13th Neural Coding

Torino, September 9–14, 2018

Aula Magna, Palazzo del Rettorato,
Via G. Verdi 8, Torino

Book of Abstracts

Neural Coding 2018

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Program

Sunday	
18:30-20:30	**Registration & Welcome**

Monday		Chair	Tuesday		Chair
8:30-9:30	**Registration & Opening**		9:00-9:30	**Stiber**	
9:30-10:00	**Lindner**	Greenwood	9:30-10:00	**Roy**	Villa
10:00-10:30	**Ditlevsen**		10:00-10:30	**Andreis**	
10:30-11:00	**Coffee Break**		10:30-11:00	**Coffee Break**	
11:00-11:30	**Diesmann**				
11:30-12:00	**Borisyuk**	Braun	11.00-12:30	**Poster presentation**	Sacerdote
12:00-12:30	**Bernardi**				
12:30-14:00	**Lunch**		12:30-14:00	**Lunch**	
14:00-14:30	**Tamborrino**		14:00-14:30	**Marsalek**	
14:30-15:00	**Di Garbo**	Shinomoto	14:30-15:00	**Nieus**	Lansky
15:00-15:30	**Quaglio**		15:00-15:30	**Christodoulou**	
15:30-16:00	**Coffee Break**		15:30-17:30	**Coffee Break & Poster Session**	
16:00-16:30	**Kilpatrick**	Christodoulou			
16:30-17:00	**Bazhenov**				

Wednesday		Chair	Thursday		Chair
9:00-9:30	Shinomoto		9:00-9:30	Kostal	
9:30-10:00	Greenwood	TBA	9:30-10:00	Pica	Jolivet
10:00-10:30	Braun		10:00-10:30	Villa	
10:30-11:00	Coffee Break		10:30-11:00	Coffee Break	
11:00-11:30	Levakova		11:00-11:30	Tezuka	
11:30-12:00	Rostami	Ditlevsen	11:30-12:00	Turova	Kobayashi
12:00-12:30	Aksenova		12:00-12:30	Tubikanec	
12:30-14:00	Lunch		12:30-14:00	Lunch	
16:20	Egyptian/Cinema Museum		14:00-14:30	Kobayashi	
			14:30-15:00	Li	Tamborrino
			15:00-15:30	Gilson	
20:00-	Social Dinner		15:30-16:00	Coffee Break	
			16:00-16:30	Jolivet	Kostal
			16:30-17:00	D'Onofrio	

Friday	
10:00-12:00	Round table (optional)

Contents

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Talks (ordered by speaker's family name)

Markov mixture of experts to decode limb trajectories from ECoG for Brain Computer Interfacing

Marie-Caroline Schaeffer, Alexandre Moly and **Tetiana Aksenova**

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Brain-Computer Interfaces (BCI) aim at interpreting brain activity patterns so as to translate user's intentions into effector actions without using the users' natural neuromuscular pathways. BCIs are particularly being investigated for the sake of severely motor-impaired patients. Most of them rely on the decoding of spiking activity patterns from invasive intercortical Microelectrodes array recordings or the decoding of neural population activity patterns acquired either by semi-invasive intracranial Electrocorticography (ECoG) arrays or by non-invasive scalp Electroencephalography arrays. In the present article, the estimation of overt movement trajectories from the activity of neuronal population acquired at the level of cerebral cortex surface (ECoG) is considered. A Markov mixture of linear experts (Markov Switching Linear Models, MSLM) is proposed [Schaffer and Aksenova, 2016] for the decoding. The MLSM is built on the assumption that linear models (experts) relate neural features and kinematic parameters of movement and are conditioned on a discrete latent variable (state). A probabilistic rule is used to combine the linear models associated with state values. The latent state variable is assumed to be generated by a first-order Markov chain. In a previous study [Schaffer and Aksenova, 2016], a MSLM was used to relate neuronal population features extracted from ECoG recordings and the corresponding kinematic parameters. A two-state MSLM was applied to decode an upper limb trajectory. States were associated with rest and movement periods. A single linear model conditioned on these states was used for mapping of neuronal features to a limb trajectory. In this case, both state sequence and trajectory were available when identifying the MLSM model on a training data set, i.e. model identification was fully supervised. Linear modelling may not be optimal for the description complex movements. Piecewise linear modelling is a way to introduce nonlinearity to decoder. A MSLM with multiple states associated with movement is considered in the present article to improve the decoding performance. Contrary to the previous study, state labels are not available during model identification, i.e. MSLM training is unsupervised with respect to state labels. An iterative Expectation-Maximization procedure is proposed for MSLM identification The proposed model was tested on a data set (http://neurotycho.org/) composed of neuronal signals (ECoG) and upper limb

movement trajectories [Shimoda et al., 2012] simultaneously acquired in nonhuman primates while they were performing a food reaching task. The performance of the unsupervised MSLM (U-MSLM, unsupervised with respect to state labels) decoder was assessed for wrist trajectory reconstruction. The U-MSLM was compared to a supervised 2-state (rest vs. movement) MSLM (S-MSLM) for the reconstruction of complex 3D multiphase movements. 3 recordings of multiphase movements were found in the data base. Time-frequency neuronal features were extracted using complex continuous wavelet transforms [Schaffer and Aksenova, 2016]. Results yield 1-10% improvement of U-MSLM vs. S-MSLM using Pearson Correlation Coefficient, Normalized Root Mean Squared Error, Normalized Mean Absolute Error performance indicators averaged over the 3 axes. The performance of the proposed algorithm is to be further investigated using a large set of recordings acquired during the "BCI and Tetraplegia" clinical research protocol which is currently in progress at CLINATEC, CEA, Grenoble, France (PI: Prof. Benabid).

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Networks of interacting components with macroscopic self-sustained periodic behavior

Luisa Andreis[1] and Daniele Tovazzi[2]

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The emergence of time-periodic self-organized collective behaviors in large communities of interacting units is of interest in neuroscience, because of its link to the mathematical explanation of neural oscillation in networks of interacting neurons. The attempt of modelling these non linear macroscopic behaviors in complex systems leads often to the choice of mean field models, since they give analytically tractable equations that may explain features which are not displayed at microscopic level. Therefore, toy models in this class have been recently used to understand how macroscopic rhythmic behavior may appear in systems where single units have no tendency to behave periodically [1, 2, 3, 4]. However, the question on how to describe in full generality the class of interactions able to give origin to oscillating behavior at the macroscopic level is still open. In this framework, we discuss some interacting mechanisms that have been proved to generate rhythmic behaviors and we focus on one particular model that shows several peculiar regimes. We will explain the flexibility of this model that, depending on the choice of the parameters, may exhibit different phase transitions and, for instance, the coexistence, at the macroscopic level, of several stable periodic orbits. The talk is based on [1], a joint work with Daniele Tovazzi.

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Continuous learning, sleep and memory consolidation

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Memory depends on three general processes: encoding, consolidation and retrieval. Although the vast majority of research has been devoted to understanding encoding and retrieval, recent novel approaches have been developed in both human and animal research to probe mechanisms of consolidation. A story is emerging in which important functions of consolidation occur during sleep and that specific features of sleep appear critical for successful retrieval across a range of memory domains, tasks, and species.

Previously encoded memories can be damaged by encoding of new memories, especially when they are relevant to the new data and hence can be disrupted by new training – a phenomenon called "catastrophic forgetting". Sleep can prevent the damage by replaying recent memories along with the old relevant memories. Though multiple evidences point to the role of sleep in memory consolidation, exact mechanisms remain to be understood. In our study, we explored the neural substrates of memory consolidation involving replay of memory and task specific sequences of neurons.

We used computer models of the thalamocortical network capable of transitions between awake, stage 2 (N2), and stage 3 (N3) sleep through implementing effects of neuromodulators. The model generated characteristic sleep spindles in N2 and slow oscillations in N3. Spike-time dependent plasticity (STDP) was implemented on excitatory connections to model synaptic weight changes associated with encoding and consolidation. We found that sleep spindles (the hallmark of N2 stage sleep) and slow oscillations (the hallmark of N3 stage sleep) both promote replay of the spike sequences learned in the awake state and neuronal replay was localized near the trained network sites. Memory performance improved after a period of NREM sleep but not after the same period in awake. When multiple memories were trained, the local nature of the spike sequence replay during spindles allowed replay of the distinct memory traces independently, while slow oscillations promoted competition that could prevent replay of the weak memories in a presence of the stronger memory traces. This could potentially lead to extinction of the weak memories unless when sleep spindles (N2 sleep) preceded slow oscillations (N3 sleep), as observed during the natural sleep cycle.

Our study predicts that spontaneous reactivation of the learned neuronal sequences during sleep spindles and slow waves of NREM sleep represents a key mechanism of memory consolidation and the basic structure of sleep stages provides an optimal environment for consolidation of competing memories.

Detecting single-cell stimulation in recurrent networks of spiking neurons

Davide Bernardi and Benjamin Lindner

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Theoretical and experimental studies suggest that cortical networks operate in a noisy chaotic regime, so that large populations are required to reliably code information [1]. This picture seems to be in contrast with experiments showing that the stimulation of a single cell in the barrel cortex can influence the behavior of an awake rat [2]. In this talk, we look for a possible theoretical explanation for this apparent contradiction: we investigate how the brief stimulation of one neuron in a recurrent spiking network can elicit a weak transient macroscopic change in the network activity and how this perturbation can be detected.

First, we consider a random network of integrate-and-fire neurons [3] with exponentially distributed synaptic weights [4]. Numerical simulations and analytical estimates show how a simple readout procedure can detect the perturbation with a reliability comparable to the experimental figures. To this end, the readout must be slightly biased toward specific neurons, a proxy for the training of the experimental subjects [5]. We discuss the role of the recurrent coupling strength and show that optimal detection is achieved for a broad range of intermediate values. Furthermore, we explore several possible implementations of the readout procedure in terms of a neural circuit and compare their performance. Remarkably, all explicit readout populations require a smaller bias to detect the stimulus than the simple readout procedure introduced before [6]. Finally, we study a recurrent network model endowed with some features of the barrel cortex (cellular heterogeneity, dense inhibitory connectivity, short-term plasticity), the system in which the effect has been experimentally observed.

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Interplay of structural and functional properties in a simple locomotor network: a probabilistic model

Roman Borisyuk[1], Andrea Ferrario[1], Robert Merrison-Hort[1] and Stephen Soffe[2]

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Although, in most animals, brain connectivity varies between individuals, behaviour is often similar across species. It is known that brain development involves multiple stochastic processes and the individual connectomes are different. Despite differences in connectivity, most individuals under normal conditions are able to demonstrate similar functionality. This means that different connectomes include sufficient key structural features to produce a common repertoire of functionalities and behaviours. What are the key connectivity properties that define the network functionality? What fundamental structural properties are shared across individual networks that define this behaviour?

Motivated by this question, we derive a probabilistic model of connectivity in the Xenopus tadpole central nervous system (caudal hindbrain and spinal cord) to study the relationship between the structure and function of the network.

Our previously developed anatomical model based on the 'developmental' process of axon growth (Li et al., 2007; Borisyuk et al., 2011; Borisyuk et al., 2014; Roberts et al., 2014) generates multiple highly variable and nonhomogeneous connectomes. To deal with this large and complex data we design a very simple mathematical metamodel expecting that this new probabilistic model will reflect (generalise) structural properties of anatomical connectomes and show proper functioning (Ferrario et al., 2018).

We generate 1000 connectomes using a biologically realistic anatomical model. To design the probabilistic model we use a universal ordering of neurons in the tadpole which allows us to map one anatomical connectome to another one and calculate the probability of directed connection for each pair of neurons as the frequency at which the connection exists among the thousand generated connectomes. Thus, the probabilistic model is the matrix of probabilities of independent Bernoulli random variables. In this way, our probabilistic model 'generalizes' structural properties of networks produced by the anatomical model.

Using the probabilistic model, we can generate an adjacency matrix representing a particular realisation of neuronal connectivity. Mapping the adjacency matrix to a functional model of spiking neurons of Hodgkin-Huxley type (Roberts et al., 2014) enables us to simulate spiking activity. We compare these simulations of the functional model to the experimental results on swimming initiated by skin touch. The crucial question is: 'Can probabilistic connectomes produce swimming?' The answer to this is not obvious. Our earlier paper (Li et al., 2007) showed that a graph of connections based on probabilities derived from small number of pairwise recordings provides swimming in about 60% of cases only.

This new study shows that probabilistic connectomes that include some elements of the structure of anatomical connectomes reliably swim in all cases. We find that all generated probabilistic connectomes mapped to the functional model generate similar swimming activity. It seems, then, that the probabilistic model contains some fundamental features of the network connectivity ('proper structure') which ensure

correct functioning of the system. Thus, we can derive an important conclusion that the two properties of the probabilistic model inherited from anatomical connectomes: (1) position of neurons along the rostro-caudal coordinates and (2) frequency of connection appearance, are sufficient for swimming generation.

We study how structural and functional features differ between detailed anatomical connectomes and those generated by our new, simpler, probabilistic model (meta-model). The probabilistic model allows calculation of structural characteristics that reflect common network properties, independent of individual network realisations. We use the structural characteristics to study examples of neuronal dynamics, in the complete network and various sub-networks, and this allows us to explain the basis for key experimental findings, and make predictions for experiments. We study how the connectivity characteristics relate to particular functional properties of the network. For instance, the average in- and out-degrees were used to predict the swimming period and to find the positions of reliably firing commissural interneurons (cINs).

It is clear that some characteristics of the probabilistic connectomes (e.g. the mean of in- and out-degrees) coincide with equivalent characteristics of the anatomical connectomes but some differ (e.g. the variances of in- and out-degrees are significantly smaller for probabilistic connectomes). Although there are some differences between the behaviour of anatomical and probabilistic connectomes, even studying these differences can provide important insights into the relationship between the structure and function of the network. For example, we find an explanation underlying a difference in swimming frequency between the two types of connectome: The anatomical and probabilistic connectomes have very different variances of cINs in-degree from the descending interneurons (dINs). It would have been hard to observe this interesting phenomenon without having the probabilistic model (where in-degree variance is much lower) to compare with the anatomical one.

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Synchronization of heterogeneous neurons of different activity patterns in a mathematical model of a gap-junction coupled network

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The nervous system is composed of neurons of enormous heterogeneity. It is well known among experimentalist that no neuron, not even from the same brain area and of the same type, reacts in exactly the same way as any other one. The possible impact of such neuronal heterogeneity on neuronal network synchronization has been examined in a mathematical model of a network of nearest neighbour gap-junction coupled neurons during increasing coupling strength.

Heterogeneity has been introduced by Huber-Braun model neurons with randomization of the temperature as a scaling factor which can generate an enormous diversity of impulse pattern, including burst discharges, chaotic activity and two different types of tonic firing – all of them also experimentally observed in the peripheral as well as central nervous system.

When the network includes all these types of neurons, randomly selected, a particular phenomenon can be observed. At a certain coupling strength the network goes into a completely silent state although all neurons have originally been spontaneously firing driven by subthreshold oscillations. When parts of the neurons with specific patterns are taken out, especially the tonic firing neurons from the lower and upper extremes of temperature range, spontaneous firing can be reinstalled with further increasing coupling strength. Reinstalled firing develops from slowly increasing subthreshold oscillations and is always of the tonic firing type and already fairly well synchronized.

Examination of voltage traces and interspike-intervals of individual neurons suggests 1) that all neurons, irrespective of their original pattern, go through a well-known bifurcation scenario as observed on current injection eventually leading to subthreshold oscillations without spikes and 2) that synchronization continues in the silent state at the level of subthreshold oscillations. These data demonstrate that neuronal synchronization is far away from being only a matter of synaptic coupling. The dynamics of the individual neurons play a major role.

Modelling the relationship between self-control and consciousness

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In this paper we investigate the relationship between self-control behaviour and consciousness. Morsella et al. (2009) demonstrated that conscious conflicts involving delay of gratification (Mischel et al., 1989) such as self-control problems (i.e., choosing of a large delayed reward over a small immediate reward, Rachlin, 2000), lead to systematic changes in subjective experience (or "consciousness"). More specifically, by conducting experiments of the Stroop (1935) and Flanker (Eriksen and Schultz, 1979) task type, they observed that the stronger the conflict in the task, the higher the level of consciousness required. Problems in exercising self-control, suggest a conflict between cognition and motivation. This has been linked to brain-imaging studies, which have demonstrated that in such situations, parts of the limbic system and regions of the prefrontal cortex compete for the decision (McClure et al., 2004). As Kavka (1991) suggests, such inner conflicts are resolved as if they were a result of strategic interaction among rational subagents. A computational model of interpersonal conflict we developed (Cleanthous and Christodoulou, 2009; Christodoulou et al., 2010) consists of two agents learning simultaneously but independently, competing in the Iterated Prisoner's Dilemma (IPD) game (Rappoport and Chammah, 1965). The IPD can be thought of demonstrating interpersonal conflict (Kavka, 1991), where the Cooperate-Cooperate (CC) outcome corresponds to the behaviour of self-control. The structure of internal conflict is represented by the IPD's payoff matrix. An internal conflict of low to moderate intensity for example, would have a Temptation payoff (T) just slightly higher than the Reward for mutual cooperation (R) and a Sucker's payoff (S) slightly lower than the Punishment for mutual defection (P), meaning that the agents would be less tempted to defect and less afraid to cooperate (Cleanthous, 2010). T represents the value of the immediate gratification, while S reflects the cost of getting the least immediate gratification. Thus increasing T while decreasing S results in an internal conflict of strong intensity (e.g., addiction) as the conflict between Cooperate-Defect (CD) and Defect-Cooperate (DC) outcomes increases. From these observations it can be deduced that the differentiation of conflict intensity in our model results from the modification of the payoff differences T-S, T-R and P-S. Given this and inspired by the work of Morsella et al. (2009) described above (where they relate the conflict level with consciousness), consciousness is represented in our model by the internal conflict and its level can be altered based on these payoff differences. In particular, the greater these differences are, the stronger the conflict becomes and thus the greater the level of consciousness. We simulated a version of our previous self-control computational model (Cleanthous and Christodoulou, 2009; Christodoulou et al., 2010) based on look up tables, one for each agent representing different parts of the brain, the limbic system and the prefrontal cortex, playing the IPD and trained with temporal difference reinforcement learning. In order to investigate the relationship between self-control behaviour and consciousness we used a simple hill climbing local search for altering the payoff values of the look up tables such that the most appropriate values are found which give the highest possible

self-control outcome (CC). We also incorporated the concept of consciousness in the model through the payoff value differences, which were modified by the hill climbing local search algorithm in order to give the agents different levels of consciousness. According to the results, while the level of consciousness was reduced by the hill climbing algorithm, the more the urge was by the agents to learn to cooperate. In other words, as the level of consciousness is reduced, the level of self-control is increased. It was also observed that in the case of very strong initial conflict indicating a very high level of consciousness, the hill climbing algorithm was able to greatly reduce the payoff value differences such that a higher level of self-control was developed. Concluding, the results from our computational model indicate that self-control and consciousness are reversely proportional, which confirm the psychological findings of Morsella et al. (2009). Effectively as self-control is learned, the level of conflict becomes weaker and so do the perturbations in consciousness. We can also say that learning in our computational model of self-control can be used for regulating a conscious conflict and thus the level of simulated consciousness.

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Multi-area models as data integrators and building blocks

Markus Diesmann

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Cortical architecture, i.e. the area-specific cellular and laminar composition of the cortical network, is related to the connectivity between areas, which forms a hierarchical and recurrent network at the brain scale. Based on earlier work on the cortical microcircuit, our recent study [1] integrates data on cortical architecture and axonal tracing data into a multi-scale framework describing one hemisphere of macaque vision-related cortex. We represent each area by the network below one square millimeter of cortical surface. These circuits are modeled with their natural number of neurons and synapses. Simulations confirm a realistic activity regime after adjustments of the connectivity within the margins of error [2] with the help of mean-field theory. At a sufficiently large coupling between the areas, spike patterns, the distribution of spike rates, and the power spectrum of the activity are compatible with in-vivo resting-state data. Furthermore, the matrix of correlations between the activities of areas is more similar to the experimentally measured functional connectivity of resting-state fMRI than the anatomical matrix. This correspondence on multiple spatial scales is achieved in a metastable state exhibiting time scales much larger than any time constant of the system.

While many anatomical and dynamical aspects of the brain are still unknown, such models integrate the available data, constitute testbeds for theories of brain function, and serve as research platforms for iterative improvements and building blocks for further studies. There are, however, two technical challenges to overcome.

First, models have reached such a complexity that only executable model descriptions enable the effective communication between scientists and the reproducibility of results. Furthermore, the information required to instantiate a model in the memory of a computer is only one aspect of the modeling process. The experimental data entering the model span multiple scales and come from different sources. Algorithms are required to collocate the data and derive the final model parameters. Often, data are only partially available such that quantitative hypotheses need to be formulated to bridge the gaps. As a consequence researchers can only add new data to the model or modify assumptions if they have access to the construction process. Therefore, the workflow of data integration also needs to be documented in an executable format. Borrowing techniques from computer science we demonstrate on the example of our multi-area model the development of a publishable executable workflow of model construction and discuss the difficulties we encountered in the process.

Second, simulating multi-area models at the level of resolution of neurons and synapses taxes the largest supercomputers available. There is a technological barrier for the further increase of network size as potentially enabled by the memory and compute power offered by exascale systems. Present simulation code distributes the activity of all neurons to all compute nodes and only subsequently filters out the

locally required information. This strategy becomes unfeasible in terms of memory for networks larger than 1 billion neurons. The number of incoming connections to a neuron in the cerebral cortex is, however, limited to the order of 10,000. Therefore, at the brain scale, connectivity is extremely sparse. The talk introduces a two-tier connection infrastructure and a framework for directed communication among compute nodes [3]. This novel technology removes the scaling of local memory consumption with network size and disburdens compute nodes from the need to filter the incoming data. Although the new algorithms and data structures address exascale computers, they do not sacrifice performance on small systems and exhibit substantial performance gains already at the petascale. The technology is presently being integrated into the next release of the NEST simulation code. As seen in the study of the multi-area model, mean-field approximations support the exploration of parameter ranges and ultimately it will be useful to simulate different parts of a network at different levels of description. For this reason NEST has been extended by the capability to integrate rate-based models [4].

Still, solving the equations for microscopically parallel system on conventional computers with their rather coarse-grained parallelism consumes considerable energy and reaching real-time or accelerated speeds is difficult. Therefore, we also explore neuromorphic computing as an alternative for brain research. The talk presents recent progress in this area [5], where a microcircuit model at full density of local synapses runs for the first time on the SpiNNaker hardware system. The finding is relevant because the model already comes close to the total number of synapses received by neurons in all larger cortical networks.

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Analysis of interspike intervals of a resonate-and-fire neural model with periodic drive

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The understanding of the basic mechanisms shaping the response of a single neuron to stimulations is a fundamental step for improving our knowledge on the functional processes underlying the coding of sensory information in neural populations [1-3]. To this aim, an important approach consists in the study of phase-locking patterns or synchronization phenomena in simple neuron mathematical models subject to periodic inputs. To partially reduce the intrinsic complexity of these problems, a useful strategy is that of employing simplified, but still realistic, neuron models, such as the integrate-and-fire class [4-9]. Therefore, in keeping with the above remarks, we studied the dynamics of a resonate-and-fire neural model in the presence of periodic driving. The adopted model was introduced in [10] and is a two dimensional nonsmooth dynamical systems with a threshold crossing firing mechanisms. This model was obtained by linearization of the well-known FitzHugh-Nagumo neural model. We studied the effects of a sinusoidal forcing on the firing discharges generated by this model and, in particular, on its phase-locking patterns. The statistical properties of the distribution of interspike intervals were investigated by studying the dynamical properties of the corresponding firing map. Lastly, the effects of the addition of noise on the synchronization properties of the system were also studied.

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Oscillating systems with cointegrated phase processes

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We present cointegration analysis as a method to infer the network structure of a linearly phase coupled oscillating system. By defining a class of oscillating systems with interacting phases, we derive a data generating process where we can specify the coupling structure of a network that resembles biological processes. In particular we study a network of Winfree oscillators, for which we present a statistical analysis of various simulated networks, where we conclude on the coupling structure: the direction of feedback in the phase processes and proportional coupling strength between individual components of the system. We show that we can correctly classify the network structure for such a system by cointegration analysis, for various types of coupling, including uni-/bi-directional and all-to-all coupling. Finally, we analyze a set of EEG recordings and discuss the current applicability of cointegration analysis in the field of neuroscience.

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On diffusion neuronal models with multiplicative noise

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The diffusion leaky integrate-and-fire (LIF) model is commonly used to study the changes in the neuronal membrane depolarization between two consecutive spikes of a single neuron and is described by an Itô stochastic differential equation of the following type (see for instance [5])

$$dY_t = \left(-\frac{Y_t}{\theta} + \mu \right) dt + a(Y_t)dW_t, \quad Y_0 = y_0, \tag{1}$$

where the diffusion coefficient $a(Y_t)$ determines the amplitude of the noise. We consider model (1) such that the function $a(\cdot)$ depends on the process itself and on postsynaptic reversal potentials. Models with different choices of $a(Y_t)$ are considered and compared. The processes have the same deterministic part but different stochastic components. The differences in the state-dependent variabilities, their asymptotic distributions, and the properties of the first-passage time across a constant threshold are investigated. Computationally easy expressions of the first moment of the first-passage time for the Feller process [2], for the Inhomogeneous Geometric Brownian Motion [1] and for the Jacobi process [3]-[4] are derived and implemented to determine the role played by the parameters involved in the model.

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Framework for estimation and interpretation of biomarkers for brain dynamics from fMRI

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The brain is a massively-connected network of neuronal populations with specialized regions that interact to process information. Non-invasive neuroimaging techniques such as functional magnetic resonance imaging (fMRI) are more and more used to explore mechanisms for cognition in healthy human subjects and alterations in neuropathologies. Functional connectivity (FC) measures the level of correlated activity between brain regions and has been demonstrated as a proxy to describe how "interactions" within the brain are modulated, e.g., when a subject engages a task. We have recently proposed a framework to estimate effective connectivity (EC), which aims to quantify directional interactions between brain areas at the whole-brain level [1]. Our current direction of research is to evaluate to which extent EC provides a biomarker for the brain dynamical state, in the sense that the estimated EC from individual fMRI sessions (5-10 minutes) can be used to discriminate between tasks performed by subjects. On the clinical side, EC can be used to aid diagnostic by characterizing patterns of alterations in EC as compared to healthy subjects. Our approach relies on a dynamic model to reproduce the propagation of fMRI activity across brain regions, for a parcellation of the brain divided in about 100 regions [1]. Importantly, this model is constrained by structural connectivity (SC), which measures anatomical white-matter projections between brain regions. All three types of connectivities are represented in Figure 1. SC determines the topology of EC, which typically corresponds to a density of 30% among all possible connections between the brain regions. For 100 brain regions, the model fitting procedure must robustly estimate 3000 EC weights, which provides a biomarker in a high dimensional space. Here we present recent results for two lines of research. First, we have benchmarked the capabilities of EC as a biomarker to identify the identities of subjects and the task they perform, using machine-learning techniques [2]. Our results show that EC is a more accurate biomarker than FC to identify subjects. In addition, we demonstrate how EC-based signatures can be extracted to identify subjects on the one hand and tasks on the other hand. This is important in a practical context such as clinical applications to avoid the contamination of pathology-specific EC signatures by subject-to-subject variability. In addition, we have recently explored how to transpose task identification at a shorter timescale in fMRI recordings (~1 minute) using dynamic FC. In essence, this is important to evaluate the stability over time of the estimated "brain dynamical state". Together, our results about classification from fMRI measurements aim to provide a well-benchmarked framework for fMRI-based biomarkers. Second, we present a network-specific analysis of EC estimates. Because of its high-dimensional nature, EC matrices are difficult to interpret at the level of single connections when comparing them across conditions. To overcome this limitation, we have developed a formalism that describe how EC weights collectively determine the propagation of fMRI activity across brain regions, bridging with graph theory [3]. It provides a consistent approach for brain dynamics from estimation

to interpretation, allowing for the characterization of the EC topology (e.g., small worldness, hierarchical modules) and detection of communities of brain regions.

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Quasi-patterns of Phase Synchronization

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A family of stochastic processes has quasi-cycle oscillations if its otherwise-damped oscillations are sustained by noise. Such a family forms the reaction part of a stochastic reaction-diffusion system when we insert a local Mexican Hat-type, difference of Gaussians, coupling on a one-dimensional and on a two-dimensional lattice. We find that the phases of the quasi-cycles synchronize rapidly at coupling strengths lower than those required to produce spatial patterns of their amplitudes. The phase patterns persist and evolve but do not induce patterns in the amplitudes. At higher coupling strengths we find quasi-patterns both of phase synchronization and of amplitude (resembling Turing patterns) corresponding to the phase patterns. Specific properties of these patterns are controlled by the parameters of the reaction and of the Mexican Hat coupling.

Energy-efficient information transfer at synapses and energy-dependent learning rules

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The nervous system consumes a disproportionate fraction of the resting body's energy production. In humans, the brain represents 2% of the body's mass, yet it accounts for 20% of the total oxygen consumption. Expansion in the size of the brain relative to the body and an increase in the number of connections between neurons during evolution underpin our cognitive powers and are responsible for our brains' high metabolic rate. Despite the significance of energy consumption in the nervous system, how energy constrains and shapes brain function is often under-appreciated. I will illustrate the importance of brain energetics and metabolism, and discuss how the brain trades information for energy savings in the visual pathway. Indeed, a significant fraction of the information those neurons could transmit in theory is not passed on to the next step in the visual processing hierarchy. I will discuss how this can be explained by considerations of energetic optimality. Finally, I will discuss how energetic considerations modulate learning and coding in neural networks, and lead to coding strategies similar to data compression algorithms, where frequently observed inputs are encoded in low energy trajectories of the neural network.

Synaptically shaping working memory codes

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In working memory tasks, the response pertaining to a particular item can be biased by distractor items presented on the current trial or even items from previous trials, a phenomenon known as interference. Subjects performing visual working memory (WM) tasks can exhibit interference in their responses in different ways. First, the recalled target location can be biased in the direction of the target presented on the previous trial. Second, the remembered location of multiple items can interact during the delay period of a WM task. We will explore how both of these effects can disrupt the WM code, and develop a theory for how such biases are shaped by changes to the synaptic efficacy of the networks in which memory states are stored.

We will begin by presenting a probabilistic inference model of history-dependent bias, and demonstrate such inference can emerge from computations of a recurrent network with short-term facilitation (STF). Applying timescale separation methods, we obtain a low-dimensional description of the interference bias based on the target history. Delay-period activity is approximated by a particle in a slowly varying potential, attracting the particle in the direction of the previous stimulus. Target angles drawn from repetitive sequences are thus encoded better retained in WM than targets drawn from uncorrelated sequences. We also show that two timescales of memory degradation emerge in the delay-period activity, indicative of the slow timescale of STF dampening fluctuations later in the delay.

We then turn our attention to studying how multiple-item WM codes can be shaped by synaptic changes. Classic conceptions of WM capacity assume a finite number of slots, but recent evidence suggests WM may be a continuous resource. Resource models typically assume there is no hard upper bound on the number of items that can be stored, but WM fidelity decreases with the number of items. We analyze a neural field model of multi-item WM that associates each item with the location of a bump in a finite spatial domain, considering items that span a one-dimensional continuous feature space. Leveraging our previous techniques, we can reduce the dynamics of bumps to that of interacting particles, whose strength of interactions is shaped by the network synaptic strength. Our analysis thus relates the neural architecture of the network to accumulated errors and capacity limitations arising during the delay period of a multi-item WM task. Networks with stronger synapses support wider bumps that interact more, whereas networks with weaker synapses support narrower bumps that are more susceptible to noise perturbations. There is an optimal synaptic strength that both limits bump interaction events and the effects of noise perturbations, leading to the most efficient code for a particular item number count. This optimum shifts to weaker synapses as the number of items stored in the network is increased. Our model not only provides a neural circuit explanation for WM capacity, but also speaks to how the capacity of the code relates to the arrangement of stored items in a feature space.

This framework can be extended to study how long-term plasticity shapes neural architecture in networks to better execute evidence accumulation, as animals learn relevant features of the environment in other cognitive tasks. Ultimately, there is

a great deal of promise in uncovering how biophysical mechanisms of probabilistic inference can determine more efficient cognitive coding.

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Estimation of synaptic connections from parallel spike trains

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Advanced techniques of multiunit spike recording started to provide us with a huge number of spike trains. From the acquired spike signal, we might infer the underlying neuronal circuitry, that is, the synaptic connections between neurons. Here we develop a method for estimating synaptic connections from spike trains recorded from multiple neurons based on the generalized linear model (GLM) [1, 2, 3]. The estimation performance of the model is evaluated by applying it to a synthetic data from a network of Hodgkin-Huxley type model neurons. Furthermore, our method is applied to rat hippocampal data.

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Neuronal population size and reliable information transmission

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Optimal information decoding serves as a guiding principle for understanding fundamental questions in theoretical neurosciences. The problem often involves analysis of the Shannon limits for information representation and transmission in neural populations. It is well known that the probability of decoding error has a phase transition at information rate equal to channel capacity. The corresponding thermodynamic limit, however, requires the coding dimension to tend to infinity, thus making the actual decoding practically impossible. In this paper we focus on the finite-size effects that occur in realistically limited neural populations. We examine the achievable information rate in dependence on the population size, and illustrate our findings assuming independent Hodgkin-Huxley neurons responding to individual stimulus patterns. We report that, remarkably, the achievable rate approaches the asymptote in a strikingly non-linear manner as the number of active neurons increases. We identify the critical population size below which reliable information transmission deviates significantly from the fundamental limit. Qualitatively, our findings do not seem to depend on the details of the neuronal model. We hope that our results will stimulate further research into non-asymptotic phenomena and their impact on optimal neural population size or structure.

Short- and long-term adaptation in moth olfactory receptor neurons

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Adaptation of a moth olfactory system to a pheromone exposure begins at the level of olfactory receptor neurons (ORNs) located at the antenna. Adaptation processes manifest on different timescales. A rapid adaptation, lasting tens to hundreds of milliseconds, emerges when an ORN is exposed to a constant stimulus. After tens of seconds, the adaptation results in an adjustment of response amplitudes to the most frequent patterns of stimulation.

The rapid adaptation can be observed in the typical phasic-tonic time course of the ORN firing rate in response to a constant stimulus. We developed a simple mathematical model of moth ORNs, which can reproduce this behavior. The model employs a simplified description of the chemical kinetics leading to the activation of olfactory receptors [1] that govern opening of ion channels. The stimulus-triggered conductance is incorporated into the leaky integrate-and-fire (LIF) model. It can be demonstrated that an adaptation mechanism in the form of an adaptive threshold [2] is necessary to reproduce real data.

In a longer perspective, the adaptation affects neuronal coding. The efficient coding hypothesis [3] predicts that sensory neurons adjust their coding resources in order to optimally represent the stimulus statistics of their environment. Stimulation by an odorant in a natural environment is characteristic by rapid fluctuations in the actual concentration and the statistics of the fluctuation timescales depends on the distance from the odorant source [4]. We analyzed encoding of a pheromone by moth ORNs using Fisher information on experimental recordings obtained in a naturalistic environment [5]. Our results are in agreement with the prediction that ORNs adjust their encoding properties to represent the timescale statistics of a given distance from the pheromone source. This is manifested, for example, in the fact that the most frequent stimulus timescales are encoded with maximum accuracy.

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Benefits of fluctuations and heterogeneity for the signal transmission in single neurons and neural populations

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It is known for quite some time that noise can have a beneficial effect on the signal transmission in nonlinear systems such as neurons or neural populations. In my talk I review a few new developments regarding this idea. I show that up-down fluctuations can boost the information flow in a generic scenario of population coding [1]. Furthermore, I compare the differential effects of dynamic noise in homogeneous populations vs parameter heterogeneity in populations of deterministic neurons [2]. Finally, I explore at the single-cell level whether the multiplicative character of synaptic background noise (which enters as a conductance noise and not as a current noise) can additionally improve the neural information transmission [3].

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Inference in complicated mixture models with application in neuroscience and visual attention

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Mixture models arise when we assume the observation is driven by a discrete number of hidden components. Most statistical and machine learning tools that tackle mixtures rely on certain parametric observation models that describe the distributions of observed data conditional on the hidden component, which, in many real applications, can be complicated distributions. Here we consider mixture models with complicated observation model where the log-likelihood objective is computationally expensive and highly non-convex. Given the observation model (with known parameters) and observed data, we aim to cluster the data according to the hidden components, as well as to estimate the parameters describing each component. Standard methods with maximum log-marginal-likelihood and the expectation-maximization (EM) algorithm using random initial parameters, are slow and perform poorly due to the expensive and non-convex objective function. In this research, we attempt to overcome the difficulties in complicated mixture models. We suggest the hard-assigned EM for complicated mixtures to save computational burden, and propose new parameter initialization schemes for the EM or the marginal likelihood procedure: one extending the k-means++ to consider arbitrary model distribution, and the other relying on novel ideas of data pre-clustering in a space of log-likelihood distances that describe relationships among data.

Simulation studies are conducted in a neuroscience and visual attention environment, under the framework of Neural Theory of Visual Attention (NTVA), which concerns the visual attentional mechanism when the eyes see multiple separated stimulus objects. The central idea in NTVA states that one neuron in the brain can only attend one stimulus object at any given time, and single objects are attended by the neuron with probabilities. Therefore, the full statistical model for the multiple unknown stimulus objects given neural observation is a mixture model. We consider the decoding (inference) problem where the model parameters are assumed known, and we aim to estimate the stimulus objects and cluster the data into categories. Depending on the data in real applications, we may have very complicated mixture model, or very large data sets. This raises the aforementioned problem of complicated mixture models. In this NTVA framework, we conduct three experiments with distinct but all widely-studied models, including leaky integrate-and-fire models, point process models and models based on directed acyclic graph structures (e.g. artificial neural networks). For these experiments, we also use different stimulus types and observation formats, with various optimization methods: Nelder-Mead, gradient descent and simulated annealing. The results show that the proposed methods provide consistently better performance over conventional approaches in all simulation experiments.

Description of sound intensity and frequency encoding in the human auditory periphery

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In the auditory nerve, sound frequency is encoded by location of the neuron along the tonotopic axis and sound intensity is encoded by the recruitment of spikes both across neurons and within the firing rate of individual neurons.

This simple textbook wisdom describing auditory periphery becomes more complicated, when we attempt to describe complex sounds ecologically relevant for human. These complex sounds are speech sounds, speech in babble noise and sounds just above the hearing threshold. In sound frequencies lower than maximum firing rate of individual neurons, sound frequency encoding uses also temporal spike timing. In the encoding of the complex sounds, a difference of single spike per second is not sufficient for encoding sound level difference discrimination observed psychophysically. Therefore more advanced encodings are taking place in the auditory periphery.

We use combined theoretical and psychophysical approach to describe the coexistence of temporal and rate code in the auditory nerve and two subsequent nuclei in the auditory periphery up to the first binaural neurons in the medial and lateral superior olive. Psychophysical data and own experiments, mathematical simulations and abstract models using the concept of the ideal observer are used.

Our aim is to arrive to a description consistent with the human auditory nerve information throughput, with the psychophysical performance and also consistent with the re-learning capabilities of impaired hearing listeners using hearing aids or cochlear implants.

PCIe: a novel data robust perturbational complexity index to assess consciousness in human subjects

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Theoretical considerations suggest that consciousness depends upon an optimal balance between functional integration and functional segregation of brain activities. In order to condense these properties in a single number, our group has introduced the Perturbational Complexity Index (PCI) in the field of TMS/EEG human recordings [1]. The PCI has been shown to [2]: 1) discriminate between consciousness and uncosciousness with 100% sensitivity and specificity on a benchmark population, 2) detect minimal conscious state (MCS) patients with a 94.7% sensitivity, 3) allow to identify a number of unresponsive vegetative state (VS) patients who might be conscious albeit unable to express it in behavior. The pipeline to compute PCI involves a series of steps that are time consuming and alternative approaches are therefore desirable to speed up its computation. Here we introduce a novel index, called PCI evoked (PCIe), in which cortical currents are calculated from averaged EEG sensor responses. The PCIe provides to be more data robust and quicker to compute than the standard PCI. The TMS/EEG data are from previous works of our group [1, 2]. The EEG responses to TMS at the sensors level were obtained as the average across repetitions of the same pulse; then, source modelling was performed on the averaged traces. In particular, we imposed a real geometry with boundary element model (BEM) with triangular tessellations for the conductive head volume and solved the inverse problem with the weighted minimum norm approach. The significant cortical activations were determined with respect to iAAFT surrogates generated from prestimulus activity. The algorithm to compute the Lempel-Ziv complexity was essentially the same of [1, 2] but we also tested different rankings and normalizations of the matrix of significant activations [3]. The data analysis pipeline we developed is based on MNE, an open source Python module for EEG data. Preliminary results on a subset of data [3] show that PCIe provides a good separation between the wake and sleep states. Therefore, the univocal ranking and novel normalization of significant activations proposed in this work significantly contribute to improve computation of complexity of TMS/EEG recordings. We will share the Python based pipeline on the HBP platform and this will extend previous softwares [3] (called "collabs") released from our laboratory (e.g. "A Theoretically Based Index of Consciousness"). Hopefully, the PCIe will simplify the use and increase the applicability of the complexity index to human data, to non-human data (e.g. cell culture, slices, and in-vivo preparations) as well as to non-biological preparations (e.g. neuromorphic circuits, computer simulations).

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Intersection information: a new mathematical concept that probes the relationship between sensory information and behavioral discrimination performance

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Determining how much of the sensory information carried by a neural code contributes to behavioral performance is key to understand sensory function and neural information flow. However, there are as yet no analytical tools to compute this information that lies at the intersection between sensory coding and behavioral readout. Here we present our work on how to address this issue. We developed a novel measure, that we termed the intersection information, that quantifies how much of the sensory information carried by a neural response is used for behavior during perceptual discrimination tasks. We derived two versions of this measure. The first [1] is defined through simple stimulus decoding algorithms and quantifies the match, within individual trials, between the stimulus decoded by neural activity and what the animal reports. The second [2] was defined through information theory. In particular, building on the Partial Information Decomposition framework, we define the information-theoretic intersection information as the part of the mutual information between the stimulus and the response that also informs the consequent behavioral choice. We illustrate the use of intersection information with the analysis of two experimental cortical datasets [3,4], to show how this measure can be used to compare quantitatively the contributions of spike timing and spike rates to task performance, and to identify brain areas or neural populations that specifically transform sensory information into choice. We also discuss how this measure could be used to assess the role of noise correlations on the behavioral performance in performing perceptual discrimination tasks.

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Behavior related precise spatio-temporal spike patterns

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Cell assemblies [1], i.e. interacting groups of neurons, were suggested as the building blocks of information processing in the cortex. Modern electrophysiological techniques allow to record hundred(s) of neurons simultaneously and thereby hopefully increase the chances to observe active cell assemblies. Their activity is assumed to be expressed by synchronous or spatio-temporal spike patterns (STPs) [2,3], i.e., temporal sequences of millisecond precision. Here we present an extension of the Spike Pattern Detection and Evaluation method (SPADE) [4,5], which allows one to detect repeated activation of STPs in parallel spike trains recordings. The method consists of two main steps: a) detection of repeated STPs (classified as pattern candidates) by using Frequent Itemset Mining (FIM) in sliding windows along the data, b) statistical testing of the pattern candidates through a bootstrap technique to distinguish STPs occurring by chance from those that are statistically significant. We show how crucial it is to perform the statistical evaluation independently for patterns of different lengths. Firing rate modulation on different temporal scales as well as using different sliding windows for pattern detection on the same data may result in different significance levels for patterns of different lengths. Therefore we evaluate now the significance of patterns of different lengths separately. We validate the method in terms of false positives and true positives using a variety of simulated point processes that model different pattern lengths and further aspects of neuronal activity (e.g., firing rate heterogeneity, correlated firing rate changes). We apply this extended SPADE version to parallel spike train data recorded from pre-/motor cortex of non-human primates [6], thereby extending the previous analysis of the same data for synchronous patterns [7] to precise patterns with temporal lags. The monkeys performed a delayed reach to grasp task: after a preparatory period, they had to pull and hold an object by using either a side or a precision grip, and using either high or low force (resulting in four different behavioral conditions). Our goal is to test the hypothesis that different cell assemblies are activated at different points in time in relation to the behavior. Therefore recordings of the same set of neurons were analyzed for the occurrence of significant STPs in different behavioral epochs and in the four different behavioral conditions. We found a variety of significant patterns that show specificity to the behavior. Altogether, these findings provide evidence for the occurrence of behavior-specific STPs.

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Inhibitory Clustering and Spike Frequency Adaptation: Crucial Features in Modeling Cortical Dynamics

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Balanced networks of inhibitory and excitatory neurons with homogeneously random recurrent connectivity are often employed to model local cortical circuits. A recent series of studies [1-3] has extended the balanced random network model to incorporate clusters of strongly interconnected excitatory neurons with no modularity in the inhibitory population. This clustered topology demonstrates a functionally desired multistability where different clusters become spontaneously activated and inactivated. The model captures a realistic high firing variability of single neurons and a reduction in trial-to-trial variability during stimulation of clusters as observed experimentally [4-5].

We recently showed that, despite the multistability and trial-to-trial variability that emerge in the clustered excitatory network, this topology leads to widely separated firing rate states of single neurons and tends quickly towards firing rate saturation, which is inconsistent with experimental observations. To overcome this problem we incorporated two biologically plausible mechanisms.

First, we introduced clusters of inhibitory neurons, which are coupled to each excitatory cluster [6]. This connectivity scheme is not directly supported by experimental findings. However, recent anatomical and physiological studies point to increased local inhibitory connectivities and possible inhibitory clustering through connection strengths [7-10]. Here we model different architectures of inhibitory circuits, based on these recent experimental studies, and investigate the role of inhibitory clusters on the multistability and trial-to-trial variability of the spiking network when excitatory clusters have strengthened connections with different portions of the inhibitory population. Our model can be reduced to the case of exclusively excitatory clusters [2], or to a one-to-one correspondence of inhibitory and excitatory clusters [6], but we explore all different architectures in between these extreme cases. Such intermediate scenarios are more consistent with recent experimental observations.

Recent studies with large-scale recordings [11] argue for the importance of spike frequency adaptation (SFA) in accounting for cortical network dynamics. Indeed SFA is a prominent feature in cortical neurons [12]. We previously showed that adaptation has a strong effect on cortical variability dynamics [13]. We, therefore, include SFA in our model and study its effect on cortical attractor dynamics.

We find that inhibitory clustering is necessary to achieve realistic spiking activity under stimulation in terms of a biologically realistic firing rate, spiking regularity, and trial-to-trial spike count variability. Inhibitory clustering achieves the desired attractor dynamics over a wide range of network parameters and thus makes networks robust against parameter fluctuations due to homeostasis or neuromodulation. Remarkably, when the stimulus is weak, without clustering of inhibitory neurons, the spiking network model fails to capture the reduction of trial-to-trial variability

during stimulation. Including cellular mechanisms of SFA adds a second temporal component to variability dynamics and similarly enhances robustness of attractor dynamics against variation in network parameters.

Acknowledgments:

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The role of network architecture in the onset of Local and Global Up states

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The spontaneous electrical activity of several brain regions – and in particular of the cortex – shows rapid transitions between periods of intense and synchronous firing (Up states) and of reduced or almost absent electrical activity (Down states) [1–3]. These transitions have been observed in vivo [4] as well as in cortical slices [5] and also when afferent cortical inputs were destroyed. These observations show that this intermittent behavior is intrinsic to the neuronal network and is not caused by the modulation of external inputs [6]. However, the role of network's architecture in this intermittent behavior has not yet been established. By means of Calcium imaging, we studied the spontaneous activity of neuronal networks in their native conformation (i.e. cortical and hippocampal brain slices) and after disruption of the original anatomical structure (i.e. dissociated cell cultures from the same tissues). We observed an intermittency between silent states (Down states), synchronous but localized states (Up states) and synchronous diffused states (Global Up states) with different properties depending on the type of network analyzed. We next developed minimal models able to describe the intermittency and differences observed between the different types of networks (i. e. slices, dissociated cultures) with a very limited number of free parameters (i. e. 3/4). This approach is complementary to those developed in current large projects as the Blue Brain Project, Human Brain Project and Allen Brain Initiative where modelling involves an extremely large number of parameters. The results of our simulations suggest that the differences between native and dissociated networks are due to the multilayer organization of the former ones, and that Global Up states could originate from long-tailed distributions of intervening biophysical parameters such as connectivity and dissipation. The long-tailed distributions of biophysical parameters implies the presence of resonances in neuronal networks. However, the specific connectivity determines the duration and intensity of these resonances. The combination of these two factors are at the basis of the ongoing properties of the nervous system and of its ability to process information.

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Inferring the source of fluctuations in neuronal activity

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Neuronal activity fluctuates greatly not only when animals are stimulated extrinsically, but also in the absence of stimulus [1,2]. We have found out recently that the Hawkes process describing self-excitation [3] may exhibit large fluctuations even in the absence of external stimulation [4,5]. Alternatively, fluctuations may be realized simply by generating point events from the inhomogeneous Poisson process that describes the extrinsic stimulus. Given a spike train recorded in vivo, we wish to estimate the relative contributions of internal excitation and external stimulation. For this purpose, we developed an Empirical Bayesian framework equipped with the self-exciting interaction term and applied it to spike trains. We shall demonstrate the result and also present related issues.

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Spatiotemporal characteristics of bursting and avalanches in cultures of cortical neurons

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Cortical cell cultures exhibit bursting behavior in which the entire culture participates [4, 3]. These cultures also produce "neuronal avalanches", which have been viewed as having scale invariance consistent with being in a self-organized critical state [1, 2]. The current work presents results from closed-loop simulations of neuron-activity-driven network development [3], and the full spiking activity of all neurons in that developing network, that suggests bursts are a separate category of behaviors that involve wave-like propagation from a single point and occur at the scale of the entire network and that the inter-burst activity is more properly viewed as scale invariant.

Figure 1: Example of a typical whole-network burst. Each image includes 10ms of activity; darker shade corresponds to large number of spikes by that particular neuron. Images are 30ms apart (entire sequence is 210ms).
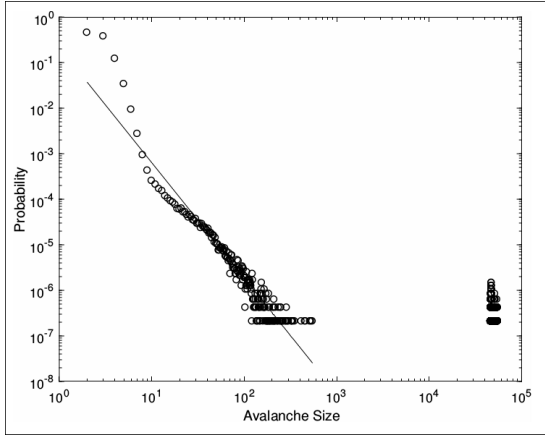
Figure 2: Probability of occurrence vs. avalanche size (number of spikes). Avalanches defined as sequences of spikes separated by interspike intervals less than overall mean. Stationary activity during last 1/4 of simulation. Line of best fit for $p = f^{-\beta}$ computed for avalanches smaller than 10^4 spikes, yielding $\beta = -2.53$. Total of 19,183,767 avalanches for full simulation, with 2 to 55,202 spikes.
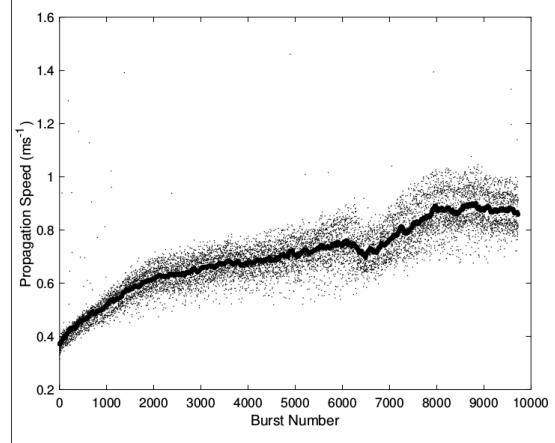
Figure 3: Burst speed during network development for individual bursts (points) and moving average of 100 bursts (line). Speeds were calculated from burst image data by identifying (x, y) centroid of initial cluster of spikes (the *origin*) and, for each window, computing distance to those neurons producing the most spikes, then averaging over the burst, excluding the first and last 50ms.
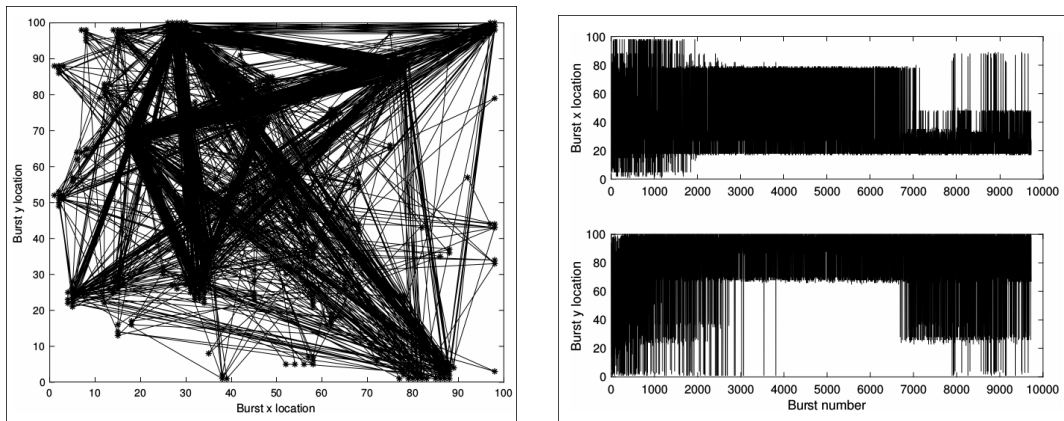
Figure 4: Burst origins (9729 bursts). **Left**: (x, y) origin of each burst ($*$) and their sequence (lines). **Right**: x (top) and y coordinates of burst origins, plotted versus burst number. Initial wide range of locations settles down to small number that alternate randomly; groups of "active origins" changes over time.

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The Jacobi diffusion process as a neuronal model

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The Jacobi process is a stochastic diffusion characterized by a linear drift and a special form of multiplicative noise which keeps the process confined between two boundaries. One example of such a process can be obtained as the diffusion limit of the Stein's model of membrane depolarization which includes both, excitatory and inhibitory reversal potentials. The reversal potentials create the two boundaries between which the process is confined. Solving the first-passage-time problem for the Jacobi process, we found closed-form expressions for mean, variance and third moment, that are easy to implement numerically. The first two moments are used here to determine the role played by the parameters of the neuronal model. Namely, the effect of multiplicative noise on the output of the Jacobi neuronal model with input-dependent parameters is examined in detail and compared with the properties of the generic Jacobi diffusion. It appears that the dependence of the model parameters on the rate of inhibition turns out to be of primary importance to observe a change in the slope of the response curves. This dependence also affects the variability of the output as reflected by the coefficient of variation. It often takes values larger than one and it is not always a monotonic function in dependency on the rate of excitation.

Gaussian process regression for decoding multineuron spike trains

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Gaussian process regression is a non-linear extension of multivariate analysis, and has been widely used in classification and regression tasks. It provides a useful mean of decoding information expressed in neural activity. Continuous signals with time-varying magnitudes such as EEG and LFP can readily be analyzed by Gaussian process using frameworks developed for time series analysis. However, since a spike train is a sequence of event occurrences, a new method to deal with such a data structure. One natural way to use Gaussian process regression for such data is to define a positive-definite kernel specific to spike trains. Various single-neuron spike trains have been proposed and used for decoding already.

One interesting generalization of this is to extend the domain to multineuron spike trains, which has become increasingly common in recent years. Some spike train kernels have been extended to multineuron spike trains, which are simultaneously recorded spike trains obtained from multiple neurons. However, most of these multineuron extensions were carried out in a kernel-specific manner. In this presentation, I introduce a general framework for extending any single-neuron spike train kernel to multineuron spike trains. The framework is based on the R-convolution kernel. A few specific subclasses of the proposed R-convolution linear combination kernel are explored as well. These subclasses have a smaller number of parameters and make optimization tractable when the size of data is limited.

The proposed positive-definite kernel was evaluated using Gaussian process regression for multineuron spike trains recorded from an animal brain. It was compared with the sum kernel and the population Spikernel, which are existing ways of decoding multineuron spike trains using kernels. The results showed that the proposed approach performs better than these kernels and also other commonly used neural decoding methods.
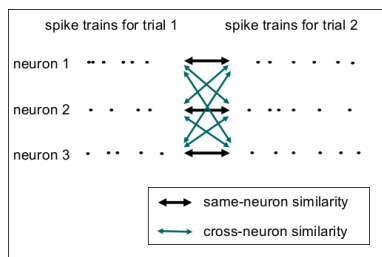
Figure 5: Same-neuron and cross-neuron similarities between spike trains.
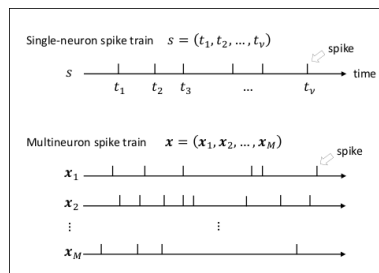
Figure 6: A single-neuron spike train and a multineuron spike train.
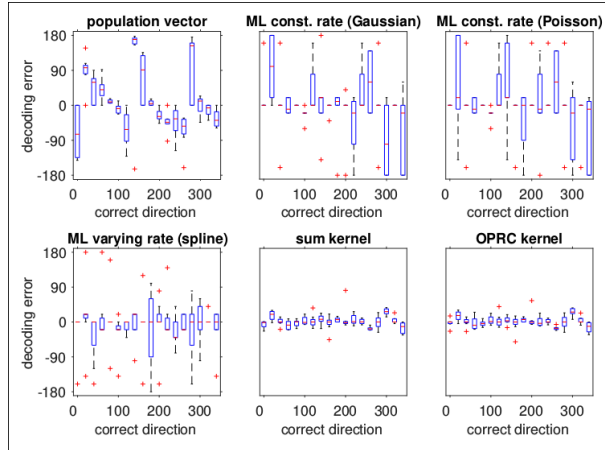
Figure 7: Decoding errors of various methods applied to CRCNS PVC-3 data set. Decoding error represents angular difference between estimated direction and correct direction in degrees. For each condition (direction), decoding errors were obtained by leave-one-out cross-validation using 4/5 of whole data set.

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Parameter Estimation through Approximate Bayesian Computation for Stochastic Neural Mass Models

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In this talk we perform statistical inference for a stochastic neural mass model using approximate Bayesian computation. Stochastic neural mass models are used to describe the electrical activity of a whole population of neurons with average properties, and have been reported to reproduce, for example EEG/MEG/SEEG data. Here we focus on a specific reformulation of the Jansen and Rit neural mass model [1] as a stochastic differential equation (JR-SDE) with additive noise [2]. We can analyse this new stochastic version of the model through its dynamical and structural properties. In particular, we are interested in estimating some parameters that have been shown to be relevant for the description of α-rhythmic and epileptic behaviour.

In [2], the authors declared that the JR-SDE can be re-formulated as a stochastic Hamiltonian equation, which enabled them to prove its ergodicity. This guarantees that the distribution of the 6-dimensional solution process $X(t) = (X_0(t), ..., X_5(t))^T$, $t \in [0, T]$ converges exponentially fast towards a unique invariant measure and allows us to extract important statistical properties from single sample paths.

Here we perform statistical inference for this stochastic model, making use of a numerical splitting scheme that has been shown to preserve the structural model properties, differently from commonly used schemes, such as the Euler Maruyama method [2]. From an experimental point of view, the solution process $(X(t))_{t \in [0,T]}$ is partially observed through the EEG-related stochastic process $Y(t) = X_1(t) - X_2(t)$, $t \in [0, T]$. Two main difficulties arise: First, due to the fact that the non-linear and multi-dimensional SDE cannot be explicitly solved, the dynamics of the signal process $(Y(t))_{t \in [0,T]}$ can be only simulated through the numerical scheme. Second, the corresponding underlying likelihood function is intractable. We tackle this last issue by considering the likelihood-free and simulation based approximate Bayesian computation (ABC) approach [3]. This is a Bayesian technique that necessitates plenty of synthetic data simulations from the original model.

In the proposed statistical analysis, the crucial part is to define reliable distance criteria to successfully compare the simulated synthetic signals with the observed reference data. Due to the large variability in the data generated by the JR-SDE, neither the calculation of distances between the data itself nor the use of standard summary statistics work. Even more sophisticated and common distances for time series fail. To overcome this difficulty, we propose to transform the signal data from time to frequency domain by considering the corresponding spectral density. The spectral density depends on parameters that directly affect the frequency as well as the amplitude and, therefore, carries significant dynamical and structural information.

By this clever use of the parameter dependent structural and dynamical properties of the system, the ABC approach, with the adopted numerical splitting method, is able to provide satisfactory estimates of the parameters of interest.

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Neurocoding via graph structure

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We study a model of random synaptic connections grown according to a biologically plausible algorithm introduced in [1]. We derive the distributions of small subgraphs in the resulting network in dimensions 2 and 3. This helps us to address the question of efficiency of storage and of transmission of information in the network. In particular, we investigate the role of small cycles and of multiple connections in the network performance.

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Attractor dynamics and spatiotemporal patterns of neural activity

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The sequence of spikes of a neuron may carry important information processed by the brain and thus may underlie cognitive functions and sensory perception, but random variation, noise, and reliability observed in the nervous system pose serious questions to the definition and meaning of neural coding [8, 10]. A substitution scheme where the message to be encoded is replaced by a special set of symbols defines the term 'coding' in information science. However, this definition seems hard to hold for representation of information in the nervous system. Firstly, substitution codes are essentially static because they are defined by fixed rules. If the rules change over time the message cannot be deciphered and will be misinterpreted. Secondly, it seems unlikely to exist a small fixed set of symbols to be encoded or decoded in the nervous system. Experimental evidence exist of spatiotemporal patterns of neuronal discharges, also referred to as preferred firing sequences, that correspond to repeated ordered and precise interspike interval relationships which recur above chance levels [9]. The possibility to fit such patterns into substitution codes appears rather remote and further evidence revealed the presence of deterministic chaotic attractors in experimental recordings [7, 3]. An association between spatiotemporal firing patterns and chaotic attractor dynamics was observed in theoretical [1] and large scale neuronal networks simulations with embedded neuro-developmental features [5]. In other words the whole time series of spike occurrences is assumed to be an expression of some fundamental process governing the activity of the neurons being recorded. When a specific input pattern activates a cell assembly, the neurons are activated following a certain mode. Then, a mode of activity defines how an information is processed within a neural network and how it is associated to the output pattern of activity that is generated. In this framework the state of the neural network is defined by a set of parameters characterizing the neural network at a certain time. Then, the state of the network at any time is represented by the values of these parameters and particular invariant states of a neural network activity are referred to as attractor states [4, 1]. Then, sequences of states determined by the network dynamics define the *attractors*, whose stability in the face of continuous perturbations is a hallmark of attractor dynamics and offer the required persistence for coding a certain function [6]. The relatively simple framework of Boolean networks has the advantage to allow a complete analysis of the attractor dynamics of the networks. In this framework the attractors correspond precisely to the cycles in the graphs of their corresponding automata, and can thus be computed explicitly and exhaustively [2]. This talk presents the latest findings of this approach and shows how theoretical information science, graph theory and computational neuroscience contribute to new insights towards the exploration of neural coding.

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Posters (ordered by presenter's family name)

Baseline-corrected space-by-time tensor factorizations for decoding population spike trains

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Populations of neurons encode sensory stimuli along the time dimension (temporal variations), the space dimension (different neuron identities), or along combinations of both dimensions (Buonomano et al., 2009; Harvey et al., 2012; Panzeri et al., 2010; Panzeri et al., 2015; Runyan et al., 2017). Consequently, understanding the neural code requires characterizing the firing patterns along these dimensions and linking them to the stimuli (Abeles et al., 1988; Haefner et al., 2013; Kristan Jr et al., 1997; Panzeri et al., 2015; Pouget et al., 2000).

Various methods were proposed for compactly representing neural activity along its most relevant dimensions. In previous work (Onken et al., 2016), we showed that space-by-time non-negative tensor decompositions performed competitively compared to other techniques both in terms of data robustness and ability to find informative patterns of salamander retinal coding. This decomposition method generalized non-negative matrix factorization (NMF)(Delis et al., 2016; Devarajan, 2008; Lee et al., 1999; Smaragdis et al., 2014) by imposing non-negativity constraints on the extracted components, temporal and spatial modules and activation coefficients, leading to a parts-based, low dimensional, though flexible representation of the non-negative data.

Although these tensor factorizations performed well on salamander retinal ganglion cells, which have almost non-existent stimulus-unrelated baseline activity, it is not clear how well the methods would perform on data with considerable spontaneous activity, which might require to explicitly correct for the pre-stimulus baseline.

In this study, we evaluated decoding performance of space-by-time decompositions using both simulated data and real auditory cortical data. Further, to tackle the potential problems generated when analysing data with high baseline activity, we derived and introduced a new variant of space-by-time tensor decompositions, termed baseline-corrected space-by-time tensor factorization, that discounts the baseline activity by subtracting the pre-stimulus baseline from each trial, and then decomposes the baseline-corrected activity using a tri-factorization that finds non-negative spatial and temporal modules, and signed activation coefficients.

To validate the methods, we simulated patterns of responses composed of ground-truth modules with high and low SNR and then we tried to retrieve the modules from both tensor decompositions. We found that only baseline-corrected space-by-time tensor decompositions recovered the ground-truth modules in both high and low SNR cases while space-by-time non-negative tensor decompositions managed to recover the modules just in high SNR cases.

We also validated the two factorization methods by decoding stimuli using the single-trial activation coefficients obtained with each considered method. We used a linear discriminant analysis decoder on a training set (half of the trials) and then used the classifier to decode the stimuli presented on a test set (remaining half of trials) of activation coefficients. We chose for all methods the number of modules that maximized decoding performance. In simulated data, we found that, while both methods performed very well, the baseline-corrected factorizations performed better than the non-negative decompositions with higher values of baseline activity, and that the methods performed similarly with lower background activity. On an auditory cortical dataset, we computed decoding performance when varying the number of trials per stimulus in the training set. Baseline-corrected tensor decompositions performed better than the non-negative ones for lower number of training trials, while the baseline-corrected decompositions gave similar decoding performances, but with most compact representations with respect to non-negative decompositions for higher number of training trials.

Our results suggest that tensor factorizations, in particular the baseline-corrected one, work robustly and efficiently when decoding neural population responses with high baseline activity.

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Functional interactions among neural assemblies based on frequency-domain analysis

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To inferring information processing mechanism in a brain, time-domain analyses and frequency-domain analyses are usually applied to time series data recorded from a brain or neuron activities. In this work, we focus on frequency-domain time series analyses to deduce the network topology in terms of information processing.

Frequency-domain analysis, such as coherence and partial coherence analyses, are applied to time series data such as spike train data and EEG and fMRI data to infer the functional relationships between neurons, and regions of interest (ROI), respectively. Especially partial coherence analysis allows us to analyze coherence of two time series data eliminating the effect of another time series data recorded simultaneously to the pair of the time series data [1]. Hence it can cancel a pseudo coherence caused by, for example, a common input. Next, the direction of functional interaction is an important target to analyze to understand the information processing mechanism in the brain. Granger-causality is applied to analyze a linear causality between two time series [2]. As the number of time series data increases, the combinations of time series data to analyze the functional interaction increase more.

Here we applied those frequency-domain analyses to simulated multivariate spike trains generated by a synfire chain model as a simple possible model of the thalamocortical circuit. The input time series are generated by nonlinear dynamical systems. In another set of data we analyze time series derived from real experiments with recordings obtained from functional brain imaging based on near infrared spectroscopy (fNIRS) in young participants. Data from virtual ROIs are used to analyze the functional interaction during various stages of sleep. We use machine learning methods at a preprocessing stage with the aim to categorize the recordings into sets of data in an unsupervised way. Then, the analysis of the functional connectivity between the sets of data will be used to infer the strength and the direction of the connections between the sets of data, which are supposed to represent a same brain state and/or brain region.

The analyses on simulated time series data are performed with reference to the known network structure in the model, which can be a basis of interpretation of the analytical results obtained from experimental data.

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Active electrosensing for spatial map encoding in a fish

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Exploration and active sensing are necessary for the acquisition of spatial information, they provide a direct measure of the type of information that is encoded. Such information includes both the intrinsic properties of the environmental items and their spatial relationships: ending up in a neural representation of the environment, often referred to as a spatial map. For this reason, we are interested in studying spatial learning in a pulse-type weakly electric fish (WEF) that uses active electrosensing to identify and localize landmarks and their spatial relation to food. Pulse-type WEF electrosense their near environment by generating electric organ discharge (EOD) pulses at variable rates and sensing spatially localized object-induced distortions of the EOD-generated electric field with a cutaneous arrays of electroreceptors. By observing active electrosensing we can infer changes in the animal's foci of attention during learning. We hypothesize that active sensing is a behavioral manifestation of attention and essential for spatial learning; the fish use spatial memory of landmarks and path integration to reach the expected food location and confine their attention to this region.

Fast Instructed Stimulus-Response Learning

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Humans are able to quickly learn new stimulus-response (S-R) rules, for instance from single verbal instructions: In situation X do action Y. We have attempted to measure how fast the learning process actually is in an experiment where a series of randomly generated S-R rules were presented visually for 200ms, e.g. "A>" means "the next time you see an A, press the key to the right". A test stimulus, e.g. "A", was then presented after a delay between 50ms and 1300ms, until the response is produced. The expectation was that if the test stimulus is presented before rule learning is completed, there should be some impairment in generating the response. To stop subjects from just producing the prepared response, we used 33% of catch trials where a different letter was presented, e.g. "B" and for which the response is a space-bar press. To test whether subjects used a serial strategy of encoding the rule first and only afterwards started processing the test stimulus, we also used 50% of masked trials, where the test stimulus was shown for only 100ms followed by a mask. The idea was that masked test stimuli may not be processed if presented during the learning process.
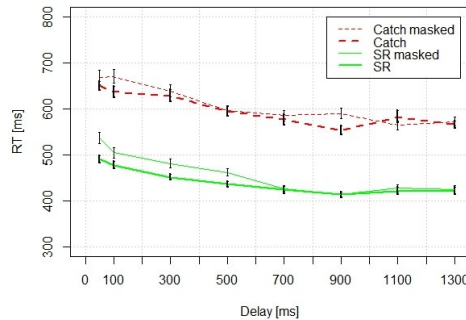
Figure 8: Response times measured from the start of the test stimulus, with standard error bars. Averages over 10 subjects.

We found longer response times (RT) for delays up to 700ms for all conditions. The errors were low for normal SR trials (<2%) and higher for catch trials, especially in the masked case for short delays (9%). Masking mainly increased the number of misclassification errors for short delays.

What do these results tell us about the speed of S-R learning? From the examination of neurophysiological data in other experiments [e.g. Wallis and Miller 2003; Muhammad R. et al., 2006; Cisek and Kalaska, 2010, Rozzi and Fogassi, 2017] , it appears that the task could be achieved without any fast synaptic learning, using fixed links between a repertoire of pre-existing sensory data processing functions in prefrontal cortex (PFC) and a repertoire of motor functions in premotor cortex (PM). Synaptic learning would only be needed prior to the start of the experiment, when subjects are explained the task, and consists of setting up appropriate connections between PFC and PM.

There are several possible ways to wire a network for the task, but the scheme most consistent with the data is that the response R is primed when the rule is presented and awaits a "match" signal as trigger, while the "space-bar" response is only activated when a "non-match" case is detected [e.g. Duque J, 2012, 2014; Katnaniand H.A. , 2013; Cisek, 2005]. This can explain the large RT cost (around 160ms) and error types in catch trials.

The next question is whether the dynamics of such a network can explain our reaction time data. This includes the fact that there is a RT cost for small delays also in catch trials, despite a longer overall RT. Such an increase in RT for small delays can have several origins, e.g. the dynamics of encoding the S identity in PFC states, the dynamics of inhibition / dis-inhibition at the start of the trial, and possibly others.

PFC is currently seen as dynamical system converging to task-dependent states, but its speed of convergence has not been documented yet. Indirect evidence suggests that it can take up to 1000ms [Cromer J.A. et al., 2012]. So, small delays could probe the PFC system during the convergence process when, e.g., match / no-match signals may be weaker or take longer to generate. This early, partially functional, state of the PFC could also explain the errors caused by masking for short delays.

The motor system comprise a number of brain areas (PFC, PM, M1, SMA, preSMA, basal ganglia, etc) providing inhibition and dis-inhibitions in various phases of action preparation and initiation, but there is still no agreement on its operation [e.g. Lebon F. et al., 2018]. In our choice RT task, it is likely that the system is inhibited until the "match" signal [Criaud M. et al., 2012] , consistent with a RT around 400ms for long delays, but it is unclear whether some extra inhibition is activated by the rule presentation and then decays within the 700ms observed here.

Future simulation work will establish whether the proposed fixed-connections network and presumed dynamics of its elements can explain our data.

A stochastic model for block-layered neuronal networks

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Front-line interacting neuronal populations, which are subjected to external stimulations and noise, transmit through networks of synaptic linkages the sensory input to a smaller ensemble of secondary-line neurons. The received information is encoded according to combinatorial schemes of the activated neurons. The overall firing activity is then modulated by the selective inhibition action of the neurons responsible for such function. A typical example is the information transmission in the olfactory system, where the sensory (front-line) neurons fire in specific way as a consequence of different odorants binding; their response is conveyed and then modulated by the olfactory bulb neurons, that are organized in reticular structures called *glomeruli*, before reaching the *mytral cells* (see, for details, [1, 2, 3]). The geometry of the network of neurons and of their synapses, together with the timing and the rate of the firing activity, are the basis of the encoding and the transmission of the information([4, 5, 6]).

Along the lines of [6] and [7], our aim is to construct a stochastic model for interacting neurons organized in a block-layered network devoted to the information processing in this kind of sensory systems. The model of a layered and modular network describes the dynamic behavior of each prototypical neuron in such systems, taking into account both its role (excitatory/inhibitory) and its location within the network. Specifically, we study the impact of selective inhibition on the information coding, also considering the relative proportion of inhibitory neurons on the neuronal population ([8, 9]).

We rely on specific results on the First Passage Time for Markov processes to obtain suitable approximations for this dynamics via the Volterra integral equation approach ([10]). Numerical approximations will be compared to the ones obtained by the simulation of stochastic differential equations describing the different kinds of neurons and their connections within the network.

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Inferring the degree of causal interactions within physical systems from their surface dynamics

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Consciousness has been linked to the functional differentiation and integration of cortical areas [1]. Understanding the nature of interactions within and across cortical areas is thus fundamental for the comprehension of consciousness and its physical substrate. For practical purposes, current empirical approaches aimed at unraveling the causal interactions between cortical areas in order to estimate a subject's level of consciousness [2] are limited to analyses of the brain's surface dynamics, i.e., neural activation patterns at rather coarse scales. However, a formal relationship between the intrinsic causal properties of a physical system and the surface dynamics (both evoked and spontaneous) it exhibits under typical conditions has not been clarified yet. Our aim is to test whether estimating the amount of structure, namely the richness, within the surface dynamics can indeed be used as a proxy for identifying structure in the underlying causal interactions.

We focus on 2D lattices of majority gates with local (*grid* network) and non-local (*random* network) interactions, as examles for simple neural networks with different amounts of structure in their causal interactions. The grid network exhibits higher degrees of shared input and output among elements, which leads to intuitively more complex dynamics with visible structure ("patches") in the relevant regime. To quantify the richness of the surface dynamics objectively, we implement two different techniques. On the one hand, we measure the deviation from statistical independence among the subsets of the system, assessed using the concepts of statistical entropy and mutual information [3]. On the other hand, we take advantage of the Minimum Description Length principle (MDL) [4], which balances a good fitting of the network's state at each time step with a simple description of it. More precisely, we use MDL implemented in the *NASSAU* algorithm [5] to tackle the optimal model order selection problem in the boolean matrix factorization. The algorithm provides the minimum description length of the surface dynamics as the sum of the description length of the identified regularities (also called *effective complexity* [6]), namely the description length of the product of the factors, and of the other features treated as incidental.

The results obtained with both techniques clearly show a higher amount of structure in the grid's surface dynamics compared to the random one. These preliminary results represent a step toward the proof that the study of the surface dynamics under typical conditions for inferring the nature of the causal interactions is well-founded. Establishing a formal connection between causal structure and surface dynamics would strengthen the link between theoretical predictions about the physical substrate of consciousness [1] and associated practical measures [2].

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Cross-sound modeling of midbrain auditory responses to two different environmental sounds

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In modeling single unit responses to different types of environmental sounds (e.g., drinking or eating sounds as commonly detected at the rearing cage of laboratory rats), results are rather satisfactory provided the same type of sounds is used in both training and testing. The performance level is high ($> 85\%$) particularly when the spectro-temporal area of strong acoustic energy is (e.g., top 30% strong energy components) fed to the model input, a finding that is consistent with the presence of broad-band amplitude transients in the environmental sounds. To predict 'cross-sound' responses (i.e., to predict the response to one type of sound after the model is trained with responses to another type of sound), model performance is typically poor ($< 25\%$), which is similar to what has been reported in the literature.

In our previous artificial neural network modeling of single unit responses to time-varying tonal stimuli (i.e., random frequency modulated tone), we found that it is critical to set in the model, a proper delay as well as a proper time window for the computation. We therefore hypothesized that the improper setting of delay and time window may lead to the poor performance for cross-sound modeling. We speculated that these delay and time window might both vary across sound types (or even across different acoustic bursts or bouts of the same sound).

We here report a novel approach to improve on cross-sound modeling. The method consisted of two parts: (a) on single sound-bout basis, we first analyzed single unit responses to each sound type (i.e., drinking or eating sounds that each consisted of multiple sound bouts) by constructing a model performance map (a 2D function of the model delay and time-window length). We then computed a 3D similarity index to compare sound-bouts based on their 3D pattern in the model performance map, and put those sound-bouts sharing similar features in one group. Within this new group that contained bouts from two different sound types, the neural model was first trained with sound bouts of one type and then tested with another type. (b) In testing responses of sound-bouts from the two sound types, we further determined their optimal threshold level at which only the stronger energy components of the sounds were fed to the model input. Results on population averages ($n = 32$ single units) showed significantly elevated model performance (up to $> 86\%$), and also improved performance of modeling within sound type to $> 92\%$. Results on individual single units also showed improvement in model performance, although not as remarkable as the population averages. The same approach was however less effective when applied to groupings of individual sound bouts in terms of their similarity in sound waveform or in their response time profile. Results further supported the sensitivity of the model delay and time window in grouping sound-bouts. We concluded that it is possible to perform cross-sound modeling for environmental sounds with rather satisfactory results, using our artificial neural

network. But two issues are important: (a) grouping of sound-bouts with similar properties, and (b) extracting high-energy components at a supra-threshold level that is sound-type dependent.

Recurrent network model for studying network dynamics in calcium imaging population recordings

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Simultaneous recordings from populations of tens to hundreds of cortical neurons have recently become possible due to technological advances in two-photon calcium imaging (Harvey et al 2012, Morcos & Harvey 2016, Runyan et al 2017). These population recordings allow the study of interactions between neurons within a network and how these interactions contribute to task performance.

It has been long known that correlations in neural activity profoundly affect how neural populations encode information (for a recent review see Kohn et al 2016). Furthermore, a recent study has shown that the strength of correlations among neurons varies between cortical areas and affects the timescales of population dynamics (Runyan et al, 2017). However, the origin of such observed correlations in neural activity remains unclear. Neural correlations could reflect a combination of factors such as anatomical recurrent connectivity, common inputs from other areas and shared covariations in excitability. Fitting a neural network model, which takes into account several of these factors, to simultaneously recorded neural activity could be a powerful way to both understand the origin of neural correlations and to better evaluate their impact on network dynamics.

Our aim is to develop recurrent neural network models that can be used to explain the patterns of correlations between the activity of different neurons simultaneously recorded within an experimental session. Recent attempts of using neural network models to fit calcium imaging data have used learning rules that do not take into account trial-to-trial correlations in neural activity, as they described only the dynamics of trial-averaged neural activity (Rajan et al 2016). To address this issue, we are developing a gradient descent learning rule for firing rate recurrent network models that can learn to infer both trial-averaged neural dynamics and trial-to-trial covariations of the recorded neural population activity. This learning rule is based on the algorithm developed by Movelland & McClelland (1993), in which neural networks are trained to reproduce multivariate continuous probability distributions. Although the techniques introduced by Movellan & McClelland (1993) were developed only for neural networks with symmetric connections, our technique is based on a moment expansion approximation, and for this reason it can be applied to recurrent networks with any topology of the synaptic connections.

We are currently validating the learning rule by training recurrent neural network models with simulated target functions, in which the ground-truth about the anatomical connectivity is known, to check its accuracy with finite data samples. We will then apply the learning rule to optimise these recurrent network models to fit two-photon calcium imaging data recorded from behaving mice, such as those reported in Morcos & Harvey (2016) and Runyan et al (2017), in order to investigate the possible relationships between functional coupling and network parameters across areas and tasks. In addition, we will extend recently developed tools to study analytically the dynamics and bifurcation structure of the recurrent firing rate networks

(Fasoli et al 2016, 2018, Fasoli & Panzeri, 2018). This approach will allow us to understand the network dynamics underlying the sequential population dynamics often observed in association cortices during cognitive tasks.

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On a stochastic model for fluctuating systems under state-dependent dichotomous noise

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Formal models in Neuroscience and Physics are often based on stochastic processes subject to fluctuating behavior due to dichotomous noise (see, for instance, Bena [1], Li *et al.* [7], Müller-Hansen *et al.* [8]). A landmark among such random processes is the (integrated) telegraph process (see Kolesnik and Ratanov [5], and references therein). Recent advances on its state-dependent generalizations have been provided by Garra and Orsingher [4]. Nevertheless, state-dependent stochastic processes deserve interest in neuronal modeling, as for diffusion neuronal models with multiplicative noise (D'Onofrio *et al.* [2]) and for processes with exponential decay subject to excitatory inputs with state-dependent effects (Di Crescenzo and Martinucci [3]).

Stimulated by the above investigations, we propose a stochastic process for the description of fluctuating behavior with variable trend, where the fluctuations follow a state-dependent alternation similar to the telegraph process. For the proposed model we aim to investigate the optimum signal determination with respect to the noise characteristics, by adopting suitable criteria as those exploited by Lansky *et al.* [6].

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A stochastically drifted model for a neuron embedded in a network: simulations and statistical analysis

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During sensory stimulations, populations of neurons work intensively to transmit the information inputs through the synapses' network to neurons of other populations. The membrane potential of each neuron, involved in this complex dynamics, undergoes variations induced by the flow of inputs (excitatory or inhibitory) coming from the neuronal network in which it is embedded. Stochastic models for this neuronal dynamics rely on diffusion processes suitable to mimic the behavior of the membrane potential of the neurons. In particular, the timing of the emission of the spike, that gives rise to the firing activity, is modeled as the first passage time (FPT) of these processes through a boundary, i.e. the firing threshold.

Our intent is to model the neuronal activity of a neuron embedded in a network and subject to the firing activity originated from surrounding neurons. Specifically, we construct a model based on a stochastic differential equation (SDE) with the drift term of stochastic nature and representative of the inputs deriving from the dynamics of the surrounding neurons. For the case of M populations of interacting neurons, we use a stochastic counting process to sum inputs (random variables) originated from each component of each population; the resultant stochastic process drives the mean of the process solution of the model SDE. Under specified hypothesis the distribution law of the stochastic drift can be considered assigned (e.g. that of a compound Poisson process). The FPT problem for these processes stochastically drifted reveals hard to be addressed. Some useful results about FPT probability density function (pdf) of approximating diffusion processes will be suitably exploited ([1],[2]). Extensive simulations of the dynamics described by this kind of SDEs will be performed; furthermore, we analyze the amount of information that can be reliably exchanged through the network, studying mutual information and channel capacity (see for instance [3], [4]). Particular attention will be given to the changes of these quantities with respect to the proportion of inhibitory and excitatory neurons constituting the network.

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A model of presynaptic KV7 channel function in hippocampal mossy fiber boutons

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In hippocampus, a type of slowly-activated and non-inactivating K+ channels, belonging to the Kv7 family, are highly localized on initial segments of myelinated and unmyelinated axons where they influence neurons' excitability. Interestingly, immunohistochemistry shows that the KV7.2 and KV7.3 subunits are localized throughout hippocampal mossy fibers. Electrophysiological recordings from mature synaptic boutons showed that the KV7/M- current is also present in mossy fiber, is active at rest and regulates the membrane conductance. This is an important issue, since these channels may be an important determinant for modulation of excitatory neurotransmitter release, and thus signal transmission, at DG-CA3 synapses. In this poster we will show the possible functional consequences of blocking Kv7 channels, by using a biophysical computational model of mossy fiber bouton (MFB). The model is able to reproduce a number of experimental findings under control and after Kv7 block by XE991. Surprisingly, the model predicts that Kv7 channel expression and activation in MFB may directly influence other channels' kinetic, which may result in a significant modulation of the action potential waveform and in potentially important consequences on synaptic transmission and signal coding.

Detecting dependences between neurons in the electric fish

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The response of two neurons to a stimulus is influenced by both their interactions and their own past activity. Since recorded spike trains exhibit patterns due to both phenomena, it is a challenge to distinguish to which of them every specific behavior should be ascribed. Here, we consider spike trains that were simultaneously recorded from two neurons of the electro-sensory lobe in the weakly pulsing electric fish *Gymnotus omarorum*. These cells respond to a specific pulsed electric stimulus, emitted by the fish's own electric organ discharge (EOD) with a nearly constant frequency. Note that, without this regular signal, the neurons are silent. To discriminate between marginal and joint behaviors, we introduce two shuffling procedures. We analyze the results with auto-correlograms and cross-correlograms as well as through the use of copulas. Besides providing information on the nature of the observed dependencies, the provided method identifies also the direction of mutual influences. In particular, we recognize the presence of both a *within* and a *between dependence* of the spike trains. Both neurons preserve memory traces of the recent past, in terms of their propensity to spike with high frequency. Moreover a mono-directional inhibitory mechanism is observed as a consequence of the direct interaction between the cells.

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Modeling event cascades using networks of additive count sequences

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We propose a statistical model for networks of event count sequences built on a cascade structure. We assume that each event triggers successor events, whose counts follow additive probability distributions; the ensemble of counts is given by their superposition. These assumptions allow the marginal distribution of the count sequences and the conditional distribution of the event cascades to have analytic forms. Based on this, we develop a statistical method for estimating the model parameters and the event cascades from the observed count sequences. We demonstrate our method on synthetioc and real event sequential data.

Statistical Definition of Bursting in Neural Spike Trains by Means of Novelty and Surprise Measure

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We present a method for calculating the statistical significance of bursts in a spike train relative to a 0-hypothesis of independent Poisson processes. Mathematically, the method is based on the calculation of novelty and surprise for bursts as defined by Palm (2012) [1,2], where a 'burst' signifies the event that a large number of spikes have occurred in a short interval of time.

Let $(X_k)_{k \in \mathbb{Z}}$ be a sequence of positive random variables (inter-spike-intervals) and $X_{i,k} = \sum_{j=0}^{i-1} X_{k-j}$ for $1 \leq i$. Obviously the distribution of $X_{i,k}$ is the same for each k and $X_{1,k} = X_k$. Let $F_i(t) = \mathbb{P}[X_{i,0} \leqslant t]$, we define the **burst novelty** at spike k as:

$$N_k := -\log_2[\min_i F_i(X_{i,k})].$$

Again the distribution of N_k is the same for each k with cumulative distribution function F, i.e. $F(x) = \mathbb{P}[N_0 \leqslant x]$. Now we can define the surprise function as:

$$S : \begin{cases} \mathbb{R}_+ \to \mathbb{R}_+ \\ x \to -\log_2(1 - F(x)) \end{cases}.$$

The **burst surprise** at spike k is defined as the random variable $S_k := S(N_k)$. It is the logarithm of the significance probability of the burst novelty at spike k.

In order to apply those measures in practice to experimentally observed spike-trains, the task is to precompute the functions F_i and S either analytically or by sampling. To this end we assume as 0-hypothesis that the spike trains are sampled from a Poisson process. For exponentially distributed X_k the F_i are well-known, and we have computed or estimated S by sampling.

This method can be easily generalized to more general inter-spike interval distributions. In addition to the characterization of burstiness the method may also be used to determine response latency of single neurons or small groups of neurons based on single trials. It is related to some previous approaches by [3,4,5].

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Channel density variability across hippocampal CA1 neurons

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Every neuron of a network exerts its function by transforming multiple spatiotemporal synaptic input patterns into a single spiking output. This intrinsic input/output function is specified by the particular passive electrical properties of the neuronal membrane, the composition and spatial distribution of ion channels, and the properties of the synaptic inputs. For a variety of physiological or pathological reasons, this function may change during a neuron's lifetime. This process results in a high variability in the observed peak conductance of ion channels across neurons. The mechanisms responsible for this variability are not well understood, although there are clear indications from experiment and modeling that degeneracy and correlation among multiple channels may be involved. Here, we studied this issue in biophysical models of hippocampal CA1 pyramidal cells and interneurons. Using a unified data-driven simulation workflow and starting from a set of experimental recordings and morphological reconstructions obtained from rats, we built and analyzed several ensembles of morphologically and biophysically accurate single cell models with intrinsic electrophysiological properties consistent with experimental findings. This modeling effort has been carried out using the Brain Simulation Platform (BSP) of the Human Brain Project (https://collab.humanbrainproject.eu/#/collab/1655/nav/28538) and two open-source packages, the Electrophys Feature Extraction Library (eFEL, https://github.com/BlueBrain/eFEL) and the Blue Brain Python Optimization Library (BluePyOpt) [1]. The results suggest that the set of conductances expressed in any given hippocampal neuron may be considered as belonging to two groups: one subset is responsible for the major characteristics of the firing behavior in each population and the other more involved in degeneracy. Analysis of the model neurons suggested several experimentally testable predictions related to the combination and relative proportion of the different conductances that should be expressed on the membrane of different types of neurons for them to fulfill their role in the hippocampus circuitry.

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On stochastic neuronal models integrating correlated inputs

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Among stochastic neuronal models the Leaky Integrated-and-Fire (LIF) model with colored noise ([1, 2, 3]) is a refined version of the classical one driven by the white noise ([4, 5]). Indeed, the colored noise is required to include a correlated input described as a stochastic (no-delta) correlated process and integrated in the neuronal dynamics. The motivation of considering such model is that the standard LIF model cannot explain the high variability in the neuronal response to stimulations and the adaptation phenomenon ([6, 7, 8, 9]).

Although this model is based on a non-Markov process, estimates of firing densities and rates can be obtained not only by means of simulation techniques but also by exploiting some properties of Gauss-Markov processes approximating the modeling process ([3]). In order to improve these results and the characterization of such kind of models, we use some recent theoretical results about integrated Gaussian processes ([10, 11]).

In addition, with the aim to focus on neuronal models with memory, a fractional Langevin equation is also considered ([2, 12]). For this case, fractional integrals of Gaussian processes turn out to be helpful to investigate the corresponding neuronal models.

Putting together the theoretical investigations, simulations and numerical approximations for the firing densities and rates, the goal is to compare the above models highlighting the specific features also respect to the classical models.

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Benefits of functional data analysis of evoked potentials

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Evoked potentials reflect neural processing and are widely used to studying sensory perception. We applied a functional approach to studying single-trial auditory evoked potentials in the rat model of tinnitus, in which overdoses of salicylate are known to alter sound perception characteristically. Single-trial evoked potential integrals were assessed using the functional principal component analysis. An analogous analysis was performed on the first derivative of the response functions. We conclude that the functional principal component analysis is capable of differentiating between the controls and salicylate treatments for each type of sound. It also well separates the response function for different treatments. The results show, that scores of the first few principal components are effective cluster predictors.

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A Pure Integrate and Fire model with Input-output Consistency

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In 1964, Gernstein and Mandelbrot proposed the Integrate and Fire model to account for the observed stable behavior of the Interspike Interval distribution. Their study of histograms of ISIs revealed the stable property and they suggested modeling the membrane potential through a Wiener process in order to get the inverse Gaussian as first passage time distribution, i.e. a stable distribution. Holden (1975) observed that stable distributions determine a simple transmission pathway.

Later many variants of the original model appeared with the aim to improve its realism but meanwhile researches forgot the initial clue for the model. The Leaky Integrate and Fire model that has not stable FPT distribution gives an example. The same holds for many other variants of this model. More recently Persi et al.(2004) studying synchronization patterns, proposed a time non homogeneous integrate and fire model accounting for heavy tail distributions. The existence of heavy tails, typical of stable distributions is well recognized in the literature (see for example Tsubo et al., Gal and Morom and references cited therin).

Signals from different neurons are super-imposed during the elaboration. Lindner (2006) [7] showed inconsistencies in the generally accepted hypothesis on a resulting Poissonian distribution. Unfortunately, this is the basic assumption of classical Integrate and Fire models and it determines a serious inconsistency in the models.

If we accept that the spiking times of a neuron should exhibit heavy tail distributions, then the post-synaptic signals should arrive to the observed neuron according to inter-times displaying heavy tails as well. Hence, the randomized random walk describing the dynamics of the membrane potential should exhibit jumps at times coherent with the superposition of the impinging postsynaptic contributions. Furthermore, the resulting dynamics should determine inter-spikes intervals (ISIs) with heavy tails. Generally the consistency between input and output signal is generally disregarded, despite the improved robustness exhibited by a code characterized by stable ISIs.

Here we rethink to the problem, taking advantage of the mathematical progresses on regularly varying random variables. Hence, we propose to formulate the model starting from its main property, i.e. the heavy tails of the ISIs distribution. Then, we follow the Integrate and Fire paradigm. However, we model the membrane potential evolution as a randomized random walk whose jumps result from the superposition of the regularly varying inter-times of the post-synaptic signals of the other neurons participating to the network. The resulting model is actually consistent, i.e. the ISIs of the considered neuron has the same heavy tail behavior as the other neurons of the network.

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A Thalamocortical Network Model for Pathological and Healthy Dynamical Regimes

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The thalamus is a crucial gateway for inputs to cerebral cortex. Thalamic dysfunction can affect cortical dynamics and lead to sensory impairment, cognitive disorders and epilepsy. A deep understanding of the thalamocortical transmission is then necessary to develop therapies for the aforementioned pathologies. Here we present a novel thalamocortical network where both areas are simulated with Adaptive Exponential Integrate-and-Fire (AeIF) spiking neurons. Starting from a recent paper [1] on spindle oscillations, we extend previous results by linking thalamic network to a cortical AeIF model reproducing the basic features of cortical information processing [2] and analyzing the relationship between thalamic and cortical Local Field Potential (LFP) both when the thalamus is isolated and when is receiving external inputs.

We simulate a network consisting of four neuronal populations divided into two different excitatory-inhibitory subnetworks. We consider 250 thalamocortical relay (TC) neurons and 250 reticular (RE) neurons for thalamic subnetwork, while 4000 pyramidal (PY) neurons and 1000 interneurons (INT) for cortical subnetwork. Ratio between populations are compatible with anatomical findings. We build RE-RE connections starting from a ring network and then randomly rewiring for a small-world-like arrangement. Synaptic connections are random and sparse with different probabilities between populations. During *asleep state* (absence of external stimuli to thalamic network) we initialize self-sustained spindle-activity of thalamic circuit as in [1]. We consider instead external Poisson spike trains with different rates to simulate sensory inputs during *awake state*. In both regimes we consider also cortical ongoing activity as external inhomogeneous Poisson spike trains with time-dependent rate described by an Onrstein-Uhlenbeck process. We described single neuron dynamics with typical AeIF coupled equations between membrane potential $V(t)$ and auxiliar current $\Omega(t)$ reproducing biophysical adaptation. We consider different set of parameters for every populations in order to capture intrinsic dynamics of thalamocortical cells. Synaptic currents are described by a conductance-based double-exponential model, with different time constants for EPSP, IPSP and axonal delay.

Out results show that during *asleep* state thalamic LFP is characterized by θ/spindle oscillations [7-14 Hz] and 2 Hz δ-oscillations with higher amplitude. The latter emerge from a wax-and-wane behaviour of faster θ/spindle rhythms. On the other hand, during *awake state* a fraction of TC neurons change their dynamics to tonic firing with linear response to sensory stimuli. So thalamic LFP shows enhancement of β-rhythms, while an amplification in lower frequency range is also visible.

We then insert thalamic relays into cortical network. We find out that cortex synchronizes in the 2 Hz δ-rhythm and filters out θ/spindle-oscillations. Thalamic network modulates cortical LFP through this slow mechanism of δ-rhythm embodied by cortical network. This occurs during both asleep and awake states. Instead,

intermediate θ/spindle-oscillations are not incorporated into cortical rhythms. Rather, low spindle inputs from thalamus enhance intrinsic cortical excitation-inhibition rhythms in the high-β [20-30] Hz range during asleep state. When sensory inputs intensify thalamic activity, cortical oscillations encode strength of thalamic afferents into amplified and faster γ-rhythms [35-40 Hz]. Even during awake state spindle frequencies are not embodied by cortical activity. Consequently, they seems to be a relay mechanism rather than an informative coupling between networks.

In conclusion, our model is able to reproduce information transfer from thalamus to cortex in terms of network oscillations. This opens new possibilities for understanding the role of thalamocortical rhythms in several physiological and pathological processes, such as perception and epileptic discharges mechanisms [3].

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Inhibitory circuits in the antennal lobe of the honey bees

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Olfaction represents an essential function for living organisms, yet it is one of the least understood of the senses. In the honey bee, olfactory information processing from the olfactory sensory neurons (OSNs) to the uniglomerular projection neurons (uPNs) of the antennal lobe (AL) and higher order centers is modulated by inhibition (via both fast, ionotropic, and slow, metabotropic, receptors). Fast ionotropic inhibition provides rapid inhibitory synaptic transmission to the central nervous system and, in the honey bee AL, is mediated by three major neurotransmitters: GABA, glutamate, and histamine. These neurotransmitters act via ionotropic receptor- chloride channels (GABAa, GluCls, HistCl), that are members of the Cys-loop ligand-gated ion channel superfamily. Particularly little is known about histaminergic Cl channels in the bee, while the subset of the LNs in AL is known to be histaminergic. Among the slow metabotropic receptors in the honey bee olfactory system are AmTyr1 and AmGluRA, both of which are known to be negatively coupled to adenylyl cyclase in a way that diminishes cAMP levels. We previously showed that AmTyr1 is expressed in the presynaptic OSNs in the glomerulus. In our new study, we describe GABAergic and glutamatergic inhibition in the honey bee AL aiming to understand how inhibition shapes responses to the odor in the AL.

In the honeybee AL, the principal inhibitory GABAergic neurons are the Local Interneurons (LNs) and multiglomerular projection neurons (mPNs). They release GABA into the all compartments of each glomerulus and act via GABAa receptors. The only group of neurons that express a GABAa subunit (rdl, part of the ionotropic GABA channels) comprises homogenous LNs that equally interconnect glomeruli. On the other hand, the source of glutamate is still unknown, but glutamatergic synapses are present in all compartment of a glomerulus. Glutamate acts on GluCl1 channels and our new data revealed that GluCl1 are expressed at high levels in uPNs. To show that, we used antibodies against GluCl1 subunits combined with the synaptic marker anti-synapsin in PNs identified using neural tracing with neurobiotin. These new results strongly suggest that glutamate is a neuroactive molecule involved in inhibition of the uPNs in the antennal lobe.

Importantly, glial cells are a critical part of the inhibitory glutamatergic circuits. They can be visualized in the antennal lobe by identifying sites containing glutamine synthetase, the enzyme that processes glutamate. We found that glial cells that surround each glomerulus have very fine arborizations in the cortex area of the glomerulus. Also, the glial cells reveal anti-glutamate staining as well as the anti- NMDR1 subunits together with mGluRA. Our new data suggest a complex distribution of the glial cells involved in the GABA and glutamate signaling in insect olfaction. Grant: Human Frontier Science Program grant for Brian H Smith as co-PI.

Can grid cell ensembles represent multiple spaces?

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SISSA

Grid cells are neurons in the Medial Entorhinal Cortex of mammals whose firing activity is tuned to the position of the animal in space, exhibiting multiple peaks of activity that span an hexagonal grid. Early work investigating the representation by these cells of multiple environments [1] showed that mutual relationships between grids of different cells where conserved between environments, suggesting that grid cells ensembles encode a single, low-dimensional, "universal" map. Such universality was only demonstrated, however, in flat, extended and empty spatial environments. Moreover, recent studies [2,3] in environments with complex geometry show a distortion of the grid pattern in response to environmental features, such as odd shapes or internal walls. These results question the universal map hypothesis, and come together with evidence that the hippocampal-entorhinal circuit can encode abstract or conceptual spaces [4] which may in principle require a complex geometrical and topological representation.

We aim to address these issue from a theoretical perspective, answering first a preliminary question: is it at all possible to conceive of multiple, hence non universal, ideal grid representations expressed in the same local network when the animal is placed in distinct flat environments?

To answer this question we estimate, with both numerical simulations and analytical calculations, the capacity of an ensemble of grid units to store and retrieve multiple uncorrelated grid maps. This ensemble is described as a neural network of firing-rate units with a threshold-linear input-output relation and recurrent connectivity. Multiple continuous attractors, corresponding to different environments, are stored in the synaptic weights of the network through a hebbian connectivity rule. The storage capacity is calculated analytically in the mean field approximation for a network with full connectivity, following the method described in [5], for three different periodic attractors: stripes, square grids and hexagonal grids. Using the self-consistent signal to noise analysis developed in [6], the calculation is extended to arbitrary values of connectivity density.

Results show a great enhancement of the storage capacity in the case of hexagonal patterns with respect to stripes and square grids, indicating that the former satisfy optimality criteria for stability and memory capacity. This enhancement persists throughout all biologically realistic values of the connectivity density. The large storage capacity for hexagonal grids suggests a mechanism of this kind could be effective in representing multiple complex and incongruent spaces, provided such representation can be established in memory in the first place. Finally, these results hint that the same basic neural circuitry could store and represent, with no extra mechanism, abstract or conceptual spaces.

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Comparison of methods for detection of spatio-temporal patterns in multivariate point processes

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Hebb's hypothesis [1] states that the information processing is performed by groups of neurons called assemblies. Correlated activity between neurons of the cell assembly is considered as the signature of its activation [2, 3]. Several methods have been designed to extract such correlation and dependency structures from massively parallel spike trains. Here we concentrate on methods that specifically detect significant repetitions of spatio-temporal spike patterns (STP), i.e. with temporal delays between the composing spikes. In particular we aim here to compare two statistical methods for STP detection, SPADE [4, 5] and CAD [6], for their statistical and computational performances to evaluate their parameter regimes. SPADE detects all possible repetitions of spike patterns with a mining technique called Frequent Itemset Mining (FIM). The found and counted patterns are then evaluated for their statistical significance by a bootstrap technique employing the generation of surrogate data by spike dithering [7]. CAD on the other hand, consists of a parametric statistical test (assuming Poisson distribution of the spike trains) applied to pairwise correlations. It builds on an agglomerative recursive algorithm similar to the accretion method [8], starting by extracting all significantly correlated pairs of neurons. The resulting correlated processes are then further correlated with individual spike trains for higher order patterns. The two methods are compared by applying them to the same artificial parallel spike trains modeled as stochastic point processes with a particular correlation model (marked point processes, see [9], supplementary material). We give an overview of the differences between the two statistical methods, both in terms of their statistical hypothesis and the required parameter input. Based on the analyses of these differently parametrized ground truth data the methods are compared in terms of the number of false positives and false negatives, in terms of the number of neurons participating in the patterns and their number of occurrences. We conclude that SPADE has overall better performance in detecting higher-order dependency structures of any size (number of neurons involved, higher than 2) and number of occurrences, whereas CAD performs well for STPs of any size, however only if they occur in high numbers. Finally, we assess their computational performance in terms of runtime in different contexts (i.e. datasets with and without STPs), concluding that CAD is computationally performing better than SPADE, since the second is based on Monte Carlo methods. Further tests will also consider more realistic non-Poisson ground truth data and evaluate the combined computational and false positive/false negative performance, expecting the latter to be less good for the CAD method.

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Associative Transitions in Language Processing

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Many studies of the neural substrates of language measure responses to semantic violations or involve unnaturally rapid stimulus presentation. While recent studies have also shed light on the distributed encoding of concepts in the brain in more ecological settings, the study of language cannot be reduced to only a description of where semantic content is stored. Related concepts tend to elicit one another, allowing for the production and expression of more complex and profound thoughts. Based on this simple intuition, we have designed a new paradigm to explore the associative neuronal mechanisms that may underlie language processes, which we have previously characterized with models of latching dynamics. Participants are asked to select words (targets), appearing on the screen, which satisfy precise rules of association with a reference word (prime), allowing us to investigate the neural signatures of latching between stored memory items. The stimuli are existing Italian words which could be associated to each other orthographically (addition, omission or change of one letter) or semantically (synonym, antonym, encyclopedic or association of ideas). Behavioral results show orthographic transitions to be 80ms faster, on average, than semantic ones. Among semantic transitions, "association of ideas" need the longest reaction times, in contrast to what other priming experiments have shown. This opposite result could be due to the diverse semantic content that has to be accessed in such trials. Networks models envisage a transition of part of the semantic units, "pivoting" around the stable activity of others. In a following EEG study we considered the Event-Related Potentials time-locked to the presentation of the target words. For this experiments we mainly focused on the differences between word-form (orthographic) and semantic transitions, comparing them with a "no association" control condition, made by target words correctly classified as not related to the prime. The data clearly show different dynamics for the different conditions. A N400 component is found for orthographic transitions only, in possible disagreement with the current dominant view of the N400 as related to the retrieval of word meaning N400. A semantic retrieval interpretation would indeed suggest the presence of this component also in "no association" trials, which we have not found. A modulation of the P600 potential appears for "word-form" and, more weakly, for "no association" transitions with respect to semantic ones. This later component, mostly investigated in sentence comprehension studies, could be the marker for a process of re-analysis/integration of top-down and bottom-up information, necessary for the decision making process. Further experimental and theoretical investigation on the specific rules of association is needed to clarify the different processing hidden in what we now observe as a N400/P600 modulation.

A study of dependency features of spike trains through copulas

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Simultaneous recordings from many neurons are possible but the underlying network is generally unknown. The existence of an underlying network determines dependencies in the neural activity, generating patterns in the spike trains. Many efforts have been devoted to the development of statistical techniques suitable to detect these dependencies. (see Kass et al. [1] and papers cited therein). Due to the importance of this problem it looks interesting to enlarge the study to alternative approaches. To do that, we propose the use of copulas, as they are able to completely capture all the information related to the joint behavior of random variables. This is a preliminary contribution, on the same direction followed by Sacerdote et al. [2]. In particular, we developed an open source software (NERVE) for this type of analysis and we use this software to generate and analyze synthetic data . We simulate leaky integrate and fire models for groups of two or three neurons, introducing dependencies among them mimicking the behavior of the surrounding networks or through direct interactions. By the use of empirical copulas we were able to discern between the two cases and to reconstruct the causal interactions among neurons.

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The Gamma renewal process as an output of a two compartment leaky integrate-and-fire neuronal model

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In a previous paper [1] we related a neuronal model based on neurophysiological data with a completely descriptive one. In particular, we considered the stochastic leaky integrate and fire (LIF) and the Gamma models. The question investigated in that paper was the possibility of getting a Gamma distributed output from a LIF model in the presence of coherent choices of the parameters. The used LIF model was the classical one-dimensional Ornstein-Uhlenbeck process; this choice implied a strong simplification of the structure of the neuron that was identified with a single point.

In [2], we proposed a different LIF model characterized by two compartments. This choice allowed us to distinguish the dynamics between the trigger and the synaptic zones.

Here we repeat the study of [1] on the two compartment model. For this aim we introduce the inverse First Passage Time (FPT) problem for multivariate Gauss-Markov processes and we investigate the boundary shape corresponding to Gamma FPT distributions for suitable choices of the paramenters.

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