e.g., genomic, imaging data, etc.)

Key Highlights

This workshop mediated ideas from both machine learning and mathematical/statistical/physical modeling research directions in the hope of providing a deeper understanding of the foundations of predictive intelligence developed for medicine, as well as an understanding of where we currently stand and what we aspire to achieve through this field. PRIME MICCAI 2020 featured a single-track workshop with keynote speakers with deep expertise in high-precision predictive medicine using machine learning and other modeling approaches – which are believe to stand in opposition. PRIME 2020 ran virtually and keynote talks were live streamed this year due to the COVID-19 pandemic. Pre-recorded videos of accepted papers and keynote presentations were posted on the PRIME web page¹. Eventually, this will increase the outreach of PRIME publications to a broader audience while steering a wide spectrum of MICCAI publications from being ‘only analytical’ to being ‘jointly analytical and predictive.’

We received a total of 20 submissions. All papers underwent a rigorous double-blinded review process by at least 2 members (mostly 3 members) of the

¹ <http://basira-lab.com/prime-miccai-2020/>.

Program Committee composed of 27 well-known research experts in the field. The selection of the papers was based on technical merit, significance of results, and relevance and clarity of presentation. Based on the reviewing scores and critiques, all but one of the PRIME submissions were scored highly by reviewers, i.e., all had an average score of above the acceptance threshold.

Diversity and **inclusion** was one of main focuses of PRIME MICCAI workshop. This year we were able to have a gender-balanced Organizing Committee. We also promoted gender balance and geographic diversity in the Program Committee. The authors of the accepted PRIME papers were affiliated with institutions in the four continents: Africa, Europe, America, and Asia. We have also provided two PRIME awards to register the papers of talented minority students in low research and developing countries (both were from Africa). The eligibility criteria of the PRIME award were included in the CMT submission system. We will strive to continue this initiative in the upcoming years and see a similar trend in other conferences and workshops.

August 2020

Islem Rekik
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Contents

Context-Aware Synergetic Multiplex Network for Multi-organ Segmentation of Cervical Cancer MRI.	1
<i>Nesrine Bnoui, Islem Rekik, Mohamed Salah Rhim, and Najoua Essoukri Ben Amara</i>	
Residual Embedding Similarity-Based Network Selection for Predicting Brain Network Evolution Trajectory from a Single Observation	12
<i>Ahmet Serkan Göktas, Alaa Bessadok, and Islem Rekik</i>	
Adversarial Brain Multiplex Prediction from a Single Network for High-Order Connectional Gender-Specific Brain Mapping.	24
<i>Ahmed Nebli and Islem Rekik</i>	
Learned Deep Radiomics for Survival Analysis with Attention	35
<i>Ludivine Morvan, Cristina Nanni, Anne-Victoire Michaud, Bastien Jamet, Clément Bailly, Caroline Bodet-Milin, Stephane Chauvie, Cyrille Touzeau, Philippe Moreau, Elena Zamagni, Francoise Kraeber-Bodéré, Thomas Carlier, and Diana Mateus</i>	
Robustification of Segmentation Models Against Adversarial Perturbations in Medical Imaging.	46
<i>Hanwool Park, Amirhossein Bayat, Mohammad Sabokrou, Jan S. Kirschke, and Bjoern H. Menze</i>	
Joint Clinical Data and CT Image Based Prognosis: A Case Study on Postoperative Pulmonary Venous Obstruction Prediction. . .	58
<i>Xinrong Hu, Zeyang Yao, Furong Liu, Wen Xie, Hailong Qiu, Haoyu Dong, Qianjun Jia, Meiping Huang, Jian Zhuang, Xiaowei Xu, and Yiyu Shi</i>	
Low-Dose CT Denoising Using Octave Convolution with High and Low Frequency Bands.	68
<i>Dong Kyu Won, Sion An, Sang Hyun Park, and Dong Hye Ye</i>	
Conditional Generative Adversarial Network for Predicting 3D Medical Images Affected by Alzheimer's Diseases	79
<i>Euijin Jung, Miguel Luna, and Sang Hyun Park</i>	
Inpainting Cropped Diffusion MRI Using Deep Generative Models.	91
<i>Rafi Ayub, Qingyu Zhao, M. J. Meloy, Edith V. Sullivan, Adolf Pfefferbaum, Ehsan Adeli, and Kilian M. Pohl</i>	

Multi-view Brain HyperConnectome AutoEncoder for Brain State Classification	101
<i>Alin Banka, Inis Buzi, and Islem Rekik</i>	
Foreseeing Brain Graph Evolution over Time Using Deep Adversarial Network Normalizer	111
<i>Zeynep Gürlü, Ahmed Nebli, and Islem Rekik</i>	
Longitudinal Prediction of Radiation-Induced Anatomical Changes of Parotid Glands During Radiotherapy Using Deep Learning.	123
<i>Donghoon Lee, Sadegh Alam, Saad Nadeem, Jue Jiang, Pengpeng Zhang, and Yu-Chi Hu</i>	
Deep Parametric Mixtures for Modeling the Functional Connectome	133
<i>Nicolas Honnorat, Adolf Pfefferbaum, Edith V. Sullivan, and Kilian M. Pohl</i>	
Deep EvoGraphNet Architecture for Time-Dependent Brain Graph Data Synthesis from a Single Timepoint	144
<i>Ahmed Nebli, Uğur Ali Kaplan, and Islem Rekik</i>	
Uniformizing Techniques to Process CT Scans with 3D CNNs for Tuberculosis Prediction.	156
<i>Hasib Zunair, Aimon Rahman, Nabeel Mohammed, and Joseph Paul Cohen</i>	
mr ² NST: Multi-resolution and Multi-reference Neural Style Transfer for Mammography	169
<i>Sheng Wang, Jiayu Huo, Xi Ouyang, Jifei Che, Zhong Xue, Dinggang Shen, Qian Wang, and Jie-Zhi Cheng</i>	
Template-Oriented Multi-task Sparse Low-Rank Learning for Parkinson's Diseases Diagnosis	178
<i>Zihao Chen, Haijun Lei, Yujia Zhao, Zhongwei Huang, Xiaohua Xiao, Yi Lei, Ee-Leng Tan, and Baiying Lei</i>	
Multimodal Prediction of Breast Cancer Relapse Prior to Neoadjuvant Chemotherapy Treatment	188
<i>Simona Rabinovici-Cohen, Ami Abutbul, Xosé M. Fernández, Oliver Hijano Cubelos, Shaked Perek, and Tal Tlusty</i>	
A Self-ensembling Framework for Semi-supervised Knee Cartilage Defects Assessment with Dual-Consistency	200
<i>Jiayu Huo, Liping Si, Xi Ouyang, Kai Xuan, Weiwei Yao, Zhong Xue, Qian Wang, Dinggang Shen, and Lichi Zhang</i>	
Author Index	211