

Special Issue on Biomedical Big Data: Understanding, Learning and Applications

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BIOMEDICAL imaging is an essential component in various fields of biomedical research and clinical practice. The study of biologists requires continuous monitoring of cell behavior under microscope. Neuroscientists detect regional metabolic brain activity from positron emission tomography (PET), functional magnetic resonance imaging (MRI), and magnetic resonance spectrum imaging (MRSI) scans. During these researching process, large amount of biomedical data will be produced for processing. The development of advanced imaging equipment and diverse applications also have driven the generation of biomedical big data. The main challenge and bottleneck for the related research is the conversion of “biomedical big data” into interpretable information and hence discoveries. Computer vision theory has a huge potential in many aspects for automated understanding of biomedical data and has been used successfully to speed up and improve applications such as large-scale cell image analysis (image preconditioning, cell segmentation and detection, cell tracking, and cell behavior identification), image reconstruction and registration, organ segmentation and disease classification. Considering the recent advance in machine learning technique, deep learning has revolutionized multiple fields of computer vision, significantly pushing the state of arts of computer vision systems in a broad array of high-level tasks. Hopefully these technique advance will help to deal problems in biomedical big data.

The first part of the special issue includes four articles that cover the area of brain imaging in biomedical applications. The technique advance in electroencephalography (EEG) and *functional Magnetic Resonance Imaging* (fMRI) have prospered the study of the function mechanism of human brain. This part includes some recent works that deal with the study of brain imaging big data.

In the paper “Graph Regularized EEG Source Imaging with In-Class Consistency and Out-Class Discrimination” by Feng Liu, Jay Rosenberger, Yifei Lou, Rahilsadat Hosseini, Jianzhong Su, Shouyi Wang, the authors proposed a supervised method to solve the electroencephalography (EEG) inverse problem. The proposed method makes use of a novel model called Laplacian Graph Regularized Discriminative Source Reconstruction which could explicitly extract the discriminative sources by implicitly coding the label information into the graph regularization term.

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Digital Object Identifier no. 10.1109/TBDA.2017.2772930

In the paper “Optimized Deep Learning for EEG Big Data and Seizure Prediction BCI via Internet of Things” by Mohammad-Parsa Hosseini, Dario Pompili, Kost Elisevich and Hamid Soltanian-Zadeh, the authors proposed a system model for epileptic seizure prediction and localization of the seizure focus from EEG big data based on an extended optimization approach on existing deep learning structure. Furthermore, they developed a cloud computing solution for real time processing, automatic computing and storage of the EEG big data.

In the paper “Low-Rank Graph-Regularized Structured Sparse Regression for Identifying Genetic Biomarkers” by Xiaofeng Zhu, Heung-Il Suk, Heng Huang and Dinggang Shen, the authors proposed a novel low-rank graph-regularized sparse regression model to find the associations between genetic features and brain imaging features. The low-rank constraint makes it possible to conduct variable selection with the low-rank representations of the data. Results on the Alzheimer’s Disease Neuroimaging Initiative dataset showed that the method could select important SNPs to estimate the brain imaging features more accurately.

In the paper “Resting-State fMRI Functional Connectivity: Big Data Preprocessing Pipelines and Topological Data Analysis” by Angkoon Phinyomark, Esther Ibanez-Marcelo and Giovanni Petri, the authors discussed recent progress of big data share projects for rfMRI dataset and presented three approaches as data preprocessing pipelines to get access to big preprocessed rfMRI data. They also proposed a number of novel methods rooted in algebraic topology to analyze rfMRI functional connectivity, referred to as Topological Data Analysis.

The second part of the special issue contains three articles that focus on the tracking and detection problem of cells in microscopy images. Continuous observation of cell behaviors in microscope is important in many biological and medical researches. Modern computer vision techniques could help to process and analyze these large amount of data generated during the observation.

In the paper “Debugging Object Tracking by a Recommender System with Correction Propagation” by Mingzhong Li and Zhaozheng Yin, the authors proposed a novel iterative recommender system with correction propagation to help humans debug (verify and correct) tracking results generated by automated object tracking algorithm. The approach is validated on different biomedical image sequences to track stem cells under microscope and fruit flies in front of camera. The results show that the proposed method could guide human annotators to debug tracking data in an efficient and collaborative way.

In the paper "Mitosis Detection in Phase Contrast Microscopy Image Sequences of Stem Cell Populations: A Critical Review" by An-An Liu, Yao Lu, Mei Chen and Yu-Ting Su, the authors reviewed the advances of techniques for mitosis detection in recent years. They described the task of mitosis detection at big data era and categorized the detection approaches into tracking based methods, tracking free methods, hybrid methods and deep learning methods. The authors also gave a comprehensive comparison of these methods at different stages of the detection pipeline as well as their performance on the real datasets.

In the paper "Modeling Temporal Information of Mitotic for Mitotic Event Detection" by Weizhi Nie, Huiyun Cheng and Yuting Su, the authors proposed an effective method to capture video-wide temporal information by learning the order information of video sequences for automated mitosis detection and recognition in phase-contrast microscopy image sequences. The method is tested on two popular dataset of phase-contrast microscopy image and achieves better performance compared with traditional mitosis recognition methods.

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Guest Editors

ACKNOWLEDGMENTS

We would like to thank all the authors for contributing their high-quality works and all the reviewers for providing thoughtful and timely reviews. We would like to thank the Editor-in-Chief, Dr. Qiang Yang for the support and advice for this special issue. Last but not least, we would like to thank Kathy Santa Maria and Leigh Ann Testa for their invaluable professional assistance in the paper review and production process.



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Mei Chen received the BS and MS degrees from Tsinghua University in Beijing, China and the PhD degree in robotics from the School of Computer Science at Carnegie Mellon University. She is an associate professor in the Computer Engineering Department, State University of New York, Albany. From 2011 to 2014, she was the Intel Principal Investigator for the Intel Science & Technology Center on Embedded Computing that sponsored research of more than 60 faculty and students from Carnegie Mellon, Cornell, Georgia Tech, Penn State, UC Berkeley, UIUC, and UPenn. Previously she held research and research lead positions at Intel Labs, HP Labs, and Sarnoff Corporation. Her work in computer vision and machine learning have been nominated finalists for 6 Best Paper Awards and won 3.



Tolga Tasdizen is an associate professor in the Electrical and Computer Engineering Department, University of Utah. He is also a member of the Scientific Computing and Imaging Institute. His research interests include the general areas of image processing, computer vision and pattern recognition. More specifically, he studies pattern recognition, supervised learning and variational methods for biomedical image restoration, segmentation and analysis. Over the last five years, the main driving application of his research

has been neural circuit reconstruction (connectomics) from large-scale electron and confocal microscopy image datasets. His research group is in the leading positions of the Segmentation of neuronal structures in EM stacks and 3D segmentation of neurites in EM images challenge leaderboards. Various parts of his work have been published in first-tier venues including the *IEEE Transactions on Image Processing*, TBE, MIA, MICCAI, ICCV, the *Journal of Neurophysiology*, the *Neuroinformatics*. He has served as the associate editor of the *IEEE Signal Processing Letters* and the *BMC Bioinformatics* and also served as the reviewers for a rich set of forums, e.g., the *IEEE Transactions on Pattern Analysis and Machine Intelligence*, the *IEEE Transactions on Image Processing*, the *Transactions on Medical Imaging*, the *IEEE Transactions on Visualization and Computer Graphics*, the *Media International Australia*, etc.



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