Random geometric graphs and their applications in neuronal modelling

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by Fioralba Ajazi

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and
Doctor in Science and Information System
Thesis advisors:
Prof. Valérie Chavez,
and
Prof. Tatyana Turova
Faculty opponent: Tom Britton

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Random geometric graphs and their applications in neuronal modelling

Abstract

Random graph theory is an important tool to study different problems arising from real world. In this thesis we study how to model connections between neurons (nodes) and synaptic connections (edges) in the brain using inhomogeneous random distance graph models. We present four models which have in common the characteristic of having a probability of connections between the nodes dependent on the distance between the nodes. In Paper I it is described a one-dimensional inhomogeneous random graph which introduce this connectivity dependence on the distance, then the degree distribution and some clustering properties are studied. Paper II extend the model in the two-dimensional case scaling the probability of the connection both with the distance and the dimension of the network. The threshold of the giant component is analysed. In Paper III and Paper IV the model describes in simplified way the growth of potential synapses between the nodes and describe the probability of connection with respect to distance and time of growth. Many observations on the behaviour of the brain connectivity and functionality indicate that the brain network has the capacity of being both functional segregated and functional integrated. This means that the structure has both densely interconnected clusters of neurons and robust number of intermediate links which connect those clusters. The models presented in the thesis are meant to be a tool where the parameters involved can be chosen in order to mimic biological characteristics.

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Dedicated to
Leonardo and Axel

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List of publications

This thesis is based on the following papers:

Paper I Ajazi, F., *One-dimensional inhomogeneous random distance graph*, in format of manuscript, to be submitted, (2018).

Paper II Ajazi, F., Napolitano, G. M., Turova, T., *Phase transition in random distance graphs on the torus*, J. Appl. Prob. 54, 1278-1294 (2017).

Paper III Ajazi, F., Napolitano, G. M., Turova, T., Zaurbek, I., *Structure of a randomly grown 2d network*, BioSystems, 136, 105-112, (2015).

Paper IV Ajazi, F., Chavez-Demoulin, V., Turova, T., *Random distance network as a model of neuronal connectivity*, to be submitted (2018).

Popular summary in English

Random graphs theory has been an important tool to model and solve problems related to real world networks. Although those problems come from very different fields, such as for example social networks, electrical power grids, and Internet network, they share an important common feature such as a very large number of elements. Due to their large and intricate structures those problems have been first studied in terms of their elements (nodes) and connections between those elements (edges).

Very often the problems are so complicated that a complete description of the dynamics happening in the whole network is impossible. Hence there has been given a lot of attention to the local properties of the network such as how many nodes are involved in a process or how to estimate the probability that the elements of the network will interact with each other in order to produce a certain result.

In this thesis we will focus the attention on a particular category of neural network, i.e., a network which mimics the dynamics and the connectivity of neurons in the brain. The nodes of the network are representing neurons, while the edges connecting them are potential synaptic connections. We propose and analyse a random graph model which may predict synaptic formation of a network and formation of connected clusters which communicate with each other. In particular, in the resulted networks the probability of connections depends on the distance.

Random geometric graphs and their applications in neuronal modelling

1 Introduction

This thesis consists of four papers concerned with the study of random graph models which mimic potential synaptic connections between neurons in brain. The random graphs introduced here have as common features the dependence on the distance between the neurons, that is the probability that two neurons are connected depends on the distance (euclidean, or graph distance) between them.

In Paper I we introduce a model of an inhomogeneous random distance graph in one dimension. The graph presents some aspects of random geometric graph as in Penrose (1993) and Cheng and Robertazzi (1989), where if the distance between any two nodes is smaller than a certain threshold r then there is a connection with probability one, otherwise the probability of the connection is a function of the distance.

In Paper II the concept of dependence on the distance is extended for a model on a two-dimensional torus, as in Janson et al. (2015), where the probability of connection between two nodes decreases with respect to the distance. In Paper III and Paper IV we keep the influence on the distance between nodes and we also introduce the concept of growing connectivity in time. This growth is meant to be a simplified model for the

formation of potential synaptic connections between nodes. In particular, results on the structure of a randomly grown $2d$ network, and in Paper IV we study connectivity properties of neurons using theoretical tools and computational simulations.

2 Graph theory

Many of the basic definitions are taken from Bollobás et al. (2007), Van der Hofstad (2017), Gut (1999) and Shiryaev (1996). Many of the statements in the introduction of this thesis can be found with respective proofs in Van der Hofstad (2017).

Definition 1 (Graph)**.** *A graph G is an ordered pair of disjoint sets (V, E), where V is the set of n vertices and E is the set of edges s.t., $E \subseteq V \times V$ is formed by unordered pairs of elements of V indicated as $e_{i,j} = \{v_i, v_j\}$, for $v_i, v_j \in V$.*

We say that a graph is *directed* when E is an ordered, i.e., if $\{v_i, v_j\} \neq \{v_j, v_i\}$, otherwise the graph is called *undirected*. If $(v_i, v_j) \in E$ then we say that the vertices v_i and v_j are connected and we denote this by $v_i \sim v_j$. Given a vertex v_i, if there does not exist any edge connecting v_i with any other vertex of V, we call v_i an *isolated vertex*.

Definition 2 (Degree)**.** *Given a graph $G = (V, E)$, the degree $D(v_i)$ of a vertex $v_i \in V$ is defined to be the number of vertices connected with v_i directly by an edge, i.e.,*

$$D(v_i) = \sum_{j \neq i, j=1}^{n} \mathbf{1}_{\{v_i \sim v_j\}}$$

When the graph is directed we define the *in-degree* and *out-degree* of a vertex v_i respectively, as the sum of incoming edges and the sum of outcoming edges.

Definition 3 (Connected component)**.** *A connected component $\mathcal{C} = \mathcal{C}(G)$ of a graph G is a subgraph of G s.t., $\mathcal{C} = (V', E')$ with $V' \subset V$ and $E' \subset E$, where any two vertices in V' are connected to each other through a path*

and which is not connected to any other vertices of G. When the size of the connected component is of the order of the entire graph, then we call it a giant component*.*

We will now recall some important stochastic processes that are used to study some of the random graphs which will be presented later on in the thesis. We will refer mainly to the definitions and results presented in Gut (1999).

In general a stochastic process with state S is a collection of random variables $\{X_t : t \in T, T \subseteq \mathbb{R}\}$, which are defined on the same probability space $(\Omega, \Sigma, \mathbb{P})$, where T is called the parameter set. If $T = \mathbb{N}$ then the process is said to be a discrete parameter process, while if $T = \mathbb{R}$ then it is a continuous process.

Definition 4 (Poisson process)**.** *A Poisson point process is a continuous parameter stochastic process $\{X(t), t \geq 0\}$, where $X(t)$ is the number of occurrences in $(0, 1]$, where:*
(i) $X(0) = 0$ a.s.,
(ii) the increments $X(t_k) - X(t_{k-1})$, for $k = 1, \ldots n$, are independent r.vs., for all $t_0 \leq \ldots, t_n$, with $t_i \in \mathbb{R}$, for all $n \geq 0$,
(iii) there exist $\lambda > 0$ s.t., $X(t) - X(s) \sim \text{Po}(\lambda(t-s))$, for all $s < t$, where λ is defined as the intensity of the process.

Let T_k be the time of the k-th occurrence of the Poisson point process $X(t)$. Let $\tau_k := T_k - T_{k-1}$ be an interval between two consecutive occurrences for any $k \in \mathbb{N}^+$. Then $\{T_k \leq t\} = \{X(t) \geq k\}$ and the following results hold:
(i) for all $k \in \mathbb{N}^+$, τ_k are i.i.d r.v, distributed as $\text{Exp}(1/\lambda)$,
(ii) for all $k \in \mathbb{N}^+$, T_k are r.v. distributed as $\Gamma(k, 1/\lambda)$.

We then introduce a stochastic process defined as a *branching process*, which is frequently used to investigate the size of connected components in random graphs. A branching process is a model for describing how a population evolves in time, or in the case of random graphs, how a graph connectivity evolves. We suppose that each individual, independently from each other, generates a random number of successors with the same offspring distribution $\{p_i\}_{i=0}^{\infty}$ where $p_i = \mathbb{P}(\text{individual has } i \text{ successors})$. Let X be a r.v. with probability function $(p_i)_{i \geq 0}$. We denote Z_j as the number of individuals in the j-th generation s.t,

$$Z_0 = 1,$$
$$Z_j = \sum_{i=1}^{Z_{j-1}} X_{j,i},$$

where $\{X_{j,i}\}$ is a double array of i.i.d. random variables. The offspring distribution of $X_{j,i}$ is the same as for X and we indicate it as $X_{j,i} \sim X$ for all j, i.

One of the most relevant results on branching processes is that when the expected value of X is smaller or equal than 1 then the populations dies out with probability 1, while when $\mathbb{E}(X) > 1$ there is a non-zero probability that the population will survive. More precisely, define $\eta = \mathbb{P}(\exists j : Z_j = 0)$ to be the probability of extinction. The following result, from Gut (1999), holds.

Theorem 1. *Given a branching process with offspring distribution X, and given G_X the probability generating function of X, i.e, $G_X(s) = \mathbb{E}(s^X)$, the following results hold.*
(i) The extinction probability η satisfies the equation $\eta = G_X(\eta)$.

(ii) η is the smallest non negative root of the equation $\eta = G_X(\eta)$.

(iii) $\eta = 1$ for $\mathbb{E}(X) \leq 1$ and $\eta < 1$ for $\mathbb{E}(X) > 1$.

Given T the total progeny of the branching process defined as $T = \sum_{j=0}^{\infty} Z_j$ then the following result holds.

Theorem 2. *Given a branching process with i.i.d offspring X and with probability generating function $G_X(s)$, the probability generating function of the total progeny T is given by*

$$G_T(s) = sG_X(G_T(s)).$$

Let X_i be independent random variables for any $i \geq 1$, with the same distribution as $X_{1,1}$. Then we define the following recursion

$$S_0 = 1$$
$$S_i = S_{i-1} + X_i - 1 = X_1 + \ldots, + X_i - (i-1).$$

Let T be the minimum t for which $S_t = 0$, i.e.,

$$T = \min\{t : S_t = 0\} = \min\{t : X_1 + \cdots + X_t = t - 1\},$$

when T does not exist then we define $T = \infty$.

The above recursion can be now read in terms of the exploration process of a connected component. Given a connected component $\mathcal{C}(v)$ containing the vertex v in graph G, we start to explore the vertices as follows. During the explorations the vertices have three different status: *active*, *neutral* or *inactive*. The status of the vertices will change during the exploration of the connected component according to the following rules. At time $t = 0$ the only active vertex is v and all the other vertices are neutral, then we set $S_0 = 1$. At time t, we choose an active vertex w in an arbitrary way and we explore all the edges (w, u) where u runs all over the neutral vertices. If there is a neutral vertex u s.t., it is connected with the active vertex w, and we say that u has become active, otherwise it stays neutral. After we have searched all the set of neutral vertices connected to w, we set w to be inactive and we set S_t to be equal to the new number of active vertices at time t.

When there are no more active vertices left, i.e., when $S_t = 0$ the process then terminates and $\mathcal{C}(v)$ is then the set of all the inactive vertices with cardinality $|\mathcal{C}(v)| = t$.

In the previous recursion the variable X_t is the number of vertices that become active after the exploration of the t-th vertex, while the t-th vertex becomes inactive. Then $S_t = S_{t-1} + X_t - 1$ represents the number of active vertices after the exploration of t vertices.

Another important measure which characterizes random graphs, and real world networks, is the clustering coefficient. This measure represents how probable in a network that two nodes share a connection, are connected with each other.

Given an undirected graph $G = (V, E)$, with $|V| = n$ we define

$$W_G = \sum_{1 \le i,j,k \le n} \mathbf{1}_{\{ij,jk \in E\}},$$

which is equal to two times the number of open triples as follows. The

factor two comes from the fact that in undirected graphs W_G counts each edge twice as (i, j) and (j, i).

Moreover we define

$$\Delta_G = \sum_{1 \le i,j,k \le n} \mathbf{1}_{\{ij, ik, jk \in E\}},$$

which is equal to six times the number of triangles in G.

Then we define $CC(G)$, the clustering coefficient of G, as the ratio of the number of triangles to the expected number of open triples, i.e.,

$$CC(G) = \frac{\mathbb{E}\, W_G}{\mathbb{E}\, \Delta_G}.$$

When G is a directed graph the computation of the clustering coefficient can be found in Fagiolo (2007), and in Rubinov and Sporns (2010). In particular in Rubinov and Sporns (2010) we can find a list of typical measures of network analysis for both directed and undirected networks.

3 Random graphs

In this section we will briefly introduce the main definitions and some of the main properties of the most known random graph models such as the classic random graph $G(n, M)$ and $G(n, p)$ presented by Erdős and Rényi (1960), the small world network introduced by Watts and Strogatz (1998) and Newman (2000), and the geometric random graph by Penrose (1993) and a model in between percolation and classic random graph by Turova and Vallier (2006), and Turova and Vallier (2010). Many of the statements can be found with respective proof also in Van der Hofstad (2017).

3.1 Erdős-Rényi random graph

Definition 5. *The classic Erdős-Rényi random graph $G(n, p)$ is the graph defined on a set of vertices $V = \{1, \dots, n\}$, where an edge between any two*

vertices is present independently with probability p, and is missing with probability $1-p$. The graph is equivalently denoted as $G(n, \lambda/p)$ where λ is a positive constant.

The degree distribution of $G(n,p)$ follows a Binomial distribution $\mathrm{Bin}(n-1,p)$, i.e., for any given $v \in V$,

$$\mathbb{P}(\mathrm{D}(v) = k) = \binom{n-1}{k} p^k (1-p)^{n-k}.$$

An important aspect studied for random graphs is the presence of connected components and the evolution of their size with respect to the increasing number of nodes in the graph. In particular the threshold of the size of the giant component in $G(n,p)$ has been studied intensively. Here we report the main result.

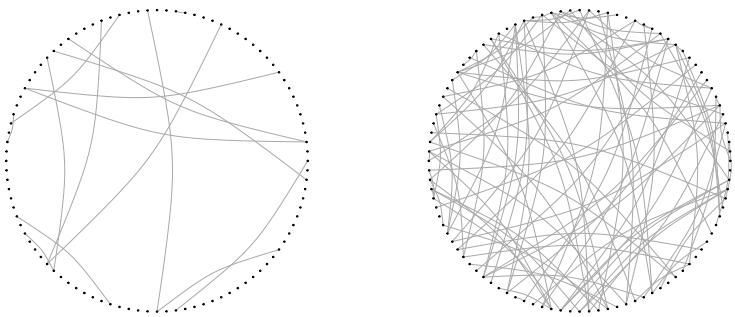

Figure 1: On the left is reproduced a realization of $G(100, 1/300)$ and on the right $G(100, 1/50)$.

Theorem 3 (Erdős-Rényi, (1960))**.** *Let $p = \lambda/n$, where $\lambda > 0$ is a constant.*

If $\lambda < 1$, *then*

$$\frac{|C_1|}{\log n} \xrightarrow{p} \frac{1}{1-\lambda-\log\lambda},$$

If $\lambda > 1$ *then*

$$\frac{|C_1|}{n} \xrightarrow{p} \beta(\lambda)$$

where $\beta = \beta(\lambda) \in (0,1)$ *is the unique solution of*

$$\beta(\lambda) + e^{-\lambda\beta(\lambda)} = 1.$$

The proof can be seen in Erdős and Rényi (1960). A characteristic which makes $G(n,p)$ not very suitable to model real world networks is the presence of low clustering coefficient. Indeed the clustering coefficient of $G(n,p)$ is $CC(G(n,p)) = \lambda/n$, which is relatively small with respect to the clustering computed on real networks Watts and Strogatz (1998).

3.2 Scale-free and small-world random graphs

Real world networks are in general complex networks with a very high dimension. Although they all have high numbers of vertices, they are mostly *sparse* networks, i.e. their degree is low with respect to the maximum possible degree. Real world network moreover are formed by considering growing precesses, as for example the collaboration network, which grows in size as time increases. Let G_n be a random graph. For any n the proportion of nodes with degree k in G_n is given by

$$P_k(n) = \frac{1}{n}\sum_{i=1}^{n} \mathbf{1}_{\{D_i^{(n)}=k\}}$$

where $D_i^{(n)}$ is the degree of the vertex i for all $i = \{1\ldots,n\}$. Then $\{P_k^{(n)}\}_{k=0}^{\infty}$ is called the *degree sequence* of G_n.

We then formalise the definition of a graph being sparse.

Definition 6. *A random graph sequence* $\{G_n\}_{n=0}^{\infty}$ *is sparse when* $\lim_{n\to\infty} P_k(n) = p_k$, *for some deterministic limiting probability distribution* $\{p_k\}_{k=0}^{\infty}$.

We can then define the property of being *scale-free* as follows.

Definition 7. *A random graph process* $\{G_n\}_{n=0}^{\infty}$ *is defined to be scale-free with exponent* τ *if it is sparse and if there exists* τ *s.t.,*

$$\lim_{k\to\infty} \frac{\log p_k}{\log(1/k)} = \tau.$$

A scale-free random graph process has a degree sequence that converges to a limiting probability distribution which has an asymptotic power-low tail.

We then define the property of a graph process as being small-world. The main characteristics of small-world networks is both the presence of a small geodetic distance and high clustering coefficient (see the results presented by Watts and Strogatz (1998) and Newman (2000)).

Let H_n be defined and the *typical distance* of G_n, as the graph distance between two uniformly chosen vertices from within a connected component of G_n. We define the general property as being small-world as follows.

Definition 8. *A random graph process* $\{G_n\}_{n=0}^{\infty}$ *is called a "small world"when there exists a constant* K *such that,*

$$\lim_{n\to\infty} \mathbb{P}(H_n \leq K \log n) = 1.$$

This indicates that the distance between nodes increases slowly as a function of the number of nodes in the network compared to the maximum possible which is of order n.

Watts and Strogatz (1998) described the classic model of building a graph G_n with the small-world property as follows.

The n nodes are placed in a ring, as in Figure 2, and m is defined to be the number of the neighborhood within which the vertices of the lattice will be connected ($m/2$ per side). Then p is set as the probability of an edge between any two pair of vertices v_j and v_j to be rewired randomly from v_j to any other node different from v_j. This means that when $p = 0$ the graph is the original G_n while for $p = 1$, we obtain a random graph $G(n, p)$.

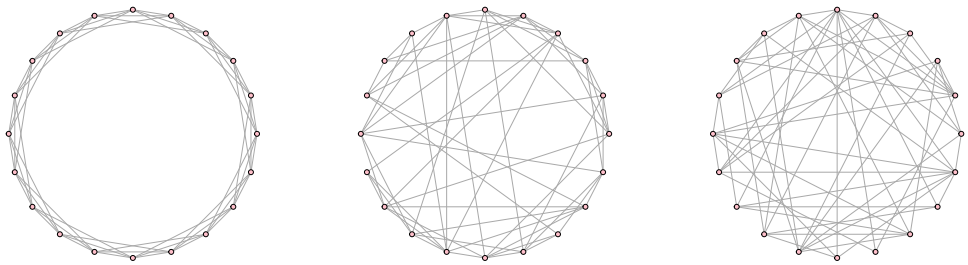

Figure 2: On the left is reproduced a realization of G_n with$n = 20$, $m = 6$ and rewiring probability 0, while in the middle and on the right the rewiring probabilities are 0.3 and 1 respectively.

3.3 Random geometric graphs

In the following section we briefly introduce the basic concepts and results of random geometric graphs (RGG) from Penrose (1993). We will primarily focus on the result on two-dimensional case although in Penrose (1993) we can find general results on the d dimensional case with $d \geq 1$. RGG have been a fundamental tool in developing solutions for wireless networks (see the results by Cheng and Robertazzi (1989), **?**, Gupta et al. (2008) and Gupta and Iyer (2010)).

Definition 9. *The random geometric graph $G(n, r)$ is defined on the set of vertices with cardinality n distributed in $[0, 1]^2$ independently and uniformly at random, such that a connection between any two pairs of vertices v_i and v_j is present with probability one if the distance between v_i and v_j is lower*

or equal than a given positive cut-off constant r, i.e., if $\| v_i - v_j \| \leq r$.

In Figure 3 we can see three simulated independent realizations of random geometric graphs with the same vertex set cardinality and three different radios of connectivity.

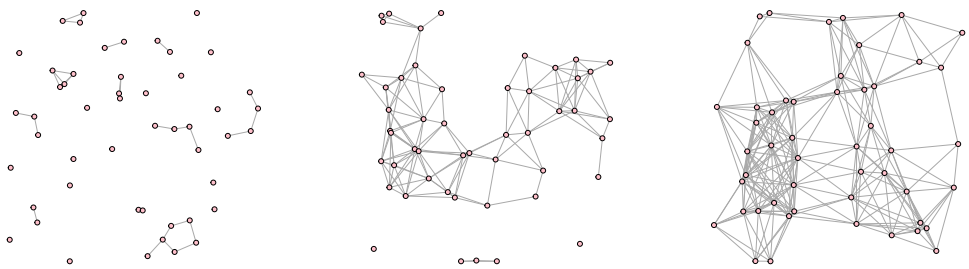

Figure 3: From left to right, computer independent realizations of three RGGs with $n = 50$, and radius 0.1, 0.2 and 0.3 respectively.

We recall that approximately the expected degree of a typical vertex is $n\pi r^2$. Hence the following result on the connectivity properties of $G(n, r)$ has been prove in Penrose (1993).

Theorem 4 (Connectivity of two-dimensional RGG)**.** *Let $(r_n)_n$ be a sequence of non negative numbers, and define $x_n = \pi n r_n^2 - \log n$, then*

$$\lim_{n\to\infty} \mathbb{P}(G(n, r_n) \text{ is connected}) = \begin{cases} 0 & \text{if } x_n \to -\infty \\ e^{-e^{-x}} & \text{if } x_n \to x \in \mathbb{R} \\ 1 & \text{if } x_n \to \infty \end{cases}$$

The following theorem describes the results regarding the threshold for the formation of the largest connected component as n goes to infinity.

Theorem 5 (Largest connected component)**.** *Let $\mathcal{C}_\infty(G(n,r))$ be the size of the largest connected component. There exists a non-decreasing continuous function $f : [0,\infty) \to [0,1)$ such that the following holds. Given the sequence $(r_n)_n$ defined as $r_n = \sqrt{\lambda/\pi n}$, then*

$$\frac{\mathcal{C}_\infty(G(n,r))}{n} \to f(\lambda), \quad a.s.$$

Furthermore there exists a critical value $\lambda_c > 0$ such that, if $\lambda \leq \lambda_c$, then $f(\lambda) = 0$, while if $\lambda > \lambda_c$ then $f(\lambda) > 0$.

It is noteworthy that the exact values of λ_c and $f(\lambda)$ for the case $\lambda > \lambda_c$ are not known but have been experimentally computed where $\lambda_c \approx 4.51$.

3.4 Between percolation and classic random graph

In the original model of percolation theory (see the results presented by Grimmet (1999)), it is considered the d-dimensional integer lattice. Chosen a probability p, each edge of the graph $\mathbb{Z}^d$ is *open* with probability p and *closed* with probability $1-p$. It has been investigated the structural properties of the obtained random graph consisting on the vertex of $\mathbb{Z}^d$ together with the set of open edges.

In the infinite dimensional lattice it is investigated if with positive probability there is a connected component of open edges. In dimension 1 there is a critical value $p_c = 1$ such that if $p < 1$ the probability that a cluster has size greater than k decreases exponentially fast to zero. In higher dimensions only for $d = 2$ the value of the critical probability is exactly known and is given by $p_c = 1/2$. If $p < p_c$ then the lattice is composed of finite open clusters separated by infinite closed clusters. If $p = 1/2$ the main question whether the infinite cluster exists with positive probability, and if $p > 1/2$ whether there is an infinite open cluster and if with probability 1 it is unique.

In the d-dimensional case it is possible to obtain approximations of the critical parameter. In percolation models the percolation transition, due

to the critical probability, can be interpreted as the phase transition in classic random graphs. In both cases indeed the size of the largest connected component increases to reach the characteristics of a giant component which will contain a positive amount of vertex of the graph. The models are defined with a very consistent difference between each others. In the classic random graph model there is no definition of distance between the vertices while in percolation theory the structural geometric distances are fundamental for the definition of the connectivity structure. The connectivity created by the nearest neighbours in the lattice do not fit many real topological structures present in real world networks.

Consider for example the model of Turova and Vallier (2006), which captures the features of both the classic random graph model and percolation model; both connectivity properties are typical for real networks.

Definition 10. *Given a graph $G_N^d(p,c)$ on the set of vertices $V_N^d = \{1,\dots,N\}^d$ in $\mathbb{Z}^d$, the edges between any two pairs of vertex i and j are present independently with probability*

$$p_{i,j} = \begin{cases} p & \text{if } |i-j| = 1 \\ \frac{c}{N^d} & \text{if } |i-j| > 1, \end{cases} \tag{1}$$

where $0 \le p \le 1$ and $0 < c < N$ are constant.

Hence the graph $G_N^d(p,c)$ is a mixed model between a random graph model where any vertex is connected to another vertex with probability $\frac{c}{N^d}$, and a percolation model where each pair of neighbours of $\mathbb{Z}^d$ is connected with probability p.

Turova and Vallier (2006) proved a phase transition along both parameters c and p when the dimension of the lattice is 1. Suppose that p is fixed, then there exists a critical value $c_{cr}(p)$ given by the following relation

$$c_{cr}(p) = \frac{1-p}{1+p},$$

such that if $c < c_{cr}(p)$ the size of the largest connected component $\mathcal{C}_1(G_N^d(p,c))$ is of order $\log N$ with probability tending to 1 as N goes to infinity. If

$c > c_{cr}(p)$ then the size of $\mathcal{C}_1(G_N^d(p,c))$ increases until it includes a positive part of the entire graph and it is such that

$$\frac{|\mathcal{C}_1(G_N^d(p,c))|}{N} \xrightarrow{p} \beta,$$

as $N \to \infty$, where $\beta = \beta(p,c)$ is defined to be the maximal solution of

$$\beta = 1 - \frac{1}{\mathbb{E}(X)}\,\mathbb{E}(Xe^{-cX\beta}).$$

The result is extended for d-dimension in Turova and Vallier (2010). Let C_0 denote an open cluster containing the origin of $\mathbb{Z}$, in the bond percolation model, and let $B(N)$ be the box of length N. Then we have that the critical parameter is the following

$$c_{cr}(p) = \frac{1}{\mathbb{E}(C_0)}.$$

If $c < c_{cr}(p)$, set y to be the root of

$$\mathbb{E}(c|C_0|e^{c|C_0|y}) = 1,$$

and let $\alpha = \alpha(p,c)$ be defined as follows

$$\alpha = (c + cy\,\mathbb{E}(ce^{c|C_0|y}))^{-1},$$

then with probability tending to 1 as $N \to \infty$ we have

$$|\mathcal{C}_1(G_N^d(p,c))| \le \alpha \log|B(N)|.$$

If $c \ge c_{cr}$ it follows that

$$\frac{|\mathcal{C}_1(G_N^d(p,c))|}{B(N)} \xrightarrow{p} \beta,$$

as $N \to \infty$, where $\beta = \beta(p,c)$ is defined as the maximal solution of

$$\beta = 1 - \frac{1}{\mathbb{E}(X)}\,\mathbb{E}(Xe^{-c\beta|C_0|}).$$

The same result can be stated for the critical value p_{cr} of the probability p for fixed c. The phase transition can be proved along both critical values

$$c_{cr}(p) = \frac{1-p}{1+p} \quad \text{and} \quad p_{cr}(c) = \frac{1-c}{1+c}.$$

The proofs of Turova and Vallier (2010) are based particularly on the theory of inhomogeneous random graphs, which will be presented in the next section.

3.5 Inhomogeneous random graphs

Classic random graph models are considered to be *homogeneous* since the degree tends to be concentrated around a typical value. Many graphs based on real world models do not have always this characteristic. Then the model introduced in Bollobás et al. (2007) is very relevant, which could include the category of *inhomogeneous* random graphs. We start reporting a basic example (from Van der Hofstad (2017)) in order to have intuition into the idea behind the definitions which will follow and we report some of the main results on the degree distribution and the formation of a giant component.

Example 1 (9.25 of Van der Hofstad (2017))**.** *We start to define an inhomogeneous model as follows. We have a graph with n nodes where to each node has been assigned a characteristic called* type*, in a certain type space $\mathcal{S}$ (clearly when the nodes can have just two types is enough consider $\mathcal{S} = \{1, 2\}$). The space $\mathcal{S}$ can be both finite and infinite. We need to know how many individuals we have of a given type. This quantity is described in terms of a measure μ_n, where for every subset A of $\mathcal{S}$, $\mu_n(A)$ measures the proportion of nodes having a type $A \subseteq \mathcal{S}$. In this model, instead of vertex weights, the edge probabilities are defined through a* kernel *$\kappa : \mathcal{S} \times \mathcal{S} \to [0, \infty)$. Then the probability that two nodes of types x_1 and x_2, are connected is approximately $\kappa(x_1, x_2)/n$.*

We will now formalize the above terms. Let us write $G(n, p_{ij})$ to indicate the random graph on vertex set $V = \{1, \ldots, n\}$, where $i, j \in V$ are connected by an edge with probability $p_{i,j}$.

Definition 11 (Kernel)**.** *(i) A ground space is a pair $(\mathcal{S}, \mu)$, where $\mathcal{S}$ is a separable metric space and μ is a Borel probability measure on $\mathcal{S}$.*
(ii) A vertex space $\mathcal{V}$ is a triple $(\mathcal{S}, \mu, (x_n)_{n\geq 1})$, where $(\mathcal{S}, \mu)$ is the ground space and $(x_n)_{n\geq 1}$ is a random sequence of points in $\mathcal{S}$ s.t.,

$$\#\{i : x_i \in A\}/n \xrightarrow{p} \mu(A),$$

where $A \subseteq \mathcal{S}$ is a μ-continuity set.
(iii) A kernel κ on a ground space $(\mathcal{S}, \mu)$ is a symmetric non negative Borel measurable function on $\mathcal{S} \times \mathcal{S}$.

Moreover we need to set some necessary conditions for the kernels. Given $E(G)$ the number of edges in the inhomogeneous graph $G_n(p(\kappa)) = G(n, p(\kappa))$ we define the expectation of this number as $\mathbb{E}(E(G(n,\kappa)) = \sum_{i<j} p_{i,j}$, so the model has a bounded expected degree, i.e., when $1/n \sum_{i<j} p_{i,j}$ is bounded. Moreover the graph should not get decomposed in two disconnected components, that is the graph should be irreducible. Those considerations explain the introduction on the following conditions for the kernel.

Definition 12 (Graphical and irreducible kernels)**.** *A kernel κ is graphical if the following conditions hold:*
(i) κ is continuous a.e. on $\mathcal{S}$,
(ii) The following integral is finite

$$\int\int_{\mathcal{S}} \kappa(x,y)\mu(dx)\mu(dy) < \infty,$$

(iii)

$$\frac{1}{n}\,\mathbb{E}(E(G_n(p(\kappa)))) \to \frac{1}{2}\int\int_{\mathcal{S}} \kappa(x,y)\mu(dx)\mu(dy),$$

Similarly the definition can be applied for a sequence of kernels (κ_n) which is set to be graphical with limit κ when if $y_n \to y$ and $x_n \to x$, than $\kappa_n(y_n, z_n) \to (y, x)$, where κ satisfies (i) and (ii) and

$$\frac{1}{n}\,\mathbb{E}(E(G_n(p(\kappa_n)))) \to \frac{1}{2}\int\int_{\mathcal{S}} \kappa(x,y)\mu(dx)\mu(dy).$$

A kernel κ is called reducible if

$$\exists A \subseteq \mathcal{S} \quad with \quad 0 < \mu(A) < 1 \quad such\ that \quad \kappa = 0 \quad a.e.\ on \quad A \times (\mathcal{S} \setminus A),$$

otherwise the kernel is irreducible.

We now introduce the main result of the degree sequence of $G_n(p(\kappa))$.

Theorem 6 (Degree sequence of IRG)**.** *Let (κ_n) be a graphical sequence of kernels with limit κ. For any fixed $k \geq 0$, set N_k to be the number of nodes with degree k then,*

$$\frac{N_k}{n} \xrightarrow{p} \int_{\mathcal{S}} \frac{\lambda(x)^k}{k!} e^{-\lambda(x)} \mu(dx),$$

where for any given type x the function $x \to \lambda(x)$ is defined as

$$\lambda(x) = \int_{\mathcal{S}} \kappa(x, y) \mu(dy).$$

Equivalently

$$\frac{N_k}{n} \xrightarrow{p} \mathbb{P}(\Xi = k),$$

where Ξ has a compound Poisson distribution with distribution F_λ given by

$$\mathbb{P}(F_\lambda \leq x) = \int_0^x \lambda(y) \mu(dy).$$

This proves that the degree of a given type x is asymptotically Poisson with mean $\lambda(x)$. The distribution for the degree of a (uniformly chosen) random vertex of $G_n(p(\kappa))$ has a compound Poisson distribution.

Let Λ be a r.v., $\lambda(U)$ where U is a r.v, on $\mathcal{S}$ with distribution μ. Let $N_{\geq k}$ be the number of vertices with a degree at least k, and let D be the degree of a randomly chosen vertex of $G_n(p(\kappa_n))$. From the considerations on the degree distribution it follows the next corollary on the distribution of the tails for the degree sequence.

Corollary 1. *Let (κ_n) be a graphical sequence of kernels with limit κ. Suppose that $\mathbb{P}(\Lambda > t) = \mu\{x : \lambda(x) > t\} \sim at^{-(\tau-1)}$ as $t \to \infty$ for some $a > 0$ and $\tau > 2$. Then*

$$\frac{N_{\geq k}}{n} \xrightarrow{p} \mathbb{P}(\Xi \geq k) \quad \text{for } k \text{ fixed, as } n \to \infty$$

and

$$\mathbb{P}(\Xi \geq k) \sim ak^{-(\tau-1)} \quad \text{for } k \to \infty.$$

As for the exploration of the connected components in homogeneous graphs, also the connectivity of inhomogeneous random graphs can be studied by the use of branching processes. In particular for the inhomogeneous model we will use a multitype branching process, i.e. a branching process which keeps track of the type of each vertex explored. The complete description of the process can be found in Van der Hofstad (2017) and for general theory on multitype branching process see Athreya and Ney (1972). Here will be presented the multitype branching process with Poisson offspring distribution, followed by the main results on the phase transition of inhomogeneous random graphs. For complete proofs we suggest to read as well Bollobás et al. (2007).

A multitype Poisson branching process with kernel κ is defined as it follows. Every individual of type $x \in \mathcal{S}$ is replaced in the next generation by a set of successor distributed as a Poisson process on $\mathcal{S}$ with intensity $\kappa(x, y)\mu(dy)$. Then the number of successor with type in $A \subseteq \mathcal{S}$ has as well a Poisson distribution with mean $\int_A \kappa(x, y)d(\mu y)$.

Let $\zeta_\kappa(x)$ be the survival probability of the Poisson multitype process, starting from the original individual of type $x \in \mathcal{S}$. Then the survival probability is defined as it follows

$$\zeta_\kappa = \int_{\mathcal{S}} \zeta_\kappa(x)\mu(dx).$$

Given the linear operator $\mathbf{T}_\kappa$ defined for $f : \mathcal{S} \to \mathbb{R}$ as

$$(\mathbf{T}_\kappa f)(x) = \int_{\mathcal{S}} \kappa(x, y)f(y)\mu(dy),$$

where f is any measurable function s.t., the integral is defined a.e., for $x \in \mathcal{S}$.

The survival probability $\zeta_\kappa > 0$ if and only if $\|\mathbf{T}_\kappa\| > 1$.

The norm of the operator can be defined as follows

$$\|\mathbf{T}_\kappa\| = \sup\{\|\mathbf{T}_\kappa f\|_2 : f \geq 0, \|f\|_2 \leq 1\} \leq \infty.$$

We also define Φ as a non linear operator as

$$(\Phi_\kappa f)(x) = 1 - e^{(\mathbf{T}_\kappa f)(x)}, \quad x \in \mathcal{S}.$$

Then it is shown that the function ζ_κ is the maximal fixed point of the non linear operator Φ_κ.

Hence the following theorem on the presence of a giant component in inhomogeneous random graphs holds.

Theorem 7. *Given the sequence of irreducible graphical kernels (κ_n), with limit κ, let $\mathcal{C}_1$ denote the largest connected component of the inhomogeneous random graph $G_n(p(\kappa_n))$, the following convergence holds:*

$$\frac{|\mathcal{C}_1|}{n} \xrightarrow{p} \zeta_\kappa,$$

in all cases when $\zeta_\kappa < 1$, while $\zeta_\kappa > 0$ exactly when $\|\mathbf{T}_\kappa\| > 1$.

4 Complex brain network

In this section we discuss the complex topological and functional structure of the brain. In particular we see how tools of random graph theory have been applied to obtain a better understanding of one of the most complicated systems.

In general the nodes in brain network structures represent brain regions, while the link between them can represent anatomical or functional connections (see the results presented by Bullmore and Sporns (2009) and Rubinov and Sporns (2010)). The activities happening in the brain are usually divided into two categories, one related to a *structural brain network* and another that creates a *functional brain network*.

In Figure 4 we can see a schematic representation of how these structures are extrapolated by experimental techniques. In Bullmore and Sporns (2009) one can find a detailed description of each steps taken to obtain the two structures. Let us briefly present those steps.

The first step consists in defining the network nodes to be considered for the analysis. For the description of a structural network this is done by anatomical parcellation, while for functional networks it is done by using recording sites which will map the transmission of signals between the selected nodes.

The secondary step estimates a continuous measure associated with the nodes. The third step generates an associated matrix by coupling all pairwise associations obtained between the nodes. Applying a threshold to every element of the matrix yields an adjacent matrix and the corresponding (usually undirected) graph. This threshold will highly influence the connectivity description of the two networks, hence several thresholds will be taken into consideration in order to have a more realistic reproduction of the feature of the real brain section selected. At the fourth step both structural and functional network properties can be investigated by graph theoretical analysis.

The main tools that are used to test the resulting networks are the degree distribution, the assortativity index, the clustering coefficient, the average shortest path length and modularity Stam and Reijneveld (2007). The values of many network measurements are very much influenced by the

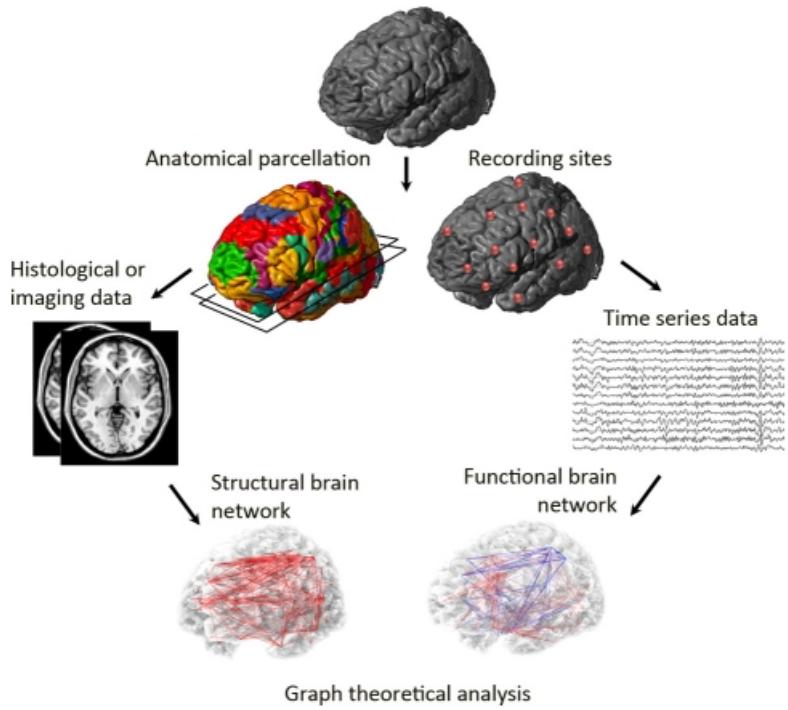

Figure 4: Graph analysis to brain networks. Structural (including either gray or white matter measurements using histological or imaging data) or functional data (including resting-state fMRI, fMRI, EEG, or MEG data) is the starting point. Nodes are defined (e.g., anatomically defined regions of histological, MRI or diffusion tensor imaging data in structural networks or EEG electrodes or MEG sensors in functional networks) and an association between nodes is established (coherence, connection probability, or correlations in cortical thickness). The pairwise association between nodes is then computed, and usually thresholded to create a binary (adjacency) matrix. A brain network is then constructed from nodes (brain regions) and edges (pairwise associations that were larger than the chosen threshold). Scientific Figure on ResearchGate available from researchgate.net/Graph-analysis-to-brain-networks-Structural-including-either-gray-or-white-matterfig2_221792911

basic structure of the network itself, hence the significance of a network statistics should be established by comparing the result with a null hypothesis network. In general the null hypothesis network is considered to be the classic random graph model where the numbers of edges and vertices are taken to be the same as the network to be tested.

Often real networks have a high clustering coefficient (CC) with respect to the corresponding $G(n, m)$ model, while the average shortest path (L) results to be in both cases being very small Sporns et al. (2002).

In Table 1, some known measurements are reported on the clustering coefficient and the average shortest path length (from Sporns et al. (2002), Rubinov and Sporns (2010) and Bullmore and Sporns (2009)).

Table 1: In the table are reported clustering coefficient CC, average shortest path length L and number of nodes N of the respective neural networks of known neural networks are reported. The values come from Sporns et al. (2002), Hilgetag et al. (1996).

Network	N	CC	L
C. Elegans	232	0.28	2.65
in vitro neural network	240	0.113	17.58
Macaque visual cortex	32	0.59	1.69
Macaque cortex	73	0.49	2.18
Cat cortex	35	0.60	1.79

In particular from Sporns et al. (2002) we can also compare the computation done for the clustering coefficient in the specific case of the Macaque visual cortex with respect to the analogous random graph model. The first network has $CC = 0.59$, while the random graph model has $CC = 0.32$. The anatomical brain connectivity structure studied until now indicates that this structure has the opposite characteristic of being both *functional segregated* and *functional integrated* Tononi et al. (1994). This means that the anatomical network combines the co existence of densely interconnected groups (clusters) with a robust number of intermodular links. The first random graph models that captured both these features are small-world networks. Since then, many other models theoretically (from Voges et al. (2010), Sporns et al. (2002), and Kozma and Puljic (2015)), and experimentally, (from Van Ooyen et al. (2014) and Stepanyants and Chklovskii (2005)), have been developed using ad hoc growing random networks which mimic the main characteristics of neuronal connectivity.

5 Main results of the research papers

5.1 Paper I

In Paper I we introduce an inhomogeneous random distance graph $G_T(c(T), \alpha)$ on an interval $[0, T] \in \mathbb{R}$. The vertex set V is given by a Poisson process with intensity λ, i.e., every vertex v corresponds to an occurrence time of this process. We assume that the probability of connection between any two nodes v_i and v_j depends on the distance between them. More precisely if $|v_j - v_i| \leq r$ then we set an edge between them, while if $|v_j - v_i| > r$ then we assigned the probability of connections to be

$$p_{v_i v_j} = c(T)/|v_i - v_j|^{\alpha},$$

where $r > 0$, $\alpha \geq 0$, and $c(T) \geq 0$ are the parameters of the model.

Observe that even in the particular case where $c(T) = 0$, the resulting model is an example within a class of random geometric graphs (RGG). Other models in this class were previously introduced and studied by Penrose (1993), Gupta and Kumar (1998) and Cheng and Robertazzi (1989). Many of the properties of RGG have applications in the fields of cluster analysis and wireless networks as i.e., in the studies of Gupta and Kumar (1998) and Cheng and Robertazzi (1989).

In Section 4.1 (Paper I) we investigate clustering properties of the subgraph induced by the short connections only. More precisely we define $X_i = X_i(T)$ to be the number of vertices in the i-th connected component (or cluster), and we let $N(T)$ be the total number of clusters. We denote the resulting graph $\tilde{G}_T(N(T), \alpha)$.

First we prove that the distribution of the size of a single cluster X_1 converges as T goes to infinity to the Geometric distribution with parameter $e^{-\lambda r}$. Then for a fixed number of clusters K we prove that as $T \to \infty$ the distribution of $(X_1, \ldots, X_K)$ converges to a distribution of a vector of i.i.d entries distributed as $\mathrm{Ge}(e^{-\lambda r})$.

We also derive the Law of Large Numbers for $N(T)$. More precisely we prove that the averaged number of clusters, i.e., $N(T)/T$ converges in L_1 and *a.s.* to a constant as T goes to infinity and we find this constant.

In Section 4.2 we consider every cluster X_i as a macrovertex i, and we define a new vertex set consisting on these macrovertices: $\hat{V} = \{1, \ldots, N(T)\}$. Then we also define a new graph $\hat{G}(\mathbf{X})$ on the vertex set $\hat{V}$, this time considering long range connections. We say that two macrovertices i and j are connected if there is at least one long range edge between two vertices belonging to these two macrovertices. Hence, the probability of this event is given by

$$\mathbb{P}(i \sim j) = 1 - \prod_{x,y}(1 - \frac{c(T)}{|x-y|^{\alpha}}),$$

where the product runs over all pairs of vertices (x, y) with x belonging to the i-th cluster and y belonging to the j-th cluster. We found approximated lower and upper bounds for this probability (see Corollary 1).

To study the degree distribution of $\hat{G}(\mathbf{X})$ we approximate the distance between vertices in the pairs (x, y) in the above formula.

This investigation led us to a definition of another RGG model (defined in Section 4.3) where the probability of edges is inspired by the bounds found for our original model (Corollary 1).

For the latter model we found for which values of $c(T)$ and α the degree distribution converges to a Poisson with constant parameter. This result allows us to approximate the degree of $\hat{G}(\mathbf{X})$ by a certain compound Poisson distribution (see Section 4.3).

We leave the question of the general connectivity of the model for the future work.

5.2 Paper II

We consider a model of a graph embedded in a two-dimensional torus. Again we assume that the probability of the connections decays with the distance between nodes as in Ajazi et al. (2015). The paper is inspired by the work of Janson et al. (2015), which introduces a model useful for studying the dynamics and the structure of the neuropil, the densely connected neural tissue of the cortex.

We consider a random distance graph G_N with vertex set V_N defined on a two dimensional discrete torus with probability of connection between any

two vertex u, v given by

$$p(u,v) = \min\left\{c\frac{W_u W_v}{Nd(u,v)}, 1\right\},$$

where W_v, $v \in V_N$ i.i.d copies of a r.v. W.

We study the size of the largest connected component. This can possibly help to understand the propagation of impulses through the network. In the study of neuronal network the parameters which influence the connectivity of the system change in time due to synaptic plasticity. Hence it is important to know the scaling of the largest connected component in order to control parameters responsible for the global connectivity.

We use the theory of inhomogeneous random graph (IRG) by Bollobás et al. (2007) to investigate the phase transition of G_N. Random distance graphs are not often studied by using IRG theory since they are mostly out of the rank-1 case. From the IRG theory we can derive the critical parameter for the formation of the giant component and also compute the size of the giant component in the supercritical case.

The subcritical phase presented in Theorem 1 is perhaps the first such result for non rank-1 case. To prove Theorem 1 we use the methods of the breadth-first search (see, e.g., Van der Hofstad (2017)) taking in to account the geometry of the graph in the exploration of connected components.

Although the random distance graph G_N is intrinsically different from the classic random graph model $G(n,p)$ proposed by Erdős and Rényi (1960), in Theorem 1 and Theorem 2 we prove that the asymptotic of the giant component of G_N is the same as in $G(n,p)$ where p is a certain function of c. This means that in the subcritical phase we have many relatively small connected components with a size of order $\log N^2$, while in the supercritical case with a high probability there is a unique giant component which includes a certain fraction of all nodes.

We do not prove, but we make a conjecture that even in the critical case G_N behaves similar similar to $G(n,p)$.

5.3 Paper III

We introduce a model which mimics the formation of synaptic-dendritic connections between neurons. The model shows how the probability of connections depends on the distance between the nodes.

The goal of our study is to describe the graph properties of a network (as e.g., probability of connections, and degree distribution) composed of randomly grown 2D neurites, which are represented by the soma together with a random tree of potential connections. Our model is a simplified version of the one proposed by Van Ooyen et al. (2014). Van Ooyen et al. (2014) models the branching of axonal tree and dendritic tree in time taking into account empirical parameters.

We assume that the nodes $v \in V$ which represent the locations of neurons are distributed according to a Poisson process with intensity μ on a square $\Lambda = [0, D] \times [0, D]$. At time $t = 0$ the network is formed by only disconnected neurons, while as $t > 0$ an initial segment grow out of every v with a randomly chosen direction and constant speed. The initial segment splits in two independent branches at a random time τ exponentially distributed with parameter $1/\lambda$. The branches are independent and start to grow a segment with the same manner as the initial branch. This creates for any node $v \in V$ a randomly growing branching tree $T_v(t)$, with spatial distribution defined by the random parameters μ, λ and t.

In Section 2.2 we define the formation of edges in the network. We derive the probabilities of these edges. These probabilities provide a complete description of the network. We find that the dependence on the distance is not monotone. Hence our model provides some theoretical explanation for the empirical results of R. Perin (2011).

In Section 3.1 we investigate the degree distribution, in particular we show that the degree is Poisson distributed with a parameter depending on the length $L_v(t)$ of a tree $T_v(t)$. We compute the moment generating function of $L_v(t)$ (see Proposition 3.1). This result allows us to approximate the tail of degree and show that it is approximately exponential.

In Section 3.2 we study the probability of connection between two neurons depending on time and distance. We prove that this probability satisfies certain integral equation. In Section 3.3 we study the marginal case of

this equation assuming $\lambda = 0$ (without branching). We obtain as well simulated results on the spatial density of the axonal arborization.

The paper is concluded with a discussion on the relevant applications.

5.4 Paper IV

We describe the network properties of the model introduced in Paper III. Our main goal is to describe the network properties as e.g., in and out degree, frequency of connections, average shortest path and clustering coefficient.

There are just few examples of randomly grown networks which are well understood analytically by now. Those networks are randomly grown classic graphs, graphs with preferential attachment and their modifications. Those models do not consider the space metric characteristics.

Experimental data (R. Perin (2011)) show the importance of the structure of connectivity and activation processes in the brain. In the last decades there has been active development of theory of random distance graphs (see Deijfen et al. (2013) and Penrose (1993)). Observe that the assumption of monotonicity and symmetry of connections is often considered to be a main characteristics. In this paper we argue that those assumptions should not be considered as invariant properties of the network. Indeed many experimental results (as e.g., Herzog et al. (2007) and Voges et al. (2010)) describe how the displacement of axonal fields can optimize the connectivity presents in the network.

We show how the geometrical properties of our model influence the probability of connections on space and on time. The results we provide are both analytical and computational. We use as a null hypothesis that the measurements are made on the classic random graph $G(n, m)$ model.

In Section 3.1 we study both the in-degree and the out-degree of a node. For the marginal case $\lambda = 0$, i.e., without branching. The maximum of those degrees exhibit the highest discrepancy between our model and the corresponding $G(n, m)$ model. When $\lambda > 0$ the branches growing from every nodes can expand until they cover the entire space. There are some particular time intervals where the properties of the network change

significantly.

In Section 3.2 we study the frequency of connection in order to prove how the connectivity changes in time and distance. We show that with respect to the increasing value of λ and time, the connectivity increase almost linearly before to reach a constant value. Moreover there is a particular distance where the connectivity reaches a maximum before to decay. In section 3.3 and 3.4 we show how the network has small-world characteristics. The presence of small average shortest path and high clustering coefficient, typical of small-warld networks, it is present in many neuronal networks as well (see e.g., Stepanyants and Chklovskii (2005) and Watts and Strogatz (1998)).

6 Conclusions and future development

In the last decade many measurements have become available for the study of topological and dynamical properties of complex networks. Advance studies have been made towards the understanding of brain disorders from a network prospective (see e.g., Dyhrfjeld-Johnsen et al. (2007)). Those are just some of the many reason why we believe that graph theory is an important framework for neuronal modelling (see Bullmore and Sporns (2009)).

It is well recognized that the key challenge for neuromodelling is to develop graph models with adequate representations of biological reality, as e.g., unambiguously assigning edge weights to the connections or interactions between the nodes (Fornit (2015)).

The aim of this study is to improve the architecture of neuronal network models, based on realistic connectivity patterns adapted from neuroanatomical observations. Therefore, we consider networks with both local connections and long-range edges. Our study was inspired by the experimental results on growing neural network analysed by R. Perin (2011), by the computational results of two-dimensional network presented by Van Ooyen et al. (2014) and by also the theoretical model presented by Janson et al. (2015). Here we describe formation of random connections in the network and derive their probabilities. The models predict when there is a formations of local and global connections and formation of a giant

component.

In this thesis we considered 2-dimensional network. Observe that is a known fact that axonal trees form essentially 2-dimensional structures Rolls (2016). Our analysis is amenable for the 3-dimensional case as well and is leave it as a open problem. Let us also mention here that a related 3-dimensional model of cylinder percolation was studied in Tykesson (2012).

Another direction for improvement modelling is to take into account both axon and denritic arborazation. Our approach should be useful to describe the axon-denritic connections as well, however the analogue of equation (4) in Paper IV will be more involved.

Finally we remark that the major challenge remain to check the impact of the macrostructures of connections that we derived here for the neurocomputations. Observe that despite the enormous amount of literature on use of random graphs there are practically no result showing advantage of random graph theory from neurocomputations. Some remarks on functioning of Hopfield neuronal network and bootstrap percolation can be found in Turova (2012).

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Paper I

One-dimensional inhomogeneous random distance graph

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Abstract

We introduce a model for an inhomogeneous random graph, where the probability of edges also depends on the distance between vertices. We investigate the degree distribution. We find for which parameters of the model the degree of a vertex converges in distribution as the size of a graph goes to infinity and we find the limiting distribution in some special cases.

1 Introduction

In the last sixty years random graphs have been an important tole to model and analyze many problems arising from real world networks [3], [4], [5]. In particular neural networks have been studied in terms of graph structures and functions in order to better understand the complicated mechanisms which are happening in the brain [10], [15]. In general a network is defined by a set of objects which are connected to each others in some fashion. In neural networks those objects represent neurons while the connections between them are synaptic and dendrite arborzations. The models based on random graphs theory, [13], [2], [1] focus the attention on the importance of the structural evolution of the system. The connectivity properties depend mostly on the distance between nodes. In [2], [1] it is shown how specific distances make behave the resulting network differently. In [11] we can see one example on how the growth of neural networks are simulated by computational tools (see for example NETMORPH or CX3D). Those programs study the characteristics of the connectivity of the network as a growing process based on a set of parameters simulated by experimental results.

The model described in this paper can be viewed as the basic case in one-dimension of the model developed in [17]. In [17] and [16], the phase transition on the giant component is studied. Here we analyze features as degree distribution and formation of clusters.

In particular, in our model if the nodes are at a distance smaller than a certain threshold r, then there is an edge with probability one, as in classic random geometric graph (RGG) (see [12], [6]), while if the distance is greater, the probability of connection is scaled by the distance itself.

In this paper we study initially the main characteristic of the clustering properties between the nodes considering only short connection smaller or equal than r as in [6]. We derive some results on the distribution of clusters. Then we incorporate long connections as well, and we use the clusters as macrovertices of the graph, to investigate the degree distribution.

2 The model

For any $\alpha \geq 0$ and $c(T) \geq 0$ we define $G_T(c(T), \alpha)$ to be a *random distance graph* on a set of vertices in $\mathbb{R}$ as it follows. For any $T > 0$, let $X(T)$ denote the Poisson point process with intensity λ, i.e. $X(T)$ has $Po(\lambda T)$ distribution. Let T_k, for $k \geq 1$, be the time of k-th occurrence and $\tau_k := T_k - T_{k-1}$ be the interval between two occurrence, with $T_1 = \tau_1$. Then the distribution of the intervals τ_k follows an $\text{Exp}(\frac{1}{\lambda})$ distribution, and T_k has a $\Gamma(k, \frac{1}{\lambda})$ distribution.

We say that at each $T_k \in \mathbb{R}$ we have a vertex, denoted by v_k, and we consider a random graph on this (random) set of vertices $\{v_1, \ldots, v_{X(T)}\}$. We assume that edges between different pairs of vertices v_i, v_j are independent and are given with probability

$$p_{v_i v_j} := \begin{cases} 1 & \text{if } |v_i - v_j| \leq r \\ c(T)/|v_i - v_j|^\alpha & \text{if } |v_i - v_j| > r, \end{cases} \tag{1}$$

where $r > 0$, $\alpha \geq 0$, and $c(T) \geq 0$ are the parameters of the model.

3 Related models

When we consider only the short connections happening with probability one between nodes at distance smaller then r, our graph is an example of RGG. In general the properties of RGG's have applications in fields like cluster analysis and wireless networks. We recall here some of the known properties when n nodes are uniformly distributed in unit circle as in [8]. It has been studied for which $r(n)$ the graph will be connected. In particular in [9] it is proved that for $r(n) = \sqrt{\frac{\log n + c(n)}{n}}$ the graph will be connected with probability that goes to one if and only if $c(n)$ goes to infinity as n goes to infinity.

Similar models on the same set of vertices as in our model, i.e. generated by a Poisson point process with intensity λ, on $[0, T]$, have been studied in [6]. Two nodes are connected with probability one if and only if the distance between them is smaller or equal than r. The paper is mainly focused on the critical transmission radii for which the connectivity between nodes in the first cluster is preserved. We can use the results of [6] to choose the minimum value of the product λr in order to have the highest percolation trough the graph. In [6] the sional case is studied as well.

In [10] and in [1] a model of random distance graph on two-dimensional discrete torus $\mathbb{T}^2 = (\mathbb{Z}/N\mathbb{Z})^2$ for $N \in \mathbb{N}, N > 1$ with vertex set $V_N = \{1, \ldots, N\}^2$ has been studied. In [10] the probability of connections between any two nodes u, v is given as it follows

$$p_{u,v} = c\frac{1}{Nd(u,v)^\alpha}, \tag{2}$$

where $d(u, v)$ is the graph distance.

The model has been studied for $\alpha = 1$, and dimension greater than one. In [10] the degree distribution and diameter have been studied. Moreover it has been defined an activation process where each vertex has two possible initial types, *excitatory* or *inhibitory*, and two possible states, *active* or *inactive*. While the types remain unchanged during the process, the states change according to some specific roles. A phase transition is proved considering the activation process of single type (excitatory) nodes. In [1] the probability of connection between two nodes u and v is given by

$$p_{u,v} = c\frac{W_u W_v}{Nd(u,v)}, \tag{3}$$

where W_u and W_v are weights associated with the nodes, $N^2 = |V|$ and $d(u,v)$ is the graph distance.

Our model can be included in the one-dimensional case of [1] as it follows. Let v_1 be the first vertex of a collection of all vertices $\{v_1, \dots, v_j\}$ such that $|v_{k+1} - v_k| \leq r$ for all $1 \leq k \leq j-1$ and $v_{j+1} - v_j > r$. Then we define the first cluster to be the collection of vertices $\{v_1, \dots, v_j\}$, and we say that the cluster has cardinality j. Consequently we define the other clusters in analogous way (see Figure 1 and Figure 2). We place the clusters on the one-dimensional discrete torus (Figure 4 (b)), where the weights of the nodes are given by the cardinalities of the macrovertices X_i, and the distance between any two macrovertices i and j is taken to be the minimum distance $d(i,j)$ with $d(i,j) > r$ such that $d(i,j) = d_T(|j-i|)$ where $d_T(i)$ is defined as

$$d_T(i) = \begin{cases} i & \text{if } i \leq T/2 \\ T - i & \text{if } i > T/2 \end{cases} \tag{4}$$

Then the probability of connection between i and j is given by

$$p_{i,j} = c(T)\frac{X_i X_j}{d(i,j)^\alpha}$$

From [1] we can investigate results on the largest connected component. Indeed from Theorem 1 of [1] for given $X_i \equiv X_j \equiv 1$ we can choose $c(T)$ such that the degree is of order constant, (see in section 4.3 details on the scaling of $c(T)$). Then we have to study for which α and $c(T)$ is it possible to apply the exploration process in order to have an analogous result of the two-dimensional case, where the asymptotic for the size of the largest connected component, in the subcrtical and supercritical case, is the same as in the classic Erdős-Rényi random graph.

4 Results

In this section we present the main results of the paper considering first just short connections and then taking into consideration the longest connections as well between clusters of nodes.

4.1 Random distance graphs on the vertices in $\mathbb{R}$.

Given $(0,T] \subseteq \mathbb{R}$, the vertices are generated by a Poisson process $X(T)$ with intensity λ. Recall that the set of vertices, or occurrences, is $V_T := \{v_1, \dots, v_{X(T)}\}$. We want to analyze the subgraph $\tilde{G}_T(N(T), \alpha)$ of $G_T(c(T), \alpha)$, where we consider only short edges between every pair of vertices v_i and v_j which are connected if $|v_i - v_j| < r$. We say that k consecutive vertices form a *connected interval* if v_i and v_{i+1} are connected for all $i \in \{0, \dots, k-1\}$ and we denote it as $v_i \sim v_{i+1}$. Then we define $X_i = X_i(T)$ to be the number of vertices in the i-th connected interval (or *i-th cluster*). Let $N(T)$ be the number of clusters.

We observe that the size (i.e. the number of vertices) of the first cluster, under the assumption that we have always at least one vertex, is $X_1 \stackrel{d}{=} \tilde{X}_1 | \tilde{X}_1 \geq 1$ where $\tilde{X}_1 = \tilde{X}_1(T)$ has the following distribution

$$\begin{aligned} \mathbb{P}(\tilde{X}_1 = 0) &= \mathbb{P}\{X(T) = 0\} = e^{-\lambda T}, \\ \mathbb{P}(\tilde{X}_1 = 1) &= \mathbb{P}\{(X(T) = 1) \cup (X(T) > 1, T_2 - T_1 > r)\}, \end{aligned}$$

$$\begin{aligned} \mathbb{P}(\tilde{X}_1 = k) = \mathbb{P}\{&(X(T) = k),\ T_{k+1} - T_k \leq r, \dots,\ T_2 - T_1 \leq r) \\ &\cup (X(T) > k, T_{k+1} - T_k > r,\ T_{k+1} - T_k \leq r, \dots,\ T_2 - T_1 \leq r)\}. \end{aligned}$$

for $k > 1$ an integer number.

Proposition 1. *As $T \to \infty$, the probability that $\tilde{X}_1(T)$ is equal to k, for all $k \geq 1$ is the following*

$$\lim_{T\to\infty} \mathbb{P}(\tilde{X}_1(T) = k) = (1 - e^{-\lambda r})^k (e^{-\lambda r}).$$

This implied that the distribution of X_1 is equal to the distribution of a r.v. Z such that $p_Z(k) = p_{X_1}(k+1)$ for all $k \geq 0$, where $Z \sim \text{Geo}(e^{-\lambda r})$.

(Proof in Section 5).

We study now the probability that the $i-$th cluster X_i has cardinality k_i given that X_j has cardinality k_j, with $k_j \geq 1$, for all $j = 1, \ldots, i-1$.

Proposition 2. *For all fixed $k_i \geq 1$, and for fixed $i \geq 1$, the distribution of $(X_1, \ldots X_i)$ converges as $T \to \infty$ to a distribution of a vector with i.i.d. entries, whose distribution is given by Proposition 1.*

(Proof in section 5).

Let t_i be the length of the i-th cluster. In particular we have

$$t_1 := \{T_k - T_1 \big| K = min\{i : T_{i+1} - T_i > r\}\}.$$

Than, as a simple corollary of Proposition 2, we get the following.

Proposition 3. *Let $K = min\{i : T_{i+1} - T_i > r\}$, we have that, as $T \to \infty$, $t_1(T)$ converges in distribution to*

$$t_1 = \sum_{j=1}^{K-1} Y_j$$

where $Y_1, \ldots, Y_{K-1}$ are conditionally i.i.d. and s.t. $Y_j \stackrel{d}{=} \tau \big| (\tau \leq r)$, with $\tau \sim \text{Exp}(\lambda)$.

We consider the distribution of $N(T)$ as $T \to \infty$. The number of clusters can be defined also as

$$N(T) = \#\{j : T_j - T_{j-1} > r, T_j < T\}.$$

Let us define $J_1 := t_1 + R_1$, as in Figure 1, which corresponds to the length of a cluster and a length of a gap between the cluster and the consecutive one.

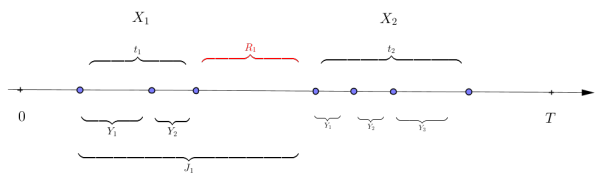

Figure 1: Random graph with two clusters of length t_1,t_2 with X_1,X_2 nodes, and with a gap R_1. The r.v. J_1 is equal to the sum of t_1 and R_1.

Knowing the length of the interval T we can expect that the number of clusters is $T/\mathbb{E}(J_1)$, i.e., if we consider an interval of given length T, and we know the length of J_1, the number of components of length J_1 that we can have in total it is given by T divided by that length. Indeed the following result holds.

Theorem 1. *We have the following convergence in L_1 and a.s.*

$$\frac{N(T)}{T} \longrightarrow \frac{1}{\mathbb{E}(J_1)}, \quad \text{as } T \to \infty.$$

(Proof in Section 5).

4.2 Inhomogeneous random distance graph.

Given a vector of clusters $\mathbf{X} = (X_1, \dots, X_{N(T)})$ we define a new graph $\widehat{G}(\mathbf{X}, c)$ as it follows. Let $\widehat{V}_T = \{1, \dots, N(T)\}$ be the set of vertices. We say that each vertex i has *type* X_i. This means that i corresponds to the i-th cluster with X_i occurrences. We call any vertex of $\widehat{G}(\mathbf{X}, c)$ a *macro vertex*.

We say that two macrovertices i and j are connected if there is at least one long-range edge between two vertices belonging to these two macrovertices. Then the probability that the i-th macrovertex is connected with the j-th macrovertex, abbreviated as $i \sim j$, is given by

$$\begin{aligned} \mathbb{P}(i \sim j) &= \mathbb{P}\{\exists \text{ at least one edge between } i \text{ and } j\} \\ &= 1 - \prod_{x,y} \left(1 - \frac{c(T)}{|x-y|^\alpha}\right), \end{aligned} \tag{5}$$

where the product runs over all pairs of vertices (x, y) with x belonging to the i-th cluster and y belonging to the j-th cluster.

Let us consider two consecutive macrovertices i and $i+1$. We can approximate the distance from any vertex of this two clusters considering the distance between the X_i-th occurrence of the i-th macrovertex and the first occurrence of the $(i+1)$-th macrovertex. We denote this distance with the random variable R_i, where $R_i \sim \tau | \tau > r$ (Figure 2) and we define the probability to have a long edge connection by $p_{i,i+1}$ as

$$p_{i,i+1} := \mathbb{P}(i \sim i+1 \big| X_i, X_{i+1}, R_i) \approx 1 - \left(1 - \frac{c(T)}{R_i^\alpha}\right)^{X_i X_{i+1}}. \tag{6}$$

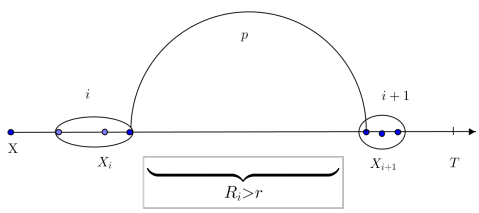

Figure 2: Connection with probability $p = p_{i,i+1}$ of two consecutive clusters i and $i+1$, with distance R_i grater than r.

Let us define the distance between two not necessary consecutive macrovertices X_i and X_j (Figure 3) as

$$R_{ij} := \sum_{k=i}^{j-1} R_k + \sum_{k=i+1}^{j-1} t_k. \tag{7}$$

Then we also define the connection probability of two macrovertices as follows

$$p_{i,j} := \mathbb{P}(i \sim j \big| X_i, X_j, R_{ij}) = 1 - \left(1 - \frac{c(T)}{R_{i,j}^{\alpha}}\right)^{X_i X_j}. \tag{8}$$

Note that (6) and (8) are an approximation of (1).

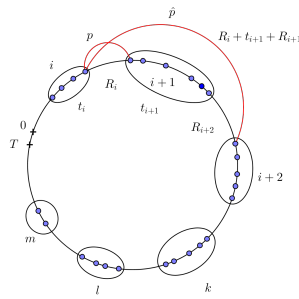

Figure 3: Connection with probability $p = p_{i,i+1}$ of cluster i with the consecutive cluster $i+1$ and connection with probability $\hat{p} = p_{i,i+2}$ with cluster $i+2$. The distance between i and $i+2$ is given by the sum of r.v.'s. $R_i + t_{i+1} + R_{i+1}$.

The probability that i is connected with j is

$$\begin{aligned} \widehat{p} = \mathbb{P}\{i \sim j\} &= \mathbb{E}(I_{i\sim j}) \\ &= \mathbb{E}(\mathbb{E}(I_{i\sim j} \big| X_i, X_j, R_{i,j})) \\ &= \mathbb{E}(\mathbb{P}(i \sim j \big| X_i, X_j, R_{i,j})) \\ &= 1 - \mathbb{E}\left(1 - \frac{c(T)}{R_{i,j}^{\alpha}}\right)^{X_i X_j}. \end{aligned} \tag{9}$$

Let us set $X_i X_j := Z$, $q := 1 - e^{-\lambda r}$ and $p := e^{-\lambda r}$.

Proposition 4. *If $c(T) \to 0$ as $T \to \infty$ then*

$$\begin{aligned} \mathbb{E}\left\{(1 - \frac{c(T)}{R_{ij}^{\alpha}})^{Z} \big| Z\right\} &= 1 - c(T) Z\, \mathbb{E}(R_{ij}^{-\alpha}) + O\left(c(T)^2 Z^2\, \mathbb{E}\left(\frac{1}{R_{ij}^{\alpha 2}}\right)\right) \\ &= 1 - c(T) Z\, \mathbb{E}\left(\frac{1}{R_{ij}^{\alpha}}\right) + O(c^2(T)). \end{aligned} \tag{10}$$

(Proof in Section 5).

Corollary 1. *The expected probability to have a connection between two macrovertices has the following bounds*

$$\frac{c(T)^2 \lambda^2}{(j-i-1)^{\alpha} e^{-\lambda r(\alpha-1)}} \leq \mathbb{P}(i \sim j) \leq \frac{c(T)}{(j-i-1)^{\alpha} r^{\alpha} e^{-2\lambda r}}. \tag{11}$$

(Proof in Section 5).

4.3 Degree distribution for the model on $\mathbb{Z}$

We compute for which values of $c(T)$ and α, fixing $N(T) = n$, the degree distribution follow a Poisson distribution as $T \to \infty$.

We can associate each macrovertex with the vertices $\{1, \dots, N(T) = n\}$ in $\mathbb{Z}$, i.e., each node i has a type X_i, for all $i \in \{1, \dots n\}$, then the probability to have a connection between two macrovertices i and j is set to be $\tilde{p} = \frac{c(n)}{|j-i|^\alpha}$. It is clear that the model has the same properties as the one above due the bounds (11).

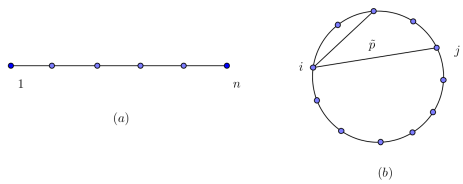

Figure 4: Macrovertices on $\mathbb{Z}$ (a) and macrovertices on a circle (b), where the probability of connection is $\tilde{p}$.

We remind that the model with $c = 0$ correspond to the percolation model on $\mathbb{Z}$. Let $\mathbb{P}_{D_n(i)}(k) = \mathbb{P}\{D_n(i) = k\}$, where $D_n(i)$ is the degree of vertex i, we have that

$$D_n(i) = \sum_{\substack{i \neq j \\ j}}^{n} \xi_{ji},$$

where $\xi_{ji} \sim \text{Be}(\tilde{p}_{ij})$, moreover ξ_{ji} for different $i, j \in \{1, \dots, N(T) = n\}$ are independent r.v.'s. First, we compute the expectation of the degree distribution:

$$\begin{aligned} \mathbb{E}(D_n(i)) &= \sum_{\substack{i \neq j \\ j}}^{n} E(\xi_{ji}) = \sum_{\substack{i \neq j \\ j}}^{n} \tilde{p_{ij}} \\ &= \sum_{\substack{i \neq j \\ j}}^{n} \frac{c(n)}{|i-j|^\alpha}, \end{aligned} \tag{12}$$

where the main term of the series is such that

$$\begin{cases} c(n)\Theta(n^{1-\alpha}), & \text{if } \alpha < 1 \\ (n-1)c(n), & \text{if } \alpha = 0 \\ c(n)\Theta(\ln n), & \text{if } \alpha = 1 \end{cases} \tag{13}$$

and function $\Theta(h(n))$ has the same order in n as the function $h(n)$. For $\alpha \geq 2$ the expected degree is given by $c(n)H(n, \alpha)$ where $H(n, \alpha)$ is the generalized harmonic number, hence as n goes to infinity $H(n, \alpha)$ converge to a Reiman zeta function $\zeta(\alpha)$ which has constant values for particular values of α.

We also compute the probability generating function of $D_n(i)$ given by

$$\begin{aligned} g_{D_n(i)}(t) = \mathbb{E}(t^{D_n(i)}) &= \prod_{j=1}^{n-1}(1-p_{ij}+p_{ij}e^t) = \prod_{j=1}^{n-1}(1+(e^t-1)p_{ij}) \\ &= e^{\sum_{j=1}^{n-1}\ln(1+p_{ij}(e^t-1))}. \end{aligned} \tag{14}$$

We can use Taylor's expansions for the logarithm if $0 \leq \alpha < 1$ and $c(n) = \frac{1}{n^{1-\alpha}}$. If $\alpha = 1$ and $c(n) = \frac{1}{\ln(n)}$ then $\sum_{j=1}^{n-1} p_{ij} \to c$, for some $c > 0$ and $\sum_{j=1}^{n-1} p_{ij}^2 \to 0$. Under these conditions we have that

$$g_{D_n(i)}(t) = e^{\sum_{j=1}^{n-1} p_{ij}(e^t-1)+O(p_{ij}^2)} \tag{15}$$

and then

$$g_{D_n(i)}(t) \overset{as\ n\to\infty}{\to} e^{(e^t-1)c}, \tag{16}$$

which is a Poisson probability generating function with intensity c.

The results of the degree distribution on the macrovertices on $\mathbb{Z}$ allows us to conjecture that the degree distribution of each macrovertx i follows a Poisson distribution with a random parameter, namely

$$\mathrm{Po}\left(\sum_{j=1}^{N(T)} X_i X_j \frac{1}{R_{ij}^{\alpha}}\right).$$

Indeed given $X_1, \ldots, X_N$ we can write the degree as a sum of Bernoulli random variables as follows

$$D(i)\big|X_1, \ldots, X_{N(T)} = \sum_{j=1}^{N(T)} \mathrm{Be}(p_{i,j}\big|X_1, \ldots, X_N),$$

where the probability of connection is the following

$$p_{i,j} = X_i X_j \frac{1}{R_{ij}^{\alpha}}.$$

From [4] we know that the degree for fixed N number of types will follow the theorem on the degree sequence of IRG, for the finite- type case, where it converges to a compound Poisson distribution where the expectation is given by

$$\mathbb{E}(D_i) = \mathbb{E}\left(\mathbb{E}(D(i)\big|X_1, \ldots, X_{N(T)})\right) = \mathbb{E}\left(\sum_{j=1}^{N(T)} P(i \sim j)\big|X_1, \ldots, X_N\right).$$

The degree distribution of this model has been also investigated in [7] for special cases of the distribution of the weights X_i and for $c(T)$ positive constant. In [7] when the degree distribution of the weights is regularly varying with exponent $1-\tau$, i.e., $\mathbb{P}(X_i > x) = x - (\tau-1)L(x)$ where the function $x \to L(x)$ is slowly varying at infinity, the degree distribution of the graph is as well regularly varying with exponent $\gamma = -\frac{\alpha(\tau-1)}{d}$, where d is the dimension of the space. In [7] can be seen results on the degree and on the existence of the giant component given the relations between the parameters of γ.

5 Proofs

5.1 Proof of Preposition 1.

The probability that in the first connected component there are k occurrence is

$$\begin{aligned}\mathbb{P}(\tilde{X}_1 = k) &= \mathbb{P}\{(X(T) = k, T_k - T_{k-1} \leq r, \ldots,\ T_2 - T_1 \leq r) \\ &\quad \cup (X(T) > k, T_{k+1} - T_k > r,\ T_k - T_{k-1} \leq r\ , \ldots,\ T_2 - T_1 \leq r)\}, \\ &= \mathbb{P}\{(X(T) = k \cap\ \tau_k \leq r\ \cap \cdots \cap\ \tau_1 \leq r)\} \\ &\quad + \mathbb{P}\{X(T) > k \cap \tau_{k+1} > r,\ \tau_k \leq r\ \cap \cdots \cap\ \tau_1 \leq r\}\end{aligned} \tag{17}$$

then we can write the first therm of (17) as it follows

$$\begin{aligned}&\mathbb{P}(X(T) = k, T_k - T_{k-1} \leq r\ \cap \cdots \cap\ T_2 - T_1 \leq r) \\ &= \mathbb{P}\{T_k \leq T, T_{k+1} > T, T_k - T_{k-1} \leq r\ \cap \cdots \cap\ T_1 \leq r\} \\ &= \mathbb{P}\{T_k \leq T, T_k - T_{k-1} \leq r\ \cap \cdots \cap\ T_1 \leq r\} \\ &\quad - \mathbb{P}\{T_k \leq T, T_{k+1} \leq T, T_k - T_{k-1} \leq r\ \cap \cdots \cap\ T_1 \leq r\} \\ &= \mathbb{P}\{(\sum_{i=1}^{k} \tau_i < T) \cap \bigcap_{i=1}^{k} (\tau_i < r)\} - \mathbb{P}\{(\sum_{i=1}^{k+1} \tau_i < T) \cap \bigcap_{i=1}^{k} (\tau_i < r)\}.\end{aligned} \tag{18}$$

As $T \to \infty$, we obtain using continuity of the probability from below we have the following limit

$$\lim_{T \to +\infty} \mathbb{P}\{(\sum_{i=1}^{k} \tau_i < T) \cap \bigcap_{i=1}^{k} (\tau_i < r)\} = \mathbb{P}\{\bigcap_{i=1}^{k} (\tau_i < r)\}. \tag{19}$$

Hence as $T \to \infty$, we have that $\mathbb{P}(X(T) = k, \tau_k \leq r\ \cap \cdots \cap\ \tau_1 \leq r) \to 0$ for any fixed $k \geq 1$.

The second therm of (17) can be written as

$$\begin{aligned}&\mathbb{P}(X(T) > k, \tau_{k+1} > r,\ \tau_k \leq r, \ldots,\ \tau_1 \leq r) \\ &= \mathbb{P}(T_k \leq T, \tau_{k+1} > r, \tau_1 \leq r, \ldots, \tau_k \leq r) \\ &= \mathbb{P}(T_k \leq T, \tau_1 \leq r, \ldots, \tau_k \leq r) \\ &\quad - \mathbb{P}(T_k \leq T, \tau_{k+1} \leq r, \tau_1 \leq r, \ldots, \tau_k \leq r) \\ &= \mathbb{P}\{(\sum_{i=1}^{k} \tau_i \leq T) \cap \bigcap_{i=1}^{k} (\tau_i < r)\} - \mathbb{P}\{(\sum_{i=1}^{k+1} \tau_i > T) \cap \bigcap_{i=1}^{k+1} (\tau_i < r)\}.\end{aligned} \tag{20}$$

Then as $T \to \infty$ we have by (19) that the probability (17) converges as it follows,

$$\mathbb{P}(\tilde{X}_1 = k) \to (1 - e^{-\lambda r})^k (e^{-\lambda r}), \quad \forall k \geq 1.$$

For $k \geq 1$, the probability distribution of X_1 is such that

$$\begin{aligned}\mathbb{P}(X_1 = k) &= \mathbb{P}(\tilde{X}_1 = k | \tilde{X}_1 \geq 1) \\ &= \frac{\mathbb{P}(\tilde{X}_1 = k)}{\mathbb{P}(\tilde{X}_1 \geq 1)},\end{aligned} \tag{21}$$

hence, as $T \to \infty$, we have that $\mathbb{P}(\tilde{X}_1 \geq 1) \to 1$ and (21) converges as follows

$$\mathbb{P}(X_1 = k) \to (1 - e^{-\lambda r})^k (e^{-\lambda r}), \quad \forall k \geq 1.$$

Given a r.v. Z such that $Z \sim \text{Geo}(e^{-\lambda r})$ for all $k \geq 0$, it follows that $p_{X_1}(k+1) = p_Z(k)$.

5.2 Proof of Preposition 2.

We prove that the distribution of X_i converges to a geometric distribution as $T \to \infty$. We start considering the second cluster X_2. In order to have a second cluster with cardinality at least one, it has to exist the cluster X_1 with cardinality $k_1 \geq 1$, and there has to be a distance greater than r between the last occurrence of X_1 and the first of X_2 (Figure 5). For any $k_1, k_2 \geq 1$, with $k_1, k_2 \in \mathbb{N}^+$, the probability of having the first two clusters of cardinalities k_1 and k_2 can be written as follows

$$\begin{aligned}&\mathbb{P}(\tilde{X}_2 = k_2, X_1 = k_1) = \mathbb{P}(X(T) = k_1 + k_2, T_{k_1+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\ &\cup (X(T) > k_1 + k_2, T_{k_1+1} - T_{k_1} > r, T_{k_1+2+k_2} - T_{k_1+1+k_2} > r, A_{k_1}, A_{k_2}),\end{aligned}$$

where for any $k_j \geq 1$, $A_{k_1} = \cap_{i=1}^{k_1-1}\{\tau_{i+1} - \tau_i < r\}$ and $A_{k_2} = \cap_{i=k_1+1}^{k_1+k_2-1}\{\tau_{i+1} - \tau_i < r\}$.

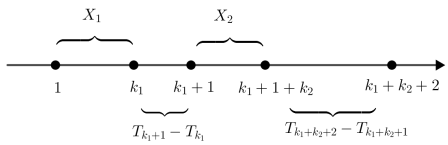

Figure 5: Representation of the clusters X_1 and X_2 with respective cardinalities k_1 and k_2. The distances $T_{k_1+1} - T_{k_1}$ and $T_{k_1+2+k_2} - T_{k_1+1+k_2}$ have to be grater than r.

We can prove with analogous computations as in Proposition 1 that for any $k_1, k_2 \geq 1$, with $k_1, k_2 \in \mathbb{N}^+$, the probability of having the clusters X_1 and X_2 with cardinality respectively k_1 and k_2 is given by the following

$$\begin{aligned}&\mathbb{P}(\tilde{X}_2 = k_2, X_1 = k_1) \\ &= \mathbb{P}(X(T) = k_1 + k_2, T_{k_1+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\ &+ \mathbb{P}(X(T) > k_1 + k_2, T_{k_1+1} - T_{k_1} > r, T_{k_1+k_2+2} - T_{k_1+k_2+1} > r, A_{k_1}, A_{k_2}).\end{aligned} \tag{22}$$

Set $K = k_1 + k_2$, we can write the first term on the right of equation (22) as it follows

$$\begin{aligned}&\mathbb{P}(X(T) = K, T_{k_1+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\ &= \mathbb{P}(T_K \leq T, T_{K+1} > T, T_{k_1+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\ &= \mathbb{P}(T_K \leq T, T_{K+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\ &\quad - \mathbb{P}(T_{k_1} \leq T, T_{k_1+1} \leq T, T_{k_1+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\ &= \mathbb{P}(T_K \leq T, A_{k_1}, A_{k_2}) - \mathbb{P}(T_{k_1} \leq T, T_{k_1+1} - T_{k_1} \leq r, A_{k_1}, A_{k_2}) \\ &\quad - \mathbb{P}(T_K \leq T, T_{K+1} \leq T, A_{k_1}, A_{k_2}) \\ &\quad + \mathbb{P}(T_K \leq T, T_{K+1} \leq T, A_{k_1}, A_{k_2}, T_{k_1+1} - T_{k_1} \leq r)\end{aligned} \tag{23}$$

As $T \to \infty$, by continuity of the probability from below we have that

$$\begin{aligned}
&\lim_{T\to+\infty} \mathbb{P}(T_K \leq T, A_{k_1}, A_{k_2}) \\
&= \lim_{T\to+\infty} \mathbb{P}\{(\sum_{i=1}^{K} \tau_i < T) \cap \bigcap_{i=1}^{K} (\tau_i < r)\} \\
&= \mathbb{P}\{\bigcap_{i=1}^{K} (\tau_i < r)\} \\
&= (1 - e^{-\lambda r})^K.
\end{aligned} \tag{24}$$

Hence as $T \to \infty$, we have that (23) goes to zero. The second term on the right of (22) can be written as it follows,

$$\begin{aligned}
&\mathbb{P}(X(T) > k_1 + k_2, T_{k_1+1} - T_{k_1} > r, T_{k_1+k_2+2} - T_{k_1+k_2+1} > r, A_{k_1}, A_{k_2}) \\
&= \mathbb{P}(T_K \leq T, T_{K+2} > r, T_{k_1+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\
&= \mathbb{P}(T_K \leq T, T_{k_1+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\
&\quad - \mathbb{P}(T_K \leq T, T_{K+2} - T_{K+1} \leq r, T_{k_1+1} - T_{k_1} > r, A_{k_1}, A_{k_2}) \\
&= \mathbb{P}(T_K \leq T, A_{k_1}, A_{k_2}) - \mathbb{P}(T_K \leq T, T_{k_1+1} - T_{k_1} \leq r, A_{k_1}, A_{k_2}) \\
&\quad - \mathbb{P}(T_K \leq T, T_{K+2} - T_{K+1} \leq r, A_{k_1}, A_{k_2}) \\
&\quad + \mathbb{P}(T_K \leq T, T_{K+2} - T_{K+1} \leq r, T_{k_1+1} - T_{k_1} \leq r, A_{k_1}, A_{k_2}).
\end{aligned} \tag{25}$$

From the observation in (24), as $T \to \infty$, we can study the limit of each terms of (25) as it follows,

$$\begin{aligned}
&\lim_{T\to+\infty} \mathbb{P}(T_K \leq T, A_{k_1}, A_{k_2}) \\
&= \lim_{T\to+\infty} \mathbb{P}\{(\sum_{i=1}^{K} \tau_i < T) \cap \bigcap_{i=1}^{K} (\tau_i < r)\} \\
&= \mathbb{P}\{\bigcap_{i=1}^{K} (\tau_i < r)\} \\
&= (1 - e^{-\lambda r})^K,
\end{aligned} \tag{26}$$

$$\begin{aligned}
&\lim_{T\to+\infty} \mathbb{P}(T_K \leq T, T_{k_1+1} - T_{k_1} \leq r, A_{k_1}, A_{k_2}) \\
&= \lim_{T\to+\infty} \mathbb{P}\{(\sum_{i=1}^{K} \tau_i < T) \cap \bigcap_{i=1}^{K+1} (\tau_i < r)\} \\
&= \mathbb{P}\{\bigcap_{i=1}^{K+1} (\tau_i < r)\} \\
&= (1 - e^{-\lambda r})^{K+1},
\end{aligned} \tag{27}$$

$$
\begin{aligned}
&\lim_{T\to+\infty} \mathbb{P}(T_K \leq T, T_{K+2} - T_{K+1} \leq r, A_{k_1}, A_{k_2}) \\
&= \lim_{T\to+\infty} \mathbb{P}\{(\sum_{i=1}^{K} \tau_i < T) \cap \bigcap_{i=1}^{K+1} (\tau_i < r)\} \\
&= \mathbb{P}\{\bigcap_{i=1}^{K+1} (\tau_i < r)\} \\
&= (1 - e^{-\lambda r})^{K+1},
\end{aligned}
\tag{28}
$$

$$
\begin{aligned}
&\lim_{T\to+\infty} \mathbb{P}(T_K \leq T, T_{K+2} - T_{K+1} \leq r, T_{k_1+1} - T_{k_1} \leq r, A_{k_1}, A_{k_2}). \\
&= \lim_{T\to+\infty} \mathbb{P}\{(\sum_{i=1}^{K} \tau_i < T) \cap \bigcap_{i=1}^{K+1} (\tau_i < r)\} \\
&= \mathbb{P}\{\bigcap_{i=1}^{K+2} (\tau_i < r)\} \\
&= (1 - e^{-\lambda r})^{K+2}.
\end{aligned}
\tag{29}
$$

As $T \to \infty$, the equation (25) converges to $(1 - e^{-\lambda r})^{k_1+k_2}(e^{-\lambda r})^2$. Hence, we have that for any $k_1, k_2 \geq 1$,

$$
\begin{aligned}
&\mathbb{P}(\tilde{X}_2 = k_2 | X_1 = k_1) \\
&= \frac{\mathbb{P}(\tilde{X}_2 = k_2, X_1 = k_1)}{\mathbb{P}(X_1 = k_1)},
\end{aligned}
$$

as $T \to \infty$, the probability of having the cluster X_2 of size $k_2 \geq 1$ given that we have a cluster X_1 of size $k_1 \geq 1$ it converges as it follows,

$$
\mathbb{P}(\tilde{X}_2 = k_2 | X_1 = k_1) \to \frac{(1 - e^{-\lambda r})^{k_1+k_2}(e^{-\lambda r})^2}{(1 - e^{-\lambda r})^{k_1}(e^{-\lambda r})} = (1 - e^{-\lambda r})^{k_2}(e^{-\lambda r}) \quad \text{as } T \to \infty.
$$

By induction on j can be proved that the probability of having the j-th cluster of size k_j, given the existence of $X_1, \ldots, X_{j-1}$ clusters of cardinalities $k_1, \ldots, k_{j-1}$, for all $k_1, \ldots, k_j \geq 1$, as $T \to \infty$, it converges to a geometric distribution with expected value $e^{-\lambda r}$, i.e.,

$$
\begin{aligned}
&\frac{\mathbb{P}(\tilde{X}_j = k_j, X_1 = k_1, \ldots, X_{j-1} = k_{j-1})}{\mathbb{P}(X_1 = k_1, \ldots, X_{j-1} = k_{j-1})} \\
&= \frac{\mathbb{P}(X(T) = \sum_{l=1}^{j} k_l, T_{k_1+1} - T_{k_1} > r, \ldots, T_{\sum_{l=1}^{j-1} k_l} - T_{\sum_{l=1}^{j} k_l} > r, A_{k_1}, \ldots, A_{k_l})}{\mathbb{P}(X_1 = k_1, \ldots, X_{j-1} = k_{j-1})} \\
&+ \frac{\mathbb{P}(X(T) > \sum_{l=1}^{j} k_l, T_{k_1+1} - T_{k_1} > r, \ldots, T_{\sum_{l=1}^{j-1} k_l} - T_{\sum_{l=1}^{j+1} k_l} > r, A_{k_1}, \ldots, A_{k_l})}{\mathbb{P}(X_1 = k_1, \ldots, X_{j-1} = k_{j-1})},
\end{aligned}
$$

and as $T \to \infty$ it converges to

$$
\frac{(1 - e^{\lambda r})^{\sum_{l=1}^{j} k_l}(e^{-\lambda r})^j}{(1 - e^{\lambda r})^{\sum_{l=1}^{j-1} k_l}(e^{-\lambda r})^{j-1}} = (1 - e^{\lambda r})^{k_j}(e^{-\lambda r}).
$$

5.3 Proof of Theorem 1

We can write the distribution function and the density function of Y_j as

$$F_{Y_j}(x) = \mathbb{P}(\tau \le x | \tau \le r) = \frac{\mathbb{P}(\tau \le x, \tau \le r)}{\mathbb{P}(\tau \le r)} = \begin{cases} 0 & \text{if } 0 \ge x, \\ \frac{1-e^{-\lambda x}}{1-e^{-\lambda r}} & \text{if } x \le r, \\ 1 & \text{if } x > r, \end{cases}$$

$$f_{Y_j}(x) = \begin{cases} 0 & \text{if } 0 \ge x, \\ \frac{\lambda e^{-\lambda x}}{1-e^{-\lambda r}} & \text{if } 0 \le x \le r, \\ 0 & \text{if } x > r. \end{cases}$$

The distribution function and the density function of R_j are

$$F_{R_j}(x) = \mathbb{P}(\tau \le x | \tau \ge r) = \begin{cases} \frac{e^{-\lambda r} - e^{-\lambda x}}{e^{-\lambda r}} & \text{if } x \ge r, \\ 0 & \text{if } x < r, \end{cases}$$

and

$$f_{R_j} = \begin{cases} \frac{\lambda e^{-\lambda x}}{e^{-\lambda r}} & \text{if } x \ge r, \\ 0 & \text{if } x < r. \end{cases}$$

Let us compute the expectation of t_1; since:

$$\begin{aligned} \mathbb{E}(t_1 \big| X_1 = n) &= \mathbb{E}(\sum_{j=1}^{n-1} Y_j) \\ &= (n-1)\,\mathbb{E}(Y_j) = (n-1)\int_0^r x f_{Y_j(x)}\,dx \\ &= (n-1)\frac{\lambda}{1-e^{-\lambda r}}\int_0^r x e^{-\lambda x}\,dx = h(n), \end{aligned} \tag{30}$$

then

$$\mathbb{E}(t_1) = \mathbb{E}(\mathbb{E}(t_1 \big| X_1 = n) = \mathbb{E}(h(X_1)) = \left(\frac{1}{e^{-\lambda r}} - 1\right)\frac{1}{1-e^{-\lambda r}}\frac{1-e^{-\lambda r}(1+r\lambda)}{\lambda}. \tag{31}$$

Moreover,

$$\mathbb{E}(R_j \big| R_j > r) = \int_r^\infty x \frac{\lambda e^{-\lambda x}}{e^{-\lambda r}} dx = \frac{1+r\lambda}{\lambda}$$

and

$$\mathbb{E}(J_1) = \mathbb{E}(R_1) + \mathbb{E}(t_1) = \frac{e^{\lambda r}}{\lambda}. \tag{32}$$

We want to prove that, as $T \to \infty$,

$$\mathbb{E}\left|\frac{N(T)}{T} - \frac{1}{\mathbb{E}(J_1)}\right| \to 0.$$

We start by considering

$$N(T) = \sum_{i=1}^{X(T)} I_i(\tau_i > r)$$

and recalling that, by the strong law of large numbers,

$$\frac{X(T)}{T} \to \lambda \ a.s. \quad as \quad T \to \infty.$$

We observe that $I = (I_1, \dots, I_{X(T)})$ is a stationary random sequence with $\mathbb{E}(|I_1|) < \infty$, and I is ergodic [14]. Here $X(T) \to \infty$ a.s. as $T \to \infty$ and one can apply the Ergodic Theorem to $\frac{N(T)}{X(T)}$ as $X(T) \to \infty$. This yields

$$\frac{X(T)}{T}\frac{N(T)}{X(T)} = \frac{X(T)}{T}\frac{1}{X(T)}\sum_{i=1}^{X(T)} I_i(\tau_i > r) \to \lambda\,\mathbb{E}(I_{\tau>r}) = \lambda e^{-\lambda r} = \frac{1}{\mathbb{E}(J_1)}, \tag{33}$$

a.s. as $T \to \infty$, and also

$$\mathbb{E}\left(\left|\frac{X(T)}{T}\frac{1}{X(T)}\sum_{i=1}^{X(T)} I_i(\tau_i > r) - \lambda\,\mathbb{E}(I_{\tau>r})\right|\right) \to 0 \ \text{ as } \ T \to \infty. \tag{34}$$

5.4 Proof of Proposition 4

Given

$$N = \frac{1}{c(T)^{1/2+\delta}} > 0, \quad \forall\ 0 < \delta < \frac{1}{2},$$

we can write the expectation as follows

$$\mathbb{E}\Big\{\Big(1 - \frac{c(T)}{R_{ij}^{\alpha}}\Big)^{Z}\big|Z\Big\} = \mathbb{E}\Big(I_{\{Z<N\}}\Big(1 - \frac{c(T)}{R_{ij}^{\alpha}}\Big)^{Z}\Big) + \mathbb{E}\Big(I_{\{Z\geq N\}}\Big(1 - \frac{c(T)}{R_{ij}^{\alpha}}\Big)^{Z}\Big),$$

where Z and R_{ij} are independent. We can use Taylor's expansion for the function

$$(1-\varepsilon)^{Z} = 1 - Z\epsilon + O((N\varepsilon)^2),$$

for all $Z < N$, therefore

$$\begin{aligned}\mathbb{E}\Big\{\Big(1 - \frac{c(T)}{R_{ij}^{\alpha}}\Big)^{Z}\big|Z\Big\} &= \mathbb{E}\Big\{\big(1 - I_{\{Z>N\}}\big)\Big(1 - Z\frac{c(T)}{R_{ij}^{\alpha}} + O\big((\frac{c(T)}{R_{ij}^{\alpha}}Z)^2\big)\Big)\big|Z\Big\} \\ &\quad + \mathbb{E}\Big\{I_{\{Z\geq N\}}(1 - \frac{c(T)}{R_{ij}^{\alpha}})^{Z}\big|Z\Big\}.\end{aligned} \tag{35}$$

If $T \to \infty$ we have that $c(T) \to 0$; then, as $N \to \infty$,

$$\mathbb{E}\Big\{(1 - \frac{c(T)}{R_{ij}^{\alpha}})^{Z}\big|Z\Big\} = 1 - c(T)Z\,\mathbb{E}\,\frac{1}{R_{ij}^{\alpha}} + O(Z^2\,\mathbb{E}(\frac{c(T)}{R_{ij}^{\alpha}})^2) + O(\mathbb{E}\,I_{\{Z\geq N\}}).$$

Since $N = \frac{1}{c(T)^{1/2+\delta}}$, for $T \to \infty$, both $O(\mathbb{E}(\frac{c(T)}{R_{ij}^{\alpha}}Z)^2)$ and $O(\mathbb{E}\,I_{\{Z\geq N\}})$ converge to zero. By the Chebyshev's inequality, we have that

$$\mathbb{P}(Z \geq N) \leq \frac{\mathbb{E}\,Z^2}{N^2} = c(T)c(T)^{2\delta}\,\mathbb{E}(Z^2) = O(c(T)) \tag{36}$$

and then, by Holder's inequality,

$$\mathbb{E}(X_iX_j)^2 = \mathbb{E}((X_i)^4)^{1/2}\,\mathbb{E}((X_j)^4)^{1/2} < \infty. \tag{37}$$

Observe that

$$\mathbb{E}\Big(\frac{c(T)}{R_{ij}^{\alpha}}Z\Big)^2 \leq \frac{1}{r^2}(c(T)\,\mathbb{E}\,Z)^2 = O\big(c(T)^2\big). \tag{38}$$

5.5 Proof of corollary 1

From (7) we can write

$$R_{ij} := \sum_{k=i}^{j-1} R_k + \sum_{k=i+1}^{j-1} t_k = \sum_{k=i+1}^{j-1} J_k + R_i,$$

and then

$$\mathbb{E}\, R_{ij} = \sum_{k=i+1}^{j-1} \mathbb{E}\, J_k + \mathbb{E}\, R_i = (j-i-2)\frac{e^{\lambda r}}{\lambda} + \frac{1+\lambda r}{\lambda}. \tag{39}$$

This, together with Jensen's inequality applied to the function $g(x) = x^{-\alpha}$, for $\alpha \geq 0$, gives us the following bound

$$\mathbb{E}\left(\frac{1}{R_{ij}^{\alpha}}\right) \geq \frac{1}{(\mathbb{E}\, R_{ij})^{\alpha}} = \left(\frac{\lambda}{(j-i-2)e^{\lambda r}+1+\lambda r}\right)^{\alpha} \geq \left(\frac{\lambda}{(j-i-2)e^{\lambda r}+e^{\lambda r}}\right)^{\alpha}$$

and, observing that $R_{ij} \geq (j-i)r$, we have that

$$\mathbb{E}\left(\frac{1}{R_{ij}^{\alpha}}\right) \leq \frac{1}{((j-i-1)r)^{\alpha}}.$$

6 Conclusions

We introduce a one-dimensional random graph model on $[0,T] \subseteq \mathbb{R}$ where the nodes are distributed according to a Poisson point process with intensity λ and the probability of having an edge between any pair of nodes is defined by the distance between them.

We study initially the model considering just the probability to have an edge between nodes that have distance less or equal than r as in [6] and in [12].

We first give a formula for the distribution of nodes in the connected components, or clusters, for finite T (with T large enough). We prove that this distribution converges, as T goes to infinity, and we obtain the limiting distribution. We give a formula for the length of each cluster and we show that the number of clusters, as T goes to infinity, converge in L_1 and a.s., obtaining also the limiting distribution.

In Section 4.2 we reintroduce the long distance edges between clusters, called macro-vertex, making our model in the framework of an inhomogeneous structure. We investigate the expected degree of macro-vertices, we give an approximation for this expectation and we specify also a upper and a lower bound of this expectation.

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PHASE TRANSITION IN RANDOM DISTANCE GRAPHS ON THE TORUS

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Abstract

In this paper we consider random distance graphs motivated by applications in neurobiology. These models can be viewed as examples of inhomogeneous random graphs, notably outside of the so-called rank-1 case. Treating these models in the context of the general theory of inhomogeneous graphs helps us to derive the asymptotics for the size of the largest connected component. In particular, we show that certain random distance graphs behave exactly as the classical Erdős–Rényi model, not only in the supercritical phase (as already known) but in the subcritical case as well.

Keywords: Inhomogeneous random graph; random distance graph; largest connected component

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1. Introduction

Random distance graphs are often designed as models of real-world systems where some of the properties of the connections between vertices are observed to be dependent on their relative distance (for some early examples, see, e.g. [1], [3], and [15]). It is generally assumed that the vertices of such models are in some metric space, most often $\mathbb{R}^d$ or $\mathbb{Z}^d$. The probability of a connection between any two vertices in these graphs is a function of the distance between them.

A great demand for this class of models is prompted in particular by developments in neuroscience. It must be noted that physiological data on the brain structure of a living organism is a highly costly exercise (see, e.g. the Blue Brain Project of [12]), hence, inevitably it has to be complemented with theoretical studies. A number of models have been developed along this line to make mathematical results accessible for applications and, in particular, random graphs have become a common tool in the exploration of neuronal networks (see, e.g. [16] and [18] and the references therein).

Recently, a model for the structure and dynamics of the neuropil has been proposed by Janson *et al.* [10]. Inspired by this work, we consider here certain random distance graphs, whose vertices lie on a two-dimensional discrete torus and the connection probabilities decay both with the distance between the vertices and the total number of vertices in the graph (see Section 2 for a precise definition). Our results deal with one of the primary questions, namely,

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the size of the largest connected component. This characteristic is very important for the study of processes on the networks, as, e.g. the propagation of impulses. In complex dynamical systems the parameters of connectivity change in time; for neuronal networks this is a known property of the synaptic plasticity. Therefore, it is important to have a complete picture of the scalings for the largest connected component on the entire parameter space, at least for some basic test networks. Such a complete description should help to fit the parameters of the connections in a neuronal model based only on qualitative information on the functioning of a network.

As a mathematical object, random distance graphs form a particular subclass of the general inhomogeneous random graph models [6]. The graphs treated in [6] have the following common feature: edges are placed independently from each other and the probability of edges is, roughly speaking, of order $1/n$, where n is the size of the graph (i.e. the number of its vertices). Briefly, each of the n vertices is assigned a type, i.e. a value in some separable metric space $\mathcal{S}$. Given a set of such values $\{x_1, \dots, x_n\}$ any two vertices i and j are connected with probability

$$p_n(i, j) = \min\left\{\frac{\kappa(x_i, x_j)}{n}, 1\right\}, \tag{1}$$

where κ is a symmetric nonnegative measurable function.

Most investigations on random distance graphs have been carried out without much use of [6] (not counting Example 4.6 of [6] itself, Bollobás *et al.* [7] is almost an exception). The reason, perhaps, is that random distance graphs are outside of the so-called rank-1 case, and thus they belong to a complicated subclass of the inhomogeneous models. The theory of [6] gives us the critical parameters for the emergence of the giant component and even describes the size of this component in the supercritical phase. However, the subcritical phase of non rank-1 models was studied only for some particular subclasses (see [19]), which do not include the present model. Furthermore, the critical phase has been studied so far only for the rank-1 cases (see [4], [5], and [20]).

The paper is organized as follows. In Section 2 we define our model and outline the connections with some random graphs models previously studied. The main theorems are stated in Section 3, whereas their proofs are collected in Section 4.

2. The model

Let $N \in \mathbb{N}$, $N > 1$, and let $V_N = \{1, \dots, N\}^2$ denote the set of vertices in the two-dimensional discrete torus $\mathbb{T}_N^2 = (\mathbb{Z}/N\mathbb{Z})^2$. Define the graph distance $d(u, v)$ between two vertices $u = (u_1, u_2)$ and $v = (v_1, v_2)$ in V_N as

$$d(u, v) = d_N(|u_1 - v_1|) + d_N(|u_2 - v_2|), \tag{2}$$

where

$$d_N(i) = \begin{cases} i, & 0 \le i \le N/2, \\ N - i, & N/2 < i < N, \end{cases} \quad \text{for } i \in \{0, \dots, N-1\}.$$

Let W be a nonnegative random variable, and let W_v, $v \in V_N$, be independent and identically distributed (i.i.d.) copies of W. Given the values W_v, $v \in V_N$, assume that between any two vertices $u, v \in V_N$ an edge is present independently of others and with probability

$$p(u, v) = \min\left\{c\frac{W_u W_v}{N d(u, v)}, 1\right\}, \tag{3}$$

where $c > 0$ is a parameter. We denote by $G_{N,W}$ the resulting random graph on V_N.

Note that, in the case of constant $W \equiv 1$, this graph is exactly the one introduced by Janson *et al.* [10] and it also has common features with other random graph models considered previously (see, e.g. [18]). Janson *et al.* [10] studied a bootstrap percolation process as a model of the spread of activation in a neuronal tissue. They also derived the size of the diameter of the graph, thus extending the corresponding results of [6] for graphs with unbounded number of types.

In the language of inhomogeneous graph theory, the model introduced by Janson *et al.* [10] can be seen as a *homogeneous* case (that is, roughly speaking, when the degrees of the vertices are asymptotically all the same; see Example 4.6 of [6]). Note, however, that the general form (3) considered here (inspired by [8]) makes the model essentially inhomogeneous.

It is worth mentioning that the model (3) is also closely related to certain bond percolation models (see [15] and, in particular, [1] and [14]). In such models, the graphs have a countable set of vertices and, as in the model we investigate here, edges between them are present with a distance-dependent probability. The main problem is whether, depending on the values of the parameters, a particular vertex belongs to an infinite cluster with positive probability. It was shown in [7] that this question for the spread-out percolation model [14] can be resolved using the theory of inhomogeneous random graphs.

3. Results

It has been already shown in [6, Example 4.6] that in the supercritical case a homogeneous distance graph has the same asymptotics for the size of largest connected component as in the classical Erdős–Rényi model. We prove that this result holds for the subcritical case as well.

Theorem 1. *Let G_N denote a random graph on V_N with probability of connections*

$$p(u, v) = \min\left\{\frac{c}{Nd(u, v)}, 1\right\}, \qquad u, v \in V_N,$$

and let $C(G_N)$ denote the size of the largest connected component in G_N. Set

$$\lambda = c4\log 2.$$

Then the following hold.

(i) *If $\lambda < 1$, we have*

$$\frac{C(G_N)}{\log(N^2)} \xrightarrow{\mathbb{P}} \frac{1}{\lambda - 1 - \log\lambda} \quad \text{as } N \to \infty. \tag{4}$$

(ii) *If $\lambda > 1$ then*

$$\frac{C(G_N)}{N^2} \xrightarrow{\mathbb{P}} \beta \quad \text{as } N \to \infty,$$

where $\beta = \beta(\lambda)$ is the positive solution of $\beta = 1 - \mathrm{e}^{\lambda\beta}$.

As we noted above, only Theorem 1(ii) follows from the results of [6].

Remark 1. One may observe a certain redundancy here, as statements (i) and (ii) of Theorem 1 are particular cases of the following Theorems 3 and 2, respectively. However, stated separately, Theorem 1 makes it clear that the largest connected component in G_N behaves, asymptotically, as the one in the Erdős–Rényi graph $G_{n,p}$, with $n = N^2$ and $p = \lambda/n$.

Furthermore, it is plausible to conjecture (but we do not study this case here) that the analysis of the critical phase in [20] can be extended to this model as well. This would yield that even

in the critical case, that is, when $\lambda = c4\log 2 = 1$, the graph G_N has the same asymptotics for the largest component as $G_{n,p}$, with $p = 1/n$ and $n = N^2$, i.e. that the largest connected component rescaled by $n^{2/3}$ converges in distribution to a certain positive random variable.

The following theorems treat the general model (3).

Theorem 2. *Assume that*

$$\mathbb{E}W^2 = \int_0^\infty x^2 \mu_W(\mathrm{d}x) < \infty.$$

Let $C(G_{N,W})$ denote the size of the largest connected component in $G_{N,W}$, and denote again

$$\lambda = c4\log 2.$$

Then

$$\frac{C(G_{N,W})}{N^2} \xrightarrow{\mathbb{P}} \int_0^\infty \beta(x)\mu_W(\mathrm{d}x) =: \hat{\beta}, \tag{5}$$

where $\beta(x)$ is the maximal solution to

$$f(x) = 1 - \exp\left(x\lambda \int_0^\infty y f(y)\mu_W(\mathrm{d}y)\right). \tag{6}$$

Furthermore, $\hat{\beta} > 0$ if and only if

$$\lambda\mathbb{E}W^2 > 1. \tag{7}$$

Note that the critical parameter $\lambda\mathbb{E}W^2$ in Theorem 2 is similar to the lower bound derived in Theorem 4.1 of [8] (in fact, it has exactly the same meaning of a certain averaged degree of a vertex as in [8]) to provide the necessary conditions for percolation.

Theorem 2 follows essentially from the general theory of [6], as we explain below. It tells us that the limit when $N \to \infty$ of the (scaled) largest component in $G_{N,W}$ coincides with the corresponding limit for the rank-1 random graph on V_N defined by the following probabilities of connections between any $u, v \in V_N$:

$$p_1(u, v) = \min\left\{\lambda \frac{W_u W_v}{N^2}, 1\right\}. \tag{8}$$

(Note, however, that for any finite N, models (3) and (8) are not equal in distribution.)

Here the largest connected component in the subcritical phase is sensitive to the tail of the distribution of W. It is known that in models of the form in (8), the size of the largest component varies between polynomial (see [9]) and logarithmic (see [17]) order depending on the distribution of W. We shall consider here a particular case of the distribution of W to show the similarities with Theorem 1.

Theorem 3. *Assume that, for some positive ε, $\mathbb{E}\mathrm{e}^{\varepsilon W} < \infty$. If also $\lambda\mathbb{E}W^2 < 1$, there exists a unique $y > 1$ which satisfies*

$$y = \frac{1}{\lambda M} \frac{\mathbb{E}(W\mathrm{e}^{\lambda M(y-1)W})}{\mathbb{E}(W^2\mathrm{e}^{\lambda M(y-1)W})},$$

where $M = \mathbb{E}W$. Let $C(G_{N,W})$ be the size of the largest connected component in $G_{N,W}$. Then we have

$$\frac{C(G_{N,W})}{\log(N^2)} \xrightarrow{\mathbb{P}} \frac{1}{\log\gamma} \quad \text{as } N \to \infty,$$

where

$$\gamma := \frac{1}{\lambda\mathbb{E}(W^2\mathrm{e}^{\lambda M(y-1)W})} > 1.$$

Finally, we remark that our analysis based on the inhomogeneous random graph theory is well applicable for models of type (3) even for different distance functions d as, e.g. euclidean distance, as long as one can justify the relations similar to (9) and (27). Also, our approach can be generalized to the similar models in higher dimensions.

4. Proofs

4.1. Random distance graph via inhomogeneous random graphs

Rescale the set V_N as follows:

$$V_N \to \widetilde{V}_N = \left\{ \left(\frac{u_1}{N}, \frac{u_2}{N} \right) \colon (u_1, u_2) \in V_N \right\}.$$

Hence, $\widetilde{V}_N$ is a set of N^2 vertices in the continuous torus $\mathbb{T}^2 := (\mathbb{R}/\mathbb{Z})^2$. Let $\mu_{\mathcal{L}}$ denote the Lebesgue measure on $\mathbb{T}^2$, and let μ_W be the Borel measure on $\mathbb{R}_+$ induced by the random variable W. Denote $\mathcal{S} := \mathbb{T}^2 \times \mathbb{R}_+$, and define the product measure $\mu = \mu_{\mathcal{L}} \times \mu_W$ on this space. Then the triple $\mathcal{V} := (\mathcal{S}, \mu, \{(v, W_v) \colon v \in \widetilde{V}_N\})$ satisfies the definition of a *generalized vertex space* from [6], i.e. for any Borel set $A \subseteq \mathcal{S}$, the following convergence holds:

$$\frac{|\{v \colon (v, W_v) \in A\}|}{N^2} \xrightarrow{\mathbb{P}} \mu(A).$$

Define now, for $u \neq v,\ u, v \in \mathbb{T}^2$, the kernel

$$\kappa_1(u, v) := \frac{1}{\rho(u, v)},$$

where, for any $u = (u_1, u_2), v = (v_1, v_2) \in \mathbb{T}^2$,

$$\rho(u, v) = \rho_1(|u_1 - v_1|) + \rho_1(|u_2 - v_2|)$$

with

$$\rho_1(a) = \begin{cases} a, & 0 \le a \le \frac{1}{2}, \\ 1 - a, & \frac{1}{2} < a \le 1. \end{cases}$$

Furthermore, let $\kappa_2(x, y) := xy$ denote the standard product on $\mathbb{R}_+^2$.

Finally, we define the kernel on $\mathcal{S} \times \mathcal{S}$:

$$\kappa((u, x), (v, y)) := \kappa_1(u, v)\kappa_2(x, y), \qquad (u, x), (v, y) \in \mathcal{S},$$

and construct the random graph $G^{\mathcal{V}}(N^2, \kappa)$ (following the notation of [6]) on a given set $\widetilde{V}_N$ of N^2 vertices in $\mathcal{S}$, by placing an independent edge between any pair of vertices $\boldsymbol{x}_i, \boldsymbol{x}_j \in \widetilde{V}_N$ with probability (see (1))

$$\widetilde{p}(\boldsymbol{x}_i, \boldsymbol{x}_j) := \min\left\{ c\frac{\kappa(\boldsymbol{x}_i, \boldsymbol{x}_j)}{N^2}, 1 \right\}.$$

Proposition 1. *The model G_N is equivalent to the inhomogeneous random graph model $G^{\mathcal{V}}(N^2, \kappa)$.*

Proof. Given a set of types $w_v,\ v \in V_N$, let $\widetilde{v} = v/N$ for any $v \in V_N$. Then the probability of connection (3) satisfies

$$p(u, v) = \min\left\{ c\frac{w_u w_v}{N d(u, v)}, 1 \right\} = \min\left\{ c\frac{\kappa_1(\widetilde{u}, \widetilde{v}) w_u w_v}{N^2}, 1 \right\} = \widetilde{p}((\widetilde{v}, w_v), (\widetilde{u}, w_u)). \quad (9)$$

Hence, given a set of types w_v, $v \in V_N$, there is a connection between any two vertices $u, v \in V_N$ of G_N if and only if there is a connection between the corresponding vertices $(\widetilde{u}, w_u)$ and $(\widetilde{v}, w_v)$ of the graph model $G^{\mathcal{V}}(N^2, \kappa)$. □

It is straightforward to check that the kernel κ is *graphical* (see Definition 2.7 of [6]), since it is continuous, $\kappa \in L^1(\mathcal{S} \times \mathcal{S}, \mu \times \mu)$, and the number of edges in the graph $e(G^{\mathcal{V}}(N^2, \kappa))$ satisfies the following convergence:

$$\frac{1}{N^2}\mathbb{E}e(G^{\mathcal{V}}(N^2, \kappa)) \to \frac{1}{2}\int_{\mathcal{S}}\int_{\mathcal{S}} \kappa(\boldsymbol{x}, \boldsymbol{y})\,\mathrm{d}\boldsymbol{x}\,\mathrm{d}\boldsymbol{y}. \tag{10}$$

4.2. Proof of Theorem 2

Proposition 1, together with (10), allows us to apply some of the results of [6] to our case. In particular, we can approximate the size of the connected component by the total progeny of a multitype Galton–Watson branching process $\mathcal{B}(\kappa)$, with type-space $\mathcal{S}$, where the single ancestor has type $\boldsymbol{x}$, and the number of offspring of type $\boldsymbol{y}$ of each individual of type $\boldsymbol{x} \in \mathcal{S}$ has Poisson distribution with intensity $\kappa(\boldsymbol{x}, \boldsymbol{y})\mu(\mathrm{d}\boldsymbol{y})$. Denote here $\beta_\kappa(\boldsymbol{x})$ and $\mathcal{X}(\boldsymbol{x})$, correspondingly, the survival probability and the size of the total progeny of this branching process with the ancestor of type $\boldsymbol{x}$.

Following [6], let us define the integral operator T_κ:

$$(T_\kappa f)(\boldsymbol{x}) := \int_{\mathcal{S}} \kappa(\boldsymbol{x}, \boldsymbol{y}) f(\boldsymbol{y})\,\mathrm{d}\mu(\boldsymbol{y})$$

for all measurable functions f (when the integral is defined) on $\mathcal{S}$, and define the norm of T_κ as

$$\|T_\kappa\| := \sup\{\|T_\kappa f\|_2 \colon f \geq 0,\ \|f\|_2 \leq 1\}. \tag{11}$$

Then, by Theorem 3.1 of [6] (whose applicability here is granted by Proposition 1), we immediately obtain

$$\frac{C(G_{N,W})}{N^2} \xrightarrow{\mathbb{P}} \int_{\mathcal{S}} \beta_\kappa(\boldsymbol{x})\mu(\mathrm{d}\boldsymbol{x}) =: \hat{\beta}. \tag{12}$$

Moreover, it was also proved in [6] that the survival probability β_κ is the maximal solution to

$$f(\boldsymbol{x}) = 1 - \mathrm{e}^{-(T_\kappa f)(\boldsymbol{x})}, \qquad \boldsymbol{x} \in \mathcal{S}, \tag{13}$$

and that $\hat{\beta} > 0$ if and only if

$$\|T_\kappa\| > 1. \tag{14}$$

Observe that it follows directly from the symmetry of our model that the survival probability $\beta_\kappa(\boldsymbol{x})$, where $\boldsymbol{x} = (u, x) \in \mathbb{T}^2 \times \mathbb{R}_+$, does not depend on $u \in \mathbb{T}^2$, but it is only a function of $x \in \mathbb{R}_+$. Hence, we shall simply write the survival probability as

$$\beta_\kappa(\boldsymbol{x}) = \beta_\kappa(x), \qquad \boldsymbol{x} = (u, x) \in \mathcal{S},$$

which, by (13), is the maximal solution to

$$f(x) = 1 - \exp\left(-\lambda \int_0^\infty xyf(y)\mu_W(\mathrm{d}y)\right), \qquad x \in \mathbb{R}_+, \tag{15}$$

i.e. (6). This together with (12) yields (5).

We are left to prove (7). Firstly, one could use definition (11) to derive straightforwardly

$$\|T_\kappa\| = \lambda \mathbb{E} W^2,$$

which together with (14) would yield (7). However, it is easier to derive (7) using direct relations between the defined above multitype branching process and a certain homogeneous Galton–Watson process which we define shortly.

Let us introduce first yet another branching process $\mathcal{B}_1(x)$ with type-space $\mathbb{R}_+$, where the single ancestor has type x, and the number of offspring of type $y \in \mathbb{R}_+$ of any individual of type $x \in \mathbb{R}_+$ has Poisson distribution with intensity $\lambda x y \mu_W(\mathrm{d}y)$. Using the same analysis as for $\mathcal{B}$, we obtain the survival probability $\beta^1_\kappa(x)$ of $\mathcal{B}_1(x)$ as the maximum solution to (15). Therefore, in the notation of Theorem 2, it holds that

$$\beta(x) = \beta^1_\kappa(x) = \beta_\kappa(\boldsymbol{x})$$

for all $u \in \mathbb{T}^2$ and for any $\boldsymbol{x} = (u, x)$.

Finally, we define a homogeneous Galton–Watson process $\mathcal{B}_2$. This process starts with one single ancestor and its offspring distribution $\widetilde{Y}$ has a compound Poisson distribution

$$\mathrm{Poisson}(\widetilde{W}\lambda \mathbb{E}(W)),$$

where the random variable $\widetilde{W}$ has the following so-called size-biased distribution:

$$\mu_{\widetilde{W}}(\mathrm{d}y) := \frac{y\mu_W(\mathrm{d}y)}{\mathbb{E}W}.$$

Let us denote $\mathcal{X}_1(x)$ and $\mathcal{X}_2$ as the total progeny of $\mathcal{B}_1(x)$ and $\mathcal{B}_2$, respectively. It was proved in Section 2.2 of [17], that $\mathcal{X}_1(\widetilde{W})$ and $\mathcal{X}_2$ are equal in distribution, i.e.

$$\mathcal{X}_1(\widetilde{W}) \overset{\mathrm{D}}{=} \mathcal{X}_2. \tag{16}$$

In the case of a homogeneous process $\mathcal{B}_2$, the necessary and sufficient condition for a positive survival probability is simply $\mathbb{E}(\widetilde{Y}) = \lambda \mathbb{E}(W^2) > 1$. Therefore, (16) yields $\mathbb{P}(\widetilde{\mathcal{X}}_1(\widetilde{W}) = \infty) > 0$ if and only if $\lambda \mathbb{E}(W^2) > 1$.

It follows by the properties of a Poisson distribution that the type of a randomly chosen offspring of the ancestor in the process $\mathcal{B}_1(x)$ has distribution $\widetilde{W}$ for any $x \in \mathbb{R}_+$. Hence, for any x, the process $\mathcal{B}_1(x)$ survives with a positive probability (i.e. $\beta^1_\kappa(x) > 0$), if $\mathcal{B}_1(\widetilde{W})$ survives with a positive probability (i.e. $\mathbb{P}(\widetilde{\mathcal{X}}_1(\widetilde{W}) = \infty) > 0$). Since β^1_κ is the maximal solution to (15), i.e. to (6), it follows that $\hat{\beta} > 0$ (see (5)) if $\lambda \mathbb{E}(W^2) > 1$.

On the other hand, if $\mathcal{B}_1(\widetilde{W})$ survives with probability 0 (i.e. if $\lambda \mathbb{E}(W^2) \leq 1$) then the equality

$$0 = \mathbb{P}(\widetilde{\mathcal{X}}_1(\widetilde{W}) = \infty) = \int_{\mathbb{R}_+} \mathbb{P}(\widetilde{\mathcal{X}}_1(x) = \infty)\mu_{\widetilde{W}}(\mathrm{d}x) = \int_{\mathbb{R}_+} \beta^1_\kappa(x)\mu_{\widetilde{W}}(\mathrm{d}x)$$

implies that $\beta^1_\kappa = 0$, $\mu_{\widetilde{W}}$-almost surely (a.s.), and, hence, μ_W-a.s. Since β^1_κ is the maximal solution to (15), i.e. to (6), it follows that in this case $\hat{\beta} = 0$.

Summarizing, we find that $\hat{\beta} > 0$ if and only if $\lambda \mathbb{E}(W^2) > 1$. In turn, this yields $\|T_\kappa\| = \lambda \mathbb{E}(W^2)$. This proves the theorem. □

4.3. Proof of Theorem 1

4.3.1. *Breadth-first search.* Let us fix a vertex $v \in V_N$ arbitrarily and let $C_v(N)$ denote the connected component containing v. We use a standard procedure to reveal $C_v(N)$, an exploration algorithm known as the *breadth-first search* (see, e.g. [2] or [21]). This is defined as follows.

In the course of exploration, the vertices of G_N can be in one of the three states: *active*, *saturated*, or *neutral*. At time $i = 0$, the vertex v is set to be active, while all the other vertices are neutral. This ends step $i = 0$.

We denote by S_i the set of active vertices at time i. Hence, $|S_0| = 1$. The state of a vertex changes during the exploration of $C_v(N)$ as follows.

At each time step $i \geq 1$, we choose an active vertex in S_{i-1} uniformly at random and denote it by v_i. Then each vertex u which is neutral after step $i-1$ becomes active at step i, if it is connected to v_i; otherwise, u stays neutral. After searching the entire set of neutral vertices the vertex v_i becomes saturated. This finishes the ith step of the exploration algorithm.

The process stops when there are no more active vertices, i.e. at the first time i when $|S_i| = 0$, that is, at time

$$T = \min\{i \geq 1 \colon |S_i| = 0\}. \tag{17}$$

At this time all considered vertices are saturated and they do not have any connection to the neutral vertices. Hence, $C_v(N)$ coincides with the set of saturated vertices, and, thus, $|C_v(N)| = T$.

Let X_i denote the number of vertices becoming active at the ith step. Then the following recursion holds:

$$|S_0| = 1, \qquad |S_i| = |S_{i-1}| + X_i - 1 = X_1 + \cdots + X_i - (i-1). \tag{18}$$

Correspondingly, we can rewrite T, defined in (17), as follows:

$$T = \min\{i \geq 1 \colon X_1 + \cdots + X_i = i - 1\}.$$

4.3.2. *Subcritical case.* In this section we assume that $\lambda < 1$ and we prove part (i) of Theorem 1.

Upper bound. We start by finding an upper bound on $C(G_N)$, the size of the largest connected component. Namely, we prove that, for any positive ε,

$$\mathbb{P}\left\{\frac{C(G_N)}{\log N} < \frac{2}{1-\lambda-\log\lambda} + \varepsilon\right\} \to 1 \quad \text{as } N \to \infty. \tag{19}$$

The proof is based on the exploration algorithm described above. We also use essentially the geometry of the discrete torus with the distance defined in (2). Recall, in particular, that the number N_r of vertices at distance r from any given vertex, for N odd, is given by

$$N_r = \begin{cases} 4r, & 1 \leq r \leq \lfloor N/2 \rfloor, \\ 4(N-r), & \lfloor N/2 \rfloor < r \leq N; \end{cases} \tag{20}$$

while for N even, it is given by

$$N_r = \begin{cases} 4r, & 1 \leq r < N/2, \\ 2(N-1), & r = N/2, \\ 4(N-r), & N/2 < r < N, \\ 1, & r = N. \end{cases} \tag{21}$$

Recall that the vertices becoming active at the ith step are connected to the vertex v_i. Let $X_{i,r}$ denote the number of vertices at distance r from vertex v_i, which become active at the ith step. Hence,

$$X_i = \sum_{r=1}^{N} X_{i,r}.$$

Let U_i denote the number of active and saturated vertices at time i (in other words, U_i is the number of vertices revealed by time i). In particular, by (18), we have

$$U_i = |S_i| + i. \tag{22}$$

Correspondingly, for any vertex u, let $U_{i,r}(u)$ be the number of active and saturated vertices at time i, which are at distance r from u. In particular, for any $i \geq 1$ and any vertex u, it holds that

$$\sum_{r=1}^{N} U_{i,r}(u) = U_i.$$

The number $X_{i,r}$ depends on the number $U_{i-1,r}(v_i)$ of active and saturated vertices at time $i-1$ which are at distance r from v_i, in the following way:

$$X_{i,r}|_{U_{i-1,r}(v_i)} \in \text{binomial}(N_r - U_{i-1,r}(v_i), p_r), \tag{23}$$

where we use the notation

$$p_r = \frac{c}{Nr} = p(u,v) \quad \text{if } d(u,v) = r.$$

Remark 2. In (23) and elsewhere, we write a random parameter for a distribution with the usual meaning that the distribution is defined conditionally on a given value of the parameter.

Let us introduce the random variables

$$Z_{i,r} \in \text{binomial}(U_{i-1,r}(v_i), p_r), \qquad X^+_{i,r} = X_{i,r} + Z_{i,r} \in \text{binomial}(N_r, p_r).$$

Then, we define

$$X^+_i := \sum_{r=1}^{N} X^+_{i,r}.$$

If a random variable ξ stochastically dominates η we denote this by $\eta \preceq \xi$.

It is clear from the above definition that $X_{i,r} \preceq X^+_{i,r}$, and, correspondingly, $X_i \preceq X^+_i$. Therefore,

$$|S_i| \preceq S^+_i := X^+_1 + \cdots + X^+_i - (i-1).$$

Note that the largest connected component has size larger than k if and only if there is a component of size at least k. Then

$$\mathbb{P}\{C(G_N) \geq k\} = \mathbb{P}\{\text{there exists } v \colon |C_v(N)| \geq k\} = \mathbb{P}\left\{\bigcup_{v \in V} \{|C_v(N)| \geq k\}\right\}.$$

It follows simply by the symmetry of the model that the random variables $|C_v|$, $v \in V_N$, are equally distributed. This allows us to derive, from the last equation, the following bound:

$$\mathbb{P}\{C(G_N) \geq k\} \leq N^2 \mathbb{P}\{|C_v(N)| \geq k\} \tag{24}$$

for any arbitrarily fixed vertex v.

By the exploration algorithm, we find that the probability for a component $C_v(N)$ to be larger or equal to k is equal to the probability of having active vertices in each of the $k-1$ steps of the exploration, hence,

$$\begin{aligned}\mathbb{P}\{|C_v(N)| \geq k\} &= \mathbb{P}\{|S_t| > 0 \text{ for all } t \leq k-1\} \\ &\leq \mathbb{P}\{S^+_t > 0 \text{ for all } t \leq k-1\}\end{aligned}$$

$$\leq \mathbb{P}\{S_{k-1}^{+} > 0\}$$
$$= \mathbb{P}\left\{\sum_{t=1}^{k-1} X_t^{+} - (k-2) > 0\right\}. \tag{25}$$

We use the coupling method described in [11] for finding stochastic bounds on X_i^{+}. It follows that $X_{i,r}^{+}$ is stochastically bounded from above by a random variable $Y_{i,r} \stackrel{\mathrm{D}}{=} \text{Poisson}(-N_r \log(1-p_r))$, i.e. $X_{i,r}^{+} \preceq Y_{i,r}$. Therefore, we can stochastically bound X_i^{+} by a Poisson random variable as follows:

$$X_i^{+} \preceq \sum_{r=1}^{N} Y_{i,r} \in \text{Poisson}\left(\sum_{r=1}^{N} -N_r \log(1-p_r)\right) = \text{Poisson}(\lambda_N), \tag{26}$$

where

$$\begin{aligned}\lambda_N &= \sum_{r=1}^{N} -N_r \log(1-p_r)\\ &= \sum_{r=1}^{N} N_r(p_r + o(p_r))\\ &= \sum_{r=1}^{\lfloor N/2 \rfloor} 4r(p_r + o(p_r)) + \sum_{r=\lfloor N/2 \rfloor + 1}^{N} 4(N-r)(p_r + o(p_r))\\ &= \lambda - \frac{2c}{N} + o\left(\frac{1}{N}\right).\end{aligned} \tag{27}$$

Let Y_i, $i \geq 1$, be i.i.d. random variables with Poisson(λ_N) distribution. Then we derive, using (25) and (26) with (27), the following upper bound for the probability in (24):

$$\mathbb{P}\{C(G_N) \geq k\} \leq N^2 \mathbb{P}\left\{\sum_{t=1}^{k-1} X_t^{+} > k-2\right\} \leq N^2 \mathbb{P}\left\{\sum_{t=1}^{k-1} Y_t > k-2\right\}. \tag{28}$$

Using Chebyshev's inequality in (28), for any $h > 0$, we have

$$\begin{aligned}\mathbb{P}\{C(G_N) \geq k\} &\leq N^2 \mathbb{P}\left\{\sum_{t=1}^{k-1} Y_t > k-2\right\}\\ &\leq \frac{N^2 \prod_{t=1}^{k-1} \mathbb{E}\mathrm{e}^{hY_t}}{\mathrm{e}^{h(k-2)}}\\ &= N^2 \exp(-h(k-2)) \prod_{t=1}^{k-1} \exp(\lambda_N(\mathrm{e}^h - 1))\\ &= N^2 \exp(-h(k-2)) \exp((k-1)\lambda_N(\mathrm{e}^h - 1)).\end{aligned} \tag{29}$$

The last equation attains its minimum at $h = \log((k-1)/k\lambda)$, where it is equal to

$$N^2 \exp(k(1 - \lambda + \log\lambda) + ko(1)).$$

Therefore, setting $k = (2/(\lambda - 1 - \log\lambda) + \varepsilon)\log N$ in (29), we find that (19) holds.

Lower bound. To complete the proof of (4), we will prove that, for any $\varepsilon > 0$,

$$\mathbb{P}\left\{\frac{C(G_N)}{\log N} > \frac{2}{1-\lambda-\log\lambda} - \varepsilon\right\} \to 1 \quad \text{as } N \to \infty. \tag{30}$$

Before proceeding to the proof of (30), we derive a useful result, which roughly speaking tells us that removing an arbitrary set of $o(N^2)$ vertices from V_N does not change (asymptotically as $N \to \infty$) the expected degree of a vertex.

Lemma 1. *Let $n_r, r = 1, \ldots, N$, with $0 \le n_r \le N_r$, be an arbitrary sequence such that*

$$\sum_{r=1}^{N} n_r = o(N^2).$$

Then

$$\frac{1}{N}\sum_{r=1}^{N}\frac{n_r}{r} \to 0 \quad \text{as } N \to \infty.$$

Proof. We prove the lemma by contradiction. Assume there exists a constant $c > 0$ such that, for any $M \in \mathbb{N}$, there exists $N \ge M$ such that

$$\frac{1}{N}\sum_{r=1}^{N}\frac{n_r}{r} \ge c. \tag{31}$$

Let $0 < \delta < \min\{4, c\}$ and define the sets $\mathcal{N}_\delta$ and its complementary $\overline{\mathcal{N}}_\delta$ as follows:

$$\mathcal{N}_\delta = \{r \in \{1, \ldots, N\} : n_r \ge \delta r\}, \qquad \overline{\mathcal{N}}_\delta = \{r \in \{1, \ldots, N\} : n_r < \delta r\}.$$

Noting that from (20) and (21), we have $n_r \le N_r \le 4r$ for any $0 \le r \le N$, from (31) it follows that

$$\begin{aligned} c &\le \frac{1}{N}\sum_{r=1}^{N}\frac{n_r}{r} \\ &= \frac{1}{N}\left(\sum_{r\in\mathcal{N}_\delta}\frac{n_r}{r} + \sum_{r\in\overline{\mathcal{N}}_\delta}\frac{n_r}{r}\right) \\ &\le \frac{1}{N}\left(\sum_{r\in\mathcal{N}_\delta} 4 + \sum_{r\in\overline{\mathcal{N}}_\delta}\delta\right) \\ &= \frac{1}{N}(4|N_\delta| + \delta\overline{\mathcal{N}}_\delta) \\ &= \delta + \frac{4-\delta}{N}|N_\delta|. \end{aligned}$$

In particular, we have

$$|N_\delta| \ge \frac{c-\delta}{4-\delta}N,$$

and, therefore,

$$\sum_{r=1}^{N} n_r \ge \sum_{r\in\mathcal{N}_\delta} n_r \ge \sum_{r\in\mathcal{N}_\delta}\delta r \ge \delta\sum_{r=1}^{|\mathcal{N}_\delta|} r \ge \frac{\delta}{2}|\mathcal{N}_\delta|^2 \ge \frac{\delta}{2}\left(\frac{c-\delta}{4-\delta}\right)^2 N^2,$$

which contradicts the assumptions. □

Now we can prove (30). We shall follow the construction used already in [17]. For any vertex v, let $V(C_v(N))$ denote here the set of vertices of the component $C_v(N)$. Observe that G_N can be decomposed into pairwise disjoint connected components as follows. Set $\tilde{v}_1 = v$. Then, given $C_{\tilde{v}_1}(N), \dots, C_{\tilde{v}_k}(N)$, for $k \geq 1$ choose a vertex $\tilde{v}_{k+1}$ uniformly in $V_N \setminus \bigcup_{i=1}^{k} V(C_{\tilde{v}_i}(N))$, unless the last set is empty, in which case we stop the algorithm. The graph G_N is thus decomposed into pairwise disjoint connected components $C_{\tilde{v}_1}(N), \dots, C_{\tilde{v}_M}(N)$, where $M = M(N)$ is a bounded random variable, $1 \leq M \leq N^2$, denoting the number of disjoint components in G_N.

Fix $\varepsilon > 0$ arbitrarily and denote $K_N = (2/(\lambda - 1 - \log\lambda) + \varepsilon)\log N$. Then we define the event

$$E_N = \{C(G_N) \leq K_N\}.$$

Recall that, from (19), it follows that

$$\mathbb{P}\{\bar{E}_N\} \to 0 \quad \text{as } N \to \infty.$$

This yields, for any $k \geq 1$,

$$\begin{aligned}\mathbb{P}\{C(G_N) \leq k\} &= \mathbb{P}\{|C_{\tilde{v}_1}(N)| \leq k, \dots, |C_{\tilde{v}_M}(N)| \leq k\} \\ &\leq \mathbb{P}\{|C_{\tilde{v}_1}(N)| \leq k, \dots, |C_{\tilde{v}_M}(N)| \leq k \mid E_N\} + o(1). \end{aligned} \tag{32}$$

Note that, since conditionally on E_N the largest connected component is smaller than K_N, it follows that $MK_N \geq N^2$. Hence, for any $m_N \leq N^2/K_N \leq M$, the following bound holds for the probability in (32):

$$\begin{aligned}&\mathbb{P}\{|C_{\tilde{v}_1}(N)| \leq k, \dots, |C_{\tilde{v}_M}(N)| \leq k \mid E_N\} \\ &\quad\leq \prod_{i=1}^{m_N} \mathbb{P}\{|C_{\tilde{v}_i}(N)| \leq k \mid |C_{\tilde{v}_1}(N)| \leq k, \dots, |C_{\tilde{v}_{i-1}}(N)| \leq k, E_N\}. \end{aligned} \tag{33}$$

Let $\mathcal{V}_0$ be an arbitrary set of $m_N K_N$ nodes, u be a vertex in $V_N \setminus \mathcal{V}_0$, and let $\tilde{C}_u = \tilde{C}_u(\mathcal{V}_0)$ denote the connected component containing u constructed precisely as the original $C_v(N)$ but on the vertex set $V_N \setminus \mathcal{V}_0$.

Then each factor in (33) can be uniformly bounded as follows:

$$\mathbb{P}\{|C_{\tilde{v}_i}(N)| \leq k \mid |C_{\tilde{v}_1}(N)| \leq k, \dots, |C_{\tilde{v}_{i-1}}(N)| \leq k, E_N\} \leq \max_{\substack{\mathcal{V}_0 \subseteq V_N : |\mathcal{V}_0| = m_N K_N \\ u \in V_N \setminus \mathcal{V}_0}} \mathbb{P}\{|\tilde{C}_u| \leq k\},$$

where we simply used the fact that on a smaller set of vertices, the components are smaller as well. Therefore, from (33), it follows that

$$\mathbb{P}\{C(G_N) \leq k\} \leq \Big(\max_{\mathcal{V}_0 :\, |\mathcal{V}_0| = m_N K_N,\, u \in V_N \setminus \mathcal{V}_0} \mathbb{P}\{|\tilde{C}_u| \leq k\}\Big)^{m_N}. \tag{34}$$

In the following, fix the set $\mathcal{V}_0 \subset V_N$ arbitrarily but so that

$$|\mathcal{V}_0| = m_N K_N = o(N^2).$$

Fix a vertex $u \notin \mathcal{V}_0$ arbitrarily, and construct the component $\tilde{C}_u$ on the vertex set $V_N \setminus \mathcal{V}_0$ as described in the exploration algorithm. Let us denote here $u_1, u_2, \dots$, the sequence of saturated vertices (which corresponds to the sequence $v_1, v_2, \dots$, in the original exploration algorithm).

Define $n_r^0(u)$ to be the number of nodes in $\mathcal{V}_0$ which are at distance r from u, so that $0 \leq n_r^0(u) \leq N_r$ and $\sum_{r=1}^{N} n_r^0(u) = |\mathcal{V}_0|$ for any u.

Analogous to the notion used previously, let $\tilde{U}_i$ here denote the number of active and saturated vertices at step i in this new exploration process on $V_N \setminus \mathcal{V}_0$ (see (22)), and $\tilde{U}_{i,r}(w)$ be the number of those vertices at distance r from the vertex w. Let also $n^0_{i,r} = n^0_r(u_i)$ denote the number of the vertices in $\mathcal{V}_0$ which are at distance r from the ith saturated vertex u_i. By this definition, and our assumption on $|\mathcal{V}_0| = o(N^2)$, we have

$$\sum_{r=1}^{N} n^0_{i,r} = |\mathcal{V}_0| = m_N K_N = o(N^2) \quad \text{for any } i. \tag{35}$$

Hence, the number of vertices activated at step i at distance r from the ith explored vertex, which we denote $\tilde{X}_{i,r}$, has the following distribution:

$$\tilde{X}_{i,r} \in \text{binomial}(N_r - n^0_{i,r} - \tilde{U}_{i-1,r}(u_i),\, p_r),$$

and the total number of vertices activated at the ith step is given by

$$\tilde{X}_i = \sum_{r=1}^{N} \tilde{X}_{i,r}.$$

Using these definitions, we derive, for any $k \geq 1$,

$$\mathbb{P}\{|\tilde{C}_u| > k\} \geq \mathbb{P}\{\tilde{X}_1 + \tilde{X}_2 + \cdots + \tilde{X}_t > t - 1 \text{ for all } t \leq k - 1\}. \tag{36}$$

To approximate the distribution of $\tilde{X}_i$ in the last equation, let us recall the following result on the Poisson approximation.

Lemma 2. (See, e.g. [21].) *On a rich enough probability space, we can define a random vector* (X, Y) *so that* $X \overset{\text{D}}{=} \text{binomial}(n, \lambda/n)$, $Y \overset{\text{D}}{=} \text{Poisson}(\lambda)$, *and, moreover,*

$$\mathbb{P}(X \neq Y) \leq \frac{\lambda^2}{n}.$$

Given the numbers $0 \leq k_{i,r} \leq N_r - n^0_{i,r}$, $r = 1, \ldots, N$, $i = 1, \ldots, k-1$, such that

$$\sum_{r=1}^{N} k_{i,r} \leq k, \tag{37}$$

let us define couplings $(\tilde{X}_{i,r}, \tilde{Z}_{i,r})$ with the Poisson random variables

$$\tilde{Z}_{i,r} \in \text{Poisson}((N_r - n^0_{i,r} - k_{i,r})p_r),$$

which satisfy the conditions in Lemma 2.

Then

$$\tilde{Z}_i = \sum_{r=1}^{N} \tilde{Z}_{i,r} \in \text{Poisson}(\lambda_{i,N}), \tag{38}$$

where

$$\lambda_{i,N} = \sum_{r=1}^{N} (N_r - n^0_{i,r} - k_{i,r})\, p_r. \tag{39}$$

To simplify the notation, define the event

$$F_N = \{\tilde{U}_{i,r} = k_{i,r}, \sum_{r=1}^{N} k_{i,r} \leq k \text{ for all } i \leq k-1,\ r = 1, \ldots, N\}$$

and consider

$$\begin{aligned}\mathbb{P}(\tilde{Z}_i > k \mid F_N) &= \mathbb{P}(\tilde{Z}_i > k, \tilde{Z}_i = \tilde{X}_i \mid F_N) + \mathbb{P}(\tilde{Z}_i > k, \tilde{Z}_i \neq \tilde{X}_i \mid F_N)\\ &\le \mathbb{P}(\tilde{X}_i > k \mid F_N) + \mathbb{P}(\tilde{Z}_i \neq \tilde{X}_i \mid F_N).\end{aligned}$$

Note that

$$\begin{aligned}\mathbb{P}\{\tilde{X}_i \neq \tilde{Z}_i \mid F_N\} &= \mathbb{P}\left\{\sum_{r=1}^{N} \tilde{X}_{i,r} \neq \sum_{r=1}^{N} \tilde{Z}_{i,r} \;\middle|\; F_N\right\}\\ &\le \mathbb{P}\left\{\bigcup_{r=1}^{N} \{\tilde{X}_{i,r} \neq \tilde{Z}_{i,r}\} \;\middle|\; F_N\right\}\\ &\le \sum_{r=1}^{N} \mathbb{P}\{\tilde{X}_{i,r} \neq \tilde{Z}_{i,r} \mid F_N\}.\end{aligned}$$

By Lemma 2, we have

$$\mathbb{P}\{\tilde{X}_{i,r} \neq \tilde{Z}_{i,r} \mid F_N\} \le p_r^2(N_r - n_{i,r}^0 - k_{i,r}),$$

which yields

$$\begin{aligned}\mathbb{P}\{\tilde{X}_i \neq \tilde{Z}_i \mid F_N\} &\le \sum_{r=1}^{N} p_r^2(N_r - n_{i,r}^0 - k_{i,r})\\ &= \frac{c^2}{N^2} \sum_{r=1}^{N} \frac{1}{r^2}(N_r - n_{i,r}^0 - k_{i,r})\\ &= O\left(\frac{\log N}{N^2}\right),\end{aligned} \tag{40}$$

uniformly in i.

Next we consider

$$\begin{aligned}&\mathbb{P}\{\tilde{Z}_1 + \cdots + \tilde{Z}_t > t - 1 \text{ for all } t \le k - 1\}\\ &\quad\le \mathbb{P}\{\tilde{X}_1 + \cdots + \tilde{X}_t > t - 1 \text{ for all } t \le k - 1 \mid F_N\} + \sum_{s=1}^{k-1} \mathbb{P}\{\tilde{X}_s \neq \tilde{Z}_s \mid F_N\}.\end{aligned} \tag{41}$$

Note that, by (40),

$$\varepsilon_k(N) := \sum_{s=1}^{k-1} \mathbb{P}\{\tilde{X}_s \neq \tilde{Z}_s \mid F_N\} = O\left(\frac{k \log N}{N^2}\right). \tag{42}$$

Therefore, (41) yields

$$\begin{aligned}&\mathbb{P}\{\tilde{X}_1 + \cdots + \tilde{X}_t > t - 1 \text{ for all } t \le k - 1 \mid F_N\}\\ &\quad\ge \mathbb{P}\{\tilde{Z}_1 + \cdots + \tilde{Z}_t > t - 1 \text{ for all } t \le k - 1\} - \varepsilon_k(N).\end{aligned} \tag{43}$$

We shall construct i.i.d. random variables $\tilde{Z}_i^-$, $1 \le i \le k$, which are a.s. smaller than $\tilde{Z}_i$, $1 \le i \le k$, correspondingly.

First, using assumption (35) and Lemma 1, we derive

$$\sum_r n_{i,r}^0 p_r = \frac{c}{N} \sum_r \frac{n_{i,r}^0}{r} = o(1). \tag{44}$$

From now on, we shall assume that

$$k = a \log N \quad \text{for some positive } a. \tag{45}$$

Under this assumption, we have

$$\sum_r k_{i,r} p_r = \frac{c}{N} \sum_{r=1}^N \frac{k_{i,r}}{r} \le \frac{c}{N} \sum_r k_{i,r} = \frac{kc}{N} = \frac{ac \log N}{N} = o(1). \tag{46}$$

Hence, from (44) and (46), we obtain the following bound for $\lambda_{i,N}$ defined in (39):

$$\lambda_{i,N} = \sum_{r=1}^N (N_r - n_{i,r}^0 - k_{i,r}) p_r \ge \sum_{r=1}^N N_r p_r + o_i(1), \tag{47}$$

where $o_i(1)$ might depend on i. Note that, by (27),

$$\sum_{r=1}^N N_r p_r = \lambda + o(1). \tag{48}$$

Hence, for any (constant)

$$\lambda' < \lambda, \tag{49}$$

(47) together with (48) yields the following uniform in $i \le k$ bound:

$$\lambda_{i,N} > \lambda'. \tag{50}$$

Recall that $\tilde{Z}_i \in \text{Poisson}(\lambda_{i,N})$ by (38). Therefore, (50) allows us to construct independent $\tilde{Z}_i^- \in \text{Poisson}(\lambda')$, $1 \le i \le k$, such that

$$\tilde{Z}_i^- \le \tilde{Z}_i \quad \text{a.s. for each } i.$$

Now we can derive the following bound:

$$\begin{aligned}\mathbb{P}(\tilde{Z}_1 + \ldots, \tilde{Z}_t > t-1,\ t = 1, \ldots, k-1) &\ge \mathbb{P}(\tilde{Z}_1^- + \cdots + \tilde{Z}_t^- > t-1,\ t = 1, \ldots, k-1) \\ &= \mathbb{P}\{\mathcal{T} \ge k\},\end{aligned}$$

where $\mathcal{T}$ denotes the total progeny of a branching process with offspring distribution Poisson(λ'). Substituting this bound into (43), we obtain

$$\mathbb{P}\{\tilde{X}_1 + \cdots + \tilde{X}_t > t-1 \text{ for all } t \le k-1 \mid F_N\} \ge \mathbb{P}\{\mathcal{T} \ge k\} - \varepsilon_k(N),$$

where the right-hand side is uniform in F_N (here we still assume conditions (37) and (45)). This yields

$$\mathbb{P}\{\tilde{X}_1 + \cdots + \tilde{X}_t > t-1 \text{ for all } t \le k-1\} \ge \mathbb{P}\{\mathcal{T} \ge k\} - \varepsilon_k(N),$$

and, therefore, by (36),

$$\mathbb{P}\{|\tilde{C}_u| \le k\} \le 1 - \mathbb{P}\{\mathcal{T} \ge k\} + \varepsilon_k(N). \tag{51}$$

Using a well-known formula for the distribution of the progeny of a branching process (see, e.g. [13]), we compute

$$\mathbb{P}\{\mathcal{T} \ge k\} = \sum_{j=k}^{\infty} \frac{(\lambda' j)^{j-1}}{j!} \mathrm{e}^{\lambda' j} \ge \frac{(\lambda' k)^{k-1}}{k!} \mathrm{e}^{\lambda' k},$$

which, together with the Stirling formula, yields

$$\mathbb{P}\{\mathcal{T} \ge k\} \ge \frac{1}{\sqrt{2\pi}\lambda'} \frac{1}{k^{3/2}} \mathrm{e}^{-\alpha k} \left(1 + O\left(\frac{1}{k}\right)\right), \tag{52}$$

where

$$\alpha = \lambda' - 1 - \log \lambda'. \tag{53}$$

Substituting (52) into (51), we obtain, using (42) for $k = a \log N$,

$$\mathbb{P}\{|\tilde{C}_u| \le a \log N\} \le 1 - \frac{1}{A_N}(1 + o(1)) + O\left(\left(\frac{\log N}{N}\right)^2\right), \tag{54}$$

where

$$A_N = \sqrt{2\pi}\lambda'(a \log N)^{3/2} N^{a\alpha}.$$

Choose now arbitrarily a constant

$$a < \frac{2}{\alpha}. \tag{55}$$

Then (54) yields

$$\mathbb{P}\{|\tilde{C}_u| \le a \log N\} \le 1 - \frac{1}{A_N}(1 + o(1)). \tag{56}$$

Observe that the value on the right-hand side of the above equation is uniform in the choice of the set $\mathcal{V}_0$ and vertex u. Therefore, we can use bound (56) in (34) to obtain

$$\mathbb{P}\{C(G_N) \le a \log N\} \le \left(1 - \frac{1}{A_N}(1 + o(1))\right)^{m_N}. \tag{57}$$

Finally, we choose

$$m_N = A_N \log N \gg A_N,$$

which by (55) also satisfies condition (35), i.e.

$$m_N K_N = o(N^2),$$

where

$$K_N = \left(\frac{2}{\lambda - 1 - \log \lambda} + \varepsilon\right) \log N.$$

With this choice of m_N, bound (57) implies that

$$\mathbb{P}\{C(G_N) \le a \log N\} = o(1) \tag{58}$$

for any fixed constant (see (53) and (55))

$$a < \frac{2}{\alpha} = \frac{2}{\lambda' - 1 - \log \lambda'}.$$

By (49), here we can choose any $\lambda' < \lambda$; therefore, it follows that (58) holds for any

$$a < \frac{2}{\lambda - 1 - \log \lambda}.$$

This proves (30), and, therefore, part (i) of Theorem 1 is proved.

This completes the proof of Theorem 1, since part (ii) follows by Theorem 2. □

4.4. Outline of the proof of Theorem 3

A proof of Theorem 3 can be obtained by following the same strategy as in the proof of Theorem 1(i), in combination with the proof of the corresponding result for the rank-1 model (8) given in [17]. Therefore, we omit the details here.

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Structure of a randomly grown 2-d network

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ABSTRACT

We introduce a growing random network on a plane as a model of a growing neuronal network. The properties of the structure of the induced graph are derived. We compare our results with available data. In particular, it is shown that depending on the parameters of the model the system undergoes in time different phases of the structure. We conclude with a possible explanation of some empirical data on the connections between neurons.

1. Introduction

Random graphs are commonly used in this century as an important tool to model and to analyse the structure and dynamics of real networks, in particular, neural networks (e.g. Bollobás et al. (2009), Bullmore and Sporns (2009)). The relations between the structure of a network and its functional properties are intensively studied. It is clear that the structure should affect the performance, especially when it concerns dynamical processes on networks, which in turn may change the network itself (consult Kozma and Puljic (2015) on a recent development in this area). These questions generate a lot of mathematical problems, answers to which might contribute to better understanding of the physiology of the brain. Although the models cannot reproduce a living brain, they may close approximate at least some experiments *in-vitro* (see the discussion on the related two-dimensional models in Eckmann et al. (2007)).

Developments in graph theory initiated on-going debates to which class of random graphs (if any) the neuronal networks might belong to. Particularly, the issue of finding scale-free properties attracted a lot of attention (see e.g., Kozma and Puljic (2015) on recent references on this topic).

Clearly, it is not just an architecture itself what is in focus, but its relation to the functioning of the networks. Perhaps the most challenging questions are:

1. How to derive the principles of geometric organization of a network using (limited) data on the activity of the network itself?
2. Or inverse question, is it possible to predict the functional properties of the network given its architecture?

For example, there is a long-standing conjecture on synfire chains as very efficient functional subgraphs in the brain. There have been a number of attempts to prove formation of such chains in an originally homogeneous complete network in a course of learning (e.g. Turova (2014)), which most often means pruning of connections according to some rules. Inevitably the resulting graph, even after some training due to external simulations, depends on the initial condition, which is most often taken as a random classical graph.

In this paper we address the issue of this initial condition: what is the initial architecture which eventually can be moulded into a functional neuronal network?

Our study is much inspired by the experimental results on growing neuronal networks reported in Perin et al. (2011), as well as by the computational results on the modelling and analysis of 2-dimensional networks presented in Aćimović et al. (2011) and Mäki-Marttunen (2013). In Perin et al. (2011) the authors collect and analyse real experimental data, which are very difficult to obtain, and hence are ought to be incomplete. Use of computer power is a natural way to compensate this incompleteness.

One of rather recently developed simulators of neuronal growth is NETMORPH (Koene et al., 2009). The program allows one to get all the necessary data and helps to develop algorithms to evaluate

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the statistical properties of the structure of simulated networks (Ačimović et al., 2011). The study carried out in Koene et al. (2009) is largely based on earlier neurite growth models introduced by Van Pelt and collaborators (see e.g. van Pelt and Uylings (2002), Uylings et al. (2002)). In particular, in van Pelt and Uylings (2002), neurons are modelled by rooted binary trees. The growth process is described by a time and state-dependent branching process, where the branching probability depends on the centrifugal order of the edge (that is the graph distance of its branching point from the tree root), the number of tips (tree leaves) at a given time, and some other factors influencing the neuronal growth. In that work, it was argued that the baseline branching rate is a monotonically decreasing function of time. An accurate description of the process of outgrowth in van Pelt and Uylings (2002) allows to assess the parameters of the model and verify them with physiological data.

A model similar to van Pelt and Uylings (2002) has been studied in Devaud et al. (2000). The model is somewhat simpler, in the sense that in this case the branching probability is a (time-independent) exponentially decreasing function of the centrifugal order only, and depends on two parameters, found by comparison with experimental data. Remarkably, the model predictions for the value of certain quantities, such as the distribution of the number of tips, are in agreement with observations.

We consider here a model of growing connections between neurons which is much simplified compared to the ones studied in Ačimović et al. (2011) (mainly computationally), in van Pelt and Uylings (2002) or in Devaud et al. (2000). Namely, we assume that the branching intensity is constant in space and time, ignoring thus the centrifugal order of the neurite and the dependence on the number of active ends. Note also the 2-dimensional restriction of our model. Taking advantage of the simplicity of the 2-dimensional setting, our approach however is not restricted to 2D and should allow for 3-dimensional extension (in a separate study though) in the spirit of the model studied in Uylings et al. (2002). The obvious advantage of studying a simpler model is that it allows analytical description. In particular, we address here the metric properties of a randomly grown tree, such as the length and thickness of its edges. Furthermore, we provide computer simulations of our model, which turn out to be to some extent similar to those obtained in Ačimović et al. (2011) with NETMORPH program.

We notice that since our model is too simple to describe any compartment of a neuron, due to its analogy with work of Perin et al. (2011) we shall say that we model terminal branches, or an axonal tree, so that our growing random tree represents a neurite growth. However, the biological limitation of our model is obvious, therefore we mostly use less specified term "connection" throughout the paper.

The goal of our study is to describe the graph properties of a network (as, e.g., probability of connection, degree of the nodes) composed of randomly grown 2D neurites, which are represented by the soma together with a random tree of potential connections. (Note here that we study only "potential connections", i.e., connections which eventually can be active or be abandoned in a course of some dynamics on a network.) One could consider biologically more plausible mechanisms of growing the random trees of (possible) connections. What is also important for our analysis, and goes well in agreement with the morphology of the neurons, is that the dimension of the trees ("thickness" of axons) are much smaller than the dimension of the soma, modelled here as a ball of a given radius around the root of the tree.

Below we identify the probability of connection between two somata with the probability that the axonal tree stemming from the soma of one neuron comes in a certain vicinity of the soma of another neuron. Notice however, that this should be considered as an initial or a preliminary structure: the functioning neuronal network is created in a course of some processes on the initial network, which modify the possible connections, as e.g., by pruning some of them and amplifying others. This learning process is not considered here. Still, we can observe even with this simple model some features reported in Perin et al. (2011) on the "real" (*in-vitro*) neuronal networks.

There are a few examples of randomly grown networks which are well understood analytically by now. These are randomly grown classical graphs, networks with preferential attachment and their modifications. However, these examples do not take into account the metric of the space. On the other hand, a subject of random distance graphs is also well-developed in the last decades (Deijfen et al., 2013; Penrose, 2003). The issue of including space characteristics into the analysis based on theory of percolation on graphs is well recognized (see the discussion in Eckmann et al. (2007)). However, in theoretical papers on this subject (e.g. Deijfen et al. (2013)), as well as in the applications for neuronal networks (Eckmann et al., 2007; Turova and Villa, 2007), usual assumptions are monotonicity and symmetry (as e.g., decay of the strength with distance). Here we shall argue that neither of these assumptions should be considered as a fundamental invariant property of a network. Our observation is in a good agreement with the results reported in Herzog et al. (2007), where it is argued that displacement of axonal fields may optimize the connectivity of a network.

We shall describe the formation of random connections in the network and derive their probabilities. These probabilities provide (at least in theory) a complete description of the network. In particular, this helps to find out the dependence of the connections on the space in time. Observe that we *derive* probabilities of the connections in a growing network, but do not *assign* probabilities which fit data or are optimal in some sense, as it is typically done in computational neuroscience. The model we consider here explains formation of local as well as global connections. The latter is considered to be an important feature of a functional network. In fact, our finding can support and provide some morphological explanation for the so-called patchy connectivity in the cortex, studied in Voges et al. (2010), Herzog et al. (2007), where it is assumed that the dendrites are centered in the soma while the center of mass of axonal fields is at some distance from the soma. In those studies it was also reported that such networks may exhibit so-called small-world properties, which are effectively seen as a relatively small graph distance between the nodes of a graph and are considered important for the efficient transmission of signals on the network and the optimization of wiring costs.

The rest of the paper is organized as follows. In Section 2 we define the model: in Section 2.1 we describe a single unit, and in Section 2.2 we define a network composed of spatially distributed units. The results are given in Section 3. In Section 3.1 we study the degree distribution. In Section 3.2 we study the time and distance-dependent probability of connection between two neurons. We show that this probability is a solution to a certain integral equation which we derive in Section 3.2. Then, in Section 3.3 we discuss one marginal case of a model without branching. Section 3.4 is devoted to the numerical analysis of the spatial density of the simulated axonal arborization. After the concluding remarks in Section 4, we provide the details of the proofs in the Appendix.

2. Model

The model presented here is a (rather crude) simplification of the one simulated and studied in Ačimović et al. (2011). We derive some functional dependencies on the parameters of the distributions of random characteristics of the model, and the degree distribution in particular.

Here we study only the geometry (or structure) of a network. We assume that each unit (neuron) of our network develops

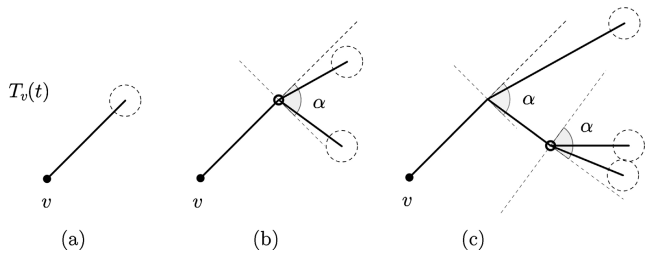

Fig. 1. Example of randomly grown tree $T_v(t)$ defined in Definition 1. (a) An edge starts growing from a vertex v. (b) After an exponentially distributed time a split occurs and two new branches grow with directions chosen independently and uniformly at random in $[-\alpha, \alpha]$. (c) After an exponentially distributed time the rightmost branch splits again, whereas the second branch keeps growing. The splitting points are indicated by an empty disc. The dashed circles denote the active ends.

independently of other units. We start with a description of the dynamics of a single unit.

2.1. A single model neuron

We assume that a neuron is represented by a random tree on a plane with a root at a given point. The root we associate with the soma and the random tree with the axonal arborization.

Let $t \geq 0$ be a parameter of time. At time $t = 0$ a neuron is represented by a point of $\mathbb{R}^2$, say $v \in \mathbb{R}^2$. At any time $t \geq 0$ the structure of the model neuron is given by a graph $T_v(t) \subset \mathbb{R}^2$ which is a random graph (with possible self-intersections) on the plane. The dynamics of $T_v(t)$ is governed by two processes: elongation and branching. This means that from a point v a segment starts to grow at time 0 in a randomly chosen direction with constant speed. We set this speed to be 1, which is not a restriction, since the time can be rescaled. This initial segment splits at some random time, say τ_0, into two segments. The random time τ_0 of splitting is distributed exponentially with mean $1/\lambda$. Then, each of the two new segments develops independently in the same manner. This means that each of the segments chooses uniformly random direction to grow, and then each splits at random times $\tau_0 + \tau_1$ and $\tau_0 + \tau_2$, where all τ_i are independent and identically distributed. Given a graph at some time t each of its ends (tips) continues to grow linearly and splits independently of others.

We consider here a uniform growth, which means that the elongation has a constant speed and the branching intensity λ does not depend on time and on position. Hence, $T_v(t)$ is a random tree on a plane with possible self-intersections, defined as follows.

Definition 1. Let $v \in \mathbb{R}^2$.

1. $T_v(0) = \{v\}$.
2. Let τ be an exponential random variable with expectation $1/\lambda$. Then as long as $t < \tau$ the graph $T_v(t)$ is an interval of length t drawn from v in a randomly chosen direction. v is called root, an interval we call a branch, and the other end of the interval we call the active end.
3. At time τ two independent branches start to grow from the active end: the directions of the new branches are chosen uniformly at random within an angle α which is the highest deviation from the direction of the splitting branch. Each of the new branches splits independently and with the same intensity λ.

Fig. 1 shows an example of the growth process defined above and Fig. 2 provides two typical computer-generated randomly growing trees with different choices of the angle α. In particular, the trees in Fig. 2 can be viewed as a simplified representation of the morphology of a neuron *in vitro*, without distinction between axonal and dendritic trees, as instead it is reproduced by NETMORPH simulations (Fig. 3.1, page 17 in Mäki-Marttunen (2013)).

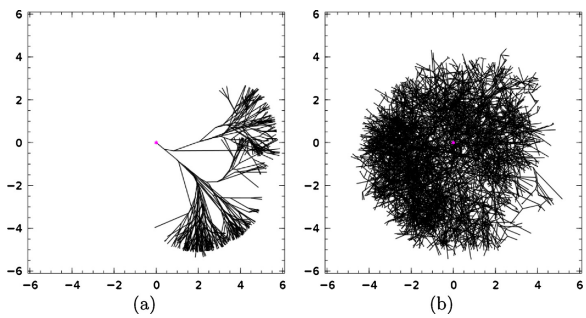

Fig. 2. Computer-simulated random trees with root at origin of the axes and parameter $\lambda = 1$, at time $t = 6$. The direction of the new branches is chosen uniformly at random (2a) in $[-\pi/6, \pi/6]$ and (2b) in $[-\pi, \pi]$.

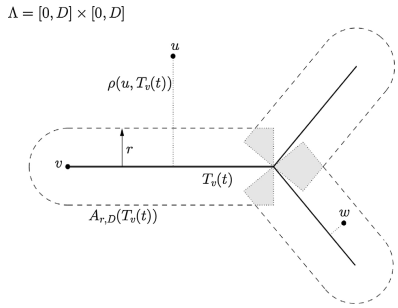

Fig. 3. Example of three Poisson distributed points v, u and w in the region Λ and a randomly grown tree $T_v(t)$ from v. The dotted lines illustrate the distances $\rho(u, T_v(t))$ and $\rho(w, T_v(t))$ from u and w to $T_v(t)$, respectively. The dashed line include the points of Λ within distance r from $T_v(t)$. Here, $A_{r,D}(T_v(t))$ is represented by the area enclosed by the dashed curve. According to the definition, the vertex w is connected with the vertex v, whereas u is not. The area of each shaded region is included twice in the upper bound formula in Eq. (3).

2.2. Network: space dependence

To define a network we assume that the origins of the neurons are placed at random points $v_1, v_2, \ldots$, on a square $\Lambda := [0, D] \times [0, D]$ which form a 2-dimensional Poisson process with intensity μ. Let $V = \{v_1, v_2, \ldots\}$ be the set of origins of neurons, and let $T_v(t)$, $v \in V$, be a collection of independent graphs each of which is defined as above.

We define a distance from neuron v to a neuron u as the smallest Euclidean distance between u and the axonal tree $T_v(t)$ of neuron v, and denote this distance by $\rho(u, T_v(t))$ (see Fig. 3).

Definition 2 *((Distance between neurons in a network at time t)).* . For each $u, v \in \mathbb{R}^2$ and $t \geq 0$, let

$$\rho(u, T_v(t)) := \min\{\|x - u\| : x \in T_v(t)\}. \tag{1}$$

In particular, $\rho(u, T_v(t)) \leq \rho(u, T_v(0)) = \|u - v\|$.

Observe that $\rho_t(u, v)$ for $t > 0$ is a random variable. In particular, even if the Euclidean distances between neurons u, u', v satisfy $\|u - v\| < \|u' - v\|$, it may happen that $\rho(u, T_v(t)) > \rho(u', T_v(t))$. We may assume that the probability of connection between neurons depends on the "actual" distance $\rho(u, T_v(t))$, rather than directly on $\|u - v\|$. This explains some non-monotonicity in the probabilities of connection, even though on average the connectivity among neurons decreases with the intersomatic distance (see e.g., Stepanyants and Chklovskii (2005)). It was also reported in Perin et al. (2011) that unidirectional connections (and this is the case in our model) show less abrupt decrease with intersomatic distance. Such non-monotone features were argued to lead to networks whose connectivity profiles are optimal for information transfer (Herzog et al., 2007; Voges et al., 2010).

Observe that the function $\rho_t(u, v) := \rho(u, T_v(t))$ is random, and the symmetry relation $\rho_t(u, v) = \rho_t(v, u)$ holds *in distribution* only.

We say that there is a synaptic (directed) connection from neuron v to neuron u at time t if u is within distance r to the graph $T_v(t)$, i.e.,

$$\rho(u, T_v(t)) \leq r, \tag{2}$$

where $r > 0$ is a parameter of the model (see Fig. 3).

3. Results

3.1. Degree distribution

For each neuron v we shall study here the (random) number $\nu_v(t)$ of neurons to which it is connected to via its axonal tree at time t.

Recall that we assume that the locations of the soma of neurons are random, it is a Poisson point process with intensity μ. This means that the number of neurons in a bounded subset of Λ with area A is distributed as a Poisson random variable with mean μA. For each neuron v we shall study the (random) number $\nu_v(t)$ of neurons to which it is connected to via its axonal tree at time t. Hence, $\nu_v(t)$ counts the number of points of the Poisson process which are at distance at most r from the tree $T_v(t)$. Denote

$$A_{r,D}(T_v(t)) = \text{area}\left(\Lambda \cap \left\{x : \rho(x, T_v(t)) \leq r\right\}\right)$$

the area of the r-neighbourhood of $T_v(t)$ within the square Λ. Then the degree ν_v of the neuron v is a Poisson-distributed random variable with a random parameter

$$A_{r,D}(T_v(t))\,\mu.$$

Remark 1. If we assume that the origins of the neurons are not forming a Poisson process, but are given with a constant density μ, then the degree of v is simply $A_{r,D}(T_v(t))\,\mu$.

Let $L_v(t)$ denote the total length of all branches of $T_v(t)$, and let $N(T_v(t))$ denote the number of active ends of $T_v(t)$ (the number of "leaves" in graph theory terminology). Observe that if $t < D$ and $|v| + t < D$ (set v at the origin, for example, in order to avoid the boundary effects) then

$$2rt + \pi r^2 \leq A_{r,D}(T_v(t)) \leq 2rL_v(t) + \frac{\pi r^2}{2}(N(T_v(t)) + 1). \tag{3}$$

The lower bound in the inequality represents the area around an edge of length t (remember that we set the elongation speed to 1) and thickness r, that is when no split occurs during the growth process. The example in Fig. 3 provides a graphical explanation of the upper bound.

Note that in our simple tree model the distribution of numbers $L_v(t)$ and $N(T_v(t))$ can be found in a closed form. We will explain below how to derive the moment generating function for $L_v(t)$. We assume here that r is a small parameter, so that $r \ll 1 \ll D$. Then as long as $t < D$ and $rL(t) = o(D^2)$ we have

$$A_r(T_v(t)) \approx 2rL_v(t),$$

in which case the distribution of ν_v is well approximated by the Poisson distribution with random parameter

$$2rL_v(t)\mu.$$

Therefore in order to derive the degree distribution we need to study first the length of the graph. Notice here that the expectation of the length of a tree is given by

$$\mathbf{E}L_v(t) = \frac{e^{\lambda t} - 1}{\lambda}.$$

This and more precise characteristics of $L_v(t)$ will be described in the Appendix.

It is worth noticing that a similar result, that is an exponential growth of the expected length of the tree, has been found in van Pelt and Uylings (2002) as a particular case of the model studied there (cf. van Pelt and Uylings (2002), eq. (17)). The similarity is made clear by noticing that the number of leaves in a binary tree is proportional to the total number of edges, hence to the total length of the tree.

Proposition 3.1. *Let v_v^* be a Poisson-distributed random variable $Po(2rL_v(t)\mu)$. Then its moment generating function is given by*

$$g_{v_v^*}(x) = \mathbf{E}[e^{xv_v^*}] = \frac{\lambda - 2r\mu\,(e^x - 1)}{\lambda - 2r\mu\,(e^x - 1)\,e^{t(\lambda - 2r\mu(e^x-1))}}, \tag{4}$$

which for every t is finite at least for all $0 \le x < c_1(t)$, for some positive $c_1(t)$.

The proof is given in Appendix.

Proposition 3.1 allows us to approximate the tail of the degree v_v, which by the argument above is

$$\mathbf{P}\{v_v(t) > K\} \approx \mathbf{P}\{v_v^* > K\}.$$

Using the generalized Chebyshev's inequality, we derive that for any $t > 0$ and $0 \le \alpha < c_1(t)$ we have that

$$\mathbf{P}\{v_v(t) > K\} \approx \mathbf{P}\{v_v^* > K\} \le e^{-\alpha K}\mathbf{E}[e^{\alpha v_v^*}], \tag{5}$$

where $\mathbf{E}[e^{\alpha v_v^*}]$ is a finite number by Proposition 3.1.

In particular this tells us that the tail of the distribution of v_v is approximately exponential here.

Notice that here we defined the degree v_v as a connection via axon to the soma of another neuron, that is from the tree to the root of another tree. Perhaps, for further studies of the network it is more justified to study connections through the neurite branches as well, i.e. from tree to tree. In this case we may observe a different distribution of the number of connections.

3.2. Geometric properties: probabilities of connection

Here we study the distribution of the tree $T_v(t)$ on the plane. We shall characterize the probability of directed connection from one neuron to another (which is a function of time and the distance between somas of these neurons) as a solution to a certain functional integral equation.

The key idea to derive this equation is based on the recursive structure of a tree. Indeed, given a tree $T_v(t)$, it can be decomposed as a segment stemming from v to the first splitting point and two other trees attached to this endpoint. Therefore, since the edge lengths and the angles are chosen independently, the probability of (not having a) connection from v to a vertex u can be written as a recursive relation according to the above tree decomposition.

We consider first dependence of $\rho(u, T_v(t))$ (see Eq. (1)) on $\|u - v\|$ and t. Due to shift and rotation invariance of the model we have

$$\rho(u, T_v(t)) = \rho(u', T_{v'}(t)), \quad \text{if} \quad \|u' - v'\| = \|u - v\|. \tag{6}$$

Therefore we introduce the probability of connection from the neuron at u to the neuron at v as a function of $\|u - v\|$ and time t. For any fixed positive r define

$$p_r(t, d) := \mathbf{P}\{\rho(u, T_v(t)) \le r \mid \|u - v\| = d\}. \tag{7}$$

Notice that $p_r(t, d)$ as a function of r for any fixed (t, d) is a distribution function of the distance $\rho(u, T_v(t))$ with $\|u - v\| = d$.

We fix r and shall derive a functional equation for

$$q_r(t, d) := \mathbf{P}\{\rho(u, T_v(t)) > r \mid \|u - v\| = d\} = 1 - p_r(t, d) \tag{8}$$

$d > 0$, $t > 0$, with boundary conditions

$$q_r(t, d) = 0, \text{ if } d \le r,\ t \ge 0,$$

$$q_r(t, d) = 1, \text{ if } d > r,\ 0 \le t < d - r.$$

Let S denote the time of first split in the tree $T_v(t)$. By definition S is an exponential random variable with expectation $1/\lambda$, and the tree $T_v(s)$ for $s \le S$ is an interval of length s drawn from v into a random direction α, where α is uniformly distributed over $(0, 2\pi)$.

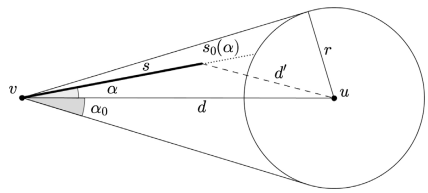

Fig. 4. Regions of integration for the integrals in Eq. (9).

Unless this interval intersects the ball of radius r with center at u (see Fig. 4), two independent processes restart at time S from the end of this interval.

Consider

$$q_r(t, d) = \mathbf{P}\{(\rho(u, T_v(t)) > r) \cap (S \le t) \mid \|u - v\| = d\} + \mathbf{P}\{(\rho(u, T_v(t)) > r) \cap (S > t) \mid \|u - v\| = d\}.$$

Here, the last term on the right is the probability of not having a connection by time t and not having any branching by time t, while the first term on the right is a probability of not having a connection by time t and having *at least one* branching by time t. Observe, that the event $\{S \le t\}$ does include all possible numbers of branching up to time t:

$$\{S \le t\} = \bigcup\nolimits_{k \ge 1} (\{S \le t\} \cap \{\text{there are } k \text{ branchings within time } [0, t]\}).$$

However, to write a recurrent relation below we need to specify only the moment S, after which the process duplicates and two branches evolve independently. Then, using the fact that

$$\mathbf{P}\{S > t\} = e^{-\lambda t},$$

we derive, for $t > d - r$ and $d > r$,

$$q_r(t, d) = \int_{-\alpha_0}^{+\alpha_0}\int_0^{s_0(\alpha)} \frac{\lambda e^{-\lambda s}}{2\pi}(q_r(t - s, d'(s, \alpha)))^2 \mathrm{d}s\mathrm{d}\alpha + \int_{\alpha_0}^{2\pi - \alpha_0}\int_0^t \frac{\lambda e^{-\lambda s}}{2\pi}(q_r(t - s, d'(s, \alpha)))^2 \mathrm{d}s\mathrm{d}\alpha + e^{-\lambda t} f(t, d), \tag{9}$$

where $\alpha_0 = \arcsin\frac{r}{d}$, $s_0(\alpha) = d\cos\alpha - \sqrt{-d^2\sin^2\alpha + r^2}$,

$$d'(s, \alpha) = \sqrt{d^2 + s^2 - 2ds\cos\alpha}$$

is the distance between $u = (d, 0)$ (in polar coordinates with pole v and polar axis $\vec{vu}$) and the first splitting point (s, α) (see Fig. 4), and

$$f(t, d) = \mathbf{P}\{\rho(u, T_v(t)) > r \mid \|u - v\| = d, S > t\}$$

is the probability of not having a connection conditionally that there is no split within time t. We shall explain now each term on the right in more details.

The first term in the right-hand side of the Eq. (9) is the probability not to have a connection, given the first split in the region defined by $-\alpha_0 \le \alpha \le \alpha_0$ and $0 \le s < s_0(\alpha)$. That is the region outside the circle of radius r centered at u and bounded by the rays from v tangent to the circle, see Fig. 4.

The second term is the probability of no connection when the first split happens in the region with $\alpha_0 \le \alpha \le 2\pi - \alpha_0$, where $0 \le s \le t$.

In both of these two first terms on the right in eq. (9) we have functions $q_r(t - s, d')^2$, where s is the moment of the first split. The square comes from the fact that after time s we have two independent branches which evolve during time $t - s$. Hence, if the

probability that a single branch does not make a connection to u is $q_r(t-s, d')$, the probability that no one of these branches will make a connection to neuron u is $q_r(t-s, d')^2$. Again, each of these branches may have any number of splits.

Finally, in the last term $f(t, d)$ is simply the probability that a segment of length s drawn from the origin v to a uniformly random direction does not intersect the circle of radii r centred in u, that is

$$f(t,d)=\begin{cases}1-\frac{1}{\pi}\arccos\frac{d^2+t^2-r^2}{2td}, & \text{if } t\in[d-r,\sqrt{d^2-r^2}];\\ 1-\frac{1}{\pi}\arcsin\frac{r}{d}, & \text{if } t>\sqrt{d^2-r^2}.\end{cases}$$

The Eq. (9) together with (8) define the probability of connection as a solution to this equation. An obvious advantage of having relations (9) is that even if it is not possible to obtain a solution in a closed form it gives a possibility to study it numerically. However, this will be a subject of separate study.

3.3. Marginal case: no branching

Let us consider a marginal case $\lambda = 0$, i.e., no branching occurs and a tree is reduced to a segment. In this case we derive that the probability that at time t there is a connection from a fixed neuron to another one chosen at distance d is

$$p_r(t,d)=\begin{cases}0, & \text{if } t<d-r,\\ \frac{1}{\pi}\arccos\frac{d^2+t^2-r^2}{2td}, & \text{if } t\in[d-r,\sqrt{d^2-r^2}],\\ \frac{1}{\pi}\arcsin\frac{r}{d}, & \text{if } t>\sqrt{d^2-r^2}.\end{cases}\quad(10)$$

This probability decays as r/d for large d or small r, but for fixed d it reaches a constant value with respect to t.

Notice however, the following spatially homogeneous property of the connections. Recall that we consider here directed graphs. Let us assume that one neuron is placed at the origin. Consider the in-degree of this neuron, which is the number of neurons which have connections to the one at the origin.

First, due to the assumptions of the network (without the boundary of the space) we compute the total number of neurons placed in the annulus

$$C_d := \{u\in\mathbb{R}^2 : d\le\|u\|\le d+1\}.$$

The area of C_d is $\pi(2d+1)$, and thus due to our assumptions the number of neurons in C_d is a Poisson random variable

$$Po(\mu\pi(2d+1)).$$

Now taking into account that each of the neurons in C_d is connected independently to the central one with probability $p_r(t, d)$, we get that for large t and d this number is approximately

$$Po\left(\mu(2d+1)\pi\arcsin\frac{r}{d}\right)\approx Po(2\pi\mu r).$$

Hence, on average there are about $2\pi\mu r$ neurons in every annulus of width 1 which are connected to the neuron placed at the origin, and this number does not depend on the distance of the annulus to the origin.

One may speculate that even when $\lambda > 0$, with a small probability some branches of the tree do not branch making a long path and then branch again, making connections to a localized set distant neurons. This might support the idea of Voges et al. (2010) on long-range patchy connections.

3.4. Density of the axonal arborization: simulated results.

We consider and analyse here the spatial properties of the simulated neurite tree for some $\lambda > 0$. One may view the results of this section as an empirical counterpart for Section 3.2, however this could be only a rough approximation.

Given the graph $T_v(t)$, let us consider the disk $D_v(t)$ of radius t centered at v. Let us fix some $n\in\mathbb{N}$, and consider the partition of $D_v(t)$ in n annuli $C_i(t/n)$, $i = 1, \ldots, n$, defined by

$$C_i(t/n)=\{x\in\mathbb{R}^2 : (i-1)t/n<\|x-v\|<it/n\}.$$

For each $i = 1, \ldots, n$, we define the partial length $\ell_v(y_i)$ of the fraction of the graph $T_v(t)$ contained in the circle of radius $y_i = it/n$ and center v. Clearly, by this definition, we have that $\ell_v(y_n) = L_v(t)$. Note that this procedure is very similar to the one described in Uylings et al. (2002) and goes back to the study carried out in Sholl (1953). Next, we set

$$\delta_v(y_i)=\left(\ell_v(y_i)-\ell_v(y_i-t/n)\right)\frac{n}{t},\qquad \text{for}\quad i=1,\ldots,n,$$

as the difference quotient of $\ell_v(y_i)$, that is the length of the graph $T_v(t)$ contained in the annulus $C_i(t/n)$ divided by t/n. We call $\delta_v(y_i)$ the density of $T_v(t)$ in the annulus $C_i(t/n)$. This quantity, as we discuss in the following, will provide an indication of the spatial distribution of the graph around the root v.

Fig. 5 shows a typical computer-generated tree $T_v(t)$ and the corresponding plots of the length $\ell_v(y_i)$ (Fig. 5b) and density $\delta_v(y_i)$ (Fig. 5c).

Hence, for each graph $T_v(t)$ for (at least some) given values t and other fixed parameters (λ is strictly positive) the density of the graph is maximal at a certain distance $d(t) > 0$ from the origin of the neuron. This non-monotonicity affects even the structure of the connections in the network: there will be more connections to the neurons in the area of the maximal density of the branches of $T_v(t)$. In turn one can express this in terms of the probability of connection: *the probability of connection has a maximum at positive distance $d(t)$ from the origin of a neuron*. It is worth noticing that this result supports the models and results reported in Voges et al. (2010), Herzog et al. (2007), although in these papers the authors assumed this type of connection while we were able to derive it from the model of random growth.

Furthermore, the observation on non-monotonicity may also provide some qualitative explanation for the experimental results reported in Perin et al. (2011). Note, however, that neurons considered in Perin et al. (2011) possess a 3-dimensional organization, whereas our model is purely 2-dimensional. On the other hand, the results presented there are obtained from cortical slices consisting of same layer neurons (layer V pyramidal neurons), therefore our model may still catch some of their organizational features.

In particular, it was reported in Perin et al. (2011) (Fig. 3), that the average number of connections in groups of six neurons, as a function of the average intersomatic distance within this group, has a maximum at some positive distance, contrary to the expected monotone decrease. Our analysis may offer the following explanation of this phenomenon. If we would model the dendrites as another random arborization stemming from the soma, then the neurons would be connected if their respective trees of axons and dendrites are overlapping. Then, the existence of a connection from a neuron v to a neuron u indicates the location of overlapping of corresponding trees stemming from u and from v. One may assume that this is the location of the most dense part of the graph and thus it is at some distance from the soma. Then, if another neuron v' has also a connection to u, this indicates that the trees stemming from v and from v' span the same location, and therefore they might form an interconnected group. Furthermore, simply

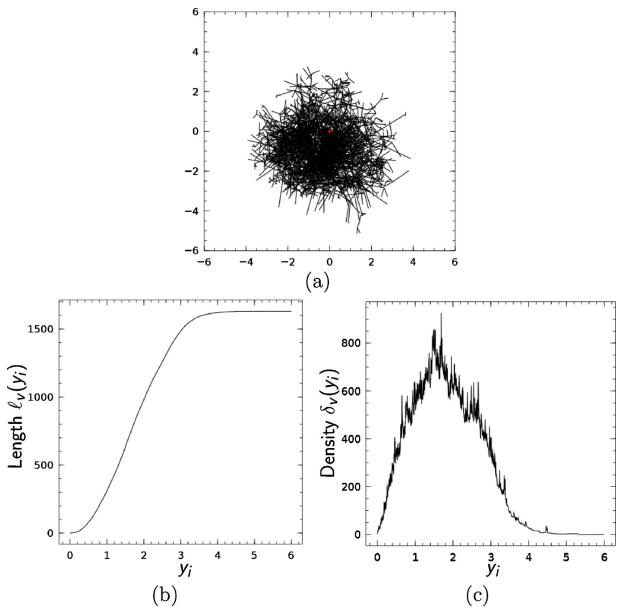

Fig. 5. (a) Computer-simulated random tree at time $t = 6$ with parameter $\lambda = 10/9$, $\alpha = \pi$ and corresponding computer-generated plots of the length $\ell_v(y_i)$ (b) and density $\delta_v(y_i)$ (5c), for $i = 1, \ldots, n$, with $n = 1000$.

due to the geometric constrain that the highest density of connections is at some given distance (say, R) from the soma, the number of neurons in a group which satisfy this condition is also determined by R and the physical size of neurons. Thus, it may well be non-monotone.

Considering connections through the arborization suggests also that the in-degrees of the neurons with overlapping trees might be highly correlated, independently of their intersomatic distance. This indicates non-trivial clustering properties, which are very important for the propagation of signals on a network.

4. Conclusions

The main question we address here is how to incorporate the space characteristics into a mathematically tractable model of a growing graph of connections between neurons. We analyse a simple mathematical model of axonal arborization. We derive some characteristics of a single unit (as the total length of random tree), and the degree distribution for the network of potential connections. We show that the probability of a connection between two neurons, which is a function of time and space, can be described as a solution to some integral equation.

We argue that a functional model of a neural network depends more on the spatial distribution of the graph which models axons and dendrites, rather than on the Euclidean intersomatic distance. In particular, we show that a growing network undergoes phases in time when the probabilities of connections may decay with distance between the origins of the neurons, but on the other hand, there are periods of time when this dependence is suppressed. Furthermore, for some parameters of time the maximal strength of the connections is achieved at a certain positive distance between the neurons.

We also argue that in our model the condition that two neurons have at least one common target neuron increases significantly the probability to have more common target units. Interestingly, this is also in agreement with the observation in Perin et al. (2011) that two neurons are more likely to be connected if they both receive an input from the same common neighbour rather than projecting to the same common neighbour. This is an important clustering property for successful propagation of impulses in a network, which requires a high in-degree. Developing further our simple model should allow to check theoretically many other experimental facts.

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Appendix A.

A.1. Length distribution

Let $L_v(t)$ be the total length of all branches of $T_v(t)$. It is easy to derive that

$$\mathbf{E}L_v(t) = \frac{e^{\lambda t} - 1}{\lambda}.$$

We shall describe the distribution of $L_v(t)$ more precisely. Let $\lambda > 0$ and $t \geq 0$. Consider the moment generating function of $L_v(t)$

$$g(x, t) \equiv g_{L_v(t)}(x) = \mathbf{E}[e^{xL_v(t)}].$$

One can derive that $g(x, t)$ satisfies the integral equation

$$g(x, t) = e^{(x-\lambda)t} + \lambda \int_0^t e^{(x-\lambda)s} g(x, t-s)^2 ds,$$

with boundary condition

$$g(x, 0) = 1.$$

Differentiating with respect to t, we obtain the initial value problem

$$\begin{aligned} &\partial_t g(x, t) = F(x, g(x, t)), \\ &g(x, 0) = 1, \end{aligned} \tag{A.1}$$

where

$$F(x, g(x, t)) = (x - \lambda)g(x, t) + \lambda g(x, t)^2. \tag{A.2}$$

Since the function $F(x, y)$ is continuously differentiable in y on $\mathbb{R}$ for any $x \in \mathbb{R}$, the Picard-Lindelöf theorem ensures existence and uniqueness of a solution to (A.1) on an interval containing $t_0 = 0$, which is given by

$$g(x, t) = \frac{x - \lambda}{xe^{(\lambda - x)t} - \lambda}. \tag{A.3}$$

Analysis of this solution shows that for every $t > 0$ there is a positive value $c(t)$ such that the moment generating function (A.3) is finite on

$$\Delta = \{(x, t) \in \mathbb{R}^2 : t \geq 0, x < c(t)\}.$$

A.2. Proof of Proposition 3.1

Let ν_v^* be a Poisson distributed random variable $Po(2rL_v(t)\mu)$. Then its moment generating function is given by

$$g_{\nu_v^*}(x) = \mathbf{E}[e^{x\nu_v^*}] = \mathbf{E}[e^{2r\mu(e^x - 1)L_v(t)}].$$

Now using the result (A.3) and the definition of function $g(x, t)$ we derive from here

$$g_{\nu_v^*}(x) = g(2r\mu\left(e^x - 1\right), t) = \frac{\lambda - 2r\mu\left(e^x - 1\right)}{\lambda - 2r\mu\left(e^x - 1\right)e^{t(\lambda - 2r\mu(e^x - 1))}}, \tag{A.4}$$

which for every t is finite at least for all $0 \leq x < c_1(t)$, for some $c_1(t) > 0$. This ends the proof.

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Paper IV

Random Distance Networks as a Model of Neuronal Connectivity

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Abstract

We provide an analysis of a randomly grown 2-d network which models dynamics of a growing neuronal network taking into account known empirical features of the brain. We estimate standard network parameters such as degree distribution, average shortest path length and clustering coefficients, considering all these parameters as functions of time. Our results show that even a simple network with just a few parameters is capable of representing a wide spectra of architecture, capturing properties of well-known models, depending on the time of the network development.

These results create a base for further study of neuronal activity on such networks as the introduced model allows not only rather straightforward simulations but it is also amenable to a rigorous analysis.

1 Introduction

Brain connectivity datasets typically represent networks of different parts of the brain connected through anatomical connections (*structural networks*) or through functional connections between the areas of the network (*functional networks*) [4], [17]) . How the brain structure affects the brain performance is an inevitable question in brain studies (see, e.g., discussion in [16]). Furthermore, as the performance may change the brain structure (learning presumably does), the question of the structure seems to be relevant only in the context of certain dynamical processes on networks [9]. Still the underlying physical connections are of the primary interest, as they provide the initial condition for a network to be developed into a functional system.

Viewing neuronal networks as abstract graphs results in numerous attempts to classify these networks using their empirical or statistical characteristics such as for example, degree, clustering coefficient or the shortest path [4]. Since there is only a few different well-studied graph models, this classification remains rather rough as it divides all networks into large classes (see discussion in [7]), most often referring to Erdos-Renyi classic random graphs, regular random graphs [5], or the so-called "small world networks" [23]. It is well recognized that the key challenge for neuromodelling is to develop graph models with adequate representations of biological reality, as e.g., unambiguously assigning edge weights to the connections or interactions between the nodes ([7]).

Classic random graphs have a low average shortest path length but also a low cluster coefficient, while regular networks have high clustering as well as a high average shortest length

path [3]. The so-called small world structure has been considered as a good model both for anatomical and functional connectivity [19] because a low average shortest path length between connected neurons yields a low wiring cost of the system. Furthermore, small world networks exhibit high clustering, which is also considered to be a property of biological networks.

Functional integration usually means existence of strongly connected different regions of the brain. Functional segregation is characterized by the presence in the network of groups called clusters or modules [15] of highly interconnected units (neurons), however the links between the groups might have a different strength. In [18] two measures called *complexity* and *entropy* have been introduced to measure those properties in a graph. To demonstrate the efficiency of such a measurement a network which has a high clustering and a low wiring cost was designed there with a help of a special technique of *graph selection*.

As far as the neuromodelling is concerned all classical random graph models miss the important characteristics, namely the dependence on space, that is, distance between the nodes, and the dependence on time (see discussion in [7]). Experimental data [13] point out that the distance between the neurons (nodes in the graph) may have an important role for the structure and therefore also for the functioning of a neuronal network.

We introduce new models of random graphs which take into consideration the distance and the time aspects. Let us also mention that mathematically tractable related models of distance random graphs have already been introduced in [12]. Recently these models got more attention due to their relation to neural networks [8]. In this paper we develop the network dynamics of the model introduced in [1]. We compare the properties of the introduced models with the general random graph model $G(n, m)$ [5]. Recall that $G(n, m)$ is a random graph with n nodes and m edges chosen at random uniformly out of all possible edges on n nodes without loops.

Here we consider the major characteristics of the graph, the degree distribution, the frequency of connection, the shortest path and the clustering coefficient as functions of the parameters of the network, which are the time, the branching parameter, and the distance between the nodes. We show that tuning the parameters yields structural changes in the model: the model may possess properties closed, e.g., to the ones of a classic random graph, or to the ones of a small world network.

We address also the question of the scalings between the parameters. Even if the size of the neuronal network is finite it is definitely large, and therefore it might be useful to consider limits when the number of the nodes (a large parameter) goes to infinity, in which case all the remaining parameters (can be small parameters as well) must be scaled correspondingly. Using data on physical sizes in a cortex ([14]) one can fit our model into a real scale of biological network.

2 Model

The network we study in this paper has been introduced in [1]. This model is inspired much by the study of dendritic trees in [10] as well as by the data gathered in [13]. The model helps to find out the dependence of the connections on the space in time, and in particular it explains the formation of local and global connections.

Recall a definition of a directed random growing network from [1]. Let the set of vertices V be a random set in a square $\Lambda = [-w, w] \times [-w, w]$, $w \geq 0$ being a parameter. Each vertex $v \in V$ represents the location of a neuron, and a ball of radius r around this vertex represents the physical size of the soma together with an area of dense dendrites of this neuron.

Assume that V has a Poisson distribution with some intensity μ. Hence, on the average there are $(2w)^2\mu$ nodes in Λ.

We assume that each neuron of a network develops its axonal tree independently of other neurons. Notice here that for a simplification we consider only axonal trees. To account for

the dendrites we set a ball of radius r around each location v to represent the physical size of the soma together with an area of dense dendrites of the neuron at v. (A model with dendritic arborization can be treated in a similar way, but this we leave for later studies.)

Let $t \geq 0$ be a parameter of time. At time $t = 0$ each neuron is simply represented by a point v. At any time $t \geq 0$ the structure of a network is given by a random graph (with possible self-intersections) $G(t)$ on Λ whose dynamics is governed by two processes: elongation and branching of each tree independently. Let us describe the dynamics of a single tree.

From a point $v \in V$ a segment, or better a ray, as we actually consider directed graphs, starts to grow at time 0 in a randomly chosen direction with constant speed. We set this speed to be 1, which is not a restriction, since the time can be rescaled. This initial ray splits at some random time into two rays. The time of splitting is exponentially distributed with mean $1/\lambda$. Then, each of the two new rays develops independently in the same manner, but the directions of the new branches are independent random variables uniformly distributed on $[-\alpha, \alpha]$, where parameter $\alpha \in [0, \pi]$ represents the highest deviation from the direction of the splitting ray. This means that each of the rays chooses an independently random direction (within α) to grow, and then each splits independently with the same intensity λ. Hence, any $\alpha < \pi$ yields some memory of direction in the model.

Denote $\mathbf{T}_v(t)$ the resulting tree at time t. Notice, that $\mathbf{T}_v(t)$ is a subset of Λ. Given a graph at some time t each of its ends continues to grow linearly and splits independently of others.

We define a distance from neuron $u \in V$ to a neuron $v \in V$ as the smallest Euclidean distance ($\|\cdot\|$) between u and the tree $\mathbf{T}_v(t)$ and denote this distance by ρ with

$$\rho(u, \mathbf{T}_v(t)) := \min\{\|x - u\| : x \in \mathbf{T}_v(t)\}.$$

We say that a neuron $v \in V$ has a connection to a neuron u at time t if the tree $\mathbf{T}_v(t)$ intersects a ball of radius $r > 0$ (representing the soma) with a center at u, or equivalently,

$$\rho(u, \mathbf{T}_v(t)) \leq r. \tag{1}$$

Finally, define a directed graph $G(t)$ on vertices $V(t)$ by setting an edge from v to u if $\rho(u, \mathbf{T}_v(t)) \leq r$. Denote a probability of this edge by

$$p_{\lambda,\alpha}(t, u, v) = P\{\rho(u, \mathbf{T}_v(t)) \leq r\}. \tag{2}$$

Observe that since every tree develops in the same manner we have

$$P\{\rho(u, \mathbf{T}_v(t)) \leq r\} = P\{\rho(v, \mathbf{T}_u(t)) \leq r\},$$

therefore the probability (2) depends only on $\|u - v\|$:

$$p_{\lambda,\alpha}(t, u, v) = p_{\lambda,\alpha}(t, \|u - v\|) = P\{\rho(u, \mathbf{T}_v(t)) \leq r\}. \tag{3}$$

Recall that in [1] the integral equation was derived for the function $p_{\lambda,\alpha}(t, d)$ for all $\lambda \geq 0$ when $\alpha = \pi$. Let $q_{\lambda,\pi}(t, d) = 1 - p_{\lambda,\pi}(t, d)$. It is derived in [1] that

$$\begin{aligned} q_{\lambda,\pi}(t, d) = &\int_{-\phi_0}^{+\phi_0} \int_0^{s_0(\phi)} \frac{\lambda e^{-\lambda s}}{2\pi} (q_{\lambda,\pi}(t - s, d'(s, \phi)))^2 \mathrm{d}s\mathrm{d}\phi \\ &+ \int_{\phi_0}^{2\pi - \phi_0} \int_0^t \frac{\lambda e^{-\lambda s}}{2\pi} (q_{\lambda,\pi}(t - s, d'(s, \phi)))^2 \mathrm{d}s\mathrm{d}\phi \\ &+ e^{-\lambda t} q_0(t, d), \end{aligned} \tag{4}$$

where

$$\phi_0 = \arcsin \frac{r}{d}$$

$$d'(s,\phi) = \sqrt{d^2 + s^2 - 2ds\cos\phi}$$

and

$$q_0(t,d) = \begin{cases} 1, & \text{if } t < d - r, \\ 1 - \frac{1}{\pi}\arccos\frac{d^2+t^2-r^2}{2td}, & \text{if } t \in [d-r, \sqrt{d^2-r^2}], \\ 1 - \frac{1}{\pi}\arcsin\frac{r}{d}, & \text{if } t > \sqrt{d^2-r^2}\ . \end{cases} \tag{5}$$

The solution to this equation for general $\lambda > 0$ remains to be an open problem, but we treat the case $\lambda = 0$ in detail below.

Our focus here is on the statistics of graph characteristics, such as degree distribution, minimum length path, clustering coefficient, of simulated $G(t)$ for different parameters $\alpha, \lambda, \mu, r, w$. Having in mind the physical interpretation of these parameters we shall assume the following scaling

$$w = \Theta(1), \quad r = o(1), \quad \mu \gg 1, \quad \mu r = o(1), \tag{6}$$

where notation $\Theta(1)$ means "of the order 1". This means that taking a size of the network in 2-dimensional space as a unit, the number of neurons is very high, the axons are very thin. This assumption is in agreement with the biological data on cortex [14] that the dendrites of cells are typically in the region of 500 μm in diameter, and their axons can distribute in patches 200-300 μm across, separated by distances of up to 1 mm ([11]). Notice that we do not fix values w, r, μ, but treat them as variable parameters of the model.

The introduced model is suitable for simulations as well as for a rigorous analysis. It satisfies demands of the neuroscientific community ([7]) to develop graph models with adequate characteristics. In particular, probability of connections defined by (4) as a function of other (biologically motivated) parameters of the model. Similar to (4) equation, however more involved can be derived for general $\alpha \in [0, \pi]$. It was shown in [1] that solution to (4) is not a monotone function of the distance between the nodes. Below we empirically confirm this fact also for $\alpha < \pi$. Observe that although this contradicts a common assumption on the monotone decay of neuronal connections with the distance, non-monotonicity between distances in space and strengths of connections between small group of neurons was already observed by measurements of [13].

We argue that depending on time t graph $G(t)$ undergoes structural transitions, as its characteristics exhibit different features depending on the time of the development. As a null hypothesis we use assumption that the measurements are made on the classic random graph model $G(n, m)$ with n being equal the number of vertices in the considered graph $G(t)$, and m being equal the number of edges in $G(t)$. Notice that one can study this model in a torus to avoid the boundary effects. We will simply consider only the nodes which are far from the boundary. Thus within time $t < w$ the trees of these nodes are less sensitive to the absence of nodes outside of Λ.

3 Network analysis

We shall quantitatively describe the connectivity properties in our model and compare them with the ones which are commonly assumed. In particular, we check what are the conditions to have "hubs", i.e., vertices with a very high degree observed in real neuronal tissue ([22]).

3.1 The degree.

The degree of a node v counts the number of edges which are connected to that node. In the case of a directed network it is natural to define *in-degree* $\nu_v^{in}(t)$ and *out-degree* $\nu_v^{out}(t)$ of a node v which counts the respective edges of $G(t)$ separately. The degree distribution has an

immediate neurobiological interpretation as it might be associated with the number of axons or dendrites.

By definition $\nu_v^{out}(t)$ counts in our model the number of points of the Poisson process on Λ which are at a maximum distance r from the tree $\mathbf{T}_v(t)$. Let $A_r(\mathbf{T}_v(t))$ denote the set of the vertices and $|A_r(\mathbf{T}_v(t))|$ denote the area of the r-neighborhood of $\mathbf{T}_v(t)$ within the square Λ. Then the out-degree of the neuron v is a Poisson-distributed random variable with a random parameter $|A_r(\mathbf{T}_v(t))|\,\mu$ that is

$$\nu_v^{out}(t) \sim \mathrm{Po}(|A_r(\mathbf{T}_v(t))|\,\mu) \tag{7}$$

(we use notation $\sim$ to denote equality in distribution here). Hence, the out-degree for our model has a "light tail", i.e., this does not imply "small-world property". However, below we show that tuning parameters one still can observe "hubs" in this model.

Notice that formula (7) for the out-degree distribution does not use the connection probabilities. However, to compute the in-degree $\nu_v^{in}(t)$ we shall make use of these probabilities. Recall the definition of edges in $G(t)$ (see (1))

$$\nu_v^{in}(t) = \sum_{u\in V\setminus\{v\}} \mathbf{1}_{\{\rho(u,\mathbf{T}_v(t))\le r\}} \stackrel{d}{=} \sum_{u\in V\setminus\{v\}} X_u(t), \tag{8}$$

where, for any t and different u, the random variables $X_u(t)$ are independent and distributed according to a Bernoulli distribution with parameter $p_{\lambda,\alpha}(t,\|u-v\|)$ defined in (3).

3.1.1 No branching case: $\lambda = 0$.

Despite being of limited interest for modelling purposes, mathematically, this specific case $\lambda = 0$ provides inside for the general one as it is exactly solvable and represents a marginal case for the model with a positive branching parameter. When $\lambda = 0$ the tree $\mathbf{T}_v(t)$ is simply a segment of length t, hence

$$|A_r(\mathbf{T}_v(t))| = 2rt + \pi r^2,$$

and in this case using formula (7) we get

$$\nu_v^{out}(t) \sim \mathrm{Po}\left(|A_r(\mathbf{T}_v(t))|\,\mu\right) \sim \mathrm{Po}\left((2rt+\pi r^2)\mu\right). \tag{9}$$

This tells us that for all t as long as $rt\mu = o(1)$ the network consists mainly of disconnected nodes.

Observe that for all $r \le t \le w$, where w is at most of order constant by the assumption (6) all the branches with high probability intersect at a positive angle. Therefore the area of the intersection of r-neighborhood of any tree with the r-neighborhood of all the remaining trees in the network is

$$\mathbf{E}\left|A_r\left(\mathbf{T}_u(t)\right) \cap \cup_{v\in V\setminus\{u\}} A_r\left(\mathbf{T}_v(t)\right)\right| = O\left(r\,|A_r(\mathbf{T}_u(t))|\right) = o\left(|A_r(\mathbf{T}_u(t))|\right).$$

Therefore the out-degrees defined by (9) can approximately be considered as independent since the respective areas of their trees have a very small overlap. Let $D_{max}(t)$ denote the maximal value $D_{max}(t)$ among

$$|V|/4 \sim \mathrm{Po}\left(\mu w^2\right)$$

i.i.d. copies of (9). Due to the properties of the Poisson distribution

$$D_{max}(t) = o_P(1), \text{ if } \mu rt \ll \frac{1}{\mu}, \tag{10}$$

$$D_{max}(t) = \Theta_P(1), \text{ if } \mu r t \sim \frac{1}{\mu}, \tag{11}$$

and with a high probability

$$\frac{\log \mu}{\log\log \mu + |\log c|} \ll D_{max}(t) \ll \left(\frac{\log \mu}{|\log(\mu r t)|}\right), \text{ if } \mu r t \gg \frac{1}{\mu}. \tag{12}$$

The last bound together with our assumptions (6) tells us that the meaningful range of parameters allowing "hubs" with high out-degree in the network requires the following condition

$$\frac{1}{\mu^2} \ll r \ll \frac{1}{\mu}. \tag{13}$$

Consider now the in-degree. First we note that by (5) (see also [1], Section 3.3) when $\lambda = 0$ the probability $p_0(t, d)$ that at time t there is a connection from a fixed neuron v to another one u at distance $d = \|u - v\| > r$ is given by

$$p_0(t,d) = \begin{cases} 0, & \text{if } t < d - r, \\ \frac{1}{\pi} \arccos \frac{d^2 + t^2 - r^2}{2td}, & \text{if } t \in [d - r, \sqrt{d^2 - r^2}], \\ \frac{1}{\pi} \arcsin \frac{r}{d}, & \text{if } t > \sqrt{d^2 - r^2}\ . \end{cases} \tag{14}$$

It is clear that for any fixed d, the function $p_0(t, d)$ increases in t, reaches its maximum when $t = \sqrt{d^2 - r^2}$, and then remains to be at this constant value which depends only on the ratio r/d.

To avoid boundary effects, assume, $r \ll t < w/3$ and consider the in-degree $\nu_v^{in}(t)$ of the vertex $v = \mathbf{0}$ at the center of Λ. Fix ε arbitrarily and define

$$V_n = \{u \in V : (n-1)\varepsilon < \|u\| \le n\varepsilon\}. \tag{15}$$

This gives us the following partition of the set of vertices V

$$V = \cup_{n \ge 1} V_n,$$

where by the definition of the set V each of V_n has also a Poisson distribution

$$|V_n| \sim \mathrm{Po}(\pi(2n-1)\varepsilon^2 \mu). \tag{16}$$

This helps us to find the following stochastic bounds for the in-degree defined in (8):

$$\sum_{n=1}^{\left[\frac{t}{\varepsilon}\right]} \mathrm{Po}\left(\pi(2n-1)\varepsilon^2 \mu p_0(t, (n-1)\varepsilon)\right) \preceq \nu_v^{in}(t) \tag{17}$$

$$\preceq \sum_{n=1}^{\left[\frac{t}{\varepsilon}\right]+1} \mathrm{Po}\left(\pi(2n-1)\varepsilon^2 \mu p_0(t, n\varepsilon)\right),$$

which yields the bounds for the expected in-degree:

$$\sum_{n=1}^{\left[\frac{\sqrt{2}w}{\varepsilon}\right]} \pi(2n-1)\varepsilon^2 \mu p_0(t, (n-1)\varepsilon) \le \mathbf{E}\nu_v^{in}(t) \le \sum_{n=1}^{\left[\frac{\sqrt{2}w}{\varepsilon}\right]+1} \pi(2n-1)\varepsilon^2 \mu p_0(t, n\varepsilon). \tag{18}$$

Let us now rewrite (14) as follows

$$p_0(t,d) = \begin{cases} 0, & \text{if } d > t + r \text{ or } d < r, \\ \frac{1}{\pi} \arccos \frac{d^2+t^2-r^2}{2td}, & \text{if } \sqrt{t^2+r^2} \le d \le t + r, \\ \frac{1}{\pi} \arcsin \frac{r}{d}, & \text{if } r < d \le \sqrt{t^2+r^2}\ . \end{cases} \tag{19}$$

Then we derive from (18) for $t + r < w$

$$\sum_{n=[r/\varepsilon]}^{\left[\frac{\sqrt{t^2+r^2}}{\varepsilon}\right]-1} 2n\varepsilon^2\mu \arcsin\frac{r}{\varepsilon n} \le \mathbf{E}\nu_v^{in}(t) \le \sum_{n=[r/\varepsilon]}^{\left[\frac{t+r}{\varepsilon}\right]+1} (2n-1)\varepsilon^2\mu \arcsin\frac{r}{\varepsilon n}. \tag{20}$$

Passing to the limit $\varepsilon \to 0$ we get

$$\int_r^{\sqrt{t^2+r^2}} 2x\mu \arcsin\frac{r}{x}dx \le \mathbf{E}\nu_v^{in}(t) \le \int_r^{t+r} 2x\mu \arcsin\frac{r}{x}dx \tag{21}$$

$$= \int_r^{\sqrt{t^2+r^2}} 2x\mu \arcsin\frac{r}{x}dx + O(r^2\mu) = 2\mu rt + O(r^{3/2}\mu),$$

which together with (17) yields

$$\nu_v^{in}(t) \sim \mathrm{Po}\left(2\mu rt + O(r^{3/2}\mu)\right), \tag{22}$$

that has the same asymptotics for small r as the out-degree (9).

Observe that despite the same value asymptotics, there is a major difference between the spacial distribution of the set of vertices contributing to the in-degree and of the set of vertices contributing to the out-degree of a vertex. Conditionally on the event that vertex v is connected to a given vertex u the location of the remaining vertices to which v is connected is restricted to the area close to the interval of length t which starts at v and passes through u. However, conditionally on the event that u is connected to v, the locations of other vertices connected to v are almost independent of the location of u. Furthermore, given the value of the in-degree these vertices are distributed almost uniformly over the ball of radius t (of order constant) around v.

Figure 1 represents histograms of in-degrees and out-degrees generated from one simulated network with $\alpha = \pi/2$, $\lambda = 1.5$, $\mu = 100$, $t = 1.5$, $w = 1$. One can observe that these maximal out-degrees exhibit the highest discrepancy between our model and the corresponding $G(n,m)$ model. When $\lambda > 0$ the differences between in-degree distribution and out-degree distribution vanish, approaching the case of the $G_{n,p}$ model where they have the same distribution. Where $G_{n,p}$ is the classic random graph with n nodes and an edge present independently with probability p between any tow pair of vertices.

Notice that when $\lambda = 0$ the values of the time t are up to the order of w, that is, bounded by a constant. After this time the network no longer changes since as soon as the "axons" pass the size of the area Λ they do not return to Λ.

3.1.2 Positive branching case: $\lambda > 0$.

The out-degree in this case follows the compound Poisson distribution as it is proved in [1].

4 Analysis of a network with branching $\lambda > 0$.

When $\lambda > 0$ the axons within area Λ may grow unbounded, or until the r-neighborhood around all the trees covers the entire area Λ. Hence, as time goes to infinity the network becomes fully connected. Therefore by analogy with phase transitions in random graphs one expects to find for each $\lambda > 0$ certain time intervals when the properties of network change significantly.

Below we provide the results of the simulated network dynamics to highlight the functions of different parameters of the network, particularly time.

We remind here as well that the out-degree in this case follows the compound Poisson distribution as it is proved in [1].

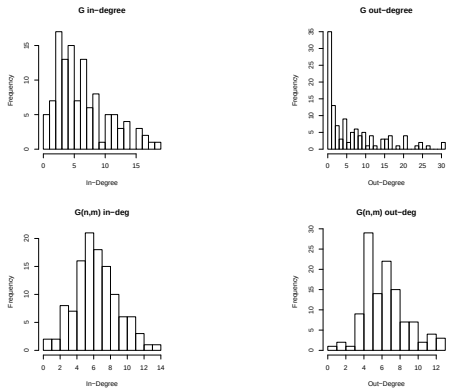


Figure 1: Frequency of degree of the graphs $G(t)$ and $G(n, m)$ with $\alpha = \pi/2$, $\lambda = 1.5$, $\mu = 100$, $T = 1.5$, $w = 1$.

4.1 Frequency of connection.

We observed already in [1] that the density in space of the axonal tree is not monotone decreasing with the distance from neuron. We expect this monotonicity to be reflected in the frequency of connections as well.

Given $\mu = 100$, $r = 0.01$, $\alpha = \pi/2$ we generate 100 graphs, with different branching intensity $\lambda = \{0, 5, 10\}$ and for different time moments t within the interval $[\sqrt{\mu}r, 3\sqrt{\mu}r]$. Furthermore, we consider different values for the size of the area, namely w. Keeping μ/w^2, the intensity of the nodes per unit area fixed, we simulate change of the distances between vertices for different values of w (Figure 2d and Figure 3).

We compute the frequency of connections in the graph for different values of the parameters μ, μ/w^2, t, setting

$$f(t) = f_{w,\mu,r,\lambda,\alpha}(t) = \frac{\#\{\text{directed edges in the graph } G(t)\}}{\#\{\text{ordered pairs of vertices of the graph } G(t)\}}.$$

Hence, $f(t)$ is an approximation for the graph probability $p_{\lambda,\alpha}(t, d)$ defined in (3). In particular, our simulated results for $\alpha = \pi$ also provide an approximation for the solution to the equation (4) averaged over the entire graph.

Figure 2 illustrates the growth of the frequencies of connections while increasing the intensity of branching:

Panel (a) for $\lambda = 0$ the number of connections increase slowly until constant;

Panel (b) for small positive $\lambda = 5$ the amount of connections is four times higher and continues to increase over time;

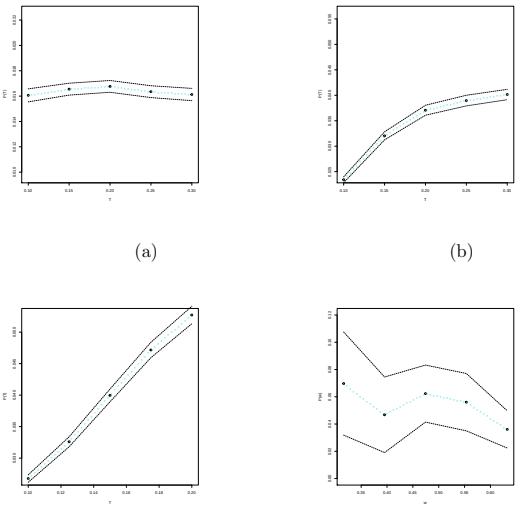
Panel (c) for higher $\lambda = 10$ the frequency of the probability grows linearly.

Panel (d) for fixed time $t = 3w$ we compute the frequency f_p depending on different distances w.

The dotted curves are the 95% confidence intervals. Connectivity increases with time (linearly, as the plot shows) while it decays with the parameter w, which reflects in our simulations the distance between nodes. The computations could have been done as well keeping the exact coordinates of the nodes but this would have created a much complex simulations and expensive in terms of time, then we decide to approximate the distance between the nodes with changing the space where the nodes could be generated i.e, the parameter w. This allowed us to simplify more the simulations keeping the characteristic of distance as a parameter which influences the dynamics of the network.

Letting fixed other parameters than w, the frequency is a function of w which reflects the distance between the vertices. The frequency is usually non-monotone indeed it attains its maximum value for a certain range of w. Figure 3 (a,c,e,g) exhibits the geometric characteristics of the network evolution for $w \in [0.5, 1, 2, 3]$ respectively and Figure 3 (b,d,f,h) reports the corresponding connectivity in the network. At the smallest distance, when $w = 0.5$ there are fewer connections than when $w \in [1, 2]$, while at $w = 1$ there is a maximum number of connections.

Our simulations confirm the following properties of the frequences
– non-monotonicity with respect to the distance (Figure 2d),
– monotone increase in time (Figures 2b and 2c),
– stabilization after a certain time (Figures 2a and 2b).



(a) (b)

(c) (d)

Figure 2: (2a)Frequency f_p with respect to t for $\lambda = 0$, with $\alpha = \pi/2$, $t = [w, 3w]$, (2b)Frequency f_p with respect to t for $\lambda = 5$, with $\alpha = \pi/2$, $t = [w, 3w]$, (2c)Frequency f_p with respect to t for $\lambda = 10$ (2d) Frequency f_p with respect to distance w , given $\lambda = 5$ given fixed time $t = 3w$. The dotted curves are the 95% confidence intervals.

4.2 Shortest path

Given an arbitrarily fixed set of parameters for our model, we now compute the average shortest path of our graph $G(t)$ and the corresponding $G(n, m)$, that is, where n and m are the same as for $G(t)$.

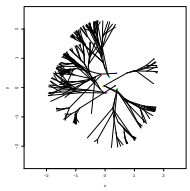
If there is at least one directed path from vertex v to vertex u in $G(t)$ we denote $d_{v\to u}(t)$ the length of the shortest path from v to u, i.e., the number of the edges it consists of. When there is no path from v to u we define $d_{v\to u}(t) = 0$. We also define the directed average shortest path length as follows

$$L_{G(t)} = \frac{1}{n}\sum_{v\in V}\frac{\sum_{u\in V:\ u\neq v} d_{v\to u}(t)}{n-1}. \tag{23}$$

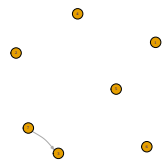
The simulations show that for a wide range of parameters our model exhibits a low average shortest path, a property similar to the classic random graph [5], [3].

Figure 4 shows the simulated ratio between the average shortest path of $G(t)$ and $G(n, m)$ depending on the time t for $\alpha = \pi/6$ (4a) and $\alpha = \pi$ (4b). For both values of α the ratio remains almost constant between 0.5 and 1.1 when the time is big enough.

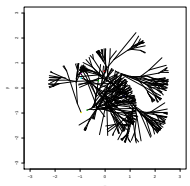
Our results show that when the time is small then the average shortest path length between any two nodes at distance bigger than t is lower in $G(t)$ than in $G(n, m)$. This is due to the geometry of $G(t)$ since here the length of an edge matters, i.e., only few short connections are



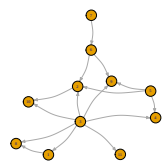
(a) $w = 0.5$, $\alpha = \pi/6$



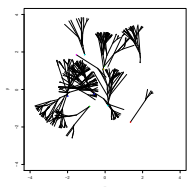
(b) $G(w = 0.5)$, $\alpha = \pi/6$



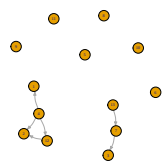
(c) $w = 1$, $\alpha = \pi/6$



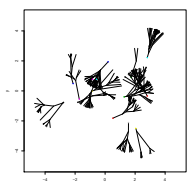
(d) $w = 1$, $\alpha = \pi/6$



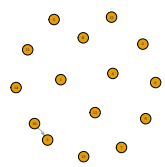
(e) $w = 2$, $\alpha = \pi/6$



(f) $G(w = 2)$, $\alpha = \pi/6$



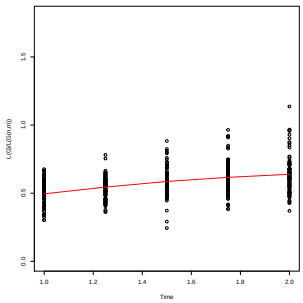
(g) $G(w = 3)$, $\alpha = \pi/6$



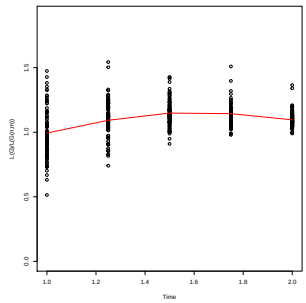
(h) $G(w = 3)$, $\alpha = \pi/6$

Figure 3: Trees structures for given value of $w \in [0.5, 1, 2, 3]$ and respective graph of connections $G(t)$.

possible, while in $G(n, m)$ the same amount of edges can be placed in longer path.



(a) Ratio between average shortest path of 100 simulations of $G(t)$ and $G(n, m)$, for $\alpha = \pi/6$, $\lambda = 1$, $r = 0.1$, $w = 1$ and $t = [1, 2]$.



(b) Ratio between average shortest path of 100 simulations of $G(t)$ and $G(n, m)$, for $\alpha = \pi$, $\lambda = 1$, $r = 0.1$, $w = 1$ and $t = [1, 2]$.

Figure 4: For every $t \in [w, 2w]$ we simulate 100 graphs and we report with the black cycles the ratio $LL(G(t))/LL(G(n, m))$, the red line represent the mean value of this ratio.

4.3 Clustering coefficient

For the resulting directed graph we will refer to the clustering coefficient defined in [6]. The number of directed triangles $t_v^{\rightarrow}$ around the node $v \in V$ is given by the following equation

$$t_v^{\rightarrow} = \frac{1}{2} \sum_{w,u \in V} (a_{vw} + a_{wv})(a_{vu} + a_{uv})(a_{wu} + a_{uw}), \tag{24}$$

and for $\nu_v^{tot} = \nu_v^{out} + \nu_v^{in}$, the directed clustering coefficient $CC^{\rightarrow}$ is defined as follows

$$CC^{\rightarrow} = \frac{1}{|V|} \sum_{v \in V} \frac{t_v^{\rightarrow}}{\nu_v^{tot}(\nu_v^{tot} - 1) - 2\sum_{w \in V} a_{vw} a_{wv}} \tag{25}$$

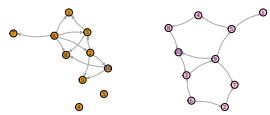


Figure 5: Given the graph $G(t)$ (on the left) and $G(n, m)$ (on the right) for chosen parameters $\alpha = \pi/4$, $\lambda = 6$, $t = 0.4$, $w = 0.2$, $r = 0.1$, we compute the respective clustering coefficients $CC^{\rightarrow}(G) = 0.19$ and $CC^{\rightarrow}(G(n, m)) = 0.041$, .

We run 50 independent simulations of $G(t)$ and $G(n,m)$ with $r = 0.1$, $\mu = 10$, for β with a range of parameter $\lambda \in \{0, 1.5, 3\}$, $\alpha \in \{\pi, \pi/2, \pi/6\}$, $t \in \{0.2, 0.66, 1.12\}$ and distance $w \in \{0.28, 0.7, 1.121\}$.

We compute the clustering coefficient for the graphs with all possible parameters combinations and we report them in Table 1, Table 2 and Table 3. The values in the tables highlighted in bold are those for which $CC^{\rightarrow}(G)$ and $CC^{\rightarrow}(G(n,m))$ are significantly different from each other at a significance level of 5%. We observe how the clustering coefficient does not always increase monotonically with time. For the value $\lambda = 0$, (Table (1)) at a fixed distance $w = 0.28$, $CC^{\rightarrow}(G)$ decreases. This fact is due to the geometry of the model. After a certain time the probability of forming single connections is higher than forming triples. The non-monotone behavior can also be seen for the parameter $\lambda = 1.5$, $\alpha = \pi/2$ and $\lambda = 3$, $\alpha = \pi/6$ respectively in Table 2 and in Table 3. The combination $(\lambda, \alpha) = (1.5, \pi/2)$ produces graphs where the tree structures have the shape of thigh cones due to the low frequency of branching. Also, despite the high intensity of branching, the pair $(\lambda, \alpha) = (3, \pi/6)$ produces as well a tree area very small due to the sharp angle of the directions of the trees growth. While when the structures of all trees grow more uniformly we can observe that the clustering coefficient increases with time monotonically.

We conclude that our model is capable to possess difference properties depending on the parameters. In particular, our simulations prove a great variability of the clustering coefficient. We highlight (in bold in each Table 1, Table 2 and Table 3) the values of the clustering coefficient which are significantly different for two graph models $G(t)$ and $G(n,m)$. Our simulations show also non-monotonicity of the value of clustering with respect to time: Table 2, $\lambda = 1.5$ and $\alpha = \pi/2$, and Table 3, $\lambda = 3$ and $\alpha = \pi/6$.

$CC^{\rightarrow}(G)$

$\lambda = 0$		w		
		0.28	0.7	1.121
t	0.2	**0.042**	0.007	0
	0.66	**0.028**	0	0
	1.121	**0.027**	0.002	0.002

$CC^{\rightarrow}(G(n,m))$

0.007	0	0
0	0	0
0	0	0

Table 1: CC comparison for $\lambda = 0$

		$CC^{\rightarrow}(G)$			$CC^{\rightarrow}(G(n,m))$		
$\lambda = 1.5$		w					
$\alpha = \pi$		0.28	0.7	1.121			
t	0.2	**0.067**	0	0.002	**0.016**	0	0.002
	0.66	**0.186**	0.019	0.007	**0.092**	0.011	0
	1.121	**0.243**	**0.091**	0.012	**0.172**	**0.031**	0.005

$\lambda = 1.5$		w					
$\alpha = \pi/2$		0.28	0.7	1.121			
t	0.2	**0.029**	0	0	**0.01**	0	0
	0.66	**0.116**	**0.025**	0.002	**0.044**	0.005	0
	1.121	**0.106**	0.022	0.007	**0.064**	0.012	0.006

$\lambda = 1.5$		w					
$\alpha = \pi/6$		0.28	0.7	1.121			
t	0.2	**0.036**	0	0	0.005	0	0
	0.66	**0.066**	**0.014**	0.002	0.03	0.001	0
	1.121	**0.074**	0.019	0.007	0.03	0.006	0.001

Table 2: CC comparison for $\lambda = 1.5$

		$CC^{\rightarrow}(G)$			$CC^{\rightarrow}(G(n,m))$		
$\lambda = 3$		w					
$\alpha = \pi$		0.28	0.7	1.121			
t	0.2	**0.062**	0	0	**0.017**	0	0
	0.66	**0.237**	**0.045**	0.016	**0.138**	**0.007**	0
	1.121	**0.467**	**0.169**	**0.065**	**0.308**	**0.094**	**0.02**

$\lambda = 3$		w					
$\alpha = \pi/2$		0.28	0.7	1.121			
t	0.2	**0.038**	0	0	0.007	0	0
	0.66	0.1	0.028	**0.01**	0.071	0.012	0
	1.121	**0.235**	0.111	0.027	0.158	0.076	0.015

$\lambda = 3$		w					
$\alpha = \pi/6$		0.28	0.7	1.121			
t	0.2	**0.047**	0.002	0	0.009	0	0
	0.66	**0.1**	0.02	0.003	0.03	0.006	0
	1.121	**0.08**	**0.03**	**0.029**	0.031	0.007	0

Table 3: CC comparison for $\lambda = 3$

5 Conclusions

We define a random graph model $G(t)$ which approximates potential synaptic connectivity between neurons. The network connectivity depends on different parameters which capture the most relevant features of potential synaptic development like intensity of branching, length, angle and speed of growth. We investigate the spatial development of those potential synapses, and show how degree distribution, frequency of connections, average shortest path and clustering coefficient evolve in time.

We show that the maximum of the in-degree of $G(t)$ does not differ much from the one for the corresponding $G(n, m)$ graph, unlike the maximum of the out-degree, which is much higher than the one in $G(n, m)$.

Our results confirm that the frequency of connection increases monotone in time, but the highest value depends on the distances between the nodes.

Our simulations show for different parameters that our network depending on the parameters may resemble the typical characteristic of small world structure, i.e., small average shortest path and high clustering coefficient, or it can be similar to the classic random graph model where both average shortest path and clustering coefficient are small.

Our study addresses also the question of scaling of the physical parameters to fit the model into real biological framework.

With this study we propose a model (simplified version of the one introduced in [10]), which is analytically tractable and allows simulations to mimic some properties of the real neural networks [2] [20]. **The code which we used to produce the simulations is open under request.**

Here we considered 2-dimensional network. Observe that is a known fact that axonal trees form essentially 2-dimensional structures [14]. Our analysis is amenable for the 3-dimensional case as well. Let us also mention here that a related 3-dimensional model of cylinder percolation was studied in [21].

Another direction for improvement modelling is to take into account both axon and denritic arborazation. Our approach should be useful to describe the axon-denritic connections as well, however the analogue of equation (4) will be more involved.

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