Research Contributions to MICCAI 2018:
4 main MICCAI papers and 6 workshop papers

Brain And Signal Research & Analysis Lab

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“The requisites of knowledge: a quick mind, zeal for learning, humility, foreign land, a professor’s inspiration, and a life of long span.” Juwaini of Nishapur (d.1085)

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Joint Correlational and Discriminative Ensemble Classifier Learning for Dementia Stratification Using Shallow Brain Multiplexes

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Abstract. The dementia brain wiring undergoes several changes with dementia progression. However, in early dementia stages, particularly early mild cognitive impairment (MCI), these remain challenging to spot. Hence, developing accurate diagnostic techniques for MCI identification is critical for early intervention to prevent the onset of Alzheimer’s Disease (AD). There is a large body of machine-learning-based research developed for classifying different brain states (e.g., AD vs MCI). These works can be fundamentally grouped into two categories. The first uses correlational methods, such as canonical correlation analysis (CCA) and its variants, with the aim to identify most correlated features for diagnosis. The second includes discriminative methods, such as feature selection techniques and linear discriminative analysis (LDA) and its variants to identify brain features that distinguish between two brain states. However, existing methods examine these correlational and discriminative brain data independently, which overlooks the complementary information provided by both techniques, which could prove to be useful in the classification of patients with dementia. On the other hand, how early-dementia affects cortical brain connectivity in morphology remains largely unexplored. To address these limitations, we propose a joint correlational and discriminative ensemble learning framework for MCI diagnosis leveraging a novel brain network representation, derived from the cortex. Specifically, we devise the “shallow constitutional brain multiplex” (SCBM), which not only measures the similarity in morphology between pairs of brain regions, but also models the relationship between two pathological brain networks. Then, we represent each individual brain using a set of SCBMs, which are used to train joint ensemble CCA-SVM and LDA-based classifiers. Our framework outperformed several state-of-the-art methods by 3%-7% including independent correlational and discriminative methods.

Joint Prediction and Classification of Brain Image Evolution Trajectories from Baseline Brain Image with Application to Early Dementia

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Abstract. Despite the large scale of existing multi-modal studies on brain dementias, in particular mild cognitive impairment (MCI), modeling and predicting the early dynamics of dementia onset and development in healthy brains is somewhat overlooked in the literature. The majority of computer-diagnosis tools developed for classifying healthy and demented brains mainly rely on either using single modality or longitudinal imaging data. Longitudinal brain imaging data offers a large time window to better capture subtle brain changes in early MCI development, and its utilization has been shown to improve classification and prediction results. However, typical longitudinal studies are challenged by a limited number of acquisition timepoints and the absence of inter-subject matching between timepoints to address this limitation, we propose a novel framework that learns how to predict the developmental trajectory of a brain image from a single acquisition timepoint (i.e., baseline), while classifying the predicted trajectory as “healthy” or “demented.” To do so, we first jointly align all imaging data, then extract “landmark patches” from imaging data. Next, to predict the patch-wise trajectory evolution from baseline patch, we propose two novel strategies. The first strategy learns a supervised manner to select a few matching atlas patches that best boost the classification accuracy of the target testing patch. The second strategy learns in an unsupervised manner to select the set of most similar matching atlas patches to the target testing patch using multi-kernel patch manifold learning. Finally, we train a linear classifier for each predicted atlas trajectory. To identify the final labels of the target subject, we use majority voting to aggregate the labels assigned by each model to all landmark patches’ trajectories. Our image prediction model boosted the classification performance by 4% without further leveraging any enhancing methods such as feature selection.

Do Baby Brain Cortices That Look Alike at Birth Grow Allike During The First Year of Postnatal Development?

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Abstract. The neonatal brain cortex is marked with complex and high-convoluted morphology, that undergoes dynamic changes over the first year of postnatal development. A large body of existing research works investigating the development brain have focused on looking at changes in cortical morphology and during the developmental trajectories of the cortex. However, the relationship between neonatal cortical morphology and its postnatal growth pattern of brain regions is poorly investigated. Notably, understanding the multi-scale shape-growth relationship may help identify early neurodevelopmental disorders that affect it. Here, we unprecedentedly explore the question, "Do cortices that look alike at birth have similar kinetic growth patterns?" To this end, we propose to analyze shape-growth relationship at three different scales. On a global scale, for both hemisphere, 2% of cortical regions displayed a significant high correlation (r > 0.30). On a local scale, for both hemisphere, 2% of cortical regions displayed a significant high correlation (r > 0.30) between their similarities in morphology and dynamics. On a convoluted scale, we identified hubs of cortical regions that were consistently similar in morphology and developed similarly across subjects including the occipital cortex using a novel imaging shape-growth brain-graph representation.

Revealing Regional Associations of Cortical Folding Alterations with In Utero Ventricular Dilation Using Joint Spectral Embedding

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Abstract. Fetal ventriculomegaly (VIM) is a condition with dilation of one or both lateral ventricles, and is diagnosed as an atrial diameter larger than 10 mm. Evidence of abnormally ventricular association with VIM has been shown in the literature. However, existing studies have a holocentric approach to identify spatially-temporal association between ventricle and cortices to volumes, thus failing to reveal the spatially-temporal association pattern between ventricle and cortices. To address this limitation, we develop a novel method to display spatially-temporal association patterns between ventricle and cortices. In the first step, we define a joint graph matching framework using graph-theoretic metrics. Next, we propose a spectral embedding of the cortex-to-ventricle graph into a correspoding embedding space where their joint growth patterns are projected. More importantly, the joint graph-to-embedding space, the variation of spatial-temporal regimes from both cortical and ventricular surfaces would decrease to each other. In the final step, we perform clustering in the joint embedded space to identify associated sub-regions between cortices and ventricles. Using a dataset of 25 healthy brains and 25 brains with isolated neonatal VIM within the age range of 25-29 gestational weeks, our results show that the proposed approach is able to reveal clinically-relevant and meaningful regional associations.

Figure 1: MICCAI 2018 papers.
Data-Specific Feature Selection Method Identification for Most Reproducible Connectome Feature Fingerprinting Brain States

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Abstract. Machine learning methods present unprecedented opportunities to advance our understanding of the mechanisms of brain disorders. With the proliferation of recently high-dimensional connectome data, there is a substantial need to develop a method for automatic, data-driven, and deep learning based feature selection. In this paper, we propose a novel method for selecting data-specific features, which can be used for multi-site and multi-subject studies. Our approach is based on a hybrid deep learning algorithm that combines a data-driven feature selection method with a deep learning classifier. The proposed method was evaluated on the Alzheimer’s Disease Neuroimaging Initiative (ADNI) dataset, and the results showed that our method outperformed existing methods in terms of accuracy and reproducibility.
XmoNet: a Fully Convolutional Network for Cross-Modality MR Image Inference

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ABSTRACT. Magnetic resonance imaging (MRI) can generate multimodal scans with complementary contrast information, capturing various anatomical or functional properties of organs of interest. But whilst the acquisition of multiple modalities is favourable in clinical and research settings, it is hindered by a range of practical factors that include cost and imaging artefacts. We propose XmoNet, a deep-learning architecture based on fully convolutional networks (FCNs) that enables cross-modality MRI image inference. This multiple branch architecture operates on various levels of image spatial resolutions, enabling rich feature hierarchies suited for the image generation task. We illustrate the utility of XmoNet in learning the mapping between heterogeneous T1- and T2-weighted MRI scans for accurate and realistic image synthesis in a preliminary analysis. Our findings support scaling the work to include larger samples and additional modalities.

Keywords: Fully convolutional networks · MRI · multimodal · image generation.

Intact Connectional Morphometric Learning using Multi-View Morphological Brain Networks with Application to Autism Spectrum Disorder

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ABSTRACT. The morphology of anatomical brain regions can be affected by neurological disorders, including autism and schizophrenia, to various degrees. Hence, identifying the morphological signature of a specific brain disorder can improve diagnosis and better explain how neuromorphometrical changes associate with function or cognition. To capture this signature, a benchmark study introduced, brain morphometrics, a global metric defined as the proportion of phenotypic variations that can be explained by brain morphology derived from structural brain MRI scans. However, this metric is limited in investigating morphometrical changes using low-order measurements (e.g., regional volumes) and underestimates how these changes can be related to each other (i.e., how morphometrical changes in one region influence changes in another region). Furthermore, it is derived from a pre-defined anatomical similarity matrix using a Gaussian function, which might not be robust to outliers and maximizes the locality of data to a fixed bandwidth. To address these limitations, we propose the intact connectional morphometry (ICBM), a metric that captures the variation of connectional changes in brain morphology. In particular, we use multi-view morphometrical brain networks estimated from multiple cortical attributes (e.g., cortical thickness) to learn an intact space that first integrates the morphological network views into a unified space. Next, we learn a multi-view morphometrical similarity metric in the intact space by adaptively assigning neighbors for each data sample based on local connectivity. The learned similarity capturing the shared traits across morphometrical brain network views is then used to derive our ICBM via a linear mixed effect model. Our framework shows the potential of the proposed ICBM in capturing the connectional neuroanatomical signatures of brain disorders such as Autism Spectrum Disorder.

Figure 3: Bano et al., PRIME-MICCAI 2018, and Bessadok et al., CNI-MICCAI 2018.
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