Diameter of the spike-flow graphs of geometrical neural networks

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Abstract. Average path length is recognised as one of the vital characteristics of random graphs and complex networks. Despite a rather sparse structure, some cases were reported to have a relatively short lengths between every pair of nodes, making the whole network available in just several hops. This small-worldliness was reported in metabolic, social or linguistic networks and recently in the Internet. In this paper we present results concerning path length distribution and the diameter of the spike-flow graph obtained from dynamics of geometrically embedded neural networks. Numerical results confirm both short diameter and average path length of resulting activity graph. In addition to numerical results, we also discuss means of running simulations in a concurrent environment.

Keywords: geometrical neural networks, path length distribution, small-worldliness, graph diameter

1 Introduction

Neural networks, while already turned out a worthy tool in machine learning, still constitute a potent source of knowledge about the nature of biological brain. Recently, a growing number of mathematical models were developed and studied in order to shed some light [9,10].

One of the most striking facts about brain networks is its sparsity. Recall, that number of neurons in human brain is put at 10^{11} while the number of synapses 10^{15}, clearly this places brain somewhere in-between regular lattice and a fully connected graph.

In [11] a flexible and mathematically feasible model of neural activity was put forward. It was mathematically proven and numerically confirmed, that its degree distribution obeys a power law, moreover the exponent value is close to results obtained from fMRI scans of human brain [7]. Continuing the research, we have decided to look closer on other commonly discussed features of the model. The aim of this work is to present strictly numerical findings (although, supported by random graph theory) about the average path length of spike-flow graphs, which tend emerge as a result of an self-organization process accompanying the dynamics of the system. Despite its sparsity, the graph turns out to

have relatively short diameter, which again bears similarity to features reported in real brain networks [3]. However complex the structure of the network might be, it still admits passing of information between any areas within just a few edge traverses. This striking feature is believed to be one of the foundations of brain's resilience to noise and random failures [2,3]. In addition to presenting obtained results, we also provide a brief discussion about numerical details of the simulation, focusing on paralleisation possibilities.

The article is organised as follows: we present the network model and the simulation dynamics in Section 2. Than we present obtained results of the path length distribution in Section 3. Numerical, technical and implementation details are discussed in Section 4 and the paper is concluded with Section 5.

2 Simulation model

We start with description of the underlying structural network $G = (\mathcal{V}, \mathcal{E})$, where $\mathcal{V}$ is a set of neurons and $\mathcal{E}$ stands for synaptic connections. Given a radius $R > 1$ of the two-dimensional sphere $S_2 \subset \mathbb{R}^3$ and the expected density of neurons $\rho \gg 1$ we pick number of neurons N in the system randomly from Poissonian distribution $\mathcal{P}(\rho \cdot 4\pi R^2)$, namely with parameter λ scaling as density times surface of the sphere. Each of N neurons v is than independently picked from the uniform distribution on the sphere surface. Additionally, it receives its initial *charge* $\sigma_v \geq 0$. The charge will be a subject to a dynamics, though we admit only non-negative integer values for σ_v.

A set of synapses is constructed in as follows: for each pair of neurons u, v a symmetric *synaptic connection* $\{u, v\}$ is added to $\mathcal{E}$ independently with probability

$$\mathbb{P}(\{u, v\} \in \mathcal{E}) = \begin{cases} d(u, v)^\alpha & d(u, v) \geq 1 \\ 1 & \text{otherwise,} \end{cases} \tag{1}$$

where $d()$ stands for euclidean distance between neurons u and v. The exponent α is fixed at the value -2.5. If successfully included, the synapse $e = \{u, v\}$ receives its *weight* w_{uv} independently generated from the gaussian distribution $w_{uv} \sim N(0, s^2)$. The weight indicates an excitatory or inhibitory (when negative) type of the synapse.

A network *energy* function depending on the charge stored in each of neurons is defined as

$$E(\bar{\sigma}) = \sum_{(u,v)\in\mathcal{E}} w_{u,v} |\sigma_v - \sigma_u|. \tag{2}$$

Having presented the structural network, we describe the dynamics. We adopt a variation of the celebrated Ising spin glass model, though extended for multiple values of σ.

– At each step we pick a random pair of neurons $u, v \in \mathcal{V}$, such that they are connected with a synapse $\{u, v\} \in \mathcal{E}$ and the charge stored in u is non-zero $\sigma_u \geq 1$,

– We try to transfer a single unit of charge from u to v through the synapse, in other words $\sigma_u := \sigma_u - 1$ and $\sigma_v := \sigma_v + 1$,
– if this transfer reduces energy of the system, it is accepted, and the dynamics proceeds to next iteration,
– if this transfer increases the energy by ΔE, then it is accepted with probability $\mathbb{P}(u \to v) = \exp(-\beta \Delta E)$ and rejected otherwise.

The parameter $\beta \gg 1$ stands for an inverse temperature and is assumed to be large. Though the dynamics can run arbitrarily long, it is terminated after hitting given number of iterations or reaching the state, where no further transfers are accepted.

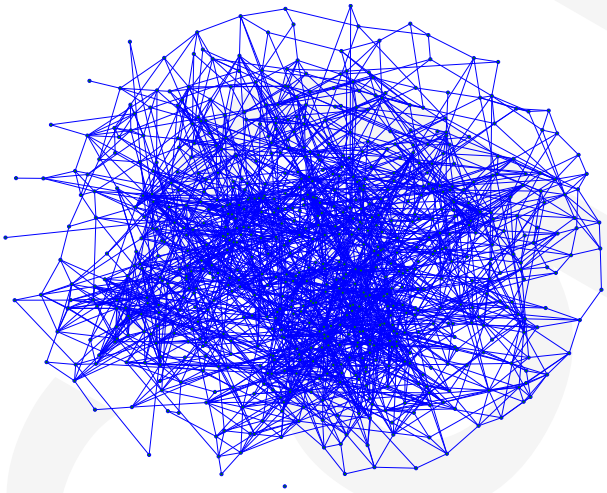


Fig. 1. A subgraph of resulting network, plot includes 719 neurons and 2500 synapses. Spatial coordinates were remapped from a sphere to a surface for better visibility. Despite a small sample, hubs (node with large degree) are clearly noticeable.

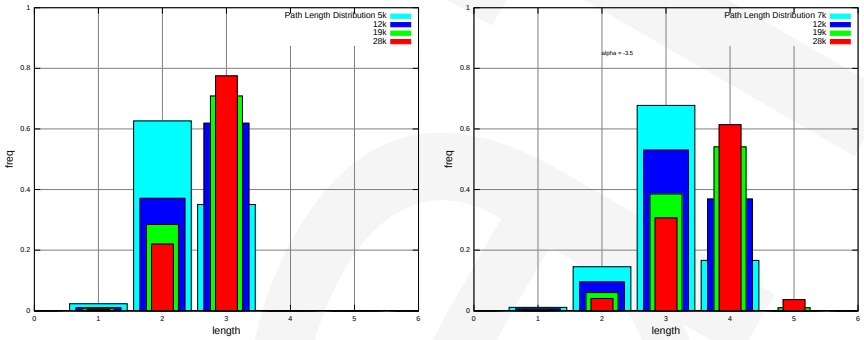
3 Path length distribution results

As pointed out in [11] the the dynamics leads to concentration of the charge in small number of nodes. For each synapse $e = \{u, v\}$ a total amount of charge which flew either from u to v or from v to u is recorded and denoted as d_e. Reaching a predefined threshold value θ qualifies an edge as a vital in the evolution process. A graph built from the vital edges will be referred as a *spike flow graph*, namely $\mathcal{G}_1 = (\mathcal{V}, \mathcal{E}_1 = \{e \in \mathcal{E} : d_e \geq \theta\})$. A value $\theta = 1$ is assumed throughout rest of the work, which results in spike flow graph consisting of all edges participating in the dynamics. A small subgraph of the resulting spike flow network is depicted on Fig. 1.

As a *minimal path length* between neurons u and v we understand classical definition, i.e. $l(u, v)$ is a minimum number of edges $(e_1 = \{u_1, v_1\}, .., e_n = \{u_n, v_n\})$, such that

- they start at u and terminate at v, $u_1 = u$, $v_n = v$,
- they are incident, $\forall_{i=1..n-1} v_i = u_{i+1}$,
- they are included in resulting spike flow graph $\forall_i e_i \in \mathcal{E}_1$.

For the sake of simplicity we assume $l(u, u) = 0$.



(a) $\alpha = -2.5$ (b) $\alpha = -3.5$

Fig. 2. A plot of path length distribution of the spike-flow graph obtained from a simulation of networks counting 5 to 28k neurons. The distribution slowly increases its mode as the number of nodes grows.

Obtained results of the path lengths are presented on Fig. 2. The results were collected from simulations of networks counting between 300 and up to $5.5 \cdot 10^4$ neurons for exponent of the connectivity function (Eq. 1) $\alpha = -2.5$ and $\alpha = -3.5$. As shown in [12] a resulting spike-flow graph obeys a power law degree distribution, this type of graphs also frequently exhibits a small world phenomenon [2].

Fig. 3 presents the dependency between the size of the simulation sample and corresponding average path value. It presents a slow growth, but in all of our cases is still bounded by 4. A slow increase of the average path length is observable, which again is in agreement with theoretical results of classical random graphs theory. Also note, that for our small samples the path length distribution is focused on 3 values. The the rest (number of paths of length up to the graph diameter — see below) is non zero, though negligible.

The *diameter of the graph* is defined as a maximum value of shortest path length $l(u, v)$ between every pair of nodes (u, v) in the graph. Its plot is provided on Fig 3. Recall that for Erdős-Réyni random graph model the diameter grows logarithmically as the network size increases, see [5] Ch. 5 and 7 for rigorous proof. Clearly the diameter can be arbitrarily larger than an average path length,

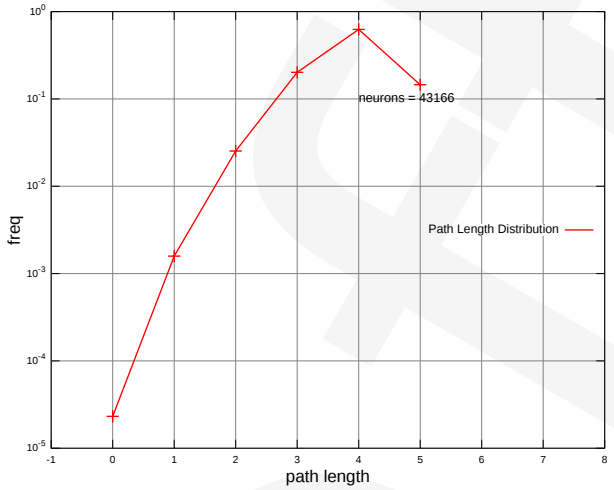


Fig. 3. A semi-log plot of the path length distribution of the spike-flow graph. The number of paths of length 0 (selfloops) and 1, though negligible, is non zero. Number of neurons $N \simeq 40\text{k}$, $\alpha = -3.5$.

however in our cases it is bounded by 6 for our samples, which means that starting in any neuron, the whole network is available in no more than 6 hops. While our model is not a ER model, this feature make it strikingly similar to WWW [1] or social graphs [6]. A few reports suggest small-worldliness to be present also in brain activity networks [3].

Small discrepancy between l for different values of α seems to originate from difference in underlying structural graphs. Lower α yields less synapses in the structural network $\mathcal{G}$, while the spike-flow graph consists exclusively of synapses present in $\mathcal{G}$. The formula of g was suggested in [7].

While the clustering coefficient is an aim of ongoing research we can provide a brief preliminary results concerning this value. After classical theory [5] we define a *clustering coefficient of the node* v as a ratio of existing edges in the neighbourhood of v to all possible edges.

$$C(u) = \frac{|\{e = (w, v) : e \in \mathcal{E} \wedge (w, u) \in \mathcal{E} \wedge (v, u) \in \mathcal{E}\}|}{|\{(w, v) : (w, u) \in \mathcal{E} \wedge (v, u) \in \mathcal{E}\}|} \tag{3}$$

The *clustering coefficient of the graph* C is defined as an average of clustering coefficients of its nodes.

$$C = \frac{1}{|\mathcal{V}|} \sum_{u \in \mathcal{V}} C(u) \tag{4}$$

Recall, that for ER graph model the clustering coefficient is relatively small (it is equal to the average connectivity of the graph). As it can be see in Table 1 for spike-flow graph in our model the actual clustering coefficient is 2-3 orders of magnitude higher then its average degree, which again is in agreement with fMRI data [3].

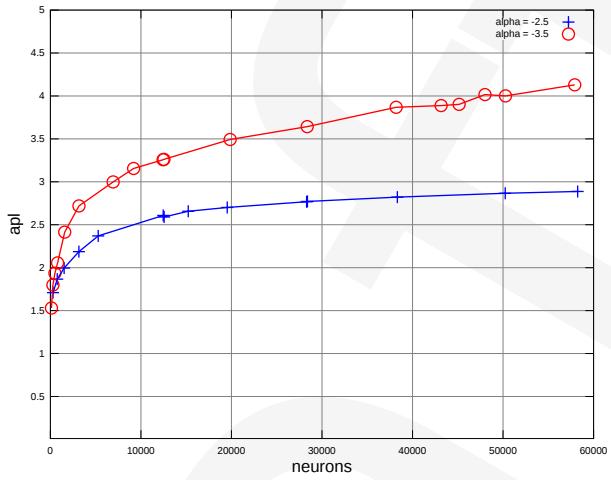


Fig. 4. A plot of the average path length of the spike-flow graph vs sample size.

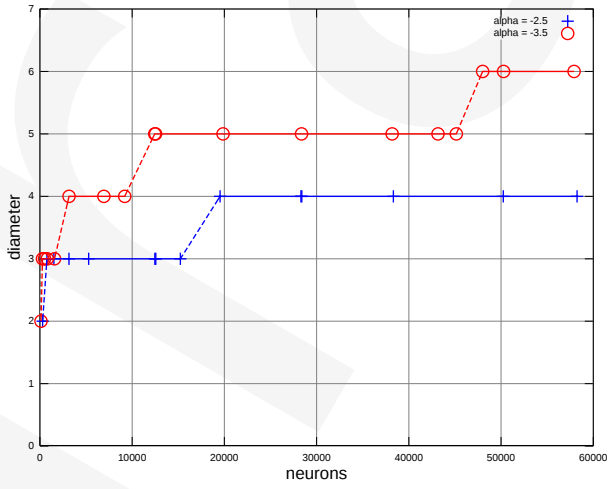


Fig. 5. A plot of the diameter (maximum path length connecting a pair of nodes) of the spike-flow graph vs sample size. Note, that slope segments indicate values, which are not known (diameter must be an integer number).

Table 1. Calculated clustering coefficient and average connectivity for obtained spike-flow graphs, $\alpha = -2.5$. Note that the *average degree* is also a theoretical clustering coefficient for equivalent ER random graph, while by *clustering coefficient* we mean an actual, numerically obtained value for our model.

Neurons	Synapses	Average degree	Clustering coefficient
3155	0.18M	0.038	0.243
12568	0.8M	0.010	0.207
19531	1.3M	0.006	0.198
24630	1.7M	0.005	0.194
28501	2.0M	0.004	0.191
38322	2.6M	0.0035	0.187
50241	3.5M	0.0027	0.183
58244	4.1M	0.0023	0.182

4 Numerical details

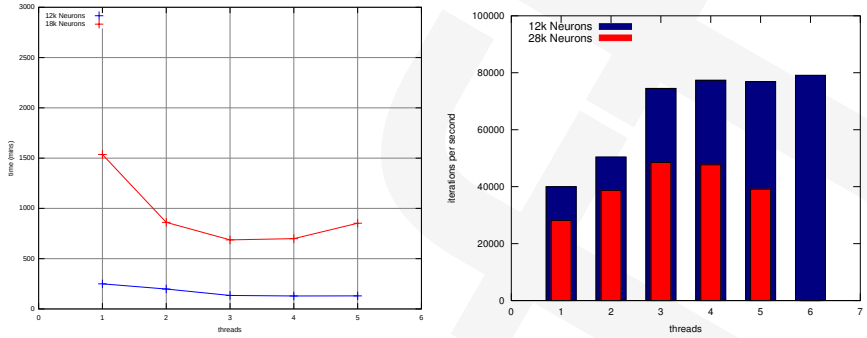
The simulations were carried on spheres with radii varying up to $R = 30$ with constant density $\rho = 10$, see Sec. 2. This yields samples counting up to 55k neurons.Additionally, we expect an average 500 units of charge amount per neuron to be present in the network. In most cases a strict limit of iterations turned out a sufficient terminating condition.

The simulation itself was paralleled to take advantage of multiprocessing environment. However, due to highly unpredictable dynamics and the usage of control-flow instructions one finds particularly demanding to put graphical computing units into a good use [12]. We decided to implement a task division, i.e. splitting the total number of iterations among parallel threads. Sparse though the resulting network might be, it still requires visiting all of the neighbour neurons before deciding whether (or not) to accept the transfer. Along with growing number of threads it increases frequency of waiting for the lock to be released and thus affects the speedup. The overall efficiency was about 66% for three threads.

For calculation of the path length distribution a classical Dijkstra algorithm has been adapted with a domain-division paralleisation. The results of calculation times are presented on Fig. 4. The computation time seems reasonable, when take into account sequential collecting data from threads. Obtained efficiency is about .78 for 4 threads, which is the number of computing cores. The results were obtained on Core Quad 2GHz CPU + 4GB RAM + Fedora 11–14 (32bit, PAE) system.

Some of the simulations were also run of the infrastructure of the PG-Grid, who kindly provided their computing resources. The timing and speedup results from those simulations, while still being collected and analysed, are beyond the scope of this work.

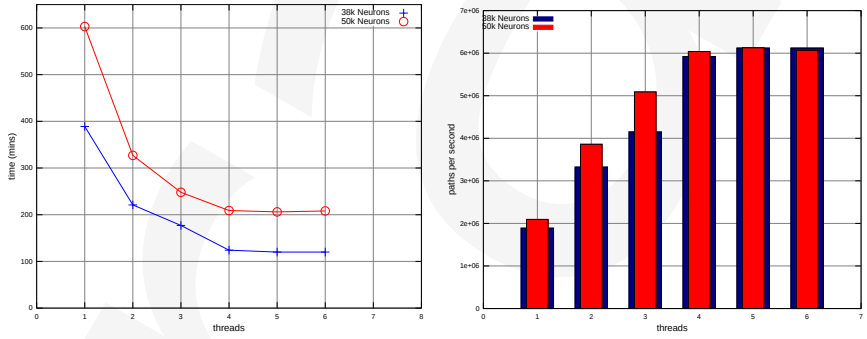
Additionally a Monte Carlo was also implemented, however we found the time, required to yield a results with a satisfactory precision, comparative to the



(a) Computation time (b) Iterations per second

Fig. 6. Computation times obtained for the dynamics. Reprinted from [12].

time required by the former algorithm. Although, for larger samples MC may turn out indispensable.



(a) Computation time. (b) Number of paths calculated per second.

Fig. 7. Computation times obtained and number of path lengths calculated per second for sample 38k neurons. The results were obtained on 4 cores CPU.

5 Conclusion and future work

In this work we have presented our findings concerning path length distribution in spike-flow graphs of neural network. The distribution turns out concentrated on few values and its mean value is relatively low, making the whole network available to reach within just a few hops. Along with high clicqueliness determined by the clustering coefficient, this suggests a complicated structure of the

resulting network, even despite not so complicated dynamics. Clearly, the network bears resemblances to social graphs or WWW networks, which also tend to exhibit a small-world phenomenon.

It might turn out interesting to see how the network evolves to its final shape throughout the simulation. This unfortunately requires either more computational power or reduction of the size of the network, in order to keep the simulation time reasonable. As an additional aim of future work, we point at considering a directed version of the spike flow graph, which is natural feature of WWW networks [1]. Since the dynamics in our network is directed, the distinction between a input and output synapses seems to be a forgone conclusion. One more vital aspect frequently discussed when working with complex networks is clustering coefficient [2,3]. While it was bearly mentioned in in Sec. 3, a coherent comparison between the results obtained from fMRI and our model is a focus of ongoing research.

Acknowledgements

The author would like to mention the unparalleled support from prof. Tomasz Schreiber, Associate Professor at Faculty of Mathematics and Computer Science, NCU, a bright young scientist, who carried researches in mathematics, computer science and physics, prematurely died in December 2010.

The author acknowledges a cooperation and a dash of red ink from dr Filip Piękniewski.

Additionally, the author is grateful to PL-Grid Project[1] for providing a computing infrastructure for simulations.

The work has been partially supported by Polish Ministry of Science and grant project 2011/01/N/ST6/01931.

The author would also like to acknowledge the support of the European Social Fund and Government of Poland as a part of Integrated Operational Program for Regional Development, ZPORR, Activity 2.6 "Regional Innovation Strategies and Knowledge Transfer" of Kuyavian-Pomeranian Voivodeship in Poland (2008-2009).

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