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BIH Type II
(Special Session/Workshop)

Abstracts

Special Session on BigNeuron Project

- S06201** 3D Axial Analysis for Neuron Reconstruction
- S06202** Efficient and Accurate Reconstruction of Neuron Morphology from Bright-Field Images of Biocytin-Filled Neurons Using an Automated Algorithm
- S06203** Automatic 3D Neuron Tracing Based on Deep Convolutional Neuron Network and Transfer Learning
- S06204** SmartTracing: Self-Learning Based Neuron Reconstruction
- S06205** BigNeuron Data Analysis for Massive-Scale, Automated Neuron Reconstructions
- S06206** Design and Implementation of Multi-Signal, Time-Lapse Digital Reconstructions of Neuronal Morphology
- S06207** Synapse Detector: Whole-Neuron Structural Input Mapping of Excitatory and Inhibitory Synapses
- S06209** Morphological Comparisons in a Vibration Sensitive Interneuron in the Dorsal Lobe of the Brain among Honeybees of Different Ages

3D Axial Analysis for Neuron Reconstruction

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Abstract. 3D neuron reconstruction is important for understanding the morphology and structure of neurons as well as for quantifying the distribution of subcellular objects such as synapses. Many methods have been studied to reconstruct neurons using 3D light imaging, among them include the contributions derived from the recent BigNeuron effort. Compared with approaches such as tracing, relatively fewer attention has been paid to methods based on 3D skeletonization, partially due to the challenge of 3D connectivity analysis in the presence of noise and staining artifacts.

Here we present a 3D reconstruction method based on 3D axial analysis. Surrounding a core of image skeletonization using 3D medial axis analysis, our approach also investigates novel methods that analyze the connectivity of skeletons, particularly when the uneven staining (such as membrane-based staining) causes hollow areas on the dendrite morphology which lead to 3D loops in reconstructed neuritis. These loops are commonly caused by splits in the skeleton that travel along both sides of a hole and then reconnect with itself on the other side. They compromise the neuron connectivity and interfere with the radius estimation. A novel algorithm based on graph analysis is proposed which consists of two steps of loop detection and loop merging. Using a 3D graph structure built from the skeleton elements, the step of loop detection detects loops that are considered mergable. The step of loop merging then derives the centerlines of the 3D loop. Compared with traditional methods that remove the excessive edges, the proposed algorithm can better preserve the original axial structure and locate the dendrite centerline. As a result, it not only potentially leads to better reconstruction, but also improves the accuracy of neurite radius estimation.

The method has been applied to BigNeuron image databases on images that cover various species and imaging modalities. It has also been used to help analyze 3D subcellular synaptic distribution in the fruitfly neurons with complex dendritic structure. The reconstruction method is implemented as a Vaa3D plugin.

Keywords: 3D Neuron Reconstruction, BigNeuron, 3D Axial Analysis, Loop Merging

Efficient and Accurate Reconstruction of Neuron Morphology from Bright-Field Images of Biocytin-Filled Neurons Using an Automated Algorithm

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Abstract. Intracellular recording of hippocampal and cortical neurons is a common technique for studying dendritic integration of input signals. Numerical simulations of the recorded neurons (e.g. NEURON), are often needed to fully understand the implications of the intracellular recordings. Accurate reconstructions of dendritic structures of the recorded neurons, including the correct diameters of dendritic branches, are required for informative simulations. Typically, neurons are filled with biocytin during recordings and imaged with bright-field optical microscopes under high magnifications (60-100X).

A traditional method of morphology reconstruction is a computer-aided manual method of clicking through the neuron image on screen while the coverslip is under the microscope. The diameters are measured by adjusting a circle on screen against the image of a branch. The coverslip moves while different parts of neurons are reconstructed. This process is tedious and time consuming, and leads to many errors, mainly due to fatigue and mechanical drifts of coverslips.

We developed a system of reconstructing biocytin filled neurons efficiently and accurately. Image stacks that cover the entire neuron are taken automatically. The stacks are stitched using the overlapping regions between them. An automated algorithm reconstructs the neuron. The algorithm measures the diameters of dendrites and the shapes of dendritic branches. It succeeds in getting the majority of the structure, especially where image quality is good. We then use a software tool to edit the structure by comparing to the underlying neuron image. This process is efficient, because the attention can be focused on difficult parts of the structure, where the branching patterns are complicated and image qualities are poor. Our algorithm consists of the following steps: projection of neuron image in 2D; detection of neurites with Hessian matrix; level-set smoothing; skeletonization; estimating depth for each node of the 2D skeleton; extension from end points in 3D. A key of the algorithm is checking the validity of the points in the created SWC structure.

Keywords: Automatic Neuron Reconstruction, Bright-field Images

Automatic 3D Neuron Tracing Based on Deep Convolutional Neuron Network and Transfer Learning

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Abstract. To advance our understandings of neural circuits, neuroscientists are generating huge volume of microscopic neural images that demand automated neuron tracing tools to help them accurately extract neuronal morphology information. We have designed a deep transfer learning approach that trains a deep 3D convolutional neural network to trace neurons in 3D microscopic images. To avoid using large set of manually labeled data, which are costly to obtain, our approach mainly trains the convolutional neural network based neuron tracer using large-scale synthetic noisy data, the ground-truth of which is known. The synthetic training dataset contains images of a large number of 3D simple lines of various widths, lengths, intensities, and directions embedded in noisy backgrounds. Our convolutional neural network architecture mainly consists of two components: one for foreground detection and the other for extracting the central lines of neurites. Each component contains several independent narrow convolutional neural networks, which are responsible for different directions. We have developed a procedure to take advantage of this architecture design and effectively train the convolutional neural network based neuron tracer. This training procedure runs dramatically faster than training a whole random-initialized deep convolutional neural network. After trained by the synthetic data, the deep convolutional neural network neuron tracer is fine-tuned by using a small amount of labeled real 3D neuronal images, which allows it to adapt to real scenarios. The experimental results on real 3D neural images show that our convolutional neural network based neuron tracer is able to accurately trace neurons of various types.

Keywords: Neuron Tracing, Convolutional Neuron Network, Neuron Tracing, Deep Learning, Transfer Learning

SmartTracing: Self-Learning Based Neuron Reconstructions

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Abstract. As a quantitative description of neuron morphology, the digital representation has been widely applied in the tasks of modern neuroscience studies such as characterizing and classifying neuron phenotype, or modeling and simulating electrophysiology behavior of neurons. In the past decade, many efforts have been given to increase the throughput of neuron morphology analysis by developing automatic or semi-automatic neuron reconstruction algorithms. In this work, we propose SmartTracing, an automatic tracing framework that does not require substantial human intervention. There are two major novelties in SmartTracing. First, given an input image, SmartTracing invokes a user-provided existing neuron tracing method to produce an initial neuron reconstruction, from which the likelihood of every neuron reconstruction unit is estimated. This likelihood serves as a confidence score to identify reliable regions in a neuron reconstruction. With this score, SmartTracing automatically identifies reliable portions of a neuron reconstruction generated by some existing neuron-tracing algorithms, without human intervention. These reliable regions are used as training exemplars. Second, from the training exemplars the most characteristic wavelet features are automatically selected and used in a machine-learning framework to predict all image areas that most probably contain neuron signal. Since the training samples and their most characterizing features are selected from each individual image, the whole process is automatically adaptive to different images. In practice, the procedure of the SmartTracing algorithm includes 4 steps. First, the initial reconstruction was obtained based on existing automatic tracing algorithms. Second, a confidence metric proposed in this paper was computed for each reconstruction segment to identify reliable tracing. Third, a training sampler and the most characteristic features were obtained. Fourth, a classifier was then trained and the foreground containing neuron morphology was predicted. Finally, after adjusting the image based on prediction result, the final reconstruction was traced. Notably, SmartTracing can improve the performance of an existing automatic tracing method. In our experiment, with SmartTracing we have successfully reconstructed complete neuron morphology of 120

Drosophila neurons. In addition, the performance of SmartTracing has been tested in the BigNeuron project (bigneuron.org). It may lead to more advanced tracing algorithms and increase the throughput of neuron morphology related studies.

Keywords: SmartTracing, Neuron Reconstruction, Neuron Morphology, Machine Learning

BigNeuron Data Analysis for Massive-Scale, Automated Neuron Reconstructions

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Abstract. BigNeuron is a worldwide community project to advance the research and applications of single neuron reconstruction, which remains to be an important challenge in brain science. So far, the BigNeuron project has bench-tested 38,769 contributed neuronal microscopy image stacks from worldwide institutes, and in the current second version of batch testing the project has generated 1,110,590 reconstructions from more than 30 contributed neuron tracing algorithms.

To evaluate the automatic tracing results quantitatively, we have calculated morphological properties/features (such as BlastNeuron metrics) and spatial distances to measure the accuracy of the reconstructions with respect to manually curated reconstructions (the gold standard) and to compare the differences between the reconstructions from the same image datasets. Due to the diversity of the BigNeuron image datasets and the different engineering designs of BigNeuron algorithms, the performance ranking of the algorithms is quite different across different image datasets. For images that are relatively challenging due to lower signal-to-noise ratio or intense imaging artifacts, the reconstructions from different algorithms tend to capture different characteristics of the underlying neuron morphology.

In order to leverage all the automatic tracing results and produce faithful representative reconstructions for all BigNeuron images, we have developed an algorithm to fuse multiple reconstructions into a single consensus reconstruction for each image based on the neuronal skeleton locations and connections agreed upon by the majority of the input reconstructions. When comparing the consensus results to individual auto reconstructions on a dataset of 166 images with gold standard reconstructions, we found that the consensus is closer to the gold standards than each and any of the individual algorithms. For another dataset more than 25,000 images, which no gold standards are provided, we found that the consensus is closer to the population center (has a smaller total distance to individual reconstructions) than the median case reconstruction for each dataset.

Keywords: BigNeuron, Neuron Reconstructions

Design and Implementation of Multi-Signal, Time-Lapse Digital Reconstructions of Neuronal Morphology

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Abstract. Mature neuronal arbors develop from growth processes regulated by complex molecular interactions. The convergence of extracellular, intracellular, and activity-dependent molecular events on the cytoskeletal effectors, primarily actin filaments and microtubules, facilitates neural development as well as maintenance of mature morphology. Several effective techniques to digitally reconstruct and analyze neuronal morphologies exist, but the quantification of their structural dynamics remains challenging. Current descriptions of neuron morphology are static and do not contain precise representations of intracellular components. Recent advances in tissue labeling and imaging techniques necessitate the co-evolution of the standard SWC format for representing digital arbor tracings. Generation of time-varying reconstructions is required, co-registering subcellular information with neuronal morphology. Additionally, large numbers of augmented reconstructions are required to develop data-driven mechanistic models of neuronal development and of structural plasticity.

Here we present the definition of a new multichannel file structure and a new Vaa3D plug-in to handle this new type of data. We also introduce a design to tag dynamic structural changes in a time-coded manner. Next, we illustrate ongoing progress in using the multichannel/time-lapse system on developing neurons in the *Drosophila* larva. Time-varying images of overall neuronal morphology along with fluorescently labeled subcellular cytoskeletal components are digitally traced into the aforementioned file structures. These new reconstructions enable complete statistical analysis of the structural changes and the underlying molecular processes. Lastly, we will demonstrate how stochastic computational simulations of neuronal growth, statistically constrained by and validated against these novel reconstructions, can help select the most experimentally promising genetic alterations to gain additional biological insight.

The designed data structure and research approach are also broadly applicable to other types of multichannel/time-lapse neuronal imaging, such as quantification of voltage changes or tracking the arbor-wide movement of any subcellular component of interest.

Keywords: Neuroinformatics, Neuronal Development, Extended SWC Format

Synapse Detector: Whole-Neuron Structural Input Mapping of Excitatory and Inhibitory Synapses

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Abstract. The proper function of neural circuits requires spatially and temporally balanced development of excitatory and inhibitory synapses. Very little is known about the molecular mechanisms coordinating the maturation and the density of excitatory and inhibitory synapses during circuit development in mammals. At this point, one of the most significant roadblocks in studying the function of proteins involved in synaptic development *in vivo* is that it is extremely challenging to quantify the distribution of all excitatory and inhibitory synapses across the entire dendritic arbor of single neurons. We recently overcame this limitation by developing Synapse Detector, a software platform capable of annotating the position and morphology of all synapses across whole neurons genetically labeled *in vivo* using sparse *in utero* electroporation. Synapse Detector takes a trace of the dendritic arbor as input to automatically isolate either excitatory or inhibitory synapses within a user-defined radius of each dendrite. Within this toolkit, spines (excitatory synapses) are classified with a Spine Detector program that identifies regions of fluorescence at the same wavelength as the cell-filler surrounding the neuron skeleton. Inhibitory synapses are identified using an IS Detector program that identifies fluorescence from an inhibitory synaptic marker at a different wavelength than the cell-filler. Notably, IS Detector has the capability to identify and measure any fluorescently labeled structure within the spatial context of a cell-filler. Synapse Detector then determines the distance between each synapse and the dendrite, volume, and the nearest tree node to each synapse. Information contained within these nodes can then be used to directly analyze the morphology of every synapse with respect to their continuous distance from the soma. We find that in wild type layer 2/3 pyramidal neurons, large excitatory synapses exhibit a high degree of structured organization across the dendritic arbor. We also used these tools to investigate the regional function of SRGAP2A, a protein our lab has previously shown to promote synaptic maturation and limit the density of both excitatory and inhibitory synapses. In SRGAP2A knockout neurons, synaptic maturation is differentially regulated in apical and basal dendrites. Our results demonstrate that synaptic distribution across pyramidal cell dendrites is more precise and spatially segregated than previously appreciated, and may in part reflect spatial and temporal differences in the maturation of specific synaptic inputs.

Keywords: Synaptic Development, Reconstruction, Input Mapping, Dendritic Spine, Inhibitory Synapse

Morphological Comparisons in a Vibration Sensitive Interneuron in the Dorsal Lobe of the Brain among Honeybees of Different Ages

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Abstract. During the waggle-dance communication of honeybees, the dancing bee sends her message indicating the direction and distance from their hive to a nectar source, and receivers follow the dancer to receive her message. Ethological studies on waggle-dance communication have suggested that airborne vibration signal generated by both abdomen-wagging and wing-vibration during the waggle dance are important cues in the dance behavior. However, the detail process of the vibratory stimuli has not been revealed yet. We have begun to analyze the neural mechanisms for encoding and decoding the vibratory message in the dance communication. The neuron morphology is strongly related to its physiological properties, and thus to the encoding and decoding functions. Various observations and analysis of neuronal structure have been performed to reveal neural morphology and connectivity in the brain. We are investigating the morphology and circuitry of neurons in the vibratory signal processing system of honeybees to understand the decoding mechanism of the waggle dance.

In this study, we present results of morphological analysis of a honeybee interneuron, DL-Int1, which is considered to be involved in the vibratory signal processing. We stained this neuron by intracellular injection of dye. Morphologies of the neurons were reconstructed from their confocal images. Our scheme for reconstruction combines several software tools, such as, Fiji (Schindelin et al., 2012) for image filtering and masking, and SIGEN (Minemoto et al., 2009) for segmentation and tracing dendritic neural structure. Segmentation software can extract structure from confocal images automatically, and selects the largest continuous object as a main structure of reconstructed neuron. One of the problems for automated segmentation is the occurrence of fragments not connected to the main structure. SIGEN takes account for this problem by connecting the fragments to the main structure based on two criteria, their volumes and distances to the main structure. Furthermore, spurious segments are removed by pruning and dendritic branches are smoothed by averaging. The reconstructed neurons were stored as the SWC format, so their morphological characteristic parameters were calculated by highly-functional visualization software, vaa3D (Peng et al., 2014). Morphological differences of DL-Int1 between newly emerged honeybees and forager honeybees were evaluated quantitatively. Principal components of morphometric parameters

of young honeybee's neurons were distributed widely, but forager neuron's ones were aggregated in a certain ranges.

Keywords: Honeybee, Dance Communication, Vibratory Sensitive neuron, Neuron Segmentation, Morphometry

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S01203 Memory Network Initialization Based on Network Motifs in Hippocampus

Memory Network Initialization Method Based on the Analysis of Network Motifs in Hippocampus

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Abstract. It is widely believed that the studies of the structural connections will reveal the functions of network communities. Recent studies have shown that the patterns of local network connectivity (network motif) are statistically over- and under- represented in various networks. Network motif has been one of the most efficient methods to understand the functions and the characteristics of the network. The analysis of motif has been used on various kinds of networks, including transcriptional regulatory networks of *Escherichia coli*, *Saccharomyces cerevisiae* network, the developmental transcriptional network of *Drosophila melanogaster*, the signal transduction knowledge environment network, the neural connection map network of *C-Elegans* and so on. The characteristics of network which are closed with the network functions, such as the property of recurrent feedback, the convergent and divergent structural connectivity, can be identified by the analysis of network motifs. In the mammalian long term memory system, one of the most intensively studied regions is hippocampus. Hippocampus plays an important role in encoding and decoding implicit contextual information from the environment. We select hippocampus network as the research network and make some analysis about the network motifs in each subregion of it, such as CA1, CA2, CA3, dentate gyrus and subiculum. The experimental results indicate that the network motif does show the functional characteristics of these subregions. For example, the recurrent motif in CA3 is more than other regions which is fit for the anatomical experiments, similar results can also be found at CA1 for convergent characteristics. Since the network motif is an efficient network description, so that we can rebuild the network characteristics by the rules of motif distribution. Many detailed network models about hippocampus formation have been proposed and they usually contain detailed neuron models (excitatory and inhibitory neurons) and synaptic types (which obey the rules of short term synaptic plasticity or spike timing dependent plasticity). However, for the most of these proposed models, the connections between neurons are randomly distributed. The limitation of anatomical experiments makes it impossible to get the detailed micro-scale anatomical network connections. But the motif will give us a new insight on the network initialization.

Based on the motif analysis results, we rebuild the connections of each subregions of hippocampus network by the rules of the motif distribution which is consistent with the anatomical results. Combining with the detailed models of neurons and synapses, the experimental result shows that: On the structural level, the new network is more closed with the biological networks. On the functional level, the new network shows more characteristics on memory storage and retrieval tasks compared with the traditional randomly connected networks.

Keywords: Motif, Hippocampus, Memory Storage and Retrieval

International Workshop on Neuromorphic Computing and Algorithms

- S05201** Implementation of a Liquid State Machine with Temporal Dynamics on a Novel Spiking Neuromorphic Architecture
- S05202** Neural Machine Learning Algorithms and Hardware for Image Analysis and Data Science Applications
- S05203** The Importance of Evolution for Learning in Neuromorphic Systems

Implementation of a Liquid State Machine with Temporal Dynamics on a Novel Spiking Neuromorphic Architecture

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Abstract. The brain is innately parallel and comprised of simple computational units (neurons) and functionality is encoded neurally by the combined effect of sparse connectivity with unique variable efficacies and temporal latencies. Utilizing these neuroscience principles, we introduce the Spiking Temporal Processing Unit (STPU) and show its applicability for attentive processing with software simulation as well as FPGA instantiation. Key to STPU architecture are leaky-integrate and fire (LIF) spiking neurons. Each neuron has a temporal stack that allows inputs to be mapped to a neuron with temporal offsets and is one key feature that differentiates the STPU from other architectures such as IBM's True North cross-bar architecture.

A liquid state machine (LSM) is a neuro-inspired algorithm composed of three general components: 1) a set of input neurons, 2) a set of randomly connected leaky-integrate and fire spiking neurons called the liquid, and 3) a set of readout nodes that read the state of liquid. Neurologically, the liquid in the LSM mimics the cortical columns in the brain that are conjectured to cast input to a higher input space where a simple linear model can learn using this richer input feature space. Practically, LSM's are designed for temporal data where input sequences are dependent on previous input data. The liquid functions as a temporal kernel, casting the input data into a higher dimension. The LIF neurons allow for temporal state to be carried from one-time step to another. LSM's avoid the problem of training recurrent neural models by only training the weights from the liquid to the readout nodes, similar to extreme machine learning that use a random non-recurrent neural network for non-temporal data.

The performance of a LSM is dependent on the parameters of the liquid. One important parameter is the synapse response function, which has been shown to improve the performance of the LSM. In the brain, when a neuron fires, the impact of spikes on

downstream neurons are not discrete binary events, but rather the spike induces a change in post-synaptic conductance that decays over time. However, implementing an exponential function is expensive in hardware and most neuromorphic spiking hardware has either binary synapses or synapses with discrete temporal impact.

Using the constructs available in the STPU, many of the expensive processes in hardware can be avoided. For example, the exponential synapse response functions are generally expensive to implement in hardware and can be avoided by taking advantage of the temporal stack in the STPU requiring no additional logic to be implemented in the hardware. The exponential function can be sampled at discrete time samples and mapped in the weights with temporal offsets. The sparse nature of a LSM also allows for a low power usage by the STPU and an order of magnitude speed up over conventional processors.

Keywords: Liquid State Machine, Neuromorphic Architecture, Spiking Neural Network, FPGA

Neural Machine Learning Algorithms and Hardware for Image Analysis and Data Science Applications

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Abstract. Neural machine learning, a fusion of traditional machine learning techniques with concepts and functionality found in neurobiological systems, is an algorithmic approach to improve the analysis of complex data in challenging pattern recognition problems. The Hardware Acceleration of Adaptive Neural Algorithms project at Sandia National Laboratories is developing algorithms and microdevice hardware for addressing applications in image processing and cyber-data analysis. Specifically, we are generating techniques that measure information content in data representations generated by neural machine learning algorithms. We hypothesize that the information content of neural networks is embodied by the configurations, representations, and computations of ensembles of neurons. By assessing the time-integrated rate of firing activity generated by a given neural ensemble, compressibility as a measure of complexity may be used in order to estimate entropy and thus information content. Using this methodology, we are developing techniques to maximize the information content in - and thus maximize the training and performance of - neural machine learning algorithms. Once algorithms are trained, we also incorporate neural-inspired methods to enhance algorithm robustness when exposed to new classes of data such that new representations can be learned without the loss of previously learned representations. As a final component of our algorithm development, we are using the hippocampus as a source of inspiration to produce a theoretical framework based upon the hippocampus's regional functionality. This includes a combinatorial mathematical model to represent the function of the dentate gyrus region and a dynamical spiking model to represent the function of the CA3 region. Our goal is to integrate this set of functionalities together to assemble a neural-inspired one-shot machine learning algorithm.

In addition to focusing on novel algorithm development, we are also designing hardware architectures to accelerate algorithm training and operation. We have designed a resistive switching crossbar architecture to perform the vector-matrix multiplication operations prevalent in neural algorithm training and operation that is focused on reducing energy consumption per matrix operation and increasing the density of weights. An additional

objective is to design and fabricate devices with switching characteristics optimized for neural-inspired analog computations. Our analysis indicates that variability in shifting a device to a particular resistance state (write noise) has a more detrimental impact on algorithm performance than the variability in measuring the resistance state of a given device (read noise). We also assessed several different resistive switching device technologies and modeled the impact of device switching symmetry and linearity on algorithm training, operational accuracy, and long-term algorithm stability in character recognition and data-file categorization tasks.

Keywords: Neuromorphic Computing, Machine Learning, Hardware Acceleration, Neural Algorithms

The Importance of Evolution for Learning in Neuromorphic Systems

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Abstract. Learning and evolution in biological brains go hand-in-hand; the brain’s overall structure has been determined by evolution, and then structures in the brain are refined and tuned over the course of an individual’s lifetime by learning processes. When developing algorithms for neuromorphic systems, most learning methods that have been considered are those that shape biological brains over an individual’s lifetime. For example, synaptic-weight based optimizations (such as spike-timing dependent plasticity), axonal growth, neurogenesis, and neuromodulation are all “learning” mechanisms that have inspired neuromorphic learning algorithms. We propose that, in addition to considering these types of mechanisms as inspiration from biology, we should also consider how high-level neuromorphic structures or networks can first be determined using evolutionary or genetic algorithms and then be refined using learning algorithms.

Evolutionary algorithms have been used successfully for different types of neural network structures for the last few decades. We have successfully applied evolutionary algorithms to determine high-level structural features of deep learning networks in combination with gradient-based weight optimization and the structure and parameters of spiking and neuromorphic networks in combination with long-term potentiation and long-term depression based weight refinements. Computationally, evolutionary algorithms have the advantage that they can work with a variety of network types or structures, and they can optimize over different characteristics of networks, making them applicable for a wide variety of problems. Moreover, they can work directly with neuromorphic hardware, potentially making them more efficient than other (off-chip) algorithms.

In practice, one of the issues associated with using evolutionary approaches is that convergence to a good solution can take a significant amount of time, especially for problems with a very large search space. As network sizes grow larger for neuromorphic systems, it may become more and more difficult to find good solutions quickly using simple evolutionary algorithms. It is likely worthwhile to examine how evolution has shaped (and continues to shape) biological neural systems, and how we may apply similar principles to evolutionary algorithms for neuromorphic systems.

Keywords: Neuromorphic Computing, Evolutionary Optimization, Genetic Algorithms

BIH Type II

Abstracts

Investigations of Human Information Processing Systems

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A Resting-State fMRI Study
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Multimodal Neural Decoding with Natural Data from Humans

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Abstract. There have been many successes in using experimental ECoG (electrocorticography) and EEG (electroencephalography) studies to decode human brain activity; however, natural data collected without a specific, controlled task has been rarely analyzed. Signals collected from humans in the wild are affected by a noisy environment and modulated by a complex range of behaviors. Implementing Brain Computer Interfaces (BCIs) outside carefully controlled experiments in laboratory settings requires adaptive and scalable strategies with minimal supervision. Indeed, fully automated decoding of human activities and intentions from direct neural recordings is a tantalizing challenge in brain-computer interfacing. Using modern advances in machine learning and computer vision, recordings of multiple modalities can be mined for information about a patient's behavior without the need of strict experimental protocols. In this project, we collected and analyzed thousands of hours of simultaneous video (including a depth channel), audio and intracranial neurophysiological data from patients undergoing clinical long term monitoring from more than 10 ECoG patients. We are able to automatically cluster behaviorally relevant categories as well as functionally map the brain from the ECoG signals without any supervision or manual labeling. Our approach to circumvent the need for manually annotated behavioral labels exploits automated techniques developed in computer vision and speech processing. Both of these fields have seen tremendous growth in recent years with increasing processor power and advances in methodology. Our unsupervised approach discovered clusters for behaviors such as moving, speaking and resting from ECoG data. Our results represent, to our knowledge, the first demonstration of automated clustering and labeling of human behavior from brain recordings in a naturalistic setting. In our ongoing work, preliminary results show that the latest state-of-the-art techniques based on deep learning can detect human poses accurately from the naturalistic patient videos. We will present functional brain mapping and decoding results from the human ECoG signals enabled by this automated pose detection from video. Our techniques overall show the suitability of natural data combined with fully automated video and audio analyses in brain activity decoding and prediction.

Keywords: Natural Data, Human ECoG, Multimodal, Neural Decoding, Computer Vision

Altered Brain Network Efficiency in Patients with Major Depressive Disorder: A Resting-State fMRI Study

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Abstract. Brain imaging studies have demonstrated that major depressive disorder (MDD) can be conceptualized as a disorder of abnormal interactions between brain regions, reflecting disrupted topological organization of functional brain networks. However, it needs more evidence to clarify the relationship between the abnormal brain activities and symptomatology of MDD. This study is focused on the small-world network topology efficiencies, and further explores how the altered topological efficiencies are associated with the depressive psychopathology. **Methods:** We collected the rsfMRI data and T1-weighted structural images from 19 MDD patients and 19 healthy control (HC) individuals with matching of age, gender and education level. All participants were assessed using a neuropsychological test battery that included 17-item Hamilton Rating Scale (HAM-D-17), 9-item Patient Health Questionnaire (PHQ-9), and Trait Anxiety Inventory (T-AI). Standardized preprocessing was applied to brain imaging data and 90 regions of interest (ROIs) were defined based on the template of Automated Anatomical Labeling. Then Pearson's correlation coefficients between all pairs of ROI time series were computed, which resulted in a 90×90 correlation matrix representing functional connectivity ($P < 0.05$, Bonferroni corrected). After that, with the method of graph theory, we calculated the brain efficiencies in the two groups, including the nodal efficiency, local efficiency and global efficiency. Paired t tests were conducted to determine the differences between the MDD and HC groups. **Results:** Compared with the HC group participants, the patients with MDD exhibited significantly reduced nodal efficiency in the left parahippocampal gyrus, right amygdala, left heschl and left temporal pole (middle temporal gyrus). Nodal efficiency measures the ability of information propagation between a given node and the rest of the nodes in a network. Higher nodal efficiency is indicative of higher integration in the brain. This reduced nodal efficiency indicates that the function of transmitting information to other regions is weakened in MDD. The local efficiency of the left medial superior frontal gyrus,

left orbital superior frontal gyrus, right rectus, left amygdala, right superior parietal gyrus, left thalamus, and left temporal pole (middle temporal gyrus) were also significantly reduced. And the local efficiency of the left medial superior frontal gyrus, left amygdala, left thalamus had negative correlation with PHQ-9. The local efficiency measures the ability of information transmission of a network at the local level. These results suggest that the communication ability of the sub-network regions in these were weakened in MDD, and weakening level might reflect the severity of depression. At last, there was no significant difference between the two groups in the global efficiency. Conclusion: In summary, graph theory analysis was applied to the rsfMRI data of MDD and HC groups. Results revealed reduced ability of network community widely in the limbic system, frontoparietal network, default mode network and the thalamus in MDD, and the correlation between the brain network information processing and depressive psychopathology. Further studies are suggested to verify these conclusions by pursue more node-specific analyses.

Keywords: Major Depressive Disorder, Resting State fMRI, Brain Network

Effect of Fatigue on Cognitive Abilities in Adolescents

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Abstract. Fatigue is generally associated with different physical, physiological and mental problems; mostly fatigue is to be the cause of the decline in activity levels following any physical activity that reaches the level of exhaustion. Although much of the evidence suggests that the relationship between acute physical activity and cognitive performance has an inverted U function, it is important to interpret these finding with some caution given that the pattern of the studies differ along several important scopes, such as the type of exercise, the cognitive functions assessed, the age groups tested, as well as the physical and health condition of the participants. In this study we are aiming to assess the effect of fatigue on cognitive abilities. A pre-test post-test design was used to measure the changes in cognitive abilities pre and post fatigue procedures ,20 normal, healthy adolescents aged between 16-18 years of age participated in this study they were assessed using the Determination test (DT) one of the test batteries enrolled in the Vienna test system, it is used in Measurement of reactive stress tolerance, attention and reaction speed in situations requiring continuous, swift and varying responses to rapidly changing visual and acoustic stimuli. The subjects were assessed for weight and height, each subject performed a pre fatigue assessment of the DT then started the fatigue protocol, on braked cycle ergometer till he/she expressed fatigue at this time he stops the exercise and take the post fatigue assessment of the DT immediately after stepping down the ergometer. Results showed that performance in the DT test has significantly declined after doing the fatiguing exercise especially the reactive stress tolerance variable.

Keywords: Fatigue, Cognitive Abilities

Phase Transitions in Dynamics Complexity of Sparse Boolean Networks and Their Implications

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Abstract. We study dynamics of several classes of Boolean Network Automata (BNA). Important subclasses of the BNA we study include classical (finite, Boolean-valued) Cellular Automata and (discrete, binary/Boolean valued) Hopfield Networks. We are particularly interested in uniformly sparse BNA, in which each node has a small number of neighbors. In terms of the node update rules, we focus on biologically inspired (linear) threshold functions, and investigate in detail their important subclass, simple threshold functions. We assume deterministic behavior to allow for rigorous and exact investigation of such BNA's dynamics. Arguably the most important problem about the asymptotic dynamics of these BNA is to identify, characterize and enumerate all of their stable configurations, called Fixed Points (FPs). Our research on characterizing and enumerating these FPs in sparse Boolean networks has resulted in establishing two fundamental phase transitions. One, in homogeneous such networks, in which every node updates according to the same rule, we have established that almost all simple threshold update rules allow for only a handful of FPs. The exact number of these FPs depends on the total number of nodes, the specific choice of an update rule, and the details of the graph topology and 'boundary conditions'. However, regardless of these details, the number of stable configurations is always of the order of $o(n)$, where n is the total # of network nodes. In contrast, such Cellular/Boolean Network Automata all of whose nodes update according to the Majority rule provably have an exponential in n number of fixed points. Importantly, while the details of the combinatorial analysis can get quite involved depending on the exact cellular space / BNA graph structure, determining the number of FPs in homogeneous CA/BNA exactly is always computationally tractable. This tractability holds both for the Majority rule that allows for plenty of FPs, and for other simple threshold update rules that allow for only a few FPs. The second fundamental phase transition takes place, when we allow some heterogeneity in the local behaviors. By heterogeneity, we mean that not all nodes in the network update according to the same local update rule. In that setting, we have established that it suffices to have a very minimal level of heterogeneity -- only two different update rules -- so that determining the exact number of FPs in such BNA is computationally intractable in the worst-case. More specifically, we show that Discrete Hopfield Networks with sparse symmetric integer weight matrices (such that the rows/columns encode simple threshold functions) may have exponentially many stable configurations. More interestingly, in general determining the number of those stable configurations is intractable in the worst-case, and that intractability already can be observed

when the Hopfield Network's nodes use only two different update rules. Thus, this second fundamental phase transition takes place when a very modest amount of heterogeneity in local interactions is permitted. This transition from tractable to intractable asymptotic dynamics has important ramifications for theoretical neuroscience as well as complexity of emerging behaviors in biological, physical and social networks.

Keywords: Asymptotic Network Dynamics,
Boolean Networks and Cellular/Network Automata, Phase Transitions in Network Dynamics,
Characterizing and Enumerating Stable Configurations,
Computational Complexity of Enumeration

Brain Big Data Analytics, Curation and Management

- B269** Automated Functional Connectivity Analysis for Multiple Brain Data Sets
- A Preliminary Study on Relationship among Cognition, Emotion, and Depression
- B256** The Computational Infrastructure for a Large-Scale Neuroinformatics Platform: Brain-CODE
- B257** Segmentation of Brain Magnetic Resonance Images Using Deep Neural Networks
- B258** Deep Learning ECG Beat Classifier Using RNN's
- B271** An Automated Python Pipeline for Modeling the Cerebral White Matter Pathways with Diffusion-Weighted Imaging

Automated Functional Connectivity Analysis for Multiple Brain Data Sets - A Preliminary Study on Relationship among Cognition, Emotion, and Depression

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Abstract. Multi-level integration of brain big data is one of the core issues of Brain Informatics. The brain big data which are characterized by its complexity and multiple aspects, such as collected collection for from multiple experimental purposes, heterogeneous multiple features of subjects, and multi-scale analyses multiple scales can be summarized as multiple aspects. Especially, human higher cognitive function brain function consisted by of multiple diverse function should be investigated by multiple aspects cognitive domains. Integrating each all the aspects of the cognition-related data brain big data about cognitive functions enables further mining of potential values hidden in the brain big data. In this study, we propose a method for the brain data integration at the information level by using an automated functional connectivity analysis system. We used Data Brain to integrate human-brain-related knowledge, information, and data, which is composed of “Knowledge Layer”, “BI Provenances Layer”, and “Brain Data Layer”, and is a knowledge graph developed for supporting brain informatics (BI) studies as well. In order to integrate human brain related knowledge, information and data, we the Data Brain consists of the knowledge layer, the BI provenances layer and the brain data layer, which is also a knowledge graph developed for supporting brain informatics (BI) studies. The Knowledge Layer is designed for modeling the multiple dimensions of brain and relevant experiments with ontologies. The BI Provenances layer contains detail information such as information about subjects, experiments, measure instruments, types of tasks, analytic tools, and results, etc. Furthermore, BI Provenances manage brain data in the form of metadata. Since the metadata are characterized by uniformity, BI Provenances can store all heterogeneous brain data by RDF (Resource Description Framework). By this method, the BI Provenances Layer connects the Brain Data Layer and Knowledge Layer through turning the brain data into

metadata and managing them as organized by the existing brain-related knowledge. Based on this knowledge graph, we developed an automated analysis system, which facilitated the integration of multi-center brain big data. The automated analysis system adopts knowledge and information integrated in Data Brain for data analysis. To integrate multiple data sets at the information level, the system compare pairs of functional connectivity graphs using the two sample t-test. Especially, we focused on the relationship among cognition, emotion, and depression. We investigated the functional connectivity of multiple sites (regions) of the brain underlying diverse brain functions, by applying automated analysis system to three data sets associated with cognitive function, emotion, and depression, respectively: (1) experiment specific to mental arithmetic; (2) experiment specific to mental arithmetic under negative emotion state; (3) experiment specific to mental arithmetic under negative emotion state in depressed patients and healthy controls. Comparisons between (1) and (2) revealed brain activities corresponding to only negative emotion in healthy subjects; comparisons between (1) and (3) demonstrated brain responses to negative emotion in depressed patients. Then, the system generated three functional connectivity graphs and showed significant differences between the data sets. By developing the automated functional connectivity analysis system based on Data Brain, the integration of multiple data sets at the information level is realized. The system accesses the Knowledge Layer for selecting brain data sets that were organized by BI Provenances. The value of brain big data will be raised greatly by converging multiple brain data. In our future study, emphasis will be put on the integration of multiple data sets at the knowledge level with help of the improved Data Brain.

Keywords: Brain Informatics, Brain Big Data, Provenances, Function Connectivity Analysis, Semantic Web

The Computational Infrastructure for a Large-Scale Neuroinformatics Platform: Brain-CODE

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Abstract. Brain-CODE is the Ontario Brain Institute's (OBI) extensible large-scale neuroinformatics platform which manages the acquisition, sharing, and analysis of multi-dimensional data for over 35 research institutions. Brain-CODE hosts a uniquely rich array of standardized data including neuroimaging, genomic and clinical research data to allow for deep analysis within and across brain disorders. The Brain-CODE platform is housed at the Centre for Advanced Computing (CAC) at Queen's University in Kingston, Ontario, Canada. The CAC specializes in providing high availability, secure, advanced computing resources and support for academic and medical researchers. The dedicated resources for Brain-CODE consist of over 500 cores and 300TB of storage. Brain-CODE also leverages CAC's general infrastructure, over 5000 cores and 30PB of storage, including specialized equipment such as large memory, highly-threaded systems, symmetric multiprocessing systems, GPUs, and hierarchical storage. Transferring research data to and from the platform from other research institutions in Ontario is facilitated by a large 10 gigabits per second (Gbps) fiber optic network provided by the Ontario Research and Innovation Optical Network (ORION). Furthermore, data transfers across Canada are facilitated via a 100 Gbps networks by the Canadian Network for the Advancement of Research, Industry and Education (CANARIE). In addition, the CAC adheres to high privacy and security standards to help maximize the usability and value of participant research data

while ensuring data is only accessed by approved individuals. Brain-CODE's data sharing model is physically built on a three tiered zoning structure which permits functional separation of sensitive data. Zone 1 is a secure space where researchers can upload raw data containing personal health information for analysis and data sharing with direct collaborators. Following a 12 month period of data exclusivity, datasets have participant identifiers removed and are transferred from Zone 1 to Zone 2 for secure long-term storage. Finally, approved researchers may access subsets of Zone 2 data through Zone 3 workspace access provided data passes re-identification risk evaluation. Brain-CODE offers familiar, yet powerful analytic tools to researchers in a high performance computing environment. Researchers may utilize software that has been provisioned on the platform, including R, SAS, Spotfire, and a MATLAB server, or bring customized analytics tools into their virtual workspaces. The computational resources, tools and data Brain-CODE makes available to the neuroscience researcher makes it a unique platform for exploring new analytical techniques and/or mechanisms underlying brain disorders. Work in the future will focus on expanding the services and computing resources of Brain-CODE to match data analytics needs for individuals contributing data to Brain-CODE, as well as for individuals seeking to make new discoveries from the data.

Keywords: Neuroinformatics, Advanced Computing, Integrated Analytics, Privacy, Sharing

Segmentation of Brain Magnetic Resonance Images Using Deep Neural Networks

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Abstract. Objectives: This work aims to utilize deep learning techniques to develop a more accurate approach to the segmentation of brain MR images into gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF). Motivation: Besides the image degradation caused by noise, intensity non-uniformity (INU) and partial volume effect (PVE), the difficulties of brain MR image segmentation can be ascribed to that (1) each image contains millions of voxels to be classified and (2) few efforts have being devoted to discover the visual descriptor that is effective for voxel classification. Due to their widely recognized abilities to handle a myriad number of data and to avoid handcrafted feature extraction in pattern classification, deep learning techniques are suitable for solving this problem. Method: We segment brain MR images on a slice-by-slice basis via supervised learning. In training, each 16*16 image patch within the brain region is, on one hand, utilized to train a deep convolutional neural network (DCNN), which is an eight layer MatConNet with three convolutional, two pooling and three fully connected layers, and, on the other hand, is divided into four 8*8 patches to train a sparse auto-encoder (SAE) neural network, which consists of four layers with 64, 250, 300 and 64 neurons, respectively, for image restoration. In the meantime, each 5*5 patch in the restored MR image is utilized to train a four-layer back propagation neural network (BPNN) with 25, 200, 250 and 4 neurons, respectively, for local information-based voxel classification. For each brain voxel in a test image, we first apply each 8*8 patch to the trained SAE for image restoration, then apply the 16*16 original image patch and 5*5 restored image patch to the train DCNN and BPNN, respectively, and finally combine the soft decisions made by both networks to classify the voxel. Evaluation: We evaluated the proposed method against the segmentation routines in the widely used FSL, GAMixture and EMS packages on 17 simulated T1-weighted brain MRI studies (INU ranges

from 0 to 40% and noise ranges from 0 to 9%, but exclude the crisp study) from BrainWeb. We randomly selected five studies (1%noise+20%INU, 5%noise+20%INU, 9%noise+20%INU, 1%noise+40%INU and 9%noise+40%INU) as test cases. When testing each study, we used other 16 studies as training cases and the percentage of correctly classified brain voxels as accuracy metrics. Results: Our results show that the proposed method achieves the highest segmentation accuracy on three test cases and the second highest accuracy on two test cases, and the FSL and GAMixture achieve the highest accuracy on one test case, respectively. On average, the proposed method achieves an accuracy of 92.81%, which is greater than that of other three approaches. Conclusion: The proposed deep neural network-based brain MR image segmentation method is more accurate than the segmentation routines in the widely used FSL, GAMixture and EMS packages on BrainWeb studies.

Keywords: Deep Convolutional Neural Network, Sparse Auto-encoder (SAE) Neural Network, Four-layer Back Propagation Neural Network, Brain MR Image, Image Segmentation

Deep Learning ECG Beat Classifier Using RNN's

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Abstract. Neural networks have been a good alternative to classic statistics on diverse fields. In the same category, deep learning has been used on several applications like self-driving cars, image processing or even avoiding obstacle while the drone is under autopilot. In this work, we use data mining techniques in a classic medical problem, heart beat classification, with the data from an electrocardiogram (ECG). This problem has been studied before using different techniques with a wide range of results, including artificial neural networks to identify different types of abnormal beats. Pursuing a different approach to face this problem, inspired by the use of recurrent neural networks for language translation under an encoder-decoder system, we used a two-stage recurrent neural network to detect abnormal beats to contribute on medical diagnosis for cardiovascular problems. A beat could be represented by different components, the main being the P wave, the QRS complex and the T wave. On the QRS complex there are different peaks and our first stage was used to detect R peaks on the ECG. We used a threshold to control the classification if a sample was a R peak or not and the output was used on the second stage. Those results were used to feed two separated RNNs on the second stage, of dimension 1,000 times and three levels of depth, to determine if a beat was normal or not. The results show that our model has difficulties to determine if a beat is normal or not, resulting in a sensitivity of 1 and a specificity of 0.016 in the classification of a normal beat. Moreover, the cost function that we created was close to the maximum on the training phase of our model. Given that, we conclude that extra efforts put on the training phase of the model would only add more time on data processing. We propose different ways in which this result could be improved on further research.

Keywords: Classification, Recurrent Neural Network, Health Informatics, Arrhythmia

An Automated Python Pipeline for Modeling the Cerebral White Matter Pathways with Diffusion-Weighted Imaging

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Abstract. Objective: Modeling of the cerebral white matter pathways is an important technique to advance our understanding of the human brain under normal and pathological conditions. To enable the big data analysis of the emerging large-scale neuroimaging data, in this study, we developed a fully automated tractography pipeline for constructing the trajectory of cerebral white matter pathways from raw diffusion-weighted imaging (DWI) data. This pipeline requires minimum prior knowledge about tractography computing for the basic users, but provides a high level of flexibility for advanced users to incorporate various neuroimaging computing packages on different platforms. Methods: Our proposed automated tractography pipeline is built on Python and configurable via command-line parameters. It consists of four parts: data importing, pre-processing, diffusion modeling and fiber tracking. We created a default source data directory to save the raw DWI data, which can be imported based on user selection. The imported data were pre-processed using the FSL package, including brain extraction (FSL_BET) and Eddy current correction (FSL_EDDY). We then estimated the diffusion tensors and fiber orientation distributions (FOD) with the MRTrix3 package. The 2nd order integration over fiber orientation distribution (iFOD2) algorithm was used to construct the tractography with the default or user-defined parameters, including minimum tract length, step length, angle threshold and maximum number of tracks. The tensor and tractography reconstructions were automatically saved into the output directories for individual subjects. To ensure file format compatibility and support multiple platforms, we implemented our proposed pipeline using the Python-based Nipype framework, which also provides the flexibility to incorporate other open-source neuroimaging computing packages. Results: The proposed tractography pipeline was tested using 5 anonymized DWI

datasets of the Human Connectome Project (HCP) MGH Adult Diffusion data package acquired on the customized MGH Siemens 3T Connectome scanner. Each dataset has 64 diffusion directions with a b-value of 1,000 s/mm². The total processing time with our pipeline was 55 minutes with no additional effort to convert the file format or save the intermediate files. We visually evaluated the tractography reconstructions from the pipeline based on the volume and accuracy of the corticospinal tracts (CSTs), which are known to be confounded by the crossing-fiber effects. The CSTs, in all 5 subjects, appeared intact with no apparent disruptions in the corona radiata, although lateral projections from the primary motor cortex were sparse. Conclusion: We propose a fully automated tractography pipeline. It can serve as a tool for the modeling of cerebral white matter pathways, with a strong emphasis on emerging trends of big data analysis for brain research, such as the human brain connectome, normal brain development and aging. It may have many potential medical applications, such as assisting the diagnosis and management of traumatic brain injury, Alzheimer's disease, schizophrenia, autism, epilepsy, and in image-guided neurosurgery.

Keywords: Diffusion-weighted Imaging, Cerebral White Matter Pathways, Tractography, Automated Pipeline, Brain Connectome

New Methodologies for Brain and Mental Health

- B222** Modeling of Pedestrian Guidance by Sensory Fusion Using Peripheral Vision Display and Vibration Device
- B255** Hybrid Emotion Analyzer: Combination of EEG-Based Features, Facial Expressions and the Degree of Attention
- B265** Efficacy of Mobile Applications to Augment Students Learning in Advanced Graduate Education
- B267** Association between Reaction Behaviour and Gross Motor Abilities in Children with Spastic Diplegia
- B268** Development of Human Behavior Recognition for Avoiding Fall Down from a Bed with Deep Learning

Modeling of Pedestrian Guidance by Sensory Fusion Using Peripheral Vision Display and Vibration Device

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Abstract. Human walking is affected by vision, vestibular, somatic and other various sensations that come through the sensory-motor loop. In previous studies, it has not been treated that a direction of self-motion sensation is to be different directions in each sense. We examined a possible affect of self-motion sensation by an optical-flow stimulus in peripheral vision with a decayed somato-sensory feeling by a vibration stimulus on leg and foot area. In this experiment, we presented the optical flow for forward direction to the peripheral vision, and then gave the self-motion sensation by changing the flow to left or right direction. In our experiments, subject's movement was "diagonally forward left and right". Cognitive process of this action is presumed as follows. All self-motion sensation are facing forward consistently for optic flow stimulation. It is considered that self-motion direction by where left and right optic flows to the peripheral visual field is presented, subject's feeling was changed to "left and right obliquely forward". If the goal of subjects is moving forward, instructions diagonally forward left and right is issued reflexively as correcting a new self-motion sensation to compensate for current self-motion. So the output of vection and other self-motion sensation, while it is not exclusively visual dominance in previous study, it is considered that integration by superposition. And in this study, guidance effect was confirmed, but the effect was temporary, pedestrian came back in a straight line trajectory in a few seconds after stimulus. If subject has changed walking trajectory by self-motion sensation, the effect should be kept be straight, but it is shown that there is a fixed action in opposite direction from this experimental results. One reason might be that there is a hierarchical control system in walking. There are three goals of upright, straight and purpose direction at least in control of our walking. It is considered to have intervened in the reflection system to realize upright walking in this study. However, different control of straight and purpose direction are working at the same time to walk, it is not possible to

ignore them. Additional experiments are needed to elucidate this, it is necessary to consider as one possibility.

Keywords: Pedestrian Guidance, Vection, Somatosensory, Sensory Fusion, Peripheral Vision Display

Hybrid Emotion Analyzer: Combination of EEG-Based Features, Facial Expressions and the Degree of Attention

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Abstract. In order to evaluate the emotional state while watching various kinds of movie-contents, 7 females and 7 males (ages 20 to 30) participants are instructed to watch movie-contents edited to give emotional stimuli in several scenarios. The 21-channel EEG data is obtained based on international 10-20 method, together with the pupil diameter measured via infrared light as well as the facial expression multi-dimensionally evaluated from facial images. For the control data of each subject, we started with the measurement in resting condition without stimuli. To find an indicator for the preference to be evaluated from EEG data, we used the joyful contents showing a baby laughing. We verified the significant features of beta wave at T3 and T4 channels. We also verified the effectiveness of dNAT method which probes the deeply seated EEG sources by means of evaluating synchronicity and variability level of combined 3 specified channels. To confirm the difference between the real and fake emotions, we made two kinds of experiments : showing happiness movie-contents and the one asking subjects to perform fake smile. Another pair is to show unpleasant movie-contents of a snake swallowing a frog in comparison with making a wry face. We found that emotional index based on EEG is slightly higher for the cases of watching actual movie-contents and the degree of attention i.e. the pupil diameter is higher in watching actual movie-contents when compared with those for pretending action. However, the facial expressions showed opposite characteristics. Therefore, we can distinguish the real and the fake emotions. We discovered the different patterns of the EEG power between males and females in several conditions, e.g. females receive better impression from the elderly person's picture, comparing to those reaction of the males. The beta wave power during the condition staring at the elderly's picture was significantly higher than the resting condition at T3 and T4 channels, which represents their preference level. On the other hand, any significant difference could not be observed from the pattern of males between the

conditions. We also found the different activity during reminding their recent memorable experience. The activity of those channels was significantly higher in females while reminding and explaining their episode. By contrast, the activity of those channels was lower in males. In the degree of attention, it shows the similar results. Those tendencies indicate that females have different interest in comparison with males and good at treating their daily experience. Among simple contents like as baby laughing the positive correlation between visual concentration and the brain activity was observed. However, in the case of more complicated situations where the context of the story is important, the visual concentration and the brain activity are often independent. For example, in the contents that the subject wept tears and was impressed, they show that the positive correlation was seen in some impressive scenes but was not shown in all such scenes. Consequently, it is possible to estimate the emotional state of the subjects while watching movie-contents quantitatively.

Keywords: EEG, Emotion, Facial Expressions, Preference, Pupil-Size

Efficacy of Mobile Applications to Augment Students Learning in Advanced Graduate Education

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Abstract. Purpose: The purpose of this study was to investigate the perceived efficacy of mobile applications as a supplement to the education of students enrolled in doctoral programs. Participants: Current students enrolled in a doctoral program of Physical Therapy in the United States were surveyed with a total of 1,040 responses. Inclusion criteria involved being a physical therapy student currently enrolled in a doctoral physical therapy program in the United States. The survey consisted of 22 questions, divided into two sections,. The first section of the survey included demographic information such as age, gender, race, state location of school attended, year in physical therapy program, and class size. The second section of the survey inquired about student utilization and opinion of mobile applications related to their physical therapy curriculum for educational purposes. This included what types of applications students are using most, which applications they find to be most helpful, which applications have been least helpful, and what were the aspects of those applications that made them either helpful or not. The survey took between 5 and 15 minutes to complete. (Mentioned the online program used for the survey (Survey Monkey) These data were then analyzed using Statistical Package for the Social Science (SPSS) Version 22. Results: General demographics: white (87.90%) females (73.84%) between the ages of 21 and 25 years (74.90%). Of the approximately 1,000 responses received, the states with the most responses included Texas (8.89%), Michigan (8.19%), Missouri (7.69%), and North Carolina (7.59%). Only 6.87% of responders reported having a background in computer science, information systems, or health information management, while a vast majority (99.10%) report having Internet access in their home. Only 52.44% of responders reported that they are willing to pay for an application rather than only using ones that are free, however, 50.20% reported that they do use mobile applications for learning the physical therapy curriculum, even though their program does not require their use. When students use these mobile applications, they are mostly used for their anatomy curriculum (94.39%), and their musculoskeletal curriculum (57.21%). The mobile application features most preferred by students, reporting they are (very helpful) include videos (60.99%), pictures (63.98%), and

3-dimensional images with rotation capability (74.29%). Written descriptions alone seem to be the least helpful format of a mobile application, with students reporting they are (very helpful) 35.97% of the time. A majority of students (51.18%) also reported that it is (very important) that a mobile application have use in the clinical setting, beyond the classroom. Participants were also given the opportunity to report aspects of mobile applications that were most beneficial to them that were not directly asked in the survey. Conclusions: Based on the results of this survey, students enrolled in a doctoral physical therapy programs in the United States prefer intuitive mobile applications with visual representations in the form of pictures, videos, and 3-dimensional images to supplement their learning of the physical therapy curriculum.

Keywords: e-Learning, Mobile Apps, Education

Association between Reaction Behaviour and Gross Motor Abilities in Children with Spastic Diplegia

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Abstract. BACKGROUND: Spastic diplegic Cerebral Palsy is the most common form of Cerebral Palsy in children born preterm which has a profound effect on the musculoskeletal system and can be accompanied by myriad symptoms affecting other body systems including cognitive dysfunction. PURPOSE: The purpose of this study was to find the relationship between Cognitive function in the form of reaction behaviour and motor abilities in children with diplegic cerebral palsy. Research design: Correlational study. VENUE: Faculty of Physical Therapy, Cairo University METHOD: Fifty children with spastic diplegic Cerebral palsy with age ranging from 6 to 12 years were randomly selected to participate in the study, subjects were included in three groups; 6-8y,8-10y and 10-12y. All participants were evaluated using Rehacom software to assess reaction behavior, and the Gross Motor Function Measure scale to assess gross motor function including standing, walking, running and jumping subscale and total scale. This study was done in cognition lab, Faculty of Physical Therapy, Cairo University RESULTS: The reaction behavior level, quartile 1 and 3 reaction time were significantly correlated with standing ,walking running and jumping, and total scores of GMFM scale at 6-8y, 8-10y and 10-12y. CONCLUSION: The outcome measures of the current study provide original evidence based of the necessity of including cognitive impairments in the examination and evaluation of children with diplegic cerebral palsy in research and clinical settings. Also, therapeutic intervention for cognitive reaction behavior should be carefully considered when designing a program to improve gross motor function for children with spastic diplegia.

Keywords: Cerebral Palsy, Diplegia, Cognition, Reaction Behavior, Gross Motor Function

Development of Human Behavior Recognition for Avoiding Fall Down from a Bed with Deep Learning

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Abstract. The purpose of this research is that a proposed system conceptually appreciates human behaviors. In this paper, we propose a new method to appreciate human behaviors by Deep Learning and Kinect. In artificial intelligence research field, deep learning is known as an AI that it is possible to learn conceptually. In this paper, to evaluate the capability of the proposed method, the proposed method adapts a system which watches for aged people to avoid fall down from a bed. The system, which is called the awaking behavior detection system, is proposed by us. The awaking behavior detection system was proposed as method of appreciating human behaviors. The awaking behavior detection system captures a target's body using Kinect. And DBN (Deep Belief Net) appreciates human behavior. Kinect has a depth sensor which is consists of an infrared leaser for measuring distance from Kinect to an object. Kinect, which is installed on the ceiling, is used to measure a target's body. A target's body is extracted by the preprocessing. Extracted data by preprocessing is normalized by one. If a distance from Kinect to subject is further than a threshold value, the measured data is convert to 0.98. When a distance is closer than a threshold value, the processing is shown as follows. The measured values are normalized at 1 between two thresholds. This value is subtracted from 0.98. The converted data are inputted in DBN to recognize subject behavior. The experimental purpose is that the recognition ability of the proposed method is verified using data which consist of unlearned subjects. First, experimental conditions are described. For inspecting differences in physique, 19 people participated in the experiment. Subject's behaviors, which are detected in the experiment. A state of lying on the bed is defined as a safety behavior. A state of falling down is defined as a dangerous behavior. For example, flapping the hands and feet behavior is a dangerous behavior. In this experiment, at the first, some safety behaviors and some dangerous behaviors of the subject are captured by Kinect from 14 subjects and saved on the personal computer. Where, the number of the learning data of the safety behavior and dangerous behavior is 50 per one subject. Therefore, the number of total learning data is 1400. Next, learning is executed on PC. Finally, recognition data is

recognized by learned DBN. The number of recognition data, which consists of safety data and dangerous data, is 200 per one subject. From the experimental result, the recognition rate of the safety behavior is 97.4%. The recognition rate of the dangerous behavior is 93.4%. In the experiment, it is confirmed that the proposed system recognizes safety behaviors and dangerous behaviors. From the results, it was verified that the proposed method is effective. This result meant that a computer conceptually appreciates human behaviors.

Keywords: Human Behavior Recognition, DBN, Kinect,
Avoiding Fall Down from a Behavior

Brain-Inspired Intelligence and Computing

- B259** Decoding Human Auditory Perceptual Switches:
 An Intracranial Electrophysiology Study
- B270** Development of Scale Decoding Technology from
 the Human Brains Auditory Cortex Using Deep Learning

Decoding Human Auditory Perceptual Switches: An Intracranial Electrophysiology Study

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Abstract. The human auditory system is confronted on a daily basis with the challenging task of separating and grouping competing sounds in natural environments into percepts called “auditory streams”. Understanding how the brain organizes sounds into perceptually meaningful objects is critical to the study of both normal and clinically impaired cognitive states. This study utilized electrocorticography (ECoG), which offers a unique opportunity to study auditory cortical processing in humans with high spatial and temporal resolution. ECoG data were obtained during an auditory streaming task that supported perceptual bistability. Subjects were neurosurgical patients undergoing chronic invasive monitoring for medically intractable epilepsy. Stimuli were 5-minute sequences of pure tones, presented in a classical ABA_ auditory streaming paradigm, where A and B are pure tones with a frequency difference ΔF , and “_” is a silent pause. Triplets presented with 2 and 12 semitone ΔF were used as control conditions to elicit stable 1- and 2-stream percepts, respectively. Triplets presented with 6 and 8 semitone difference ΔF were used as perceptually bistable stimuli. Subjects reported perceptual switches between 1 and 2 streams using a button press. ECoG recordings were made simultaneously from depth electrodes implanted in the superior temporal plane and subdural grid electrodes implanted over perisylvian cortex. Auditory cortical activity was analyzed using a template projection method. This method placed neural responses from different cortical sites into a common feature space, allowing for direct comparisons across sites. The templates of averaged evoked potentials (AEPs) were constructed for stable 1- and 2-stream conditions and were projected onto ECoG time series data. Feature points were calculated on a triplet-by-triplet basis. Fisher linear discriminant analysis was used to classify the feature points for each triplet and posterior probability was estimated at every time point. Feature points revealed distinguishable differences between 1- and 2-stream percepts in multiple sites within auditory and auditory-related cortex, including Heschl’s gyrus, planum temporale, superior and middle temporal gyri. The method captured certain aspects of neural activity related to auditory perception and allowed for

further classification of percepts. Classification analysis of responses to the control, 6- and 8 semitone ΔF stimuli yielded 90%, 70% and 65% accuracy, respectively. In summary, the projection template technique can decode perception from continuous data stream and predict specific perceptual states. The current study lays a foundation for further analyses addressing the link between changes in brain state in real time and the emergence of perception using data-driven dynamic models.

Keywords: Auditory Cortex, Electrocorticography, Perceptual Bistability, Template Projection

Development of Scale Decoding Technology from the Human Brains Auditory Cortex Using Deep Learning

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Abstract. In this study, we develop the scale decoding technology from image data captured by fMRI. It has been reported that frequency localization was detected when hearing the 4 sounds of 2 octaves interval (125Hz, 500Hz, 2kHz, 8kHz) of Western musical scale as auditory stimuli, using fMRI. However, given the expansion of the scale decoding, it is required to further increase the frequency resolution. Previous experiments by our group have shown that brain activity shows a significant difference when a stimulus of semitone difference C7 (2097Hz) and C#7 (2217.46Hz) are presented in the spatial resolution (3.0*3.0*3.0mm) of fMRI. In this paper, as the first phase of our study, we propose a method of scale decoding technology where identifies the frequency using a deep learning that from the image data of the captured the primary auditory cortex of human brains. Outline of the proposed method: Images of the auditory cortex (120 scans) are captured in the fMRI. The t-statistics which corresponds to the primary cortex coordinates with C7 and C#7 stimulus is attained from every scan. The t-statistics of each scan is normalized to the continuous value of [0.0, 1.0]. The normalized data are used as input for the deep learning. The Deep Belief Networks (DBN), one of the deep learning methods is used to identify the frequency. An arbitrary threshold to learning error (Target_error_rate) is set so that the over-fitting can be prevented and the output value does not come close to the teacher value of each output cell. In order to examine the validity of the proposed method, experiments were conducted using data obtained by imaging at fMRI. 4 healthy Japanese men who have no hearing impairment participated as subject. C7 and C#7 were randomly presented 60 times as auditory stimuli with fMRI. 40 learning data from C7 and C#7, and 20 evaluation data from C7 and C#7 are randomly set. Target_error_rate is set to "0.1". Individual learning of all the subjects was successfully finished, however Target_error_rate not reached 0.1 in group learning. The best identification rate of deep learning was 67.5% in the individual learning and 55.0% in the group learning. The best identification rate is usually attained according to number of cells in

RBM 2 layers. In this study, the number of cells were 800~450(1st layer) and 650~350(2nd layer) in the individual learning, and 500~450(1st layer) and 520~400(2nd layer) in the group learning, which was predictable to some extent. However, the identification rate in the individual learning was not successfully finished and 55.0%, which was low. This could be because the size of the primary auditory cortex in each subject were different. When 2 subjects who have the same number of input cells were chosen, successfully finished and the identification rate and 92.5%. Thus, it is assumed that the input cell number matching is related to the recognition rate. In conclusion, it is likely that the proposed method using deep learning is useful in developing scale decoding.

Keywords: Auditory Cortex, Deep Learning, fMRI, Frequency Localization