Emergence of Scale-free Graphs in Dynamical Spiking Neural Networks (paper 1215)

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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] and numerical simulations presented in this article, 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.

INTRODUCTION

This research is based on previous results presented in [3], which dealt with a discrete model, that resembled to some extent Hopfield model. In this previous work 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 (normally distributed weights), and equipped with an energy function as follows:

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

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 units (σ_i, σ_j), $i \neq j$, and denote by ϑ^* the network configuration resulting from the original configuration ϑ 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 $\mathcal{H}(\vartheta^*) \leq \mathcal{H}(\vartheta)$ we accept ϑ^* as the new configuration of the network whereas if $\mathcal{H}(\vartheta^*) > \mathcal{H}(\vartheta)$ we accept the configuration ϑ^* with probability $\exp(-\beta[\mathcal{H}(\vartheta^*) - \mathcal{H}(\vartheta)])$, $\beta > 0$, and reject it keeping the original configuration ϑ 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 :

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

This model given by a set of differential equations above 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 our 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.
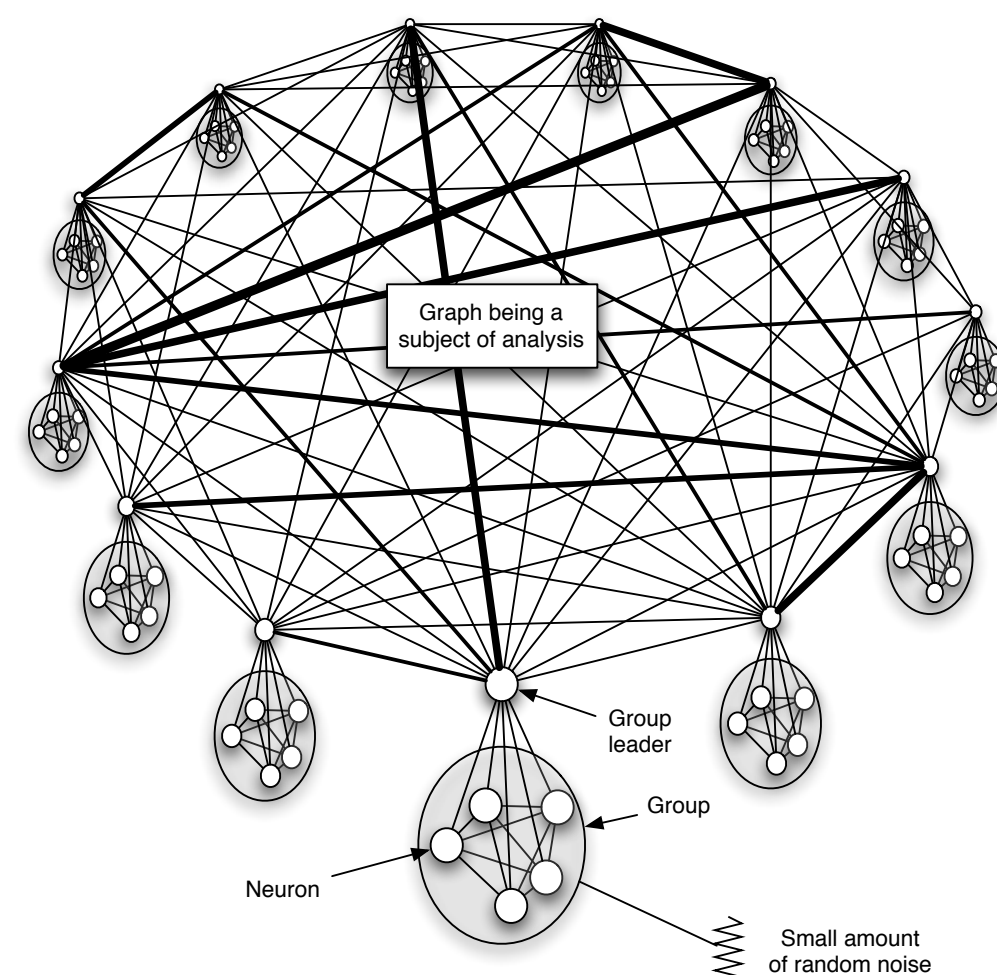

Fig. 1. A schematic presentation of the model investigated in this paper. The model consists of a number (about 1000-3000) of neuronal groups, connected randomly (weights chosen from Gaussian distribution $N(0,1)$) by the group leaders - neurons chosen to interconnect every group with others. The group's 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.
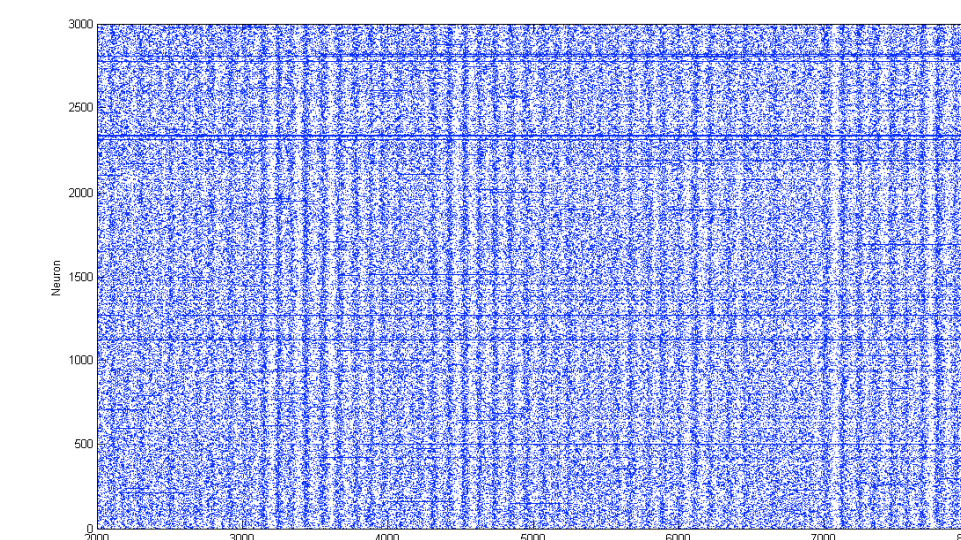

Fig. 2. Example of spike activity plot of 3000 group leaders during 6000ms timeframe (only the activity of group leaders is plotted). Note the global synchrony episodes as well as bursting of single units.
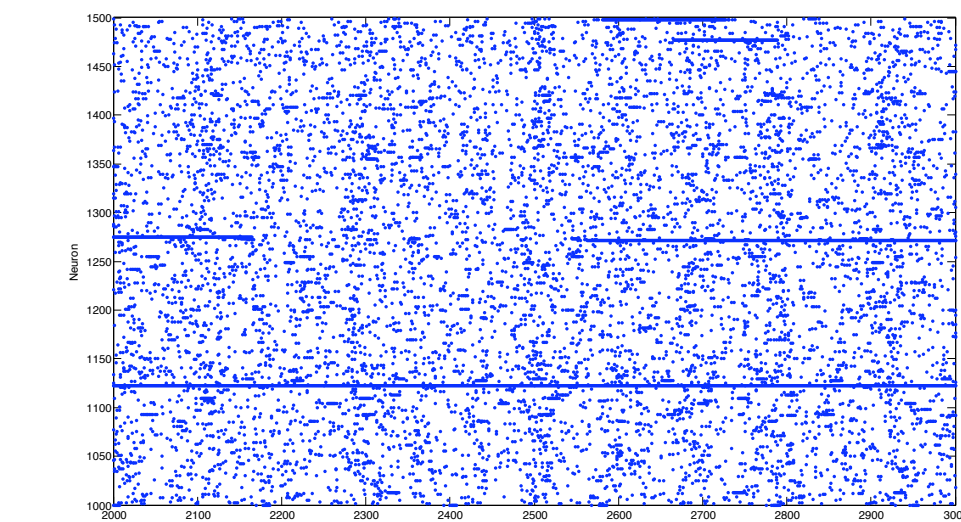

Fig. 3. Magnified segment of figure 2 showing neurons 1000 to 1500 within 2000ms-3000ms timeframe. Please note the similarities of these plots (actually it is a self-similarity). The number and length of straight horizontal lines (each symbolizing a bursting activity) in both plots is approximately the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

DYNAMICS

The simulation was carried out on two levels, on both of them synchronously:

- Initialization phase - each group was simulated synchronously over one time step (1ms). The initial input to every group was 0 plus some small Gaussian noise (applied to every neuron independently).
- After this phase, weighted summation of group leader output activities is performed and given as input activity to group leaders in the next step.
- 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.
- 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:

- Each spike train was blurred by a convolution with kernel $\exp\left(-\left(\frac{t}{t_0}\right)^2\right)$, see figure 2.
- The transformed spike train of every two neurons was then multiplied and integrated. The integral (real number) 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 several 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.

DETAILS

One of the first objectives of this research was to confirm that single neurons do not posses enough memory[1] to exhibit a scale-free synchronization graph (informally, 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 thresholding[2]. It seems that 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 - 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 those 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 - figure 5 strongly supports the claim that the degree distribution of a graph received from this numerical experiment follows a power law (similar plot was obtained in a number of simulations).

As mentioned in preceding paragraph, 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. Note that this construction was not based on any particular biological inspiration since the goal of this research was rather to find a link between the simple discrete model and more complex continous dynamical one, than mimicking the biological complexity. The next steps of this project would be to create more and more biologically feasible models that would still exhibit the scale-free property, for that however, it is essential to know what dynamical features of these models are responsible for emergence the scale-free phenomenon.

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

[1] In the sense discussed above.

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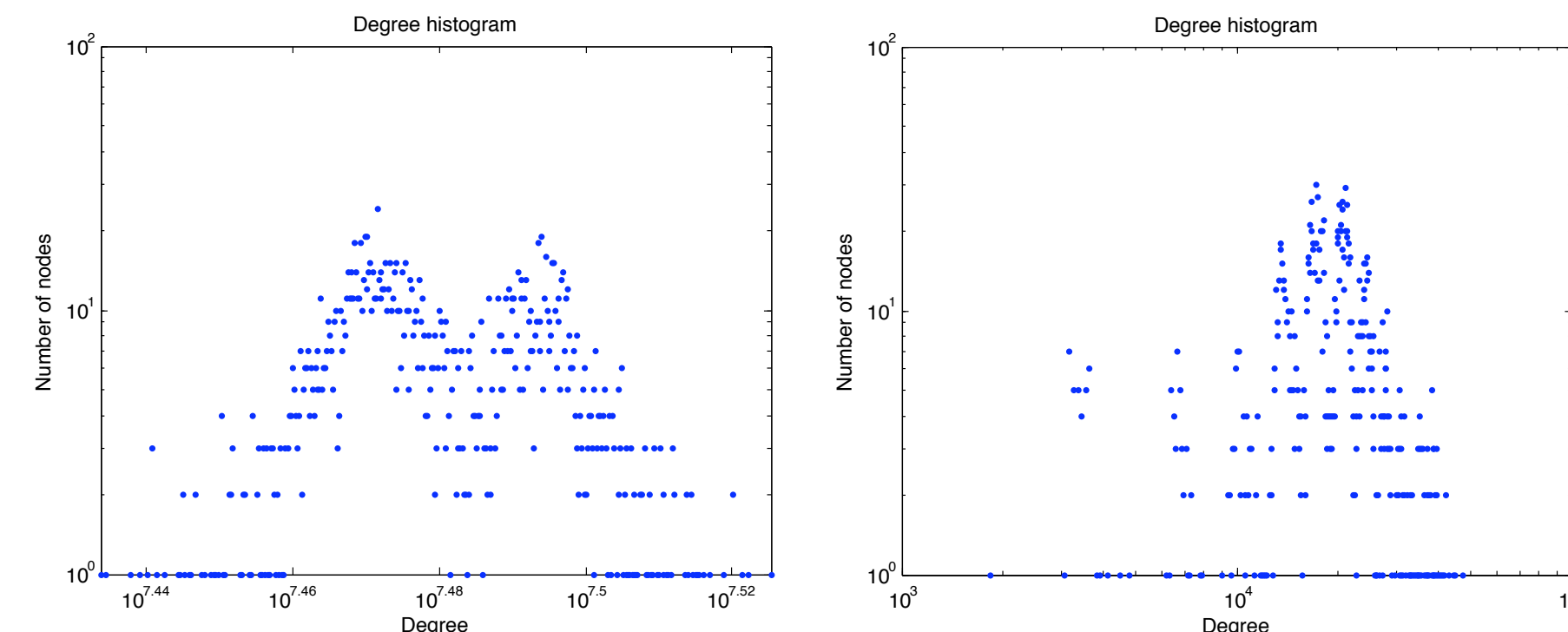

Fig. 4. Example degree distributions of synchronization graphs produced by a network of spiking neurons for different coupling regimes. Certainly these graphs do not exhibit a scale-free property.
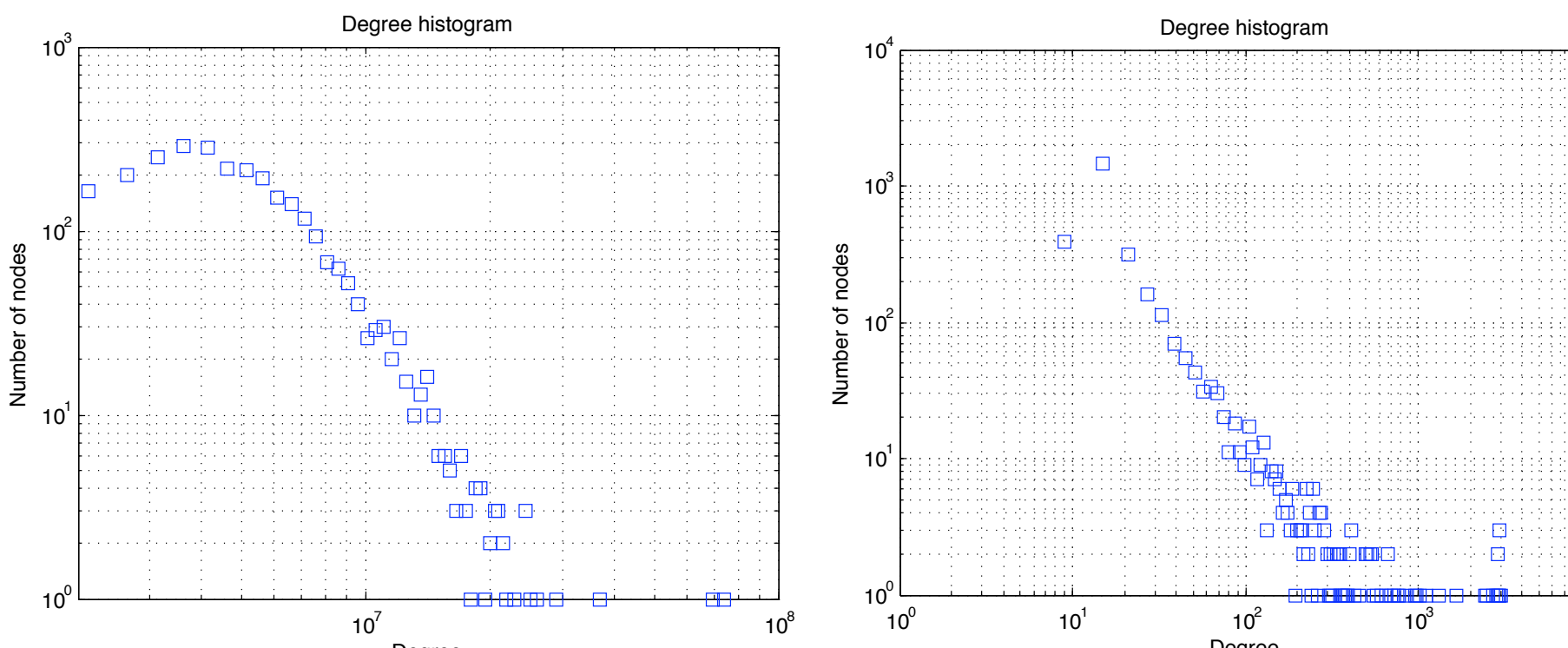

Fig. 5. The degree distributions of a network received from the model (left), and one obtained by thresholding original network at an average weight (right) in order to produce an unweighted graph. In either case the presence of a power law with exponent of about 2 is quite clear. Note the significant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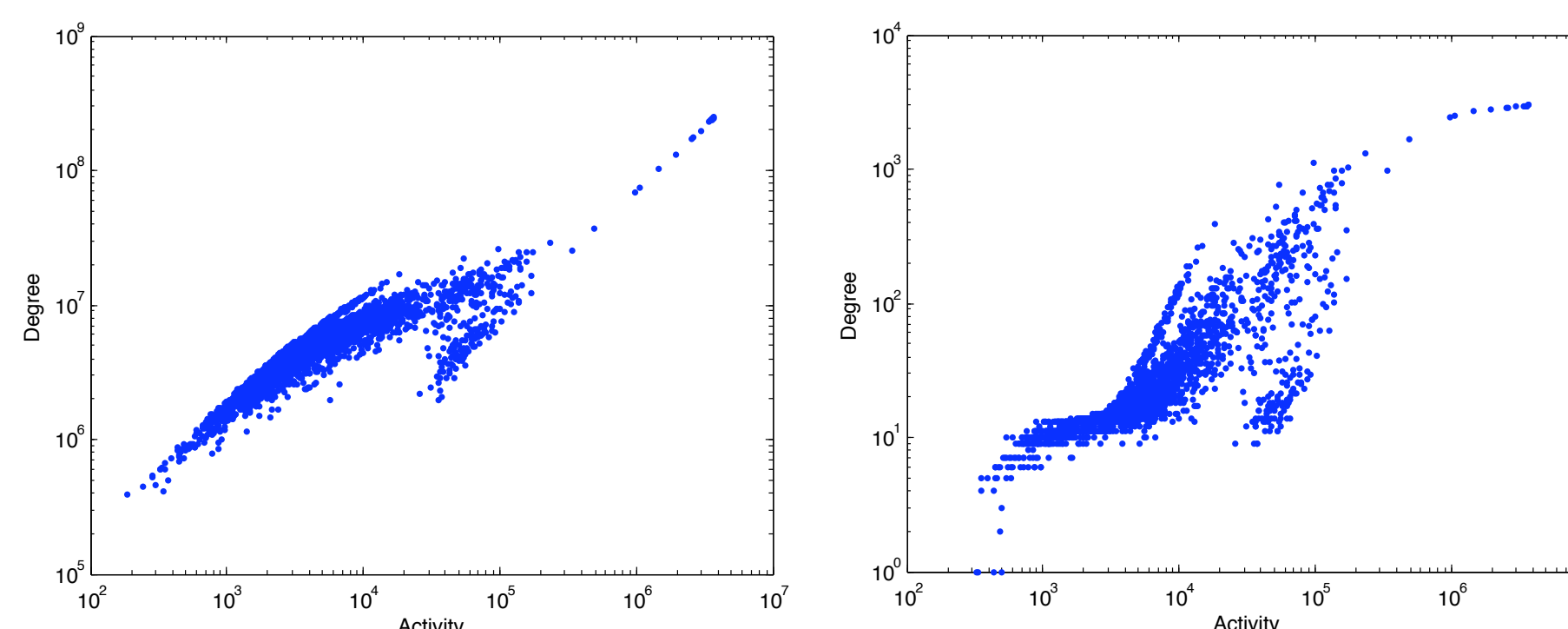

Fig. 6. The dependency between synchronization activity and vertex degree before (left) and after thresholding the graph (right). In either case we observe a clearly monotone dependency which supports our preferential attachment hypothesis.

RESULTS AND CONCLUSIONS

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 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 (and avoid possible statistical disturbance), the simulation was repeated a number of times (about 30 for each set of parameters), the results were always very similar.

Note that as expected - more active units (the activity is measured as an integral of spike train convolved with $\exp\left(-\left(\frac{t}{t_0}\right)^2\right)$ 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 single 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 graph with similar connection density), which suggests that lower degree nodes are nearly fully clustered but after reaching certain degree threshold (in the case of presented

simulation the threshold is about 10^2, but this value most probably depends on the system size), 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 graphs.

It is worth noting that the resulting graph also had a small world property - high clustering coefficient as discussed above (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 results [18] and the fact that scale-free networks exhibit small world phenomenon quite naturally.

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 raises this activity for some period of time, depending on the initial excitation*. We claim that this property, used 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 that 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. It is important to note that these results were obtained in simulation, theoretical foundations of presented phenomenon (as well as combining the discrete and continuous models) are now being a subject of ongoing research. Further investigation is required to determine, whether spontaneously developing neuronal groups [17] inherit similar properties (this as well 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 give empirical support to this theoretical/computational analysis.

Fig. 8. Spike activity convolved with $\exp\left(-\left(\frac{t}{t_0}\right)^2\right)$ 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.

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.

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