

# SPROJ

Derek Low

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## 1 Introduction

### 1.1 The Neuron

Neurons are fundamental to human cognition, and encode for a large range of activities such as movement, speech, decision making, and learning among many other functions in the human body. The interactions between neurons throughout the human body have been studied at microscopic levels, observing the specific mechanisms of the neuron and the dynamics between components of the neuron that allow for propagation of communication from one neuron to the next neuron. Additionally, networks of neurons are studied at macroscopic levels, observing where certain regions of the brain are responsible for certain functions of the body, such as the relationship between the brain and human capabilities of cognitive control and activity, or the specific activity of particular regions of the brain. However, the precise connectivity patterns of neurons, and the relationship between this organization and its possible functions, are not fully understood. Analysis of the patterns of connections in populations of neurons indicate that these cells are characterized by certain network properties. Therefore, understandings of these connections may provide insight to the function and activity of these populations of neurons, and possible implications of a relationship between functional and structural connectivity.

The activities of neurons are partially mediated by the electrical potential between the neuron and its surrounding environment, known as the membrane potential. The earliest and most influential studies concerning the effects of ions in neurons were conducted by Hodgkin, Huxley, and Katz nearly 70 years ago, and clearly indicated the relationship between ion concentration and the activity of neurons; giant squid axons in lower sodium environments demonstrated a lower resting

potential, as well as a weaker and delayed action potential (Hodgkin and Katz, 1949). Changes in concentrations of ions, distributed in varying concentrations throughout the nervous system, mediate neuron activity by changing this membrane potential. In a state of low activity, this membrane defaults to a polarized state of negative electrical potential, referred to as the resting membrane potential (Purves et al., 2004). Communication between neurons occur at the synapse, a structure of connection between two neurons. The communication occurs via a synaptic potential, a signal from the pre-synaptic to the post-synaptic neuron, and is initiated by the release of neurotransmitters from the presynaptic neuron to receptors in the postsynaptic neuron. Synaptic potentials are either excitatory, increasing the membrane potential of the neuron towards positive values (depolarization), or inhibitory, reducing potential towards negative values (hyperpolarization). The resulting depolarization due to the excitatory post-synaptic potentials (EPSPs) increases the membrane potential towards higher positive values, until a specific threshold is reached. Once this threshold potential is reached, an action potential is generated, and propagates along the neuron until it reaches another synapse, at which point the cycle of neurotransmitter release, synaptic potential, and action potential propagation cycle may be repeated.

The propagation of action potentials involves constant changes to the electrochemical gradients of the neurons by the opening and closing of ion channels in the membrane. The sections of neurons mediating and raising membrane potentials towards distinct states of polarization are the voltage-gated ion channels, a collection of channels that include the sodium ( $\text{Na}^+$ ), potassium ( $\text{K}^+$ ) and calcium ( $\text{Ca}^{2+}$ ) channels. However, while these channels serve similar purposes of allowing passage to certain ions and restricting passage to other ions, the time of activation of each type of channel demonstrated their distinct impacts on propagation. The depolarization of the neuron, and consequent upswing in membrane potential towards positive values, is caused by the influx of sodium from the extracellular medium into the cell; this influx is caused by the opening of sodium channels following an EPSP, prior to the membrane potential reaching the threshold potential and the initiation of an action potential. (Hodgkin and Katz, 1949; Hodgkin and Huxley, 1952). The resulting repolarization and hyperpolarization stages preceding the return to resting membrane potential result from the efflux of potassium; this efflux is a delayed response to the initiation of the action potential, indicating a delayed opening of potassium channels following the opening of sodium channels (Hodgkin and Huxley, 1952).

## 1.2 Network Neuroscience

Understanding the organization of neurons is paramount to neuroscientific research due to the biological functions and implications of these networks. One primary area of focus in studying these networks is the mammalian cerebral cortex, a region of the brain comprised of several subregions: the motor, sensory, and associative areas. The majority of the cortex is referred to as the neocortex, explicitly defined as the layers of the cortex comprised of six cellular layers (Purves et al., 2012). While the significance of the six cellular layers largely remains a mystery, the neocortex is a focus region for studies of cortical structure and function. Research focused in the neocortex refer to and observe corticle circuits, a general term for larger neuronal networks located in the cortex and corticle ensembles, referring to coactive networks of neurons that possibly comprise cortical circuits (Carrillo-Reid et al., 2016; Hamm et al., 2017; Bock et al., 2011). Due to the involvement of the neocortex in a variety of functions, such as movement, sensation, and cognition, the cerebral cortex is a significant target for study.

Some studies concerning the cerebral cortex focus on disease and the derivative corticle ensembles that are representative of the disease. One such example is schizophrenia, a disorder characterized by hallucinations, delusions, disordered thoughts, and loss of emotional expression (Purves et al., 2012). As a neurological disorder accompanied with altered neuromodulation, excitatory and inhibitory neuron balance, and development, as well as altered connectivity at a higher scale, schizophrenia is a target of research concerned with the effects of these neurological changes on the presentation and characterization of the disorder. For example, a study conducted by Hamm et al., observed cortical ensembles in mice models that displayed symptoms of schizophrenia via administration of ketamine or were genetically dispositioned towards development of schizophrenia. Imaging of awake mice models allowed for analysis of activity in cortical ensembles, and the relationships and recurrent patterns in sub-ensembles (local neuronal networks). The results of the study indicated several alterations to cortical activity of the symptomatic mice, such as impact of altered dynamics of local networks on cortical ensembles, and the necessity of long-term changes to cortical connectivity to initiate changes in cortical ensemble reliability in propagation of patterns of activity consistent with schizophrenia (Hamm et al., 2017).

The relationship between functionality and connectivity has been demonstrated in further additional contexts, such as in motor neurons of human patients by relating the movement of fingers

on each hand to the fluctuations in signal intensity of the sensorimotor cortex during echo-planar functional magnetic resonance imaging (fMRI) (Biswal et al., 1995). Additionally, between two related, yet distinct, activities, the functional connectivity of neurons can overlap; such is the case in the instance of motor imagery, or the mental performance of certain motor acts not accompanied by physical performance of these acts, and the accompanying physical performance of the same motor acts (Porro et al., 1996). The hippocampus of the human brain demonstrates a similar relationship of functional connectivity with particular activities; young adults display higher levels of activity in the ventral prefrontal and extrastriate regions of the cortex correlated with higher levels of hippocampus activity during encoding of words and pictures of objects. In contrast, older adults display higher levels of activity in the dorsolateral prefrontal and parietal regions of the cortex with comparable levels of activity in the hippocampus to younger adults during similar trials (Grady et al., 2003). The higher activity in particular regions implies different manners by which adults of differing ages process information concerning similar tasks, where hippocampus and brain activity are related to better recognition in younger adults, and improved memory performance in older adults. These findings indicate a shift in explicit connectivity between portions of the brain, and changes to functional connectivity related to human aging (Grady et al., 2003).

Network science provides a framework through which populations of neurons may be analyzed for their structural and functional connectivities by expanding and formalizing the terminologies and definitions for the purposes of neuronal network analysis. For example, cliques, or all-to-all connected networks, of neuronal populations have been studied as a method of relating structural and functional connectivities of neuronal populations; in the context of neuronal networks, cliques are observed under a specific definition, the directed clique. Where cliques are bidirectional, allowing a single connection for both information transfer from a source neuron to a target neuron and information transfer in the inverse direction, directed cliques do not allow for bidirectional information transfer. (Reimann et al., 2017). For a given connection in a directed clique from a source neuron to a target neuron, there is no direct connection from the target neuron to the source neuron, though there may be an intermediary neuron allowing for a connection in the inverse direction. The reconstruction and viewing of networks as compositions of cliques suggests that, in neocortical microcircuits, information is processed by the formation and disintegration of these cliques, depending on the nature of the stimulus (Reimann et al., 2017). The small world

characteristic is another such definition originating from network science and applied in analysis of neuron populations, where the small world network is a network with a short average path length, indicating a large number of paths, and a high degree of local clustering, the tendency of nodes in a graph to cluster together (Sporns et al., 2004).

Analysis of these patterns of connectivity, or microcircuitry, of neurons in regions of the brain indicate the possibility of the scale-free nature of microcircuits. In cases of such networks, the degree distribution, defined as the distribution of number of connections to each node in a give network, follows a power-law, where the majority of nodes in the network have a high number of connections, and a fraction of the population with a comparatively low number of connections (Sporns et al., 2004, Tetzlaff et al., 2010, Massobrio et al., 2015). This power-law distribution is also observed in frequency of neuronal avalanches, periodic bursts of activity from a population of neurons, where avalanches falling short of the power-law distribution is subcritical, falling on the power-law distribution is critical, and falling above the power-law distribution is supercritical (Massobrio et al., 2015)

### **1.3 Representing Networks of Neurons**

Deriving the organization of neurons in networks is difficult at lower populations of neurons, and the difficulty increases significantly as the population of neurons increases. The organization of neurons can be represented as a matrix, typically referred to as an adjacency or weight matrix; whether the matrix is an adjacency or weight matrix depends on how these connections between neurons are represented, and what information is useful and preserved. Weight matrices assign values based on the strength of connections between neurons, and whether the source neuron is an excitatory or inhibitory neuron, while adjacency matrices are representative of whether or not there is a connection, and ignores the strength of these connections. For example, the following matrix describes connections between a population of three neurons:

	Neuron 1	Neuron 2	Neuron 3
Neuron 1	0	1	1
Neuron 2	0	0	0
Neuron 3	1	1	0

**Figure 1:** Sample Adjacency Matrix of a Population, Size 3. Diagonal indices represent self-connections. Labels along the columns represent the target, and labels along the rows represent the source e.g. the connection at Row 3, Column 2 (value of 1) is a connection from the pre-synaptic Neuron 3 to the post-synaptic Neuron 2. Note the lack of the inverse connection from Neuron 2 to Neuron 3 (value of 0).

Matrices such as the one above describe the connections between different neurons in an observed population, with observed being an important keyword; these neurons could have incoming connections from sources outside of the observed population, depending on the context of the observations. One standard feature of network matrices is the zero value along the diagonal, representative of a lack of a connection from a neuron to itself. In the example above, there is a directional connection between the outward axonal connection of Neuron 3 and the incoming dendritic connection of Neuron 1; therefore, assuming a positive value to represent an excitatory connection, spikes in Neuron 3 result in a voltage increase of Neuron 1. By this method of representation, the matrix can describe the relative strength and nature of all connections between neurons in the observed population.

Why is it important to characterize networks of neurons? Currently, our methods of studying neurons and brain activity relies on techniques that observe activity at macroscopic (e.g. fMRI, PET, CAT, calcium imaging) or microscopic scales (e.g. electrodes and membrane potentials, patch clamp). However, there is no method of accurately imaging and representing larger networks of neurons in areas of the brain, or outgoing pathways from the brain. While machine learning algorithms may not provide exact mappings of networks, implementation of these algorithms is an opportunity to generate hypotheses.

## 1.4 Calcium Imaging

A commonly employed method of recording activity of neurons is calcium imaging. Neuron activity . At every spiking event, these ions travel through the cell membrane of each neuron by movement through voltage-dependent ion channels, which are functionally altered by the voltage changes that occur in neurons.

The versatility and presence of calcium in neurons can be described by the large variety of neuronal processes related to it. Calcium performs several major roles in the function and management of biological cells; most notably, in the presynaptic neuron, an influx of calcium into the neuron triggers the release of neurotransmitter to the synapse via exocytosis (Katz and Miledi, 1967). Furthermore, presynaptically, residual calcium results in neural facilitation, a period in which a successive depolarization of the presynaptic neuron, following the first depolarization event and release of neurotransmitter, raises the likelihood of neurotransmitter release (Katz and Miledi, 1967; Zucker, 1999). Postsynaptically, calcium is responsible for activating the synaptic plasticity cascade. These changes to the synapse, functionally initiated by interactions between calcium and the N-methyl-D-aspartate receptor (NMDA) and  $\alpha$ -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor (AMPA), result in changes to the sensitivity and, by extension, the interactions between the pre- and postsynaptic neurons (Zucker, 1999). The changes enhance or diminish the strength of the connection (potentiation and depression), in various temporal manners (short and long-term). For example, in the case of long-term potentiation (LTP), the influx of calcium into the postsynaptic neuron, and the resulting depolarization, result in the unblocking of the NMDA receptors, allowing for a further influx of calcium into the postsynaptic neuron and inducing LTP (Zucker 1999). Functions of calcium extend further than synaptic activity, and the ion is additionally responsible for biological functions such as cell apoptosis (Orrenius et al., 2003). Therefore, the abundance and utility of calcium, and the deeply integral relationship between calcium and neuron activity, suggest it to be a strong candidate for the purpose of imaging populations of neurons.

### 1.4.1 Calcium Indicators

As mentioned, calcium activity is dependent on the voltage changes of neurons and the responses of voltage-gated channels to voltage changes, and concentration is higher extracellularly until spike time. Therefore, introducing into the neurons an indicator that fluoresces when bound to calcium

allows recording of calcium concentration and activity. Among the first discovered and applied calcium indicators is the protein aequorin (Shimomura et al., 1962), where the binding of the calcium to the three binding sites located on the protein results in photon emission (Grienberger and Konnerth, 2012). The necessity of the three calcium molecules, in combination with a controlled amount of indicator injected into these neurons, allows for a controlled fluorescence method that is directly related to the calcium concentration within the cell. However, the particular drawbacks of aequorin, such as a low protein stability and a relatively low fluorescence rate with regards to the amount of decomposition in the concentration of the protein, result in development of several superior and modern alternatives (Grienberger and Konnerth, 2012).

Modern calcium indicators are typically categorized as high-affinity or low-affinity, where high-affinity indicates the most commonly used indicators with wide varieties of application. One such high-affinity calcium indicator is fura-2 (Grynkiewicz et al., 1985); this indicator operates by excitation with ultraviolet light, resulting in a fluorescence shift of the indicator; the fluorescence level changes when the molecule is bound to calcium, a property referred to as ratiometric, dual-wavelength, or dual-excitation (Grienberger and Konnerth, 2012). This particular indicator is applied to a variety of microscopy methods, including two-photon microscopy (discussed below), requiring slight modification by inclusion of green fluorescent protein (GFP) in the latter case (Grienberger and Konnerth, 2012).

#### **1.4.2 Microscopy**

The second component is the imaging, recording, and approximation of recorded data as a measurement of brain activity. There are several technologies employed in the recording of calcium indicator fluorescence; the technique used widely depends on the subject being recorded and quality of the imaging required. However, an equally wide range of techniques are available, and have particular benefits and drawbacks relating to the method and observed sample.

All microscopy techniques result in the photobleaching and phototoxicity of the observed specimens, resulting in photodamage (Svoboda et al., 2006). Another restricting factor in microscopy is photon scattering, a process in which a photon is absorbed by a molecule and re-emitted in a distinctly random direction, resulting in the blurring of the resulting microscopy image (Ntziachristos, 2010). Therefore, one aim relevant to employed microscopy techniques is the highest accumulation



of imaging data with the lowest possible amount of photodamage to the observed specimen, and lowest photon scattering for image accuracy and clarity. Prior to the development of two photon microscopy in the 1990's (Denk et al., 1990), most microscopy methods used, such as confocal and wide-field fluorescence microscopy, suffered from the major drawback of having low tissue penetration depth due to photon scattering and, in the case of confocal microscopy, tissue degradation (Svoboda et al., 2006).

## **1.5 Current Approaches to Reconstruction**

Several different frameworks of reconstruction have been offered to tackle the problem of inferring connectivity of neurons. While these reconstruction methods use different methods for evaluating activity and connectivity, they are typically applied to simulated neuron populations, where the ground truth of the activity is known, allowing evaluation on the accuracy of the model.

### **1.5.1 Cross-Correlation**

### **1.5.2 Granger Causality**

Zhou et al., 2014 uses Granger Causality as the primary method of inferring connectivity of conductance-based integrate-and-fire neuron models; the analysis method states that if the variance in prediction error for a particular time series is reduced by incorporating knowledge of another time series, then the second time series has some causal effect on the first time series. In other words, if incorporating information about event X allows prediction of event Y beyond prediction concerning event Y without any additional information, then event X and event Y are causally related. In brief, the researchers demonstrate that using Granger Causality allows the construction of a causality matrix, which can then be mapped to the structural connectivity matrix of the population and be observed for relationships between the activity and structure of the network.

### **1.5.3 Transfer Entropy**

Stetter et al., 2012, incorporates information theory as a reconstruction method from calcium imaging data. This particular method of reconstruction focused on in vitro calcium imaging fluorescence levels, with a slightly variant version of the Generalized Transfer Entropy formula:

$$TE_{Y \rightarrow X}(\hat{g}) = \sum P(x_{n+1}, x_n^k, y_{n+1}^k | g_{n+1} < \hat{g}) \log \frac{P(x_{n+1} | x_n, y_{n+1}^k, g_{n+1} < \hat{g})}{P(x_{n+1} | x_n^k, g_{n+1} < \hat{g})}$$

The major difference between the Generalized Transfer Entropy formula and the presented formula is the presence of  $\hat{g}$ , a predefined threshold of fluorescence, where  $g_t$  is the average fluorescence of the network at a particular time  $t$ .

The researchers use Transfer Entropy to evaluate the information transfer, where information transfer can be understood as how likely the activity of neuron Y indicates the activity in neuron X, between all possible directed pairs of neurons in the network. Afterwards, the researchers use a threshold Transfer Entropy to prune the the connections with the lowest values of information transfer, and reconstruct the network based on the remaining neurons, finding Transfer Entropy to reconstruct network properties more accurately than previous reconstruction methods, and at varying levels of visual noise in the data, or light scattering.

## 1.6 The Relevance of Advances in Machine Learning

The story concerning the invention and development of machine learning is one of constant juxtapositions with human intelligence. For example, the perhaps one of the most famous early experiments in artificial intelligence research is the Turing Test. The Turing Test, devised by Alan Turing, was originally named "The Imitation Game" by Turing in the 1950 paper "Computing Machinery and Intelligence". The experiment was devised with the proposed definition of artificial intelligence as the ability of a machine to replace a human counterpart in repeated rounds of questioning and answering; in other words, is the machine capable of imitating a human to the extent that participants are fooled by its answers? The performance evaluation of the machine is defined as a comparison with human intelligence, and as an antagonist to human interaction. Naturally, in the consistent comparison with human intelligence as benchmarks for machine intelligence, artificial intelligence research eventually developed methods of machine learning loosely based in the fundamental biological unit of human intelligence: the neuron.

As discussed previously, neurons are the fundamental units that allow what we understand to be human intelligence. As discussed by Steels in the paper "Fifty Years of AI: From Symbols to Embodiment", the field transitioned through several methods and approaches to AI before arriving at the neural network in the 1980s (Steels, 2007). These neural networks were developed with the

intent to model the biological mechanisms of the human brain as closely as possible, primarily the neurons, which the nervous system is composed of. Even in the short history of neural networks, the method has transitioned through varying degrees of discovery and standardization concerning their usage and applicability.

### **1.6.1 Supervised and Unsupervised Learning**

While the studies of machine learning have developed a variety of methods to encompass an ever-growing scope of questions to answer, the methods and questions fall into one of two categorizations: supervised and unsupervised learning. Supervised learning methods rely on the "completeness" of a data set, in which all inputs have correspondingly labelled outputs. Therefore, the output of a supervised learning algorithm is similar in type to the actual outputs  $Y$  presented in the training data set for every  $X$ ; in other words, there is a corresponding dependent output on the independent input. The natures of the inputs and outputs are variable, and need not necessarily be of the same type; for example, an input of an image can result in a categorization of the image contents, such as "dog" or "human". They can also be numerical, such as a prediction of grade based on the input amount of time studying (Hastie et al., 2009). In these two examples, the prior is an instance of qualitative, or categorical, prediction, while the latter is a quantitative, or regression, prediction.

Unsupervised learning differs in that there is no input-output; while there are  $X$  labels, there are no corresponding  $Y$  labels. Some neural networks fall under this classification of algorithms; for example, Pandarinath et al. 2017, introduces an algorithm that uses sequential auto-encoders to infer underlying patterns of spike trains. Auto-encoders are one example of unsupervised learning, where the network receives an input  $X$ , attempts to represent underlying patterns in the data, and recreate the input as the network's output.

### **1.6.2 Artificial Neural Networks**

As discussed, neural networks are based on the morphology of human brains, and the neurons that the brain is composed of. These networks are composed of some number of nodes, or neurons, that are connected to each other in some fashion, depending on the task the particular network is designed for. These nodes are typically categorized into one of three layers: input, hidden, and output layers. Neurons of the input layer have no predecessor neurons, and neurons of the output

layers have no following neurons; instead the the input neurons receive input information of a particular data set, and the output neurons displayed the expected outputs based on the inputs to the network and the corresponding hidden layers.

The general theory behind Artificial Neural Networks can be described as a metaphor to learning; just students prepare for exams by thoroughly studying and applying knowledge repeatedly prior to the exam, neural networks typically train on large data sets by taking an input  $X$ , and producing some inferred output  $Y$ , then comparing to the actual output that is provided by the corresponding input in the data set to calculate the error between the prediction and the true output reflected in the data set. This data set is referred to as the "training set", on which the neural network metaphorically prepares for the exam. The goal of this training is to adapt the system to handle situations that are not contained within the training set, and predict these outputs with accuracy based on the training information provided to the network (Werbos, 1990).

### **1.6.3 Hidden Layers**

### **1.6.4 Backpropagation**

Backpropagation is one of the most recognized techniques in the study of neural networks. Developed by Paul Werbos in the 1970's, backpropagation is the primarily used method of learning in neural networks. The method is so named because the updating of weights at every layer begins at the final layer, and propagates backwards to every node and weight until all weights of all nodes in each layer have been updated to correct for the calculated error in the network.

### **1.6.5 Gradient Descent**

## **1.7 NEST: Generating Training Data**

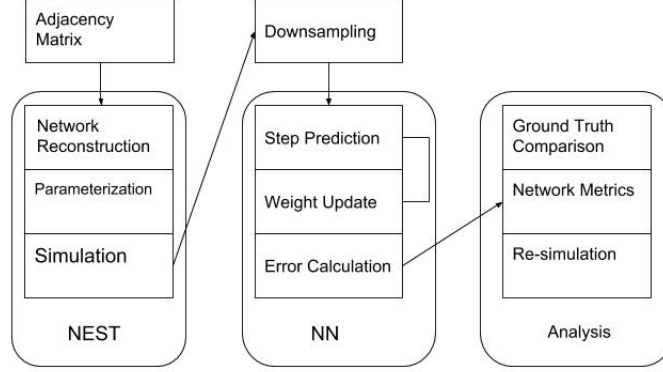
There are several reasons for generating simulated calcium imaging data for the purposes of network reconstruction. First, generation of simulated calcium imaging data allows for benchmarking of the reconstruction methods employed. In typical calcium imaging data, the ground truth is not known, resulting in a lack of comparison between the reconstructed network and the network targeted for reconstruction. By generating simulated networks and recreating calcium imaging data, we ensure access to the ground truth for comparison with the model. Simulation of training data also

permits programming of particular characteristics to the network, and observing the changes of this reconstruction in both the simulated data and the reconstruction of these networks.

Machine learning methods are typically trained on some prior data set; simulation of calcium imaging data provides a easy method of accessing data for training and testing the machine learning based model, due to unconstrained and unrestricted access to training data, before allowing the model to analyze recorded data that would be ideally used as testing data. Additionally, including a training set ensures that the algorithm is able to remain “generalized”; that is, the algorithm does not learn to represent that single data set exceptionally well, and fail when a different pattern is presented to the algorithm.

The simulations presented here are performed in NEST simulator, a tool maintained by the NEST initiative. The NEST simulator was selected for the purpose of simulations that maintain biological realism and complexity, with emphasis on simulation of large neuronal networks. The advantage NEST has over other simulators is the capability to simulate large networks with varying facets, such as synapse and neuron types, while retaining accurate representation of the individual neurons.

## 2 Methods



**Figure 2:** Experimental Pipeline. We start with a pre-generated adjacency matrix detailing the connections of a population of neurons, and pass it to the NEST simulator program. The NEST simulator reconstructs the network defined by the matrix; at this stage, poisson noise is added to the population via a connection from a 'noise generator' NEST object to all neurons in the population. The simulation is then run for 10000 timesteps (milliseconds), and the generated data is output as a spiketime matrix of  $n \times t$  dimensionality,  $n$  = population size and  $t$  = timesteps. The output is then downsampled to reflect realistic calcium imaging frame duration of 10 ms, reducing the data set to  $t = \text{timesteps}/10$ .

The downsampled data is then trained in the neural network via comparison of previous timestep to next timestep, using mean squared error and backpropagation. After some predetermined iteration value or conditional is reached (such as error convergence), the network outputs the resulting weight matrix, which can then be analyzed with respect to the ground truth adjacency matrix passed in the first stage of the pipeline.

### 2.1 Simulation of Neurons for Spike Train Generation

The NEST simulator is used for the purposes of generating spike train data. NEST Izhikevich neurons are used as the model neurons, due to the increased complexity over leaky integrate-and-fire neurons, and the reduced computational complexity over models of significantly more numerous compartment models, such as the Hodgkin-Huxley models (Brette, 2015). NEST implementation dynamics of Izhikevich neurons are provided by the following :

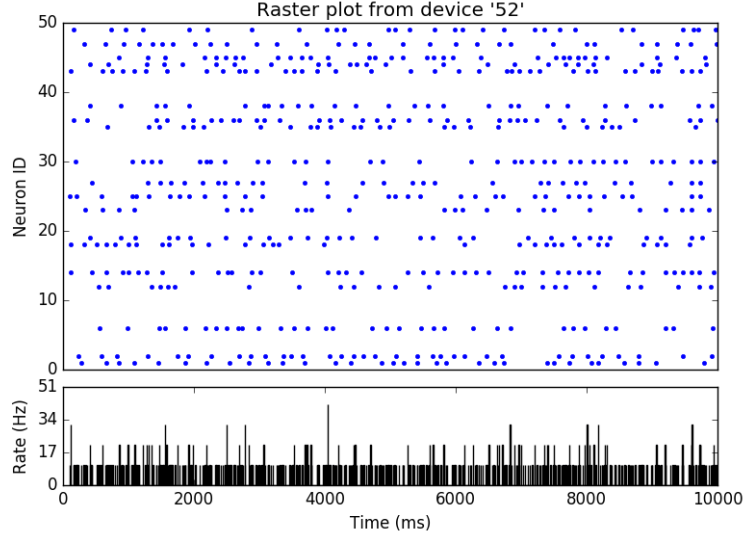
$$dv/dt = 0.04v^2 + 5v + 140 - u + I$$

$$du/dt = a(bv - u)$$

$$\begin{aligned} \text{if } v \geq V_{th} : \{ \\ v = c \\ u = u + d \} \end{aligned}$$

where  $v$  represents the membrane potential of the neuron and  $u$  the membrane recovery variable. The membrane recovery variable captures the responses of  $K^+$  and  $Na^+$ , and is a source of negative feedback to  $v$ . Coefficients for change in membrane potential, are based on scale, with membrane potential at  $mV$  and time as ms, as are  $a$  and  $b$ .  $I$  is the input current to the neuron, and  $c$  and  $d$  are the post-spike reset values of the neuron (Kunkel et al., 2017, Izhikevich et al., 2004).

To simulate a population of neurons with  $n$  population size over  $t$  time, a file containing an  $n \times n$  adjacency matrix is provided to the simulation program, which then creates a NEST neuron population with the exact number of neurons and connections between the neurons in the population, using the corresponding weight of the connection stored in the adjacency matrix. Interactions with neurons in NEST must be achieved through the creation of new node objects, made to represent and achieve the results of physical instruments and devices; therefore, we create a poisson generator node to add noise to the population, and connect a spike detector node to record all spikes in the population during simulation. The population is then recorded over 10000 simulation steps, or 10000 ms. The corresponding output of the simulation is converted to a matrix of  $n \times t$  dimensionality.



**Figure 3:** Raster Plot via NEST Simulator. The plot is generated by simulating a population of 50 neurons over 10000 time steps (ms), and graphically represents two distinct arrays output by the simulation: one array consisting of neuron IDs in the population, and another array with the corresponding spike times of the spiking neurons stored in the indices of the former array. The NEST simulator connects each neuron based on the input adjacency matrix and attaches additional noise and spike detection objects to every neuron in the population. Device 52 is the NEST spike detection object; all neurons are connected by the NEST simulation program for the purposes of spike detection. Device 51 is the noise generator object, and Devices 1-50 are the neurons in the population.

## 2.2 PageRank

The PageRank-based algorithm takes a weighted adjacency matrix as an input; a non-weighted adjacency matrix would result in no change in the PageRanks of each neuron, and no change in the resulting adjacency matrix. The PageRank for each neuron is then calculated based on the following formula:

$$PR_i = (1 - d) + d(\sum(\frac{PR_j}{C} * W_{ij}))$$

Where PR is the PageRank of neuron  $i$ ,  $d$  is the standard damping factor of 0.8,  $PR_j$  is the PageRank of incoming neuron  $j$ , and  $W_{ji}$  is the weight of the connection from neuron  $j$  to  $i$ . The summation calculates for all incoming connections to neuron  $i$ . The formula is recalculated until convergence, where the PageRanks no longer change, at which point the weights are updated such that the weight of each connection is multiplied by the PageRank of the source of the connection. The network is then pruned by comparing the weights between neuron  $i$  and  $j$ , or  $W_{ij}$  and  $W_{ji}$ ,



and the the lower value is reduced to 0, while the higher value is set to 1, preserving the higher connection. The process is then repeated, using the new weights, for an arbitrary number of times.

### 3 Results

### 4 Conclusion

### 5 Works Cited

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