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**ABSTRACT BOOK**

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# **Neuroinformatics 2010**

## **3rd INCF Congress of Neuroinformatics**

Program and Abstracts

August 30 to September 1, 2010  
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## Decorrelation of neural-network activity by inhibitory feedback

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Spatial correlations in spike-train ensembles can seriously impair the en- and de-coding of information in the population rate [1] or in the fine spatio-temporal structure of these spike trains [2]. Recent theoretical and experimental studies showed that spike correlations in neural networks can be considerably smaller than expected based on the amount of shared presynaptic input in such systems [3,4,5]. Here, we demonstrate by means of a simple linear model and simulations of networks of integrate-and-fire neurons that pairwise correlations and hence population-rate fluctuations in recurrent networks are actively suppressed by inhibitory feedback. To investigate the role of feedback, we calculate the power- and cross-spectra of the network response for the intact recurrent system and for the case where the 2nd-order statistics of the feedback signals is perturbed while the shared-input structure and the 1st-order statistics are preserved. In general, any modification of the feedback statistics causes a shift in the power and coherence of the population response. In particular, the neglect of correlations within the ensemble of feedback channels or between the external stimulus and the feedback can amplify population-rate fluctuations by orders of magnitude. This effect can be observed both in networks with purely inhibitory and in those with mixed excitatory-inhibitory coupling. In purely inhibitory networks, shared-input correlations are canceled by negative correlations between the feedback signals. In excitatory-inhibitory networks, the responses are typically positively correlated. Here, the suppression of input correlations is not a result of the mere existence of correlations between the responses of excitatory (E) and inhibitory (I) neurons [4], but is instead a consequence of the heterogeneity of response correlations across different types of neuron pairs (EE, EI, II). If correlations between EE, II and EI pairs were identical, input correlations could not fall below the level imposed by the amount of shared input [6]. We further show that the suppression of correlations and population-rate fluctuations in recurrent networks is in general frequency (time-scale) dependent. The affected frequency range is determined by the population-rate transfer properties: The population response of integrate-and-fire neurons, for example, exhibits low-pass characteristics [7]. High-frequency fluctuations are therefore not affected by feedback.

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## Random compositional networks of synfire chains dynamically self-tune to the critical state for ongoing percolation of activity

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Synfire chains are spiking networks with a sequential pool structure that supports the robust propagation of a 'wave' of precisely timed spikes and have been proposed as a mechanism for cognition in which component chains represent features and feature composition (binding) is accomplished by links between chains (Abeles et al. 2004).

Recent spiking network simulations (Trengove et al. 2010) show that a large number of synfire chains can be embedded in a network the size of a cortical column (~1000 chains of length ~100 in a network of ~100,000 neurons). Activity is stabilized by feedback in the form of balanced excitatory and inhibitory recurrent input ('noise') which limits the number of co-active waves. This set-up opens the door to simulating large-scale compositional systems of synfire chains in which many feature relationships can be represented. As a first step in exploring the dynamics of large compositional systems, we study a compositional network formed by random pair-wise composition of chains. We consider two types of pair-wise composition (as illustrated): Type 1: longitudinal (end-to-end) composition, which results in a feed-forward branching chain structure; and Type 2: lateral composition (with a longitudinal offset) using excitatory cross-links, which supports lateral ignition of waves leading to simultaneous activation of coupled chains by synchronised synfire waves.

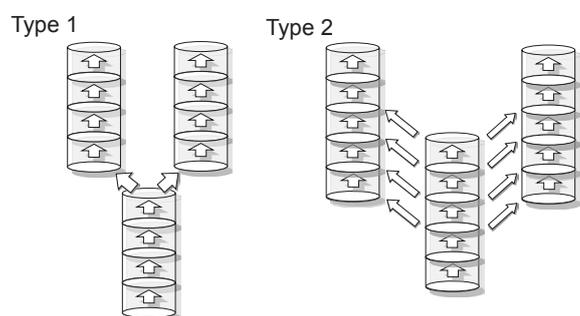
Both topologies in principle allow wave activity to multiply and spread through the network. However, due to the regulation by noise, we find that both types of network support a stable equilibrium state that is sustained without external input.

When a distribution of chain strengths is used in the Type 1 model, the equilibrium level of synfire wave activity is tuned to a near-critical level in which the number of chains strong enough to propagate activity is just enough to support ongoing percolation of synfire wave activity through the system. This is because the amount of noise which a propagating wave can tolerate increases monotonically with the strength of the chain. The Type 2 model parameters can be set so that the noise limit for lateral ignition is lower than that for wave propagation, and hence the effectiveness of lateral ignition determines the spread of wave activity through the system. The model can therefore be understood as a random directed graph in which chains are nodes, cross-links are edges, and the effectiveness of an edge is conditional on the global mean activity level. Thus, with a distribution of cross-link strengths, the system equilibrates at the activity level where the effective connectivity is at the percolation threshold: the mean effective out-degree of each node is 1. This dynamic self-tuning to a critical level may relate to the criticality of spike-avalanche phenomena observed both in neural cultures and in vivo (Petermann et al 2009).

The dynamics of the stable state in our models is consistent with observed electro-physiological data, both in terms of the low firing rate and the approximate statistics of membrane potential fluctuations. In simulated recordings replicating the under-sampling of present experimental techniques, the spiking appears irregular and asynchronous, and the precisely organised synfire chain structure and spike timing relationships are not detectable.

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Pairwise composition: Type 1 (longitudinal) versus Type 2 (lateral + offset)

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## The Schema of the European EPILEPSIAE database for seizure prediction

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### Purpose:

With a prevalence of about 1%, epilepsy is considered to be one of the most common serious brain disorders with profound physical, psychological and social consequences. Characteristic symptoms are seizures caused by abnormal neuronal activity that can lead to temporary impairments of motor functions, perception, speech, memory or consciousness. The possibility to predict the occurrence of epileptic seizures, typically by recording and monitoring the electroencephalographic activity (EEG), could enable new therapeutic strategies for the considerable fraction of epilepsy patients that are not treatable by any state of the art therapeutics like anticonvulsive medication or brain surgery.

Funded by the European Union, the EPILEPSIAE project, a 7th Framework Programme with seven clinical, academical and industrial partners in Portugal, Germany, France and Italy, was established to develop and advance prediction algorithms and to deploy these algorithms on a small transportable alarming device. So far, the main concern for the development of prediction algorithms have been limitations in the quality and duration of long-term EEG data that are important for the statistical evaluation of prediction methods. Accordingly, the EPILEPSIAE project is currently gathering the largest and most comprehensive epilepsy database existing worldwide to collect and organize a substantial amount of characteristic patient data for research on seizure prediction methods.

### Method:

In contrast to previously existing, by orders of magnitude smaller EEG data collections, the EPILEPSIAE database is a relational database, designed for efficient data organization and access and offering extensive searching capabilities.

Therefore, the 250 surface and 50 intracranial epileptic patients datasets are collected and integrated into the database as common effort of all clinical partners. The datasets comprehend multimodal data including raw data as well as different types of metadata:

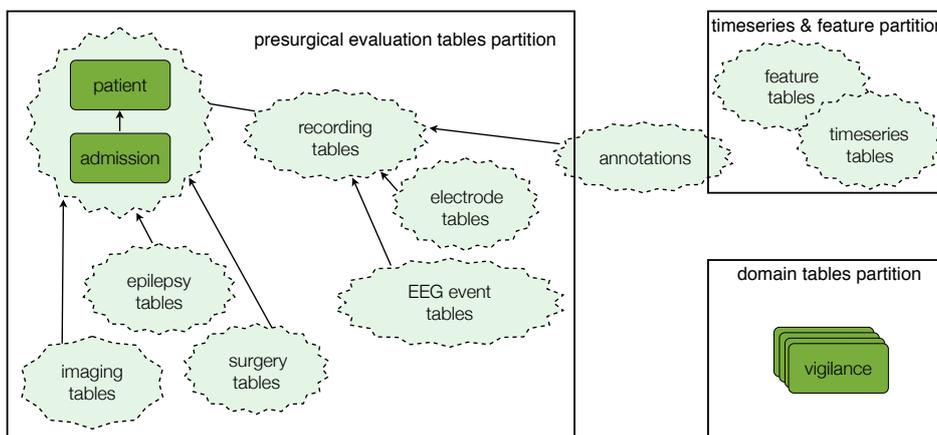
- raw EEG data recorded from all clinical partners during long-term monitoring of epilepsy patients
- feature data: features derived from the EEG recordings, which are important for the development and testing of prediction algorithms.
- magnetic resonance imaging (MRI) data (skull stripped for reasons of data anonymization)
- standardized EEG annotations covering information visually perceived by experts about the EEG, e.g. about seizures and interictal events
- clinical metadata: information about patients and their diseases including medical history, imaging findings, anti-epileptic therapy, seizure semiology as well as information about EEG recordings and therefore used electrodes
- feature metadata: supplementary information about the feature algorithms and calculations

### Results:

Currently, there are working databases at the partner's sites, all in sync with a replicated content of already more than 150 datasets. This makes the EPILEPSIAE database already the by far largest epilepsy database. Although all project partners use an Oracle database, the schema, as it is presented here, is agnostic of the underlying database system and can easily be adapted to other relational databases. We here only outline the general structure of the schema of the EPILEPSIAE database in Figure 1. The complete schema will be visually presented in full detail on the poster.

### Conclusions:

Although still work in progress, the EPILEPSIAE database is already the most comprehensive and complete epilepsy database currently existing. Interest for access to the database as well as participation requests from all over the world already give evidence of the emerging acceptance of our database as the de facto standard for databases in the field of epilepsy. This acceptance of our database schema and content is probably the most important impact of the EPILEPSIAE database.



## NEST: Science-driven development of neuronal network simulation software

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NEST is a simulator for heterogeneous networks of point neurons or neurons with few compartments (e.g. stick-and-ball models) [1]. It is suited for a broad range of neuronal network modeling approaches and computer architectures: from single- or multi-threaded simulations of small and medium sized networks on standard desktop computers, to distributed simulation of large networks on computer clusters or HPC facilities such as BlueGene. Distributed simulations exhibit excellent scaling up to the order of one thousand processors, and research is ongoing to extend the scalability into the range of ten thousand processors and beyond [2,3]. NEST is developed by the NEST Initiative, an international contract-based collaboration between academic and industrial research institutes.

NEST is subject to continuous development to provide its users with cutting-edge features and respond to the demands of current questions in neuroscience. Recent features include the incorporation of new neuron models such as the MAT(2) model [4] and spike-timing and neuromodulation dependent plasticity [5,6]. To increase its user-friendliness and exploit software trends in the neuroscience community, NEST enables users to extend its functionality through dynamically linked modules and interact with the software using a Python-based user interface PyNEST in addition to the native simulation language SLI [7]. NEST also supports the MUSIC interface to communicate with other simulators [8] and provides visualization tools [9] and a topology module that facilitates concise specification of spatial structure [10]. The developers also continually improve the underlying algorithms, e.g. for the calculation of 'off-grid' spike times and the integration of non-linear neuron models such as the AdEx model [11,12,13].

Frequent releases of the NEST software provide the users with the newest technology and the developers with feedback about bugs and potential improvements. Release stability is supported by an automated test suite [14]. The NEST user community is active and growing, in part due to its use in large national and international projects, such as the Next-generation supercomputing project of MEXT and FACETS as well as at summer schools, for example, the Advanced Course in Computational Neuroscience and the Okinawa Computational Neuroscience Course. A list of neuroscientific publications that use NEST is available on the website, as is the current release of the source code ([www.nest-initiative.org](http://www.nest-initiative.org)). A convenient option for those wishing to try out NEST is the LiveCD, which enables easy, platform-independent testing of our simulation software.

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## Brain-scale simulations with NEST: supercomputers as data integration facilities

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Neural network simulations are currently making a qualitative leap, leaving the regime of highly specialized “single-scale” models that incorporate only limited aspects of biological data, but focus on the multi-scale nature of the brain. These developments are fueled by the advent of computing power at the peta-scale which is increasingly becoming available to computational (neuro-)scientists all over the world (see e.g. <http://www.prace-project.eu/>, <http://www.nsc.riken.jp/>, <http://www.ncsa.illinois.edu/BlueWaters>). In order to optimally employ this computing power in the context of neural network modeling, we identify two main requirements:

- (1) Suitable simulation technology has to be made available that can efficiently represent multi-scale brain networks on supercomputers and rapidly solve the network's activity dynamics.
- (2) A new class of models needs to be developed comprising multiple scales from the local microcircuit to the macroscopic brain network consistently with available data.

In the past years, simulation technology development focused on the representation of the local cortical network consisting of approximately 100,000 neurons and 1 billion synapses on standard HPC clusters (<http://www.nest-initiative.org>). The construction of models resolving the layer- and type-specific connectivity structure of the cortical microcircuit integrated a large body of experimental data ranging from anatomical and electrophysiological studies to photostimulation and electron microscopy [1]. The comparison of the simulated network activity and experimentally observed *in vivo* cell-type specific activity reveals the consistency as well as potential shortcomings of the available data and models. We show that this class of models successfully captures prominent microscopic activity features such as layer-specific spike rates and the interplay of excitation and inhibition in the propagation of transient feed-forward inputs as observed *in vivo* (e.g. [2]).

In order to address the activity dynamics and the function of the local network in the context of the embedding in a network of multiple cortical areas, next generation multi-scale neural network simulations have to simultaneously represent the local microcircuit and the macroscopic connectivity structure (e.g. [3]). These brain-scale network simulations approach a regime where the number of cores is larger than the number of synapses per neuron. Therefore, corresponding data structures for the network representation have to make use of the sparseness of connections but nevertheless allow rapid network construction and spike delivery to target neurons. Models on this scale drastically increase their self-consistency and explanatory power because they explicitly incorporate most of the long-range inputs to neurons that were previously modeled as abstract external inputs but make up around 50% of all synaptic inputs. The advanced data integration now not only combines multiple methods but also multiple scales, linking microscopic and macroscopic connectivity.

Here, we present the scale-up of the NEST simulation tool (<http://www.nest-initiative.org>) up to tens of thousands of processors on the JUGENE supercomputer (<http://www.fz-juelich.de/jsc/jugene>) and quantify time-memory trade-offs. Furthermore, we summarize our efforts in the construction of brain-scale network models that integrate a vast amount of data on multiple scales. In this concept supercomputers are utilized as data integration facilities.

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## Practically trivial parallel data processing gives neuroscience laboratories easy access to advanced analysis methods

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In addition to the increasing amounts of data gushing out from neuroscientific experiments, the complexity of modern data analysis techniques places new demands on the computing infrastructure required for data processing. In particular, the observation that neuronal data typically exhibit non-stationary statistics complicates the task of finding the correct null-hypothesis to assess the significance of a variety of test parameters. Modern computer resources enable a data-based approach to tackle significance estimation: surrogate techniques. In this framework the original data is modified in a specific way so as to keep some aspects of the data (e.g., the non-stationary nature of the data), while deliberately destroying others (i.e., those described by the test parameter). Repeating this procedure many times estimates the distribution of the test parameter under the null hypothesis.

However, the required resources exceed the speed and memory constraints of a classical serial program design and require scientists to parallelize their analysis processes on distributed computer systems. Here, we explore step-by-step how to transform on-the-fly a typical data analysis program into a parallelized application. This approach is facilitated by the observation that a typical task in neuronal data analysis constitutes an embarrassingly parallel problem: the analysis can be divided up into independent parts that can be computed in parallel without communication. In particular for surrogate-based analysis programs, finding the decomposition of the analysis program into independent components is often trivial due to the inherent repetition of analysis steps. On the conceptual level, we demonstrate how in general to identify those parts of a serial program best suited for parallel execution. On the level of the practical implementation, we introduce four methods that assist in managing and distributing the parallelized code. By combining readily available high-level scientific programming languages and techniques for job control with metaprogramming no knowledge of system-level parallelization and the hardware architecture is required. We describe the solutions in a general fashion to facilitate the transfer of insights to the specific software and operating system environment of a particular laboratory.

The details of our technique accompanied by concrete examples form a chapter of the new book "Analysis of parallel spike trains" edited by Sonja Grün and Stefan Rotter and published at Springer 2010.

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