

Emergence of Scale-free Graphs in Dynamical Spiking Neural Networks

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Abstract—In this paper we discuss the presence of a scale-free property in spiking neural networks. Although as argued in [1], [2], some biological neural networks do not reveal scale-free nature on the level of single neurons, we believe, based on previous research [3], that such structures should emerge on the level of neuronal groups as a consequence of their rich dynamics and memory properties. The network we analyze is built upon the spiking model introduced by Eugene Izhikevich [4], [5]. It is formed as a set of randomly constructed neuronal groups (each group to some extent resembles the original model from [4]), connected with Gaussian weights. Such a system exhibits rich dynamics, with chattering, bursting and other forms of neuronal activity, as well as global synchronization episodes. We analyze similarities of spike trains of neurons coming from different groups, and build a weighted graph which approximates the similarity of activities (synchronization) of pairs of units. The output graph reveals a scale-free structure giving support to our claim.

I. INTRODUCTION

Connectivity plays essential role in neural models. This fundamental property has been investigated for many years, and now with advanced neural models and huge computational power available, its importance is even more noticeable. Connectivity is unavoidably combined with graph theory, and therefore research breakthroughs in the one discipline have influence on the other. Random graph theory has experienced a large progress in recent years with new ideas like small world networks [6] and scale free networks, and therefore it is important to investigate these results in context of neural networks. The concept of scale free networks introduced in [7], [8] provides a unifying description of a wide variety of networks displaying the evidence of strong structuring principles coexistent with considerable degree of randomness. A distinctive feature of a scale-free network is that the degree distribution of its nodes follows a power law, thus lacking a characteristic scale in the language of statistical mechanics, hence the name. The presence of such power laws has been observed for a broad class of networks, prominent examples including the World Wide Web [9], science collaboration networks [10], citation networks [11], ecological networks [12], linguistic networks [13] as well as cellular metabolic networks [14] and many other ones, see [15]. With so many examples of information processing networks displaying scale-free structure it was rather surprising, that biological neural networks on the level of single neurons and synapses did not

obey any power laws [1], [2] rather exhibiting exponential decay, thus lacking scale-free property. In this paper we argue that by switching to appropriate level of observation (neuronal groups instead of single neurons), the result might change, and reveal scale-free structures.

The key property required to build a scale-free network is preferential attachment combined with model growth (see [7]). Preferential attachment imposes that units already well connected should have a higher probability of being attached to other nodes. In terms of neurons this property might be translated as follows: *the more activity a unit receives, the more active becomes and retains this activity for some period of time, depending on the initial excitation*. It is essential in this formulation that a unit possesses a non trivial memory of its state (amount of activity already received, and therefore ability to become active). Although single neurons (even single compartment dynamical models) do possess some amount of state memory (stored in current vector of parameters in the phase space), this is not enough to clearly exhibit preferential attachment in the sense defined above. In the following sections we argue that things change if we move from single neurons into neuronal groups. Such groups have opportunity to stay active for a longer period of time, and have some ability to *store* received activity by continuous excitation of a number of units within the group and therefore have some sort of memory of their past excitation. This property (although not easy to clearly distinguish from other dynamical behaviors of such a group), should lead to a certain kind of synchronization that would result in a scale-free network of synchronizations between the groups. These informal statements will be specified more precisely in following sections.

Theoretically speaking, for infinite simulation runs the model growth is required, because otherwise the network would saturate and lose scale-free property. With the models discussed in this paper though, the over saturation can be to a large extent neglected due to relatively short time of simulation, therefore our model is static, although it is also worth noting that in biological reality there are processes of decay and growth that prevent neural networks from saturation.

In a previous work [3] we examined a model of a *spike flow graph*, with simple units whose states were in \mathbb{N} . A system consisting of number of such units was randomly wired (normal distribution), and equipped with an energy function as

follows:

$$\mathcal{H}(\bar{\sigma}) := \frac{1}{2} \sum_{i \neq j} w_{ij} |\sigma_i - \sigma_j|. \quad (1)$$

Initially every unit was given some amount of *potential* (some small natural number), which could be later on exchanged between any two units under stochastic dynamics defined as follows: at each step we randomly choose a pair of neurons (σ_i, σ_j) , $i \neq j$, and denote by $\bar{\sigma}^*$ the network configuration resulting from the original configuration $\bar{\sigma}$ by decreasing σ_i by one and increasing σ_j by one, that is to say by *letting a unit of potential transfer from σ_i to σ_j* , whenever $\sigma_i > 0$. Next, if $\mathcal{H}(\bar{\sigma}^*) \leq \mathcal{H}(\bar{\sigma})$ we accept $\bar{\sigma}^*$ as the new configuration of the network whereas if $\mathcal{H}(\bar{\sigma}^*) > \mathcal{H}(\bar{\sigma})$ we accept the new configuration $\bar{\sigma}^*$ with probability $\exp(-\beta[\mathcal{H}(\bar{\sigma}^*) - \mathcal{H}(\bar{\sigma})])$, $\beta > 0$, and reject it keeping the original configuration $\bar{\sigma}$ otherwise, with $\beta > 0$ standing for an extra parameter of the dynamics, referred to as the inverse temperature conforming to the usual language of statistical mechanics. Note that this simple model has a state memory in a sense discussed above - each unit "knows" exactly how much potential it possesses as well as amount of potential it receives/gives from/to other units. The more potential a unit gains the more likely it will become more active. By labeling each edge that was used to exchange a unit of potential one receives a weighted graph, which displays a scale free property as well as some other interesting properties (see [3] for details as well as [16]).

Encouraged by this result we asked a question - is this behavior general and can it be reproduced with spiking neural models? For this investigation we have chosen a simple spiking model introduced by Eugene Izhikevich in [4]. This model given by a set of differential equations :

$$\begin{cases} v' &= 0.04v^2 + 5v + 140 - u + I \\ u' &= a(bv - u) \end{cases} \quad (2)$$

has been carefully tuned to be as simple and efficient as possible (in terms of computational requirements), and yet to resemble most of known neuronal spiking patterns and behaviors. This computational simplicity lets one carry out simulations with a large number of this fairly complex (in terms of possible dynamical behaviors) spiking neurons reasonably fast, and therefore it fit perfectly requirements of the presented research project.

One of the first objectives of this research was to confirm that single neurons do not possess enough memory¹ to exhibit a scale-free synchronization graph (roughly speaking the weight of an edge in synchronization graph is high if the spike trains of two units are similar and low in the other case, this concept is explained more formally in next section). We carried out a number of simulations with different weight matrices, and did not obtain any graph that would exhibit a scale-free nature (figure 4), either before or after thresholding². Roughly speaking, such simple systems either synchronize too

well, or don't synchronize at all, whereas scale-free property requires something in between.

Since, as expected, single neurons are not complex enough, our second step was to construct a model of neuronal groups. This approach is not very far from real life, since it is well known that neurons form well connected groups, and such phenomena were observed before even in the model we use in the present paper (see [17] for example). For simplicity we have constructed the groups randomly, with respect to some basic properties like distinction between excitatory and inhibitory neurons etc. (a project based on spontaneously forming groups is currently under development). The connectivity within a single group (about 10 to 20 neurons) was quite similar to that presented in [4], with appropriately scaled weights to ensure activity within a group. In every group, one neuron was chosen to play a special role (in the sequel we will refer to it as the *group leader*). This special neuron connects the group with other groups, it forms a kind of a gateway between the group and the rest of the model. Group leaders were connected randomly with normal distribution (see figure 1 for conceptual schema). The simulation was carried out with about 3000 groups (that gives about 45000 neurons) for more than 10000 steps (the coefficients in the model are tuned, so that each step corresponds to approximately 1 ms in real time, this however is not a key issue, since the presented model does not resemble any particular biological network). The output seemed quite promising right from the beginning - one look at figure 2 and 3 reveals rich neuronal behavior with global synchronization episodes, some amount of units exhibiting bursting activity. The striking feature of this plot is its self-similarity - in some ways it looks like a fractal. This detail, although interesting, was not a part of this research project - the goal was to translate synchronizations into real numbers, use these number as graph weights, and determine whether this graph has a scale-free property or not. The details are yet to be described in further sections, however this section can be concluded by giving a positive answer to the preceding question - one glimpse at figure 5 strongly supports the claim that the degree distribution of a graph received from this numerical experiment follows a power law.

II. MODEL DETAILS

As mentioned in preceding section, the simulation was carried out for a set of 3000 groups (each consisting of 10-20 neurons - the number was chosen randomly with uniform distribution), represented by the group leaders. The connectivity within a single group was quite similar to the one from [4], with appropriately scaled weights, to ensure synchronization. The ratio of excitatory/inhibitory neurons was also chosen randomly from uniform distribution. This construction was not based on any particular biological inspiration, the goal was to create groups that would exhibit large variety of dynamical behaviors. The simulation was carried out on two levels, on both of them synchronously:

- 1) Initialization phase - each group was simulated synchronously over one time step (1ms). The initial input

¹In the sense discussed above.

²The obtained graph is weighted, thresholding is a way of creating corresponding unweighted graph.

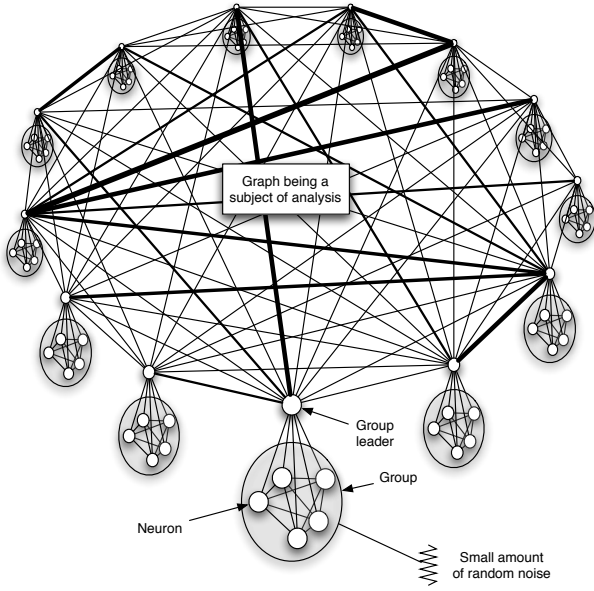


Fig. 1. A schematic presentation of the model investigated in this paper. The model consists of a number (about 1000-3000) of neuronal groups, connected randomly (weights chosen from Gaussian distribution $\mathcal{N}(0, 1)$) by the group leaders - neurons chosen to interconnect every group with others. The group's synchronization depends on the input received from the group leader and, on the other hand, the activity of the leader resembles the activity of the group.

to every group was 0 plus some slight Gaussian noise (applied to every neuron independently).

- 2) After this phase, weighted summation of group leader output activities is performed and given as input activity to group leaders in the next step.
- 3) Each group was simulated synchronously over one time step, with the group leader activity and a slight Gaussian noise as an input for every neuron.
- 4) Steps 2 and 3 were repeated until the end of simulation (in this case up to 12000 steps).

As an output, the simulation produced a significant number of spike trains (3000 neurons, each over more than 10000 time steps) that had to be compared with respect to a measure of synchronization computed in the following manner:

- 1) Each spike train was blurred by a convolution with $\exp\left(-\left(\frac{x}{10}\right)^2\right)$ kernel, see figure 8.
- 2) The transformed spike train of every two neurons was then multiplied and integrated. The integral was interpreted as a measure of synchronization.

The blur was necessary, to assure similarity between two spike trains that were in fact roughly similar, but corresponding spikes were shifted by a couple of time steps in either direction. It is worth noting that this measure strongly supports bursting - two units giving continuous spike response in the same time gain much similarity in the sense above. Note that this measure is significant only if spikes actually occur, two empty spike trains are similar in some sense, but in terms of a proposed measure their similarity is zero.

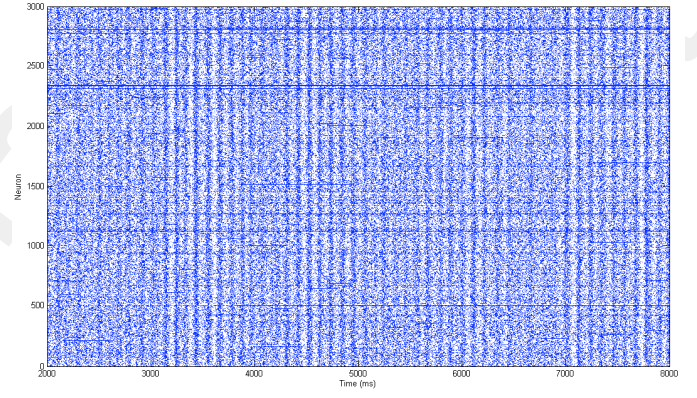


Fig. 2. Spike activity plot of 3000 group leaders during 6000ms timeframe. Please note the global synchrony episodes as well as bursting of single units.

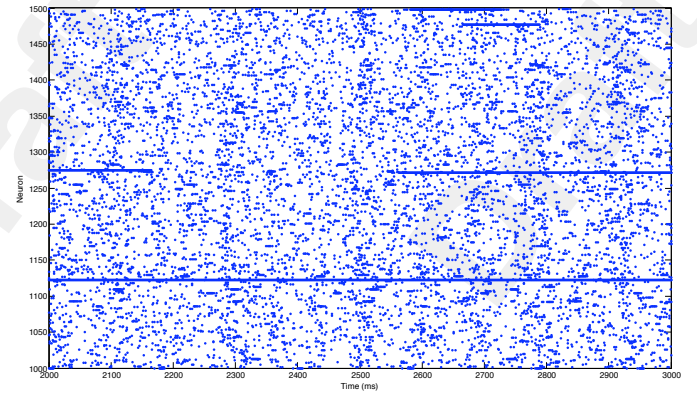


Fig. 3. Magnified segment of figure 2 showing neurons 1000 to 1500 within 2000ms-3000ms timeframe. Please note the similarities of these plots (actually it is a self-similarity). The number and length of straight horizontal lines (each symbolizing a bursting activity) in both plots is approximately the same.

Based on the similarity measure above a symmetric weight matrix corresponding to a weighted graph was built. The obtained graph was a subject to further analysis, based on a typical tools from random graph theory like degree distribution, average path, number of connected components and clustering coefficient.

III. RESULTS

The obtained graph was weighted which had its advantages and disadvantages. We used some analytical tools for weighted graph, and then continued with an unweighted one created by thresholding original graph over a certain value (in this case the average weight in a graph). The essential feature being in the scope of this article - the scale free property was observed in either case. For the weighted graph the node degree was defined simply as sum of weights of edges adjacent to that node. For the unweighted graph we used the usual definition (number of edges adjacent to a node). In both graphs the degree distribution followed a power law, with exponent of about 2, in the weighted case there were some slight deviations - the power law was slightly violated near the plot limits. This however is not very surprising, since such disturbances are

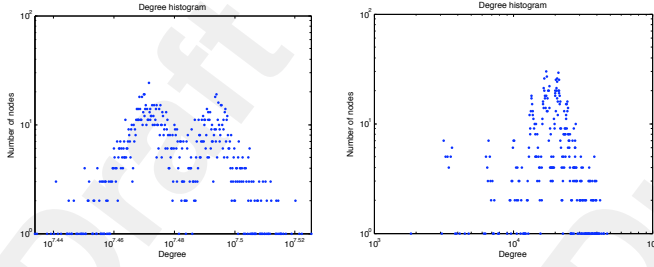


Fig. 4. Example degree distributions of synchronization graphs produced by a network of spiking neurons for different coupling regimes. Certainly these graphs do not exhibit a scale-free property.

present in a number of other scale free networks, especially of medium size like the one investigated in this paper. These artifacts appear due to under/over saturation of high/low degree nodes, due to finite time of simulation. In the unweighted case these fluctuations are even less significant due to thresholding. In order to gain confidence, the simulation was repeated a number of times, the results were always similar.

The power law exponent is roughly 2, but some further computations and averaging is required to provide a better estimate.

Note that as expected - more active units (the activity is measured as an integral of spike train convolved with $\exp\left(-\left(\frac{x}{10}\right)^2\right)$ kernel, as previously) gain more neighbors in the output graph (either weighted or unweighted). This is clearly visible in figure 6 and evidently supports our hypothesis of the presence of preferential attachment principle in the model.

The unweighted graph formed a single³ connected component (possibly with some number of abandoned nodes).

The interesting feature of the thresholded graph is its very high clustering coefficient - this graph is very well clustered. What's more, the clustering coefficient exhibits a surprisingly regular dependence on degree (see figure 7, which displays this dependency as well as the corresponding dependency obtained from Erdős-Rényi random graph with similar connection density), which suggests that lower degree nodes are nearly fully clustered but after reaching certain degree threshold, the clustering coefficient drops dramatically leaving high degree nodes almost unclustered. This gives an interesting insight into graph structure, but it is not yet obvious whether this dependency is an artifact of graph thresholding or is it some general property of these networks.

It is worth noting that the resulting graph also had a small world property - high clustering coefficient (about a magnitude higher than in corresponding Erdős-Rényi random graph) combined with short average path length (depending on the thresholding level, the average path varied from about 2 to 4 nodes, so the connectivity is nearly perfect). Again this might not be very surprising in context of already published

³This obviously depends on the thresholding level. As the threshold grew, the more nodes became abandoned ("abandoned" in the sense "not connected to anyone"), but still a single giant connected component was present.

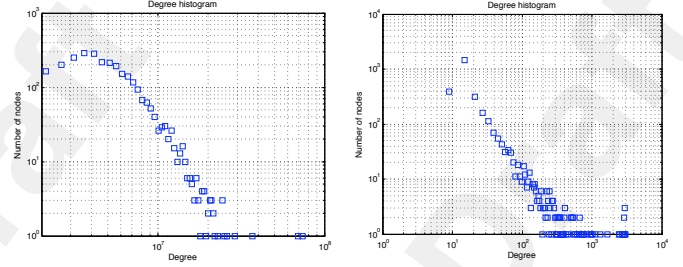


Fig. 5. The degree distributions of a network received from the model (left), and one obtained by thresholding original network at an average weight (right) in order to produce an unweighted graph. In either case the presence of a power law with exponent of about 2 is quite clear. Please note the significant difference between these plots and the ones showed in figure 4.

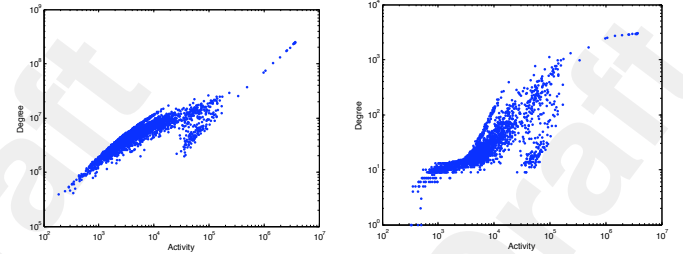


Fig. 6. The dependency between spiking activity and vertex degree before (left) and after thresholding the graph (right). In either case we observe a clearly monotone dependency which supports our preferential attachment hypothesis.

results [18] and the fact that scale-free networks exhibit small world phenomenon quite naturally.

IV. CONCLUSION

In this paper an interpretation of preferential attachment for dynamical behavior in a spiking neural network was introduced. This interpretation sets the following constraints to dynamic behavior: *the more activity a unit receives, the more active it becomes and retains this activity for some period of time, depending on the initial excitation.* We claim that this property, first analyzed in discrete setup in [3], cannot be successfully reproduced with single neurons (even fairly complex dynamical spiking neurons e.g. those introduced in [4]). Artificially created neuronal groups however, seem to have dynamics rich enough to exhibit such property, since they clearly constitute a scale-free network of spike train similarities as presented in previous sections. It is worth noting that the state memory property discussed above might not be easy to observe in direct analysis of the group dynamics - it can be hidden behind rich dynamical behavior of the group, and reveal itself only in terms of statistics. A further research is required to determine, whether spontaneously developing neuronal groups inherit similar properties (this is a subject of ongoing examination). Additional analysis of connectivity in biological neural networks on the level of neuronal groups of an appropriate size (or synchronization properties) should give more insight into issues discussed in this article, and possibly

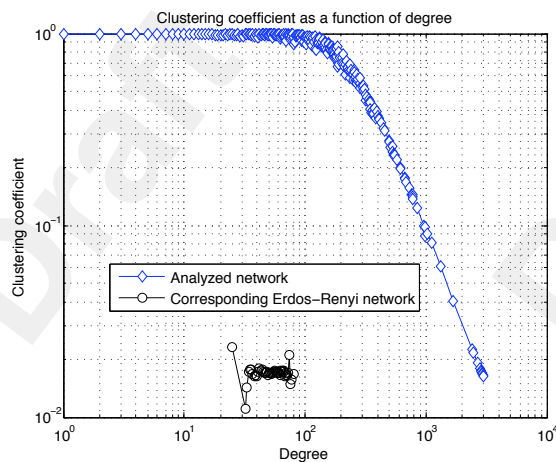


Fig. 7. Clustering coefficient as a function of degree in the investigated network. This plot is interesting, since such behavior of clustering coefficient is rather rare - the nodes of small degrees are well clustered whereas those with high degree are not. Compare with box 2 in [19]. The black-circle plot depicts this dependency obtained from Erdős-Rényi random graph with similar number of edges.

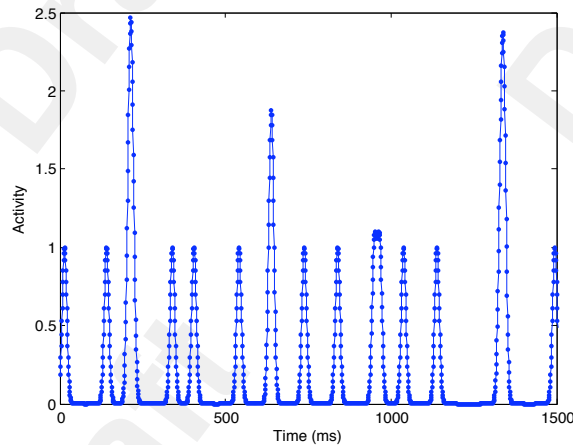


Fig. 8. Spike activity convolved with $\exp\left(-\left(\frac{x}{10}\right)^2\right)$ kernel. This procedure blurs the spike train significantly, but lets one receive non zero product of two of such trains even if corresponding spikes are shifted. The product is later integrated to obtain *synchronization strength*, a measure we introduced to describe similarity between spike trains.

give empirical support to this theoretical/computational analysis.

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