Exponential First Passage Time Approximations of Neuron Model with Conductance-Based Dynamics
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[Introduction/Motivation:]
The first-passage time problem of the stochastic leaky-integrate-and-fire (SLIF) neuron model remains a challenge despite a large amount of work on the topic (Burkitt, 2006). Apart from the work on escape noise in the time-homogeneous case (see e.g. Gerstner et al., 2014, chapter 9) most approaches focus on numerical methods (Buonocore et al., 2011). Large Deviation Theory (LDT) and in particular the Freidlin-Wentzell Theory (Touchette, 2009a, Freidlin and Wentzell, 1984) provides a framework in which we can treat stochastic processes such as the SLIF analytically in the small-noise limit, i.e. when large deviations from the deterministic path become rare. In this work, we apply the LDT to a leaky integrate and fire model with conductance-based dynamics to analyse one of its major qualitative features, as described in Kuhn, Aertsen, and Rotter, 2004: the non-monotonic firing rate response to balanced scaling of input firing rates.

[Methods:]
We use a diffusion approximation of the leaky integrate and fire model with conductance-based dynamics (Richardson and Gerstner, 2005) and investigate its firing response curve under balanced excitation and inhibition with simulations in NEST and R, see Figure 1. We then cast the resulting Itô diffusion process into a normal form which induces an action functional. This functional associates to each possible voltage trajectory a cost, measured by how much the trajectory deviates from the unperturbed dynamics. Freidlin-Wentzell-Theory now tells us that the probabilities of certain events F, such as a first passage through a constant boundary, scale as the most likely, i.e. least costly, event from this set. Effectively, this reduces to solving an optimal control problem with constrained end-points.

[Results and Discussion:]
We derive an expression that explains the non-monotonic response described by Kuhn, Aertsen, and Rotter, 2004, see Figure 2. Unser some additional simplifying assumptions, this expression reduces to
\[ E(T^\sigma) \approx \exp \left\{ \frac{V_{th}^2 (2R_E + 1)^2}{2R_E} \right\} . \]

Despite the asymptotic nature of the estimator, the resulting expressions manage to capture the qualitative characteristics to a high level of accuracy. However, most quantitative features concerning the exact scaling of the curve are not represented correctly. The diffusion approximation and some additional approximations in the derivation cause this scaling discrepancy, but they do not interfere with the qualitative characteristics. This hints at a stronger theoretical relationship between optimal control and neuron models than the Freidlin-Wentzell theory predicts and this connection warrants further investigation.
Figure 1: $\lambda_E$ is the rate of incoming excitatory spikes. For these plots, the inhibitory rate $\lambda_I$ was varied accordingly to maintain balanced input. Left: The free mean potential was kept constant at approximately -55 mV. Right: The free variance displays the same non-monotonic behaviour as the shot-noise model, albeit at a very different time scale.

Figure 2: Left: LDT approximation of the First Passage Time Cumulative Distribution Function. Expected Value $E(T^{E})$ in red and $1/E(T^{E})$ as an inset for comparison with Figure 1. Right: Same for Probability Density Function.
References:


Communication optimisation in distributed Spiking Neural Network simulations

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[Introduction/Motivation:]
In the context of distributed computation, higher parallelism is desirable to split the computation into parts that can be independently executed. The ideal scenario is that such parts do not require any level of synchronisation to speed-up execution time. In Spiking Neuron Network (SNN) simulations, this is not realistic due to the high level of interconnectivity amongst neurons. Thus, higher parallelism results in increased communication overhead, often limiting scalability [1].

There are two ways of mitigating the parallel communication overhead in neuronal simulations: communicating more efficiently (spike propagation); and decreasing the amount of data to be sent (number of spikes that need to go across partitions). This work proposes solutions to the scale of communication overhead at both levels.

[Methods:]
Sending every spike to all processes has been shown to scale poorly for large parallel sims and be wasteful because not all partitions require all spike data [3,4]. Thus, by only sending the relevant data to the interested processes, communication volume can be reduced. Two alternative point-to-point strategies are proposed, (P2P and Subscriber), based on how the inter-process messages are coordinated at each simulation time step.

Parallel simulators that have considered the mapping of neurons to processes have focused on computational load balance alone [5]. To date, state-of-the-art parallel simulators are not considering communication amongst neurons to inform the mapping of neurons to processes. Authors have suggested the impact of neuron connectivity would have [2,6], but not on actual network activity. The proposed approach models the SNN as a graph, where the vertices (neurons) are weighted proportional to their activity during simulation (neurons with high activity spike frequently, hence communicating more often with post-synaptic neurons). Multilevel k-way partitioning is used to minimise the volume of communication between vertices and map them to processes. To gather results, 500ms simulation of a Cortical Microcircuit model [7] is performed across both experiments.

[Results and Discussion:]
Figure 1 shows poor scalability of the collective all-to-all communication strategy and the reduction in communication volume when using point-to-point strategies with respect to an all to all pattern. Not only the communication is reduced, but it scales linearly with the number of processes (level of paralellisation).

The distribution of workload based on the communication volume of neurons is shown to reduce communication in distributed simulations in figure 2. Two baselines are shown: random allocation and static partitioning (graph partitioning with equal weights for all edges and vertices). Repartitioning based on network activity shows an improvement of ~40% over random and ~12-15% over static partitioning.
As the total communication during simulation is reduced, simulations are expected to run faster, particularly given the scale of the communication volume in spiking neuron simulations (20-25MB for a 500ms simulation with 48 processes). Further work could look into dynamic partitioning and graph analysis to inform partitioning in heterogeneous architectures (where processes can accept different workload).

Figure 1: Scaling of the number and weight of messages sent across during distributed simulations using three different communication strategies

Figure 2: Communication costs with different workload allocation strategies (SNN model is scaled with the number of processes)

References:
Cultured neuronal networks as complex systems

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[Introduction/Motivation:] Having simulated various network topologies, as well as having dealt with several dynamical models taking into account the spiking character of neurons, the next natural step is to culture real neuronal networks.

The goal of this line of research is to compare the theoretically-based simulations with the experimental data acquired, both from electrical activity and from structure; moreover, the idea is then to compare the interrelation, which we found in our simulations, between the dynamical output of a particular neuron and its place in the network.

[Methods:] For the first part of the work (i.e., the simulation part), we used numerical integration of several nonlinear models of neuronal spiking (specifically: Morris-Lecar, Fitzhugh-Nagumo and Rössler), for various network dispositions (Scale-Free, Erdös-Rényi, Star and Geometric), based on physiological observations of the brain and mathematical simplifications.

Regarding this part, we have cultured neuronal networks extracted from \textit{Schistocerca gregaria}. We remove every part of the connective tissue and let the neurons “find each others” to explore and record the growth of the network. We let the network grow in a Petri dish about 200 electrodes inserted in it (called Micro Electrodes Array, i.e. MEAs), which enable us the recording of the electrical activity of small groups of neurons.

[Results and Discussion:] In this ongoing experiment we will compare and, ideally, try to classify: firstly to which of the selected network topologies, if to any, the cultured version corresponds; secondly, we want to discriminate between oscillatory models in this particular species, hopefully achievable with some complexity analysis techniques.
Figure 1: Example of a cultured neuronal network (left) and a zoomed version (right). We notice the electrodes (solid black lines) and the neurons (greenish blobs) with their connections clearly.

References:

Synaptology of the mesial temporal cortex in Alzheimer’s disease

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Alzheimer’s disease (AD) is the main cause of dementia, accounting for 60–80% of all cases. During the course of the disease, three main neuropathological alterations occur: cerebral atrophy, intracellular neurofibrillary tangles and extracellular amyloid plaques. Early loss of episodic memory in AD patients is closely associated with the progressive degeneration of medial temporal lobe structures, including the hippocampal formation and adjacent cortex. In addition, neurofibrillar tangles are first observed in the transentorhinal (TEC), entorhinal cortex and hippocampal CA1 field. Synapse loss has also been reported, but relatively few detailed studies have been performed using electron microscopy. This is important because elucidation of the changes that affect synapses is crucial for better understanding the pathogenic mechanisms underlying AD.

Brain tissue from 5 AD patients and 6 control subjects with no neurological alterations were used in this study. These human brain samples had less than 3h postmortem delays. A 3D ultrastructural analysis of the neuropil in layer II of the TEC and superficial pyramidal layer of the medial CA1 was performed. We used an instrument that combines a high-resolution field-emission SEM column with a focused gallium ion beam (FIB), which mills the sample surface on a nanometer scale. The sequential and automated use of FIB milling and SEM imaging allows us to obtain large image stacks that represent a three-dimensional sample. Customized analysis software was used for the reconstruction of synapses, which allowed their number, morphology (surface area of the synaptic apposition surface) and spatial distribution to be calculated. These spatial and morphological data are of great interest in terms of synaptic function.

Our preliminary results show that the total number of synapses per volume in AD patients was lower than in controls, both in CA1 and TEC. However, we have not found differences in the morphology of the synapses in AD patients compared with control subjects. Furthermore, the spatial organization of synapses showed a nearly random 3D distribution, regardless of the subject group and the region analyzed. In conclusion, these data show a decrease in the density of synapses in these brain regions in AD patients but both the spatial distribution and size of the synapses remain unchanged. Further studies will be performed to extend these observations to other brain areas of AD patients and to try to elucidate the functional consequences of these synaptic changes.
Feature Aware Domain Adaptation for Robust Medical Signal Processing

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Introduction

Unlike most machine learning systems, the human brain is able to transfer knowledge between tasks and reliably process incoming data under a great variety of conditions. One core property enabling robust signal processing in the brain is likely the use of feedback mechanisms and integration of high level knowledge in low level processing streams. In this work, our goal is to explore ways of transferring this methodology to deep learning systems.

We propose the use of techniques developed in the context of artistic style transfer to provide new means for domain adaptation in medical data, in particular images and electrophysiological recordings. The code will be made available at stes.github.io/fan.

Methods

Domain Adaptation

In this work, we adapt the notion of domain adaptation also given in the review by [6]. A domain is denoted as a tuple $(\mathcal{X}, P_\mathcal{X})$ of a space $\mathcal{X}$ and a distribution $P_\mathcal{X}$. In our setting, we do not only deal with a single source and a single target domain, but rather with a set of domains $\{\mathcal{X}_k\}_{k=1}^N$ which are part of a common signal space $\mathcal{U} \supseteq \mathcal{X}_k \forall k \in [N]$. We consider each domain here to be fully defined as a set of samples directly given by $\mathcal{X}_k := \{x(j)\}_{j=1}^{N_k}$ drawn i.i.d. from $P_\mathcal{X}$. As a last requirement, we assume that a feature space $\mathcal{V}$ and measurement functions $\Phi_k : \mathcal{V} \rightarrow \mathcal{X}_k$ exists such that for each $x \in \mathcal{X}_k$, there exists $v \in \mathcal{V}$ with $\Phi_k(v) = x_k$. This view can also be extended in a probabilistic way by adding noise to the measurement process. For a subset of domains with $k \in I$, labels $Y_k = \{y(j)\}_{j=1}^{N_k}$ are available. Goal of the adaptation is to be able to apply an algorithm fitted to $(\mathcal{X}_I, Y_I)$ on all data domains by transforming $x \in \mathcal{X}_k$ to $x' \in \mathcal{X}_I$ such that the latent representation $v \in \mathcal{V}$ (the content) of both samples is preserved.

Adaptive Normalization Techniques

We propose the use of techniques known from style transfer [2] to perform domain adaptation for medical data. While the original algorithm was based on an iterative optimization algorithm, recent work has trained a deep neural network to perform feed-forward stylization. Interestingly, it was shown that it is sufficient to retrain the parameters of the network’s Batch Normalization [4] layers. Inspired by this technique, Instance Normalization [8] and Adaptive Instance Normalization [3] were developed. In the context of color normalization for domain adaptation in digital pathology, Feature Aware Normalization (FAN) [1] was developed using similar underlying principles.

Building on the work of [1], we investigate FAN for artifact removal and normalization of EEG signals and other electrophysiological recordings. For training, the domains $\mathcal{X}_k$ can be chosen to match patients (subject-to-subject transfer), time (session-to-session transfer) or the signal acquisition equipment.

The FAN module can be applied at any feature level in the network and normalizes each feature map $k$ of the signal representation $y$ by using features $z_j$ computed from the input $x$, yielding

$$y_k = \frac{y_k - \mu_k(y)}{\sqrt{\sigma_k^2(y) + \epsilon}} \cdot (\sum_j W_{M_k}^{(k,j)} \cdot z_j) + \beta (\sum_j W_A^{(k,j)} \cdot z_j).$$ (1)

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Here, $\mu_k(y)$ and $\sigma^2_k(y)$ denote mean and variance computed over the spatial and batch dimension of feature map $k$. Suitable choices for $\gamma$ and $\beta$ are sigmoid and ReLU units, respectively [1].

**Acquiring Features** While [1] used a pre-trained neural network from computer vision research for feature extraction, this might not always be possible in neuroscience. In this work, we adapt the technique proposed by [7] for training a transcription network generating features useful for artifact removal and modeling of the signal. We evaluate FAN in this context on the MASS sleep dataset [5] and datasets for session-to-session and patient-to-patient transfer from research on brain computer interfaces.

**Results and Discussion**

Context based normalization in deep neural networks has been shown to offer superior performance in both style transfer [3] and domain adaptation in medical image processing [1]. Building on these results, we show preliminary results on EEG classification tasks and highlight the applicability of these approaches in neuroscience research.

One interesting aspect of this approach is the use of high level feature information for low level signal processing, which might be motivated by principles such as spatial or color constancy in the visual system.

**References**


Synaptology of the somatosensory cortex in the adult mouse

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Most cortical synapses are established in the neuropil, which is composed of dendrites, axons and glial processes. There are two basic types of synapses: asymmetric or type I synapses, usually excitatory (glutamatergic), and symmetric or type II synapses, usually inhibitory (GABAergic). Most synapses in the neuropil (75-95%) are excitatory, while a minority (25-5%) are inhibitory. Synapses can be established either on the dendritic spines of excitatory neurons or on the dendritic shaft of both excitatory and inhibitory neurons. It is important to describe the morphology of excitatory and inhibitory synapses, as well as their density and location, because these parameters have a functional correlate. In addition, we have studied the possible correlation between mitochondria, multivesicular bodies (MVBs) and synapses.

For that purpose, we used three-dimensional electron microscopy with combined focused ion beam milling and scanning electron microscopy (FIB/SEM), a method that allows us to obtain long series of consecutive sections in an automated way. These stacks of serial sections can later be examined and segmented in 3D. We obtained seven stacks of serial sections from the neuropil of the six layers of the mouse somatosensory cortex. Using dedicated software (Espina), we have studied over 3550 synapses within these stacks.

Preliminary data show that the mean synapse density is 1.43 synapses/µm³, ranging from 0.93 synapses/µm³ in layer I to 1.69 synapses/µm³ in layer Vb. We found that most synapses were excitatory (95%). Regarding the location of synapses, the vast majority of them were excitatory synapses located on spines (83%), followed by excitatory synapses on dendritic shafts (12%), inhibitory synapses on dendritic shafts (3%) and inhibitory synapses on spines (2%). Therefore, it is to be noted that there are different preferences on synapse location depending on the type of synapse.

This work provides accurate quantitative data that helps understand the mouse cortical circuitry and will be useful to refine current cortical models.
SpiNNakEar - Auditory pathway modelling on neuromorphic hardware

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Introduction

The aim of this research is to investigate the mechanisms in which mammalian brains interpret sound stimuli and to replicate such mechanisms in a neuromorphic system.

The mammalian ear extracts many useful features from a sound stimulus that have been essential in evolutionary survival. Such attempts to replicate these capabilities using various methods of frequency analysis and computer algorithms currently cannot match human performance in a range of hearing tasks [DS17] [Lip97] [SM12]. We believe this is due to the adaptive biological representation of sound stimuli in the brain.

Method

The SpiNNakEar system has been developed to run existing, biologically faithful auditory pathway models [Med06] on a SpiNNaker machine [FGTP14]. This hardware implementation allows for a real-time simulation platform to a biological scale. The SpiNNakEar system is made up of a pipeline of event driven applications running across a network of microprocessor cores on a SpiNNaker machine. Each of these applications runs a small part of the full model of the auditory pathway: starting at the outer and middle ear, through the inner ear cochlea and finally ending as spiking action potentials on the auditory nerve.

Results

The results shown in Fig. 1 show the time varying auditory nerve spike rates across 1 ms windows to a 6.9 kHz sinusoidal 68 dBSPL stimulus, first in Fig. 1a from physiological data gathered by Westerman and Smith [WS87] and then from Matlab Auditory Periphery (MAP) and SpiNNakEar implementations of the auditory periphery model in Fig. 1b. These results show both model implementations produce a biologically similar response consisting of a pre-stimulus response of approximately 50 sp/s, followed by a peak response at stimulus onset at around 800 sp/s, decaying to an adapted rate in the region of 170 sp/s. Finally at stimulus removal rates significantly drop during an offset period before returning to spontaneous firing rates of approximately 50 sp/s.

Discussion

The human auditory nerve consists of approximately 30,000 fibres arranged tonotopically to represent the incoming sound stimuli. We suggest that this large number is important in representing salient sound information to the brain.

A major advantage of the SpiNNakEar system over alternative hardware is that simulations can achieve these levels of scaling without incurring a performance penalty. Another advantage of using this computational resource is that we are able to easily interface the auditory pathway models with subsequent theoretical spiking neural networks of cortical regions of the brain running on the same machine.

The main disadvantage for this implementation is the limitation in the digital sampling rate of the incoming sound stimulus to 22 kHz for real-time processing. This does limit the maximum stimulus frequency that can be simulated to $\approx 10$ kHz. This can be increased by paying a penalty of simulating at slower than real-time speed.

Future work will be investigating the role of descending projections in the auditory pathway using the SpiNNakEar system. We will attempt to replicate experimental results of a Pavlovian conditioning study on enhancing the receptive field of auditory pathway neurons [FSEK03].

References

Figure 1: Post stimulus time histogram responses to 352 repetitions of a 400 ms 6.9 kHz 68 dBSPL stimulus from experimental data obtained by Westerman and Smith [WS87] of an HSR AN fibre in a gerbil (1a) and the same experiment repeated for MAP and SpiNNaker implementations (1b).


Fighting Inactivity to Prevent Cognitive Decline: The Role of Dopamine in Modulating Physical Activity Levels in Older Adults

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Introduction: Alzheimer’s Disease (AD) is the world’s leading cause of dementia. AD is a devastating neurodegenerative disease that progressively impairs cognition and ultimately results in dependence and death. Although great efforts have been made in the pursuit of a pharmaceutical compound effective at changing the course of disease, to date, these have failed. We now know that the neuropathological process underlying AD starts up to 20 years before the first clinical symptoms of the disease manifest. This could be one of the reasons behind the lack of progress in the search for a pharmacological treatment, since by the time AD is diagnosed, the extent of the damage is so widespread that little can be done. For these reasons, attention has moved towards AD prevention. Several different modifiable lifestyle factors have been identified as potential tools to prevent AD or at least delay its onset. Physical activity is one of the most widely studied lifestyle factors, with evidence emerging from both cross-sectional and intervention studies. It is now widely accepted that physical activity is associated with reduced risk of AD and changes in AD markers such as brain volume, amyloid-beta deposition and cognitive performance. Furthermore, it is also imperative to identify individuals who are at greater risk of developing AD, such as carriers of the Apolipoprotein E gene (APOE) ε4 allele, and whether this genetic carriage alters the level of benefit gained from physical activity.

Methods: The purpose of the current study is to investigate the interaction between genetic factors and physical activity, and their contribution to risk of cognitive decline and AD. More specifically, efficient dopamine transmission has been claimed to be a powerful predictor of physical activity in several animal studies and a few human studies. We will calculate a genetic risk score of poor dopamine transmission, through the combination of different risk genotypes for genes encoding proteins involved in dopamine synthesis, transport and reception. Once we have calculated the dopamine genetic risk score, we will apply moderation and mediation statistical analyses to examine the relationship between our genetic risk scores and different AD risk indicators (such as neuropsychological scores, amyloid-beta deposition or AD susceptible brain structure volumes) and whether such relationships are mediated (or moderated) by the amount of physical activity that the individual practices. APOE genotype, age, body mass index and sex will be included as possible confounding variables in the analyses. The sample used for these analyses will be cognitively healthy older men and women aged 60 years and over, from the Australian Imaging, Biomarker and Lifestyle study (AIBL). We will utilise genetic data, cognitive scores and self-reported measures of physical activity from a set of 883 participants, which have been followed up every 18 months for up to 9 years. Amyloid-beta (Aβ) deposition data (derived from Positron Emission Tomography Imaging), volumetric data (derived from Magnetic Resonance Imaging) and actigraphy data are also available from limited subsamples (259, 233 and 233 respectively).

Results: Expected results are outlined in Figure 1.
We hypothesize that people with more efficient dopamine transmission (as a result of the carriage of a greater number of beneficial alleles in genes involved in dopamine synthesis, transport and reception) will engage more in physical activity, which will reduce the risk of developing AD pathology (indicated by lower Aβ deposition, greater hippocampal volume and better cognitive performance).

References:


Detecting cognitive decline through dialogue processing

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[Introduction/Motivation:] Due to the severe incidence of dementia across the world, its care and prevention are increasingly demanded by public health [1], with a focus on early detection and improved caregiving. As language impairment is a common symptom of dementia and a good source of clinical information for its assessment [2-4], our research aims to characterise potentially disrupted communication patterns related to cognitive function and decline. Identifying such features will ultimately help us design assistive technologies able to automatically monitor cognitive status (i.e. adaptive interfaces, social robotics), in order to allow older people to live at home longer, and as independently as possible [5, 6]. In the present work, our hypothesis is that patients suffering from Alzheimer’s Disease (AD) will show identifiable patterns during dialogue interactions (i.e. disrupted turn-taking patterns, differences in speech rate).

[Methods:] We employ spontaneous, conversational data gathered by the Carolina Conversations Collections [7] to train a machine learning model to differentiate AD and non-AD patients. Here, we included 21 patients and 17 controls, over 65 years old. The data was pre-processed to generate vocalisation graphs (figure 1) and extract speech rate information. These and the diagnostic annotations (AD vs. non-AD) were used for the supervised learning training of the model. Then, this classifier was evaluated on its ability to predict such annotations (AD vs. non-AD), implementing 10-fold cross-validation.

[Results and Discussion:] The classifier reached up to 83% accuracy, based on turn-taking patterns and speech rate. Precision, recall and $F_1$ scores were also calculated (figure 2). These are preliminary results of a research in progress, as we are currently pre-processing the rest of the dataset and will be trying different methods for dialogue analysis and natural language processing in the short term.

All in all, there are several linguistic parameters that are promising to be helpful in the assessment of cognitive functioning [2-4]. Our approach does not rely on speech transcription content, but on speech-silence patterns and basic prosodic information extracted from spontaneous spoken dialogue. Still, it obtains levels of accuracy comparable to state-of-the-art systems that rely on more complex features. This opens the possibility of devising mental health monitoring methods which would be non-invasive and low-cost in terms of time and resources.

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Figure 1: Vocalisation graph example

(Markov diagrams describing the transition relationships between events like speech, pauses, joint talk, switching pauses).

Figure 2: ROC curve representing precision and recall (sensitivity) of the classifier.

References:


Towards Grasping with Spiking Neural Networks for Anthropomorphic Robot Hands

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I. Motivation

The way movement is represented and executed in biology is an active field of research. The human hand is a complex system that can perform a wide range of motions with great flexibility and adaptation, for example, playing the piano or grasping unknown objects. Humans can remember grasp motions and modify them during execution based on the shape and the interaction with objects. However, studies show that only a small grasp repertoire is actually used [2]. Furthermore, a principle component analysis revealed that the first two components determine the 80% of the variance of all grasps [3]. A generally accepted hypothesis is that the central nervous system (CNS) uses motor building blocks when performing motion tasks [4]. These building blocks are called motor primitives [5] and are formed by muscle synergies [6]. In this context, the term synergy refers to the coupling of motor activation. A common assumption is that these primitives are linearly combined by the CNS in a hierarchical manner to compose complex motions [7]. These insights have been successfully transferred in robotics, for instance in the concepts of eigengrasps [8] and dynamic movement primitives [9].

Spiking neural networks (SNN) focus on biological plausibility [10]. Plasticity is used for learning by changing the synaptic weights. In a neuro-robotics context, there are approaches of SNNs using spike time dependent plasticity (STDP). For instance, to learn transformations of spatio-temporal data between coordinate systems [11], [12]. Inspired by this research, approaches for learning robot kinematics in simulation [13] and with a real robotic arm [14] were developed.

II. Methods

Our SNN approach is inspired by the biological concepts of hierarchical motion representation [7] and motor primitives [4] for grasping using muscle synergies [6]. We make the following assumptions for the fingers and for the hand. The hand makes different types of grasp motions when picking a pen from a table (pinch) than when holding a tennis racket (cylinder). The motion of a single finger, in the examples above, is represented by the synergies between its joints and defines a motor primitive.

Consequently, the motion representation and control movements are modeled using two types of networks, one for the fingers and one for the hand (see Fig. [1]). The finger networks control the movements of single fingers independent of the task, while the hand network coordinates the activation of the finger networks to resemble a specific grasp motion. Training data is recorded from human demonstration to train the SNN.

III. Results and Discussion

In this work, we present a model of a hierarchical SNN with a biologically inspired architecture that is able to learn and perform different grasp motions. Our model combines two different network types, one for the fingers and one for the hand. The finger networks learn different motor primitives as synergies between the joints. The hand network efficiently represents different grasp types coordinating the finger networks reusing the learned motor primitives. Both, the hand and the finger networks, are trained independently using STDP. Finally, we incorporate a mechanism for tactile feedback in the finger networks to stop the motion on contact. We evaluate our model with two different grasp types, i.e. pinch and cylinder [2]. After learning from human demonstration, the SNN is evaluated in simulation and on a real anthropomorphic robot hand.

* Presentation of the work in Tieck et al. [1]
Fig. 1: Complete architecture. The hand network (left) receives the proprioception of all fingers and a grasp type signal to generate fingertip targets. Each finger network (middle) receives its proprioception and fingertip target to generate motor commands.

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REFERENCES

The impact of music on the brainwave oscillations in children

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Motivation
The purpose of this study was to investigate the impact of music on the bioelectrical activity of the brain in children with genetic epilepsy and in healthy control group.

Methods
The prospective randomised study was carried out in the Department of Neurology, in Children's Hospital, Affiliate of Vilnius University Hospital Santaros klinikos. Children with generalised or focal genetic epilepsy and also healthy controls were investigated. All patients underwent electroencephalograms with auditory stimulation of W. A. Mozart's Sonata for Two Pianos in D major, K.448. The absolute spectral power of brainwaves in delta (1-4Hz), theta (4-8Hz), alpha (8-13Hz) and beta (13-25Hz) frequencies in both periods of silence and music was compared. The data was analysed in all electrodes together (hereinafter referred as E), as well as in groups of electrodes: frontal (F), central (C), temporal (T), parietal (P) and occipital (O). Demographic and clinical data of the patients were also analysed. Data analysis was carried out using Matlab software with EEGLAB toolbox.

Results
Data of 52 patients, aged 12,2 ± 3,7 years old, 28 females, 24 males was analysed. There were 32 patients in the epilepsy group (18 with focal and 14 with generalised epilepsy) and 20 healthy controls. There was no statistically significant difference between the demographic data of the groups.
Comparing the periods of silence and music, the epilepsy group had a significantly reduced absolute brainwave power during music in theta (E, P, O), alpha (E, F, P, T, O) and beta (E, P, O) frequencies. In the control group, the absolute brainwave power also reduced in delta (P, O), theta (E, F, P, T, O), alpha (E, F, P, T, O), beta (E, P, T, O) frequencies while listening to music. No significant correlations with age, gender, type of epilepsy or antiepileptic medications were observed.

Discussion
Listening to music significantly reduced absolute brainwave power both in epilepsy and control groups, mostly in parietal and occipital areas. However, this effect included a wider range of frequencies and electrode groups in the control group. To better understand this phenomenon, a further investigation of the differences in the brainwave oscillations between healthy population and patients with epilepsy would be needed.
Ordinal Synchronization: A novel approach for quantifying synchronization

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[Introduction/Motivation:]
We propose Ordinal Synchronization as a new measure of synchronization, based on the correlation of temporal ordinal patterns extracted from any pair of time series, in a natural development from Bandt and Pompe’s method¹. We test the performance of Ordinal Synchronization with datasets coming from unidirectionally coupled electronic Lorenz oscillators and brain imaging datasets obtained with magnetoencephalographic recordings. Given the fact that more often than not, brain signals are very noisy and nonstationary [²], and its synchronization calculation very demanding, OS seems to provide a fast and robust-to noise tool to assess synchronization, without any implicit assumption about the distribution of data nor its dynamical properties. Nonetheless, as it ranges from [-1, 1], it captures inverse synchronization, where two coupled nodes act synchronously in an inverse fashion, a neglected but plausible mechanism in the brain. The goal of this study is a better characterization of the advantages and pitfalls of Ordinal Synchronization in the presence of different noise perturbations and different levels of coupling strength, in electronic oscillators and brain imaging datasets, trying to understand what the best length of the patterns is to account for the synchronous state. 

[Methods:]
To assess the validity of the measure, and to unveil which is the best length of the ordinal patterns extracted to quantify synchronization, two Lorenz oscillators will be studied (in Master-Slave configuration), varying the strength of the coupling and perturbing the system with different noise signals in different conditions: equal noise in both oscillators, noise in the Master node, and noise in the Slave node. Comparisons with Spectral Coherence (SC), Mutual Information (MI), Phase Locking Value (PLV) and Pearson Correlation (Rho) will be provided, to assess the extent to which Ordinal Synchronization (OS) is able to capture synchronization in a similar manner. Different length of the patterns will be tested, and a Generalized Linear Model will be fitted to decompose the variance of OS and predict its value depending on the level of noise and level of coupling.

The final goal of OS is to serve as a synchronization measure in real datasets. Thus, resting-state MEG data will be analysed, studied broad-band and filtered in the most common frequency bands: θ, α₁, α₂, β₁ and β₂. Then, results will be compared with SC, MI, PLV and Rho, and, with an estimation of the SNR in the empirical data, the bias due to noise will be corrected.
[Results and Discussion:]
The experiment is ongoing, and for now, we have found a relation between the width of the studied frequencies and the length of the patterns, as well as a good concordance between OS and the other classical synchronization measures. OS seems to be robust to noise and give a good resolution capturing synchronization. The effect of the perturbation depending on the node is still a matter of debate.

References:


Detection of normal speech development using artificial neural networks

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[Introduction/Motivation:] Speech is defined as the production of complex coordinated movements of meaningful sounds through respiration, phonation, and articulation. Infants (0-12 months of age) process auditory inputs from their environments, and produce random vocal sounds (vocalizations) as explorations during speech development. Cooing, goosing, squealing and babbling are some of these vocal sounds [1][2][3]. Recognition of speech patterns gives information about the normal development. Currently, pediatricians and other professionals use global scale assessments (GSA) or clinical observation to distinguish between normal and non-normal speech development. Eventhough, early diagnosis of speech delays are rarely done. Moreover, in most cases parents are unable to recognize speech problems in their kids [4]. Infant’s vocalization can be recorder and study with computational models to understand speech behavior and development. Nevertheless, more data and research are needed in order to design models that can analyze the vocal sounds produced by infants [5]. Artificial neural networks are learning methods that has been successfully applied in speech recognition [6]. Consequently, the detection of normal speech development is proposed as an artificial neural network model train with infant’s vocal sounds and data of standardize speech development assessments, tests, and questionnaires.

[Methods:] Infants (between 0 and 12 months of age) of Antioquia-Colombia are going to be study to understand the speech development (SD). The SD characteristics will be divided into two groups: vocal sounds, defined as babbling or vocalization types; and other characteristics which help in the description of the stage development. The data needed will be collected by the application of the GSA shortened version standardized for colombian children [4], an auditory discrimination test, a questionnarie about sociodemographic information, and a questionnarie based on the LittlEARS® Early Speech Production Questionnaire [7]. Furthermore, vocal sounds recordings will be performed in order to collect data to train the neural network [5]. With the acquired data we will classify the infants into two classes: normal and non-normal speech development. Initially, the artificial neural network will be train to classify the infants into these classes using the vocal sounds recordings as input. Then, we will try the questionnaires data to improve the classifier.

[Results and Discussion:] We aim to design an artificial neural network model with the ability to process infant’s vocal sounds and the biological age to identify whether the infant has a normal speech development or not. Design an accurate real data based system will help health professionals and parents monitor speech development. Ultimately, improving early diagnoses of delays in speech development will increase timely treatments [5].
References:
Reservoir Computing (RC) is one of the rare computing paradigms which can be used both as a theoretical neuroscience modelMaass et al. [2002] and as a machine learning toolJaeger and Haas [2004]. The key feature of the RC paradigm is its reservoir a directed and weighted network that represents the connections between neurons. Despite extensive research efforts, the impact of the reservoir topology on the RC performance remains unclear. Here we explore this fundamental question and show, both analytically and computationally, how structural features determine the type of tasks that these recurrent neural networks can perform.

We focus on two network properties: First, by studying the correlations between neurons we demonstrate how the degree distribution affects the short-term memory of the reservoir. And second, after showing that adapting the reservoir to the frequency of the time series to be processed increases the performance we demonstrate how this adaptation is dependent on the abundance of short cycles in the network.

Based on our previous results we create an optimization strategy to improve time series forecasting performance. We validate our results with various benchmark problems, in which we surpass state-of-the-art implementations. Our approach provides a new way of designing more efficient recurrent neural networks and to understand how the computational role of common network properties.

References


Figure 1: **Relationship between memory capacity, neuron correlation and the network spectrum.** (a) Short-term memory capacity $M$ vs neuron state correlation $S$. (b) Neuron state correlation $S$ vs average eigenvalue modulus $\langle |\lambda| \rangle$. The different lines represent various network topologies with a wide range of parameters, but a fixed number of nodes.

Figure 2: We plot the ESN error $\sigma$, for the tasks of forecasting Mackey-Glass (a, d, g), Laser Intensity (b, e, h), and recognizing Spoken Arabic Digits (c, f, i). The variable $\rho$, accounts for fraction of cycles. Our figure shows that the optimal $\rho$, while different between tasks and cycles is not 0, as it is in all previous literature. Spectral analysis allows us to obtain an heuristic.
Detection of pathological ageing with artificial neural networks

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[Introduction/Motivation:]
Gradual decline in cognitive functions is common during normal ageing. However, some learning impairment derive in cognitive impairment, which represents a transition between normal ageing and dementia. It is highlighted that prevalence and incidence of dementia has increase in the past few years. This is defined as a cognitive disease that interferes with the functioning of daily life affecting the autonomy and independence of patients, and has a gradual and progressive development [1]. Drawings are used to diagnose different forms of dementia through the analysis of the shapes, organization, components, spatial relationships and tendencies to omit parts or to perseverate in elements. The most commonly used drawing assessments are the rey complex figure, interlocking pentagons, cube, and clock [3]. Clock test shows high sensitivity both for mild dementia, and for the differential diagnosis between cognitive impairment and dementia. Moreover it has been used to identify cognitive impairment six years before it becomes dementia [4][5]. However, some researchers exclaim that it should not be used as an exclusive test to diagnose [6]. Furthermore, it has been proved that the rey complex figure is a more accurate instrument of diagnose [7]. Over the last few years, artificial neural networks (ANN) has been design using neural imaging, questionnaires and clock drawings data to estimate medical diseases as dementia, building predictive models to identify cognitive dysfunctions [2][8]. We propose an ANN to classify into normal and pathological ageing using as inputs only the rey complex figure and the clock draws done by patients.

[Methods:]
Elderly adults with and without pathological ageing diagnoses (cognitive impairment and dementia) are going to be asked to draw the rey complex figure and the clock assessments. To avoid biases in the application instruction we are going to used Ardila’s handbook [9]. Additionally, we will have data about the medical diagnosis of each patient, collected directly by professionals and with the standardized scales of both applied assessments [10]. The ANN will be train to classify the patients into two groups: normal and pathological ageing. For the training we will used draws data as inputs. The architecture for the ANN will be convolutional neuronal network (CNN) since it has shown good properties for images analysis [11].

[Results and Discussion:]
Diagnosis of dementia is usually a problem, and early diagnoses are needed in order to give treatments with better prognosis for the patient quality of life [2]. Therefore, we aim to design an ANN model with the ability to process elderly adults draws to identify whether the adult has a normal or pathological ageing. This is intended to improve diagnosis accuracy at early stages.
References:
Integrating multiple data sources for predicting the mouse mesoconnectome

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One of the original goals of the Human Brain Project was the development of a large-scale cellular level model of the human brain which could be used for understanding fundamental mechanisms of brain diseases and cognition. The achievement of such a goal requires sufficient information about the brain structure, including structural connectivity. Extensive research reporting the connectome of various species has been made, with the closest to the human brain being the mouse connectome at a mesoscale level. However, the connectivity coverage is not complete for all brain areas. The goal of this study is the integration of multiple brain data sources for predicting missing connectivity data by employing machine learning classification techniques and a bayesian framework.

A structural connectivity dataset was used in the analysis in which information about the connectivity strength between sending and receiving mouse brain areas was estimated using the anterograde tracing method. Gene expression data corresponding to the receiving areas and estimated with the in situ hybridization (ISH) method was used as further data source. Both sources were registered into the Allen Brain Atlas. The connectivity strength was binarized in order to indicate connection or non-connection between the areas. Before utilizing multiple data sources, connectivity between brain areas using gene expression data was investigated. Classification models based on the Random Forest and Logistic Regression methods were constructed at which combinations of gene expression values were trained to match the known connectivity patterns. The classification performance of the models was tested with the leave-one-out cross validation method, while the evaluation measures used were average accuracy and area under the ROC curve (AUC). A satisfactory classification performance would then lead to utility of the models for missing value imputation.

The classification models were constructed and evaluated for each sending area separately. The average accuracy over all sending areas estimated was 84% for Random Forest and 87% for Logistic Regression. The average area under the roc curve over all sending areas was 89% for Random Forest and 92% for Logistic Regression. For some areas, both measures exceeded 95%. Single cell RNA-sequence data will be incorporated to make the mesoconnectome cell-type specific with respect to the layered structure of neocortex. Diffusion tensor imaging (DTI) data will also be used for data fusion. A Bayesian framework will be implemented for estimating the posterior probabilities of brain region pairs being connected given the distributions of multiple data sources like the single-cell RNA data, known connectivity patterns and DTI data, while the posteriors will be used to impute the missing values. Taken together, these approaches demonstrate how different sources of information can be combined into a single estimate of the mesoconnectome and lead to its completion.
Figure 1: 3D plot displaying average prediction accuracy of the surface brain areas. The colors to the right represent the prediction accuracy according to the legend. The plotted surface areas are receiving ones. The classification model used is Random Forest. The accuracy of an area is estimated by averaging the prediction accuracy of the model for the connection between the corresponding area and all sending ones.

Figure 2: Area Under the ROC curve (AUC) values for all sending brain areas. X-axis: the two classification approaches: Random Forest (left) – Logistic Regression (right). Y-axis: AUC values.

References:
A software pipeline for efficient processing of 3D high-resolution microscopy images of large brain samples

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[Introduction/Motivation:]

Imaging large biological specimens or whole organs such as whole mouse brains through state of the art microscopy techniques – such as Light-Sheet Fluorescence Microscopy (LSM) and Two-Photon Fluorescence Microscopy (TPFM) – poses significant challenges in terms of data processing and analysis. In particular, high-resolution tomographies acquired with such techniques can produce datasets as big as $10^{12}$ voxels, or several TB in terms of storage. To extract meaningful information out of these datasets, high-throughput analysis tools are needed. As a first step, the mosaic of volumetric data produced by these instruments needs to be stitched and fused to produce a reconstructed global volume. Depending on the specific specimen, the fused volume can then be either aligned to a reference atlas, or undergo further analysis such as vasculature segmentation, cell classification, cell counting, etc.

[Methods:]

We focus primarily on imaging whole mouse brains and human brain tissue. To meet the unique needs of processing this kind of datasets, we have put in place a high-throughput software pipeline for image analysis. In particular we have developed a stitching tool that allows us to reconstruct and query the fused volume. The software is written in Python and is able to cope well both with teravoxel-sized datasets and multichannel datasets. A public Application Programming Interface (API) can be used to perform queries on the stitched datasets and extract subvolumes for further processing. After stitching, we perform manual annotation of cell centroids, cell contours and cell classification. This data is used as the ground truth to train a neural network on the GPU that allows us to perform automatic segmentation and classification. Finally, we are also exploring both lossless and lossy video compression (H.265/MP4) for permanent storage and easier processing of the experimental datasets.

[Results and Discussion:]

The stitching software is currently being used successfully on production datasets. We are able to produce high-resolution tomographies of whole mouse brains and human brain tissues (see figures below). Through machine learning we are able to reconstruct 3D maps of selected cell types in the whole mouse brain, highlighting the spatial distribution of neurons in a macroscopic cerebral volume. Besides being a valuable reference for neurobiologists, these datasets can be used to build realistic point-neuron simulations of the entire brain inside the HBP. In the human brain cortex, we reconstruct the 3D structural organization of neurons to investigate how cells, dendrites and axons are distributed throughout the cortex. The microscopy techniques that we use represent a remarkable advance, in that they allow to acquire 3D images of the cellular spatial distribution in whole mouse brains and of the cellular and laminar structures in the human brain, with the molecular specificity that is needed to build accurate models and atlases.
Figure 1 Left: a single frame of a high-resolution tomography of a whole mouse brain. Right: Purkinje cells automatically localized in the cerebellum of a L7-GFP mouse using semantic deconvolution.

Figure 2 Left: a 2 x 7 x 0.5 mm³ volume of human brain cortex stained with NeuN (red) and DAPI (green). Right: automatic cell segmentation.

References:
Cortical feedback to superficial layers of V1 contains predictive scene information.

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Introduction:
A central characteristic of brain function is the ability to merge sensory input with internal representations of the world [1-3]. Many experiments have progressed our understanding of the feedforward features that modulate early sensory areas, but relatively little is known about the feature space that drives cortical feedback channels. Accessing and describing these internal feedback information channels is central to fully understanding neural computations [4].

To study feedback, one must disentangle feedforward and non-feedforward sources of input, which involves independent stimulation or inactivation of feedback and feedforward pathways. This can be achieved by pairing single- or multiunit recordings with electrical stimulation, pharmacological intervention, cooling or optogenetics [5-6], but these methodologies are generally too invasive for studying the healthy human brain. A non-invasive strategy to measure feedback is to homogenize feedforward input using visual occlusion.

Methods:
We blocked feedforward input to subsections of human retinotopic visual cortex by occluding one quarter of the visual field [7-8]. Participants viewed 384 real-world scenes while we record V1 responses using high-resolution 7T fMRI (0.8mm isotropic). By occluding a portion of these scenes in combination with recordings from high-resolution fMRI, we were able to compare depth-specific V1 responses to computational models of feedforward and feedback processes.

For each V1 voxel (a volumetric pixel in fMRI), we calculated the collective receptive fields of its contained neurons [9] and defined voxel-specific feedforward and feedback models with varying levels of computational complexity. Neurons received meaningful sensory input during non-occluded scene presentations, but not during occluded scene presentations. Therefore, feedforward models were defined as responses related to scenes as they were presented. Feedback models were defined as responses related to scenes as they would be predicted.

Results & Conclusions:
Results from these models show that in superficial layers of cortex, V1 responses exhibit predictive (and higher-level) response properties unique from feedforward orientation and spatial frequency properties typically associated with V1 processing. Our findings suggest that feedback terminating in superficial layers provides V1 neurons with contextual information not available via localized feedforward input. We are now developing more complex models in order to specify the level complexity in feedback to V1. We are also expanding this dataset, which will be available to the HBP community.
Figure 1: **Creation of voxel-specific feature timecourses.** The process of creating feature-based predicted timecourses is shown for one voxel (the pRF of this example voxel is shown in red). Each stimulus image was decomposed into feedforward and feedback Weibull and Gist feature maps. Feedforward maps were based on the image as it was presented, with the occlusion in place. Feedback maps treated the image as if it had not been occluded, and therefore feedback features were based on possible predictive voxel responses. Additionally, a high-level category model based on the SUN database hierarchy was included (Xiao et al., 2010). Feature responses were used to create predicted timecourses, which were convolved with a hemodynamic response function. These feature timecourses were used for encoding models.

Figure 2: **Depth-specific feedforward and feedback voxel tuning.** Voxel tuning histograms are shown for each cortical depth separately. Tuning was calculated by contrasting the unique information encoding of feedforward models to that of feedback models for each voxel. Probability density functions were defined for each cortical depth ROI using kernel density estimation.

**References:**


A dynamic complex network framework to model cognition: unveiling correlation structures from network centrality metrics

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Introduction
Unveiling the secrets of human cognition, developmental processes and learning is still an open question and one of the main goals for many researchers, mainly psychologists and neuroscientists. Such scholars seek for understanding the complex nature of the brain and countless processes it brings about, as well as identifying potential catalysts of individual and collective differential traits, among others [1, 2]. Our research concerns cognitive modelization as an approximation to human cognitive processes, although can be easily extended to other fields. Instead of being focused on a single cognitive process, an alternative approach is gaining ground: dynamic network models of human development and intelligence [3, 4]. Historically, the most outstanding contributions, which may even entail changes on education policies, are mostly based on observation and large batteries of psychometric tests. Statistical analysis techniques, such as exploratory and confirmatory factor analysis or structural equation modelling (SEM) applied to covariance or correlation matrices, which are inferred from experimental data, have led to most well-known theories [5]. However, the meaning and implications of such theories are still a matter of controversy and debate [6-10]. In the framework of dynamic systems, several models have been put forward which unwrap an alternative explanation to former proposals. We build upon them and stress the results of being, actually, a complex network. We show that the temporal evolution of the system and the ultimate correlations structure between processes are undeniably linked to the topology of the network and its coupling with the underlying dynamic process [11]. This framework may be an open door for neuroscience or health science among others, which, at the same time, can provide meaningful and significant data to work with [12-15].

Methods
The most general equation of such dynamic systems can be written in the following way:

\[ \dot{x}_i = F(x_i, t) + \sum_{j \in \text{neighbors}} A_{ij}(t) \cdot G(x_i, x_j, t) \]

We obtain analytical results of two models to further understand the role of network topology and its coupling with the dynamic model and characteristic parameters: we analyse the stability of the system and the corresponding covariance matrices. Moreover, numerical simulations are performed using python as well as statistic multivariate analysis of synthetic data using R.

Results and Discussion
Considering the described models, the final state of each variable is given by a measure of centrality in the network (Figures 1 and 2), equivalent to a biased random walk along the network with rescaled weights. This result and its stability conditions are linked to the structure obtained for covariance matrices (Figure 3). If we consider different network topologies, unlike several intelligence models, no explicit assumptions of underlying constructs or intercorrelations are needed to reproduce observed matrix structures which can be analysed through factorial analysis or SEM (Figure 4).
Figures:

Figure 1: Heterogenous network of 50 variables

Figure 2: Temporal evolution of heterogenous network

Figure 3: Correlation matrix of Erdös-Rényi network. We plot the lower triangular part of the symmetric matrix.

Figure 4: Correlation matrix of heterogenous network. We plot the lower triangular part of the symmetric matrix.

Figure 5: Mean correlation as a function of probability of edge creation for an Erdös-Rényi network

Figure 6: Mean correlation as a function of power law exponent for an heterogenous network

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Bio-inspired Cat Robot: Closed-Loop Locomotion with Neural Central Pattern Generators
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Research on adaptive locomotion has been conducted for many years, especially through neurophysiological and biomechanical studies generally carried independently. However, those complex motor behaviours originate from interactions between the neural system, the musculoskeletal system and the environment which makes exhaustive research in vivo hard to realize in practice. In this work-in-progress, we are developing different a robotic platform embedding classical hardware or a neuromorphic SpiNNaker board to investigate emergence of gait patterns on a quadruped and their relation with body morphology. In opposition to most of the classical robots, animals use tendon-driven actuators whose dynamical properties like stiffness or damping can be tuned in real-time depending on the usage and present unequalled performance in energy consumption and robustness. This aspect is mainly rendered by using compliant deformable and soft parts in the robot mechanics inspired from the cat. A simple model of brain functions is realized with Central Pattern Generators (CPGs) that are modelled with recurrent neural networks.

Technical details
The design process of the platform have been guided considering three main features for the robot: compliance, cheapness, versatility. The compliance is a key element in this research as it is believed to add efficiency and robustness to locomotion, like what we can see in biology. However, it also challenges classical control techniques as the dynamics of the robot is now governed by equations with a higher complexity level. On the current platform, the compliance is mainly ensure by using springs in the legs knee instead of actuating them. This version also works using classical processing hardware (relying on a RaspberryPI computer board and an OpenCM control board for sensing and actuation) and is a step toward a version integrating a spiNNaker board. A view of the mechanical state and the electrical architecture is presented on Figure 1.

\textit{Figure 1: the Tigrillo robot in its current configuration}
Semantic Annotation of Data on Neurodegenerative Diseases in Patients using Ontologies

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In this work, we propose a mid-level ontology for representing various types of data on patients with neurodegenerative diseases. The proposed ontology can be used for semantic annotation of datasets that contain different diagnostic data (clinical, imaging, biomarker, etc) about neurodegenerative diseases and its progression, collected on patients by the hospitals. Having an ontology for describing data on patients with neurodegenerative diseases is important from two different perspectives: (1) from a viewpoint of ontology-based data access (ODBA) [1] it would allow federation queries on data produced and stored at different hospitals; (2) from viewpoint of data analytics it would allow (semi) automatic creation of data analysis workflows based on the datatypes that occur in the datasets, annotated with ontology terms.

The proposed ontology was constructed following best practices from ontology engineering. This involved the use of a top level ontology (Basic Formal Ontology [2]) as a template, and a set of standard formally defined relations. We heavily reused classes and identified mappings to domain terms that are defined in previously developed biomedical ontologies and vocabularies available at BioPortal (http://bioportal.bioontology.org/). This included domain terms from ontologies and vocabularies covering general medicine (such as SNOMED, NCIT, MESH, LOINC, ICD10), neuroscience (such as NIF, BRCT, NeuroMorpho.org) and neurodegenerative diseases (such as ADO, PDON).

The ontology was constructed in a hybrid fashion (see Figure 1). For this purpose, we used two instances of datasets on patients with neurodegenerative diseases [3,4], originating from two well-known studies concerning neurodegenerative diseases: Alzheimer’s Disease Neuroimaging Initiative (ADNI) [5] and Parkinson’s Progression Markers Initiative (PPMI) [6]. We also used the domain terms that appear documentation of ADNI and PPMI studies (study objectives, study protocols, study procedures, schedule of activities and others) [7-11], as we believe that the data produced by the hospitals in the project will most probably be subsets of types of data that occur in ADNI and PPMI studies. To address the data analytics perspective, we also reused and extended our previously developed ontology of data types (OntoDT) [12] and ontology of core data mining entities (OntoDM-core) [13] to represent specific domain datatypes that occur in the datasets from the domain of neurodegenerative diseases. The ontology construction and the semantic annotation of the two instances of neurodegenerative diseases datasets was performed using semantic web technologies (RDF, OWL, RDFS), which are currently a popular solution to data and knowledge sharing and integration.

* Student author
Figure 1. Part of the structure of the constructed ontology for representing data on patients with neurodegenerative diseases. The arrows that are not labeled represent IS-A relations.

Acknowledgements:
Data used in this work were obtained from the Alzheimer’s Disease Neuroimaging Initiative (ADNI) database (adni.loni.usc.edu). As such, the investigators within the ADNI contributed to the design and implementation of ADNI and/or provided data but did not participate in analysis or writing of this report. A complete listing of ADNI investigators can be found at https://goo.gl/43TsVJ. Data used in the preparation of this work was also obtained from the Parkinson’s Progression Markers Initiative (PPMI) database (www.ppmi-info.org/data). For up-to-date information on the study, visit www.ppmi-info.org. “PPMI – a public-private partnership – is funded by the Michael J. Fox Foundation for Parkinson’s Research and funding partners, including list the full names of all of the PPMI funding partners found at www.ppmi-info.org/fundingpartners. We also acknowledge the European Commission’s support through the Human Brain Project (Grant No. 604102).

References:
Learning Movements by Imitation from Event-Based Visual Prediction

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1 Introduction

Prediction is believed to play an important role in the human brain. Indeed, the brain is capable of predicting future sensory input originating from its own actions (forward model), as well as estimating what action it should take to reach a specific sensory input (inverse model) [1]. It has also been stated that the brain learns new forward models faster than associated inverse models [2]. However, it is still unclear how predictions are used in the process of learning new movements. In this paper, we present a biologically inspired method to learn movements from visual prediction. The method consists of two phases: learning a visual prediction model, then optimizing the visual prediction error. To demonstrate the method, we learn a visual prediction model from a demonstration where only visual input is sensed. We then learn to reproduce the seen motion by minimizing the visual prediction error while exploring our own actions. Unlike previous work, we represent visual information with event streams as provided by a Dynamic Vision Sensor [3].

2 Method

An overview of our method is presented in Fig. 1. In the first phase, we train a liquid state machine that can predict future visual input from a single demonstration [4]. This prediction model represents the memory of the demonstrated movement. In the second phase, the robot tries to find the movement most visually similar to the demonstrated one. The similarity between demonstrated and performed movements is evaluated from the visual prediction error. We rely on Covariance Matrix Adaptation Evolution Strategy (CMA-ES) [5] to minimize the prediction error. At each iteration, CMA-ES samples final goal joint positions which are executed by the robot through dynamic movement primitives [6]. For each sample, we evaluate the visual prediction error and use it as a fitness function. After a given number of iterations, the robot learned a movement visually similar to the demonstrated one.

3 Result and discussion

We realize two experiments both in simulation and reality. Demonstrations are recorded either in reality with a Dynamic Vision Sensor (DVS) [3] using the ROS interface [1] or in simulation using the gazebo DVS plugin [2] presented in [7]. We initialize a robot with a similar starting pose as in the demonstration, and initialize CAM-ES with a null movement. The first experiment is a proof of concept where a schunk arm LWA 4P learns to move its arm to a pose demonstrated in simulation, see Fig. 2. After 12 iterations, precise joint goal positions are recovered by our method. For the second experiment, we show that the method is also able to learn from a human demonstration and for more joints. In this experiment, an iCub robot learns to move its arm closer together. Twelve joints are used to perform the motion - for each arm: elbow, wrist prosup, shoulder pitch, shoulder yaw, shoulder roll and wrist pitch. The iCub manages to learn a similar movement to the demonstrated one after 30 iterations.

Figure 1: Our method to learn movements by imitation from event-based visual prediction.

Figure 2: Visualization of the demonstration for the first experiment.

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References


cuHinesBatch: Solving Multiple Hines systems on GPUs *

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Today, we can find multiple initiatives that attempt to simulate the behavior of the Human Brain
by computer simulations [7, 3, 5]. This is one of the most important challenges in the recent history
of computing with a large number of practical applications. One of the ways in which the scientific
community attempts to simulate the behavior of the Human Brain consists of computing the next 3
major steps [4]: The computing of 1) the Voltage on neuron morphology, 2) the synaptic elements in
each of the neurons and 3) the connectivity between the neurons. In this work, we focus on the first step
which is one of the most consuming time steps of the simulation. Also it is strongly linked with the rest
of steps. All these steps must be carried out on each of the neurons. The Human Brain is composed by
about 14 thousand million of neurons, which are completely different among them in size and shape.

The standard algorithm used to compute the Voltage on neurons’ morphology is the Hines algo-
rithm [6]. This algorithm is based on the Thomas algorithm [2], which solves tridiagonal systems. Al-
though the use of GPUs to compute the Thomas algorithm has been deeply studied [10], the differences
among these two algorithms, Hines and Thomas, makes us impossible to use the last one as this can not
deal with the sparsity of the Hines matrix.

Previous works [1] have explored the use of other algorithms based on the Stone’s method [8]. Unlike
Thomas algorithm, this method is parallel. However, it is in need of a higher number of operations
(20n log 2n) with respect to the (8n) operations of the Thomas algorithm to solve one single system of
size n. Also, the use of parallel methods present some additional drawbacks to be dealt with.

Unlike the work presented in [1], where a relatively low number of neurons (128) is computed using
single precision operations, in this work we are able to execute a very high number of neurons (up to
hundreds of thousands) using double precision operations. We have used the Hines algorithm, which is the
optimun method in terms of number of operations, avoiding high expensive computational operations,
such as synchronizations and atomic accesses. Our code is able to compute a high number of systems
(neurons) of any size in one call (CUDA kernel), using one thread per Hines system instead of one
CUDA block per system. Although multiple works have explore the use of GPUs to compute multiple
independent problems in parallel without transforming the data layout [9], the particular characteristics
of the sparsity of the Hines matrices forces us to modify the data layout to efficiently exploit the memory
hierarchy of the GPUs (coalescing accesses to GPU memory). These modifications have not been explored
previously, which are deeply described and analyzed in the present work.

To carry out the experiments, we have used an heterogeneous node³ composed of 2× Intel Xeon
E5-2630v3 (Haswell) with 8 cores and 20 MB L3 cache each, and 2× K80 NVIDIA GPU (Kepler) with
a total of 4992 cores and 24 GB GDDR5 of global memory each. Each K80 is composed of 2×logic
GPUs similar to K40. This node is a Linux (Red Hat 4.4.7-16) machine, on which we have used the next
configuration (compilers version and flags): gcc 4.4.7, nvcc (CUDA) 7.5, -O3, -fopenmp, -arch=sm_37.
The code evaluated in this section is available in a public access repository⁴.

To evaluate the different implementations, we have used real configurations (neurons’ morphologies)⁵.

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itiveness under the project Computación de Altas Prestaciones VII (TIN2015-65316-P) and the Departament
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Economy and Competitiveness under Juan de la Cierva fellowship number IJCI-2015-23266.
⁴ MinoTauro, https://www.bsc.es/es/marenostrum/minotauro
⁵ BSC-GitLab, https://pm.bsc.es/gitlab/imartin1/cuhinesbatch
¹ http://www.neuromorpho.org/
their sizes and number of branches. More details are described in Table 1. We have considered these 6 different morphologies, as a wide range of the neurons fall into the chosen morphologies.

<table>
<thead>
<tr>
<th>Name</th>
<th>Size</th>
<th>#Branches</th>
<th>Code Name</th>
<th>neuron ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>small-low</td>
<td>76</td>
<td>7</td>
<td>299-DG-IN-Neuron2</td>
<td>NMO_00076</td>
</tr>
<tr>
<td>small-high</td>
<td>76</td>
<td>29</td>
<td>202-2-19nj</td>
<td>NMO_00076</td>
</tr>
<tr>
<td>medium-low</td>
<td>305</td>
<td>30</td>
<td>59D-40X</td>
<td>NMO_00302</td>
</tr>
<tr>
<td>medium-high</td>
<td>319</td>
<td>157</td>
<td>Culture-9-5</td>
<td>NMO_00319</td>
</tr>
<tr>
<td>big-low</td>
<td>695</td>
<td>66</td>
<td>28-2-2</td>
<td>NMO_00695</td>
</tr>
<tr>
<td>big-high</td>
<td>691</td>
<td>341</td>
<td>HSE-fluo02</td>
<td>NMO_00691</td>
</tr>
</tbody>
</table>

Table 1. Summary of the neurons used.

Finally, we evaluate the impact on performance of the particularities of each of the morphologies (Table 1). Both approaches, Multicore and Full-Interleaved (GPU), show a similar trend in performance independently of the neurons’ morphology (Figure 1). In particular the peak speedup achieved on the different morphologies does not vary significantly ($47 \times -55 \times$ on GPU).

After comparing the performance achieved by Multicore and GPU, now we focus on evaluating the efficiency of our GPU implementation. To do that, we make use of `nvprof`. We do not obtain results very different depending on the input (number and shape of neurons). In all cases, we obtain more than 99% of efficiency (sm_efficiency). It is also achieved a bandwidth (Global Load Throughput) close to 160 GB/s, being the theoretical peak equal to 240 GB/s and the effective about the bandwidth achieved by our implementation.

References


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* `nvprof -m` achieved occupancy, sm_efficiency, gld_throughput, gst_throughput, gld_efficiency, gst_efficiency . /run
Fig. 1. Performance (speedup over sequential execution) achieved for computing multiple (256, 2,560, 25,600, 256,000) neurons using different morphologies: small-low (top-left), small-high (top-right), medium-low (center-left), medium-high (center-right), big-low (bottom-left) and big-high (bottom-right).
Dynamic Resource Management for Interactive Supercomputing in Neuroscience

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Supercomputers, as High Performance Computing systems grow in complexity every year. These systems are composed of many nodes interconnected with a very fast network, which allows to use them together for very complex computations. Nowadays we see that the capacity of each node is also growing: much more cores are available (e.g. up to 72 in Intel KNL [1]), specific purpose computing units such as GPUs [2], and also different memory hierarchies (e.g. Non-Volatile Memories [3]). Having so many resources available in a single node makes very unlikely that a single application is able to exploit all of them, and if the node is reserved for that application, the situation ends up in a poor utilization of the system. This is something system administrators want completely to avoid, since the ideal case is that the supercomputer is used at its 100% capacity. Considering this, it is clear that sharing resources between applications becomes a must in the near future.

In addition, commonly used techniques these days to enable Interactive Supercomputing capacities to applications (i.e. the ability to interact with a running simulation, analysing partial results with visualization or intermediate results processing, and even steer the running simulation according to these partial insights) do not care much about where resources are obtained, for instance to run the in-situ visualization or the analytics [4]. The most common assumptions are that “extra” resources are available somehow to do these interactive tasks, or that the main application is halted so the interactive tasks can proceed, at the penalty of stopping the original application. In the Interactive Supercomputing scenario, sharing resources also becomes ideal, since a big simulation using all available resources can lend some of them to the interactive task to be started immediately, and when the interactive task finishes, resources can be given back to the big simulation, as it can be seen in Figure 1.

To achieve the resource sharing we mention, our proposal is to enable what we call Dynamic Resource Management (malleability) in the different layers of the system: Job level, Node level, Application level and Kernel level. We have especially worked in the Job level, by modifying the SLURM job scheduler to include malleability options [5], and at Node level, providing a library called DLB (Dynamic Load Balancing) that is able to share resources between different applications running in the same node, or even in the same application to speed up the processing [6]. We have successfully applied DLB in the CFD domain [7].

Our modifications made to SLURM enable jobs to increase or decrease the number of resources they are using, so a reduction of resources used by a job can allow a new job to enter to run in the system, decreasing its wait time. With respect to DLB, it is a library linked with the application that is able to lend the unused CPUs from an application to another one running in the same node, therefore speeding up the execution of the second one. DLB keeps a fair control of resources, returning them to the original owner when they are needed. Besides, DLB is able to interface with the job scheduler with its DROM API, to exchange knowledge about resource needs and resources available.

In the framework of the HBP, in particular in WP7.4, we have been able to enable malleability for both NEST [8] and CoreNeuron [9] simulators, allowing them to change the resources they use at runtime. The use case motivating this need comes from CDP2, where CoreNeuron is used as a service, and when many different users start to submit different simulations (e.g. typically in a course or tutorial), the wait time in the queue becomes a problem due to the lack of capacity of the jobs to share resources. Our tests demonstrate that on one hand, adding malleability to the simulators does not cause a penalty in their execution time, and on the other hand, malleability helps to reduce wait time of the jobs, ending up in a better response time for users, and a higher system utilization.
Acknowledgements

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References:

Big data for HPC: the Human Brain Project
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Motivation

In the HBP project, a typical workflow consists of applying different analytics to a dataset obtained from the real world or through simulation. Given the nature of the problem, high volumes of data are used, causing this workflow to span for hours. Consequently, being able to verify the results while generated or assess that the parameters defined are appropriate can save hours of computation.

Traditionally, mechanisms to store and organize data have been based on plain text or HDF5\textsuperscript{1} files among others. They imply that the user knows the storage backend and the particular interface which can be complex, for instance, when writing in parallel. Inevitably, checking the partial results during executions is hardly possible or requires the use of locks. Other issues affecting the availability of data or the risk of corruption are of the utmost importance in this context.

For all the reasons mentioned above, distributed storage systems are currently being evaluated in the WP7.2. As a starting point, we identified the structure of the data used in the HBP project, shown in Figure 1. Then, defined nice-to-have features to evaluate storage systems including horizontal scalability, ease of use, good performance on handling continuous data such as time series, space indexation, mechanisms to avoid corruption and maintain coherence, high availability and portability between backends.

\[(x, y, z) = (value_0, value_1, ..., value_{n-1})\]

Figure 1: Common structure of the data used by HBP applications.

Proposed solution

In the context of storage, the BSC has proposed an architecture comprised of a <key, value> distributed storage system with a simple interface to handle data transparently. One of its main benefits is early access to the results since they can be analyzed while generated. As a consequence, accelerating the traditional workflow is possible by performing analysis while storing the data. In concrete, control and verification of the correct execution are applied by inspecting the partial results.

Our proposed interface allows access to the data as regular memory objects. In this way, it is not necessary that the users have any knowledge of the backend and programs are adjusted by doing minor changes. The system named Hecuba is designed to be run with Cassandra\textsuperscript{2}, a NoSQL database, though it is compatible with ScyllaDB\textsuperscript{3} with whom they share the interface. They are designed with the aim of making data available without corruption obtaining a good performance.

Results

We successfully applied this solution to an HBP use case based on a Python program responsible for analyzing brain sections and individualize neurons. The proposal proved to fulfill the requirements expressed above. During the execution, we have been able to access and verify the results. Moreover, there hasn’t been a penalty on performance, and the adaptation of code implied merely minor modifications.
References

Analysing Dialogue to Support Detection of Alzheimer's Disease

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[Introduction/Motivation:]
As well as memory loss and linguistic impairment, changes in behaviour and decreased interactional skills in conversation are also symptoms for Alzheimer’s Disease (AD). Recent work has shown that linguistic features can be used within natural language processing (NLP) and machine learning (ML) methods to provide computational tools with potential for automatic detection of AD [1]; however, few studies have applied these techniques to investigate the predictive power of interactional symptoms. Automatic diagnosis of AD aids assessment and allows for earlier diagnosis. Interactional features are linguistically and culturally independent, allowing the automation to be applied across languages and borders.

[Methods:]
We investigate the use of interactional features (IFs) from to predict AD, and compare performance against and in addition to known predictive linguistic (but non-interactional) features [1]. The data used was the DementiaBank Pitt corpus [2]; IFs used were chosen to encode known symptoms of AD such as turn-taking, filler term frequency and trailing-off mid-sentence. Classification accuracy was assessed using logistic regression, following [1]. Non-IF’s & IFs were compared by ranking the features based on ANOVA F-value. IF’s were hierarchically grouped by 3 umbrella features; ‘Fillers’, ‘Unintentional Silence’ and ‘Dialogue’. Correlation analysis was carried out on the interactional features as a sense check and to investigate the direction in which each variable correlates with the diagnosis.

[Results and Discussion:]
Interactional features (IFs) can assist in computationally classifying AD. The top three features in terms of predictive power were IFs. The best feature combination improved accuracy by nearly 5% over the state of the art [1], and was composed of over 50% IFs. Dialogue-based features, together with features encoding clarification behaviour between speakers, were the most predictive group.

References: